

25-29 August 2013

Perth Convention Exhibition Centre
Western Australia



24th International Conference of the World Association
for the Advancement of Veterinary Parasitology
Hosted by **The Australian Society for Parasitology Inc.**

Abstracts

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Welcome

Dear Friends and Colleagues

On behalf of the World Association for the Advancement of Veterinary Parasitology and our host, the Australian Society for Parasitology, we warmly welcome you all to Perth, the capital of the largest state in Australia, and the most readily accessible Australian capital to South East Asia and beyond.

We are delighted that WAAVP2013 has brought together so many parasitologists from around the world to present and discuss your latest advances in research as well as important issues relevant to parasitology. Over the next few days we will look to the future as well celebrate successes over the last 50 years as past of WAAVP's 50th Birthday! We have a diverse and interesting scientific programme that encompasses all areas of veterinary parasitology, particularly the important emerging areas of aquaculture, food security, one health and wildlife diseases. We have also given emphasis to poster presentations, providing, we hope, opportunities for more exposure, discussion and social interaction. Indeed, beyond posters, we trust you will all enjoy the many social activities that the next few days will bring.

As you will discover, Western Australia offers a fresh perspective for conferences with plenty of open space for delegates to think, breathe and connect. We also hope you will take advantage of the breathtaking and unparalleled beauty of our natural attractions in the regional areas of Western Australia. Some of you have already taken this opportunity before the meeting and we hope those of you that linger after the meeting have an enjoyable time.

Andrew Thompson & Brown Besier

WAAVP 2013 Co-Convenors

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KEYNOTE PRESENTATIONS



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MONDAY 26 AUGUST

OPENING SESSION

WAAVP: The 50th anniversary in 2013 - History, Achievements and Future Perspectives

Johannes Eckert

University of Zurich

Veterinary parasitology in Australia – a short history

Brown Besier

Department of Agriculture and Food Western Australia

Veterinary parasitology in Australia – a short history

Ian Beveridge

University of Melbourne

PLENARY SESSION: ONE HEALTH

One World Health: Socioeconomic burden and parasitic disease control priorities

Paul Torgerson

University of Zurich

One World Health: Whose world, whose health?

Yaowalark Sukthana

Mahidol University

PLATINUM SPONSOR SESSION: BAYER

Long-term efficacy of an imidacloprid 10% / flumethrin 4.5 % polymer matrix collar (Seresto®, Bayer) in dogs and its potential to prevent canine leishmaniasis in a hyper-endemic

Domenico Otranto

University of Bari

Prevention of tick-borne diseases in dogs using an imidacloprid / flumethrin collar

Filipe Dantas-Torres

Aggeu Magalhães Research Centre (Fiocruz-PE)

TUESDAY 27 AUGUST

PLENARY SESSION: COMPANION ANIMALS

Future Challenges for Parasitology: Vector Control and One Health in the Americas

Susan Little

Oklahoma State University

Future Challenges for Parasitology: Vector Control and One Health in Europe

Norbert Mencke

Bayer - Germany

NOVARTIS SPONSORED SESSION

Cestode zoonoses: a one health perspective

Susan Little

Oklahoma State University

Effecting cestode impacts on human and veterinary patients

Calum Macpherson

St. George's University

WEDNESDAY 28 AUGUST

PLENARY SESSION: PROPHYLACTICS AND THERAPEUTICS

Immunomodulatory Molecules of F. hepatica: Candidates for Both Vaccine and Immunotherapeutic Development

John Dalton

McGill University

Worms - A "License to Kill"

Ronald Kaminsky

Novartis - Switzerland

ASP/ELSEVIER SESSION

Filling the gaps: expression profiling of zoonotic Apicomplexa in definitive hosts

Adrian Hehl

University of Zurich

Specific and/or unspecific mechanisms of anthelmintic resistance: How could we tackle this conundrum?

Georg von Samson-Himmelstjerna

Freie Universität Berlin

Wildlife parasitism in a changing climate: Shifting boundaries, barriers, and paradigms

Susan Kutz

University of Calgary

THURSDAY 29 AUGUST

PLENARY SESSION: ANIMAL PRODUCTION AND FOOD SECURITY

Parasitology for the hungrier, warmer, riskier world

Doug Gray

ACIAR

Global food security – the impact of veterinary parasites and parasitologists

Julie Fitzpatrick

Moredun Research Institute

PLATINUM SPONSOR SESSION: ZOETIS

Pesticide Resistance: From Theory to Practice

The Evolutionary Biology of Pesticide Resistance

Jeff Scott

Cornell University, Ithaca, NY USA

Lessons from agriculture on adaptive resistance management

Tom Walsh

CSIRO



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Session Details:	8/26/2013 Opening Session 815 - 1000 Riverside Theatre
Oral Presentation Details:	World Association for the Advancement of Veterinary Parasitology (WAAVP): The 50 th Anniversary in 2013 - History, Achievements, and Future Perspectives J. Eckert* ¹
Authors:	J. Eckert* ² c/o Institute of Parasitology, University of Zurich, Winterthurerstr. 266 a, 8057 Zurich, Switzerland

In 2013 the World Association for the Advancement of Veterinary Parasitology (WAAVP) can celebrate its 50th anniversary. At this occasion in this article selected historical data are updated, and the achievements and future perspectives of the WAAVP are discussed. Although the WAAVP is a small association with only a few hundred members, it was able to develop remarkable activities. Between 1963 and 2011 the WAAVP has organized 23 international scientific congresses, the 24th conference will take place in Perth, Western Australia, in 2013. These conferences have achieved a high degree of international recognition as indicated by relatively large numbers of participants (up to ~ 800). Furthermore, the WAAVP has promoted veterinary parasitology in various ways, such as publishing international guidelines (efficacy evaluation of antiparasitic drugs; parasitological methods; standardized nomenclature of animal parasitic diseases), stimulating international discussions on teaching and continued education (« colleges of veterinary parasitology ») or by supporting the high quality journal « Veterinary Parasitology » which is the official organ of the WAAVP. In retrospective the development of the WAAVP can be classified as very successful. New challenges associated with global changes (growth of the world population, urbanization, climate change, new developments in animal and plant production etc.) will require new efforts in research

in various fields, including veterinary parasitology, and a better exposure of the WAAVP to parasitology from hitherto neglected regions of the world.

1. Introduction

The World Association for the Advancement of Veterinary Parasitology (WAAVP) was founded in 1963. Its history has been briefly described at the occasion of the 30th anniversary (Slocombe, 1993; Soulsby, 1994) and comprehensively reviewed after the 40th anniversary (Malone at al. 2004). The intension of this article is to update selected historical data of the association, to assess its achievements and to discuss some future perspectives.

2. Foundation of the WAAVP and Aims

The formation of the World Association for the Advancement of Parasitology (WAAVP) was initiated shortly after the World Veterinary Congress (WVC) in Madrid in 1959. During the following WVC held in August 1963 in Hannover (Germany) at the School of Veterinary Medicine (now University of Veterinary Medicine) the WAAVP was formally established on the 16th August 1963 at a meeting with 24 participants present under the leadership of E.J.L. Soulsby, then Professor at the University of Pennsylvania (USA) and now Professor Lord Soulsby Baron of Swaffham Prior and a member of the House of Lords in the United Kingdom. An



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Executive Committee (EC) was formed with E.J.L. Soulsby as founding President, K. Enigk (Germany) and R.D. Turk (USA) as Vice Presidents, S.M. Gaafar (USA) as Secretary-Treasurer and five Directors from various countries around the globe. Details of the foundation of the WAAVP have been described by Malone et al. (2004). The major aims of the WAAVP are “to encouraging research in veterinary parasitology and promoting the exchange of information and material amongst researchers, veterinary practitioners and animal health investigators” (WAAVP, 2012). To achieve these goals biennial conferences are organized and other activities performed. The WAAVP is an associated member of the World Veterinary Association (WVA).

In conjunction with the WVC in Hannover the first WAAVP scientific conference (“symposium”) was organized under the heading “The Evaluation of Anthelmintics” on August 22-23, 1963 by K. Enigk and his co-workers of the Institute of Parasitology, including my colleagues D. Düwel, K. T. Friedhoff and me, thus becoming witnesses of the inauguration and first activities of the WAAVP.

A keynote speaker of the symposium was the famous taxonomist and helminthologist Professor K.I. Skrjabin (1878-1972), Academy of Sciences of the former Soviet Union (SU). He presented a lecture in German on "Problems in the control of helminthoses" and concluded with the following statement: "Ladies and gentlemen, my scientific 'credo' consists [of the opinion] that mankind inevitably sooner or later will reach a helminth-free existence and that the highly pathogenic helminthes will be objects of the palaeontological science. Only by this can I imagine the progressive development of the common as well as the sanitary culture" (cited in Soulsby, 1964; translated by K. Wolff). On the other hand E.J.L. Soulsby expressed the following view: "This Symposium on the 'Evaluation of Anthelmin-tics' is the first of what it is hoped will be a *series* of symposia held by the World Association for the Advancement of Veterinary Parasitology" (Soulsby, 1964) (Figs. 1 and 2).

Whereas the helminths-free existence of mankind envisaged by Skrjabin remained an illusion up to date, the hopes of Soulsby for a *series* of symposia have been fulfilled. Let us look back to these symposia and other activities of the WAAVP, starting with some remarks on the situation of veterinary parasitology and the general circumstances in the early days of the association.

In the early 1960ties research in parasitology, including veterinary parasitology, was predominantly based on “classical” methods and focused inter alia on parasite taxonomy, morphology and biology, on pathology of parasitic diseases, epidemiology, ecology and aspects of control. Only relatively few research groups around the world were able to perform more basic studies, such as parasite biochemistry, immunology, genetics, and pathophysiology. Sophisticated research techniques of immunology, molecular biology, epidemiology etc. or computer technologies were not available at that time. Although “classical” studies had provided solid epidemiological data on important livestock parasitoses, their control was difficult due to the lack of effective and safe antiparasitic compounds. For example, the toxic carbon tetrachloride was still in use for the control of fasciolosis in sheep and phenothiazine for nematode control in ruminants and horses.

The political situation was characterized by the “cold war” with the “Berlin wall” put up in August 1961 and the “Cuba missile crises” in October 1962 which brought mankind close to an atomic war. The world was divided into the blocks “East” and “West”, visualized by the “iron curtain” separating Europe. Passing the borders between east and west was difficult and represented a special challenge for the civil societies, including international scientific associations.

With these remarks in mind, the development and achievements of the WAAVP will be briefly described and assessed in the next section.





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3. Development and Achievements of the WAAVP

3.1. Membership

After the beginning with approximately 125 members from 25 countries (Soulsby and Baily, 1962) the membership of the WAAVP has grown considerably to numbers between 510 and 633 in the period 1993 – 1999, representing approximately 60 (31%) of the 193 member states of the United Nations (Sources: WAAVP Membership Directories 1990/91, 1995, 1999). Thereafter, there was a decline to a current low number of approximately 225 registered members (Pomroy, pers. comm., 2102). However, uncertainties exist about the mode and reliability of the registration system. The data, available to the author, suggest that the WAAVP needs and increasing registered membership and a better participation of parasitologists from more regions of the world, especially from developing countries. Up to 2011 the WAAVP has elected 41 honorary members from 16 countries in recognition of their outstanding contributions to veterinary parasitology, thus underlining the internationality of the association (Table 1). In addition, the WAAVP has currently some Corporate Members (WAAVP, 2012).

3.2. Affiliations and Cooperations

Several national or international scientific societies are affiliated with WAAVP, indicating their special interest for a close cooperation with the WAAVP. These are the *Hungarian Society of Parasitologists*, the *Asociacion Argentina de Parasitologia Veterinaria*, the *Brazilian College of Veterinary Parasitology*, the *Cuban Society of Veterinary Parasitology*, the *Indian Association for the Advancement of Veterinary Parasitology*, the *Parasitological Society of Southern Africa*, the *Danish Society of Parasitology*, the *British Association of Veterinary Parasitology*, and the *European Veterinary Parasitology College (EVPC)*.

3.3. Governance

The WAAVP is headed by the Executive Committee (EC) consisting of the President, two Vice-Presidents, the Secretary-Treasurer, five Directors and the Past-President. The editor-in-chief of the journal “Veterinary Parasitology” is an advisory, non-voting member of the EC. In a revised version of the statutes published in 1991, the EC term was defined as the current five biennial meetings, or 10 years. Every two years, the seats of the two officers who have served for the longest period become available for election. A re-election of a President is excluded (Malone et al., 2004). This system combines continuity and innovation and has proven to be successful over the years. A geographical listing of the officers having served during 13 election periods between 1963 and 2013 shows that North America, Europe and Australia/New Zealand were always represented in the EC, Central and South America in 10 periods, but Asia and Africa only in 6 and 3 periods, respectively. This fact should be considered in future elections.

The EC officers with their terms of office between 1963 and 2005 are listed in the publication of Malone et al. (2004). Therefore, in this article only the officers of the period 2005 to 2013 are presented (Table 2), but all Presidents are depicted in Fig. 3. All of them and their helpers deserve special credit for their engagement.

3.4. Relations of the WAAVP with Industries and Sponsoring Bodies

Since the early 1960ies the pharmaceutical industry has developed and introduced a whole series of efficient and safe antiparasitic compounds, belonging to at least 16 different chemical classes, including endoparasitocides, ectoparasitocides and endectoparasitocides. Furthermore, new techniques of drug application have been invented, such as the topic or intraruminal application of anthelmintics or the drug release from insecticide-





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impregnated plastic devices in collars for dogs and cats or ear tags for cattle. Companies are also involved in the development of vaccines. To date, only a few vaccines are available on the market (examples: Paracox®, Livacox®, Novibac Piro®, Leishmune®, Hidatil EG95®, TickGuard®) and some are in the “pipeline”. In general, the development of vaccines was slower than initially hoped. Members of industrial companies have provided first-hand scientific information on drugs at WAAVP congresses, either during “corporate symposia” or within the ordinary program, thus facilitating the transfer of knowledge. The application of new drugs on the basis of solid epidemiological knowledge has revolutionized and significantly improved the control of many parasitoses of food-producing and companion animals. These advances indicate that a close cooperation between companies and the WAAVP was of mutual interest and will also be needed in the future for solving existing problems, such as drug resistance of parasites or coping with new challenges (see 4).

International conferences depend on the financial support of sponsoring bodies belonging for example to governmental institutions, foundations, or non-profit and profit organizations. I am pleased to express our thanks to all sponsors at the occasion of the 50th anniversary of WAAVP.

3.5. Conferences

Between 1963 and 2011 WAAVP has organized 23 biennial conferences and will hold its 24th meeting in Perth (Western Australia) in 2013. Two further conferences scheduled for 1979 in Moscow (SU) and for 1991 in Rabat (Morocco) had to be cancelled due to special circumstances (Table 3). Among others, an indicator of success is the number of attendants which increased gradually from only 24 in 1963 to more than 800 at conferences in recent years (Table 3). Eleven of the 24 conferences were held in Europe, four each in North-America and Australia/New Zealand, two in South America, and one each in Central America, Africa and Asia. From my point of view more countries in Asia, Africa and Eastern Europe should be included into the list of potential sites for WAAVP conferences. Plans for a congress in Malaysia 2017 are a good signal in this sense. Furthermore, the WAAVP has contributed parasitological sessions or lectures to several World Veterinary Congresses.

The actuality of the themes, the quality of the presentations, the combination of basic and applied science, the organizational structure, the family-like atmosphere and interesting social programs can be regarded as reasons for the attractiveness of the WAAVP conferences (Table 3). During the conference in Montreal 1987 the EC approved “Guidelines for the Preparation and Conduct of WAAVP Conferences” which were revised in subsequent conferences. Recommendations for the conduct of conferences include inter alia a plenary paper on the host country and its parasitology (examples: Slocombe, 1989, 2009), the organization of plenary sessions, submitted paper sessions, workshops, poster sessions, and special symposia performed by corporations (companies) in which concise review papers on drug development and other topics are presented. Over the years, the corporate symposia had a very positive impact to the WAAVP conferences. Traditionally, the conferences are opened by ringing the cow-bell, dedicated to the WAAVP at the 1981 conference in Budapest by the Local Organizing Committee and the Hungarian veterinary parasitologists (Malone et al., 2004; Malone et al., 2006). Papers of the early conferences (1963 to 1975 and 1983) were published as books, and since 1977 the keynote-lectures are documented in “Veterinary Parasitology” (Tab. 3).

Many developments and events were associated with the various conferences. Only a few can be mentioned here, some have been described by Malone et al. (2004). Characteristics of the conference **1963 in Hannover (Germany)** were the foundation of the WAAVP, reports (during a joint WVA symposium) on thiabendazole, a





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broad-spectrum anthelmintic belonging to the new class of the benzimidazoles, and a great “birthday” party celebrated at the “Westfalenhof”, the site of the Institute of Parasitology (Fig.2). At the conference in **Sydney 1977 (Australia)** the participants received first-hand information on another innovation, the macrocyclic lactones, represented by ivermectin. S.M. Gaafar, then President of the WAAVP, appointed the first “guideline committee” under the chairmanship of K. G. Powers (see 3.8.). Two post-conference excursions to centres of parasitological interest combined with tourist attractions were offered. For example, a “northern tour”, guided by Dr. H. McL. Gordon, included visits to a sheep and cattle farm, a CSIRO Pastoral Research Station (Chiswick) near Armidale, the CSIRO Long Pocket Laboratories and the Department of Parasitology (head: Professor J.F.A. Sprent), University of Queensland in Brisbane, field stations of Merck, Sharp & Dohme, ICI, Bayer and Ciba-Geigy at various locations, and a vineyard in the Hunter Valley. At the conference in **Budapest (Hungary) 1981** a revision of the statutes of our association was initiated, the famous “cow-bell” was donated to the WAAVP, and the attendants had the opportunity to get a glance of the beautiful country and its culture during an excursion to the Puszta. At the conference **1983 in Perth (Western Australia)** a resolution was adopted in which the World Veterinary Congress was asked to promote the acceptance of the WAAVP anthelmintic guidelines (see 3.8.) in all countries. This conference was of special significance for me as I was elected to WAAVP President. During the first South American WAAVP conference in the beautiful environment of **Rio des Janeiro (Brazil)** initiatives were discussed for improving the links of the WAAVP with the World Health Organization (WHO) and with the Food and Agriculture Organization (FAO). At the conference **1987 in Montreal (Canada)** a proposal for holding the next conference in August **1989 in East Berlin** was first controversially discussed, but finally supported by a majority of the WAAVP members at the General Assembly with the intention to provide an opportunity for young scientist from eastern countries to get access to information presented at a WAAVP meeting. Professor Th. Hiepe, then 1st Vice President of the WAAVP, was appointed as chairman of the Scientific Program and the Local Organizing Committees. At this time Berlin was divided by the “Berlin wall”, and its eastern part regarded as capital of the so-called “German Democratic Republic” (GDR) with a communistic government. Under these circumstances some difficulties could be expected, and they occurred. For example, an initial agreement of the authorities to allow persons from all countries, including Israel, to attend the conference was later withdrawn, and could only be re-affirmed after several energetic interventions of Th. Hiepe at a high governmental level. Special care had to be taken that financial support in western currency was not deviated to the funds of the state. Nevertheless, Th. Hiepe got the permission that attendants of the conference could visit state farms which were normally not accessible for foreign visitors, as already mentioned by Malone et al. (2004). At the closing dinner a high ranking veterinary officer of the GDR told us, that a re-unification of East and West Germany is unthinkable, but a few months later, in November 1989, the wall in Germany was turned down leading to far-reaching international consequences. At the conference in **Cambridge (UK) 1993** the 30th anniversary of the WAAVP was celebrated (Slocombe, 1993; Soulsby, 1994). The subsequent conference in **Yokohma (Japan) 1995** was the first one in Asia, offering insights to the great national culture including an excursion and a Japanese banquet. **Sun City (Republic of South Africa)** hosted the first WAAVP conference in Africa. It was opened with a colorful folkloristic show and an impressive historical review presented by R. C. Krecek and B.L. Penzhorn. At this conference R. C. Krecek was elected to WAAVP President, the first from Africa and the first woman. During a visit of the famous Faculty of Veterinary Science, University of Pretoria, in Onderstepoort, the attendants could pay a spiritual tribute to Sir Arnold Theiler (1867-1936), a veterinarian of Swiss origin, the first Dean of the Faculty and “father of veterinary research” in South Africa. Although the attendants of the conference had heard for the first time, that even crocodiles can harbor *Trichinella*, some of them enjoyed to eat heated! crocodile meat at a nocturnal bush party. The conference **1999 in Copenhagen**





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(Denmark) is associated with the unforgettable Professor Peter Nansen, who had organized a great meeting and regrettably died prematurely a few months later. The conference held **2001 in Stresa (Italy)** at the beautiful Lago Maggiore provided a platform for further discussions on teaching and the foundation of a European College of Veterinary Parasitology (see 3.9. and 3.10.). The following conferences in **New Orleans 2003 (USA)**, **Christchurch 2005 (New Zealand)**, **Ghent 2007 (Belgium)**, **Calgary 2009 (Canada)** and **Buenos Aires 2011 (Argentina)** were well attended and equally successful, characterized by an increasing number of contributions from national or international research networks. The broad spectrum of themes can only be characterized here by a few keywords, such as genomics, proteomics, transcriptomics, molecular aspects of parasitism and diagnosis, new classes of anti-parasitic drugs, drug combinations, management of drug resistance, nanomedicine, alternative methods for sustainable parasite control (biological control, non-chemical control, nutraceuticals), immunology and vaccine development, emerging zoonoses, influence of globalization and climate change on parasites and vectors, modeling of complex epidemiological interactions, food safety, and parasites of wildlife and exotic animals.

Fig. 4

3.6. Veterinary Parasitology and the WAAVP Newsletter

The international journal “Veterinary Parasitology” has been published since 1975 by Elsevier. Over the first pioneering 15 years S.M. Gaafar - then Professor of Parasitology at the Department of Veterinary Microbiology, Purdue University, West Lafayette (USA) – was its editor-in chief. From 1963 to 1991 he was also a member of the WAAVP Executive Committee, including 8 years as President (Malone et al., 2004). He and his successors (S.D. Folz, USA; S.M. Taylor, UK; J.C. Williams, USA, L.S. Mansfield, USA; R.C. A. Thompson, Australia; C. Genchi, Italy , and others) were able to develop “Veterinary Parasitology” to a high quality journal with a current (2011) impact factor of 3.256 and a 4th ranking out of 143 Elsevier titles (Elsevier Health & Medical Science impact factors, Internet). Today “Veterinary Parasitology” is the official organ of the American Association of Veterinary Parasitologists, the European Veterinary Parasitology College and the WAAVP. I want to express special recognition to S.M. Taylor who has served for 20 years as editor-in-chief.

The WAAVP Newsletter, now edited by Maggie Fisher and her team, has evolved from rather simple beginnings to a very useful source of information on the activities of WAAVP.

3.7. Research and Awards

The WAAVP is dedicated to encouraging research and other activities in veterinary parasitology by various means, such as organization of congresses, publications and preparation of guidelines. The prestigious awards for “Excellence in Research” and for “Excellence in Teaching” or “Service”, conferred by the WAAVP, are acknowledgements for out-standing individual contributions and simultaneously encouragements for future activities. These awards were implemented together with corporate members and are denominated as “WAAVP/Pfizer Animal Health Award” and “WAAVP/ Bayer Health Care Award”, respectively. A list of awardees is presented in Table 4 (see also 3.9.). The “Peter Nansen Young Scientist Award” was introduced in 2001 to commemorate the renowned Danish parasitologist, Professor Peter Nansen (Table 4). It has always been his deep obligation and desire to promote young scientists in their academic career. Another example of promoting young scientists is the “WAAVP/African Foundation”, established after the 16th WAAVP conference held 1999 in South Africa and based on a financial surplus generated by this meeting. According to data published in 2011 a total of 110 scholarship applications have been screened and 51 full or partial





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scholarships awarded to young African parasitologists to attend biennial conferences of the WAAVP (Krecek et. al., 2011). Travel scholarships have also been awarded by the organizers of WAAVP conferences and some universities, for example by the Louisiana State University.

3.8. Guidelines

During the 8th WAAVP conference in Sydney, Australia, in 1977, President S. M. Gaafar appointed a committee to prepare international guidelines for evaluating the efficacy of anthelmintics. According to Powers et al. (1982) “the goal was to develop uniform testing standards and registration requirements to expedite the testing approval of effective products with a minimum of labor, money, and experimental animals without sacrificing scientific validity”. Under the chairmanship of K.G. Powers (USA) a first guideline for evaluating the efficacy of anthelmintics in ruminants (bovine and ovine) was prepared by five authors from four countries, assisted by the advice of 29 experts from 13 countries, including the former SU (Powers et al., 1982). This guideline - approved by the membership at the general meeting of the 9th WAAVP Conference in Budapest 1981 and published in 1982 - was an encouraging example of a fruitful international cooperation crossing political and administrative borders. By 2012 a further 16 guidelines for evaluating antiparasitic drugs in ruminants, pigs, equines, dogs, cats and poultry and a guideline for the detection of anthelmintic resistance in nematodes of veterinary importance have been published (Table 5). Further guidelines are in preparation (Anon, 2011): efficacy evaluation of ectoparasiticides in fish, anticoccidial drugs in mammals, drugs against non-coccidial protozoa, combinations of anthelmintics in livestock, and faecal egg count reduction test. This work is coordinated by a “Standing Committee” with J. Vercruysse as chairman and P. Holdsworth and M. Fisher as members (WAAVP, 2012). Undoubtedly, these guidelines are an important achievement of WAAVP. They are consulted by the scientific community, as indicated in the literature by the average annual numbers of citations (Table 5). Two of the guidelines have reached remarkable citation indices of 25 and 12, respectively, but the majority ranges between 0.14 and 5. In judging these indices one has to consider the relatively low number of persons working in the field of drug evaluation, the concerned animal species and other factors. Of special significance is that WAAVP guidelines are used by drug registration authorities in various countries, for example the guideline “Parasiticides for the treatment, prevention and control of flea and tick infestation in dogs and cats” (Krieger, pers. commun, 2012.)

The “Standardized Nomenclature of Animal Parasitic Diseases (SNOPAD)” published by WAAVP in 1988 (Table 5) is a guideline for a uniform terminology to denominate animal parasitic infections and infestations (Kassai et al., 1988). Drafts of this guideline induced controversial discussions culminating in the accusation that the SNOPAD-committee ignores the “basic rules of the English language”. However, the guideline was approved by the EC of the WAAVP. Subsequently, the Council of the World Federation of Parasitologists (WFP) endorsed the same principles for all parasitic diseases (Kassai and Burt, 1994). From my experience a uniform nomenclature is advantageous for teaching, textbooks (Kassai, 1999; Hiepe et al., 2006; Schnieder, 2006; Palmer et al. 2011; Deplazes et al., 2012) and for scientific journals. A review published in 2006 has revealed that 73.8 % of 126 national language parasitological textbooks or compendia from 21 European countries, published since 1990, have adopted a consistent disease terminology with the ending “-osis”, the rest used a mixture between “-osis” and “-iasis” (Kassai, 2006). The instructions for authors of the journal “Veterinary Parasitology” request to follow SNOPAD. From my point of view the application of the SNOPAD nomenclature by other parasitological journals is strongly recommended.



3.9. Teaching

Promotion of teaching veterinary parasitology belongs to the obligations of the WAAVP. In previous years, several members of the WAAVP have published their views on teaching veterinary parasitology (Cordero del Campillo et al., 1986; Verster, 1994), and congresses offered opportunities for discussing this issue. The discussion was enhanced by the endow-ment of the WAAVP/Pfizer Award on “Excellence in Teaching of Veterinary Parasitology” in 1993 (Table 4) and the lectures delivered by the awardees at WAAVP congresses (Soulsby, 1994; Euzéby, 1996; Nansen 1999; Eckert, 2000). In view of the fact that veterinary education, including veterinary parasitology, has to respond continuously to new developments and challenges, the General Assembly of the WAAVP adopted a formal resolution on teaching veterinary parasitology at the occasion of the 18th WAAVP conference in Stresa (Italy) in which minimum requirements of contact hours and a “disciplinary approach” in undergraduate teaching of veterinary parasitology are defined (Krecek, 2002). Furthermore, the WAAVP decided to publish lectures on teaching veterinary parasitology presented at workshops at the 17th and 18th WAAVP conferences 1999 in Copenhagen (Denmark) and 2001 in Stresa providing information from North and South America, Africa, Europe, and Australia (Eckert, 2002; further publications in Vet. Parasitol. 2002, 108, 265-331). How veterinary parasitology is taught in China was described in 2006 (Huang et al., 2006). These publications revealed large differences in teaching approaches and contact hours. For example, at 20 veterinary faculties in European countries parasitology was represented in the undergraduate curriculum of veterinary medicine with an average of 105 core contact hours ranging between 48 and 156 hours (Vercruysse and Eckert, 2002). Concern is expressed in the literature, that, if the present trends continue, there will be a lack of teachers with broad knowledge and experience in veterinary parasitology and the skills to relate their teaching to problems in the field (Barnish et al., 2006; Huang et al. 2006; Genchi et al., 2007). Another concern is the frequent disproportion between student numbers, teaching personnel and financial resources.

Since the Bologna Declaration from June 1999 adopted by 29 European countries the structure of education in veterinary medicine has been changed and adapted to new requirements. The introduction of Bachelor and Master courses, the integration of new disciplines, education of students in smaller groups, teaching of veterinary parasitology in a disciplinary approach combined with animal species- and organ-oriented approaches, and the inclusion of parasitology into clinical courses are some characteristics of this system. The new system has led to a reduction of contact hours in several disciplines, including parasitology. However, this loss may be compensated – at least partially - by an intensified education, the use of text books and computer-based devices for self-education (virtual microscopy, electronic teaching programs, e-books etc.) (Alcala-Canto et al. 2011; Hertzberg et al., 2011) and post-graduate training in “Colleges of Veterinary Parasitology”(see 3.10.). An integration of major parts of parasitology teaching into clinical or other courses can be associated with the risk that the self-determination of the discipline in teaching as well as in research and the allocation of resources may decline.

3.10. Colleges of Veterinary Parasitology

Following an initiative taken at the 18th WAAVP Conference in Stresa (Italy) by Prof. Ph. Dorchie, at that time President of the French Society of Parasitology, a group of 20 founding members from 12 European countries established a European Veterinary Parasitology Col-lege (EVPC) which received provisional recognition by the European Board of Veterinary Specialisation (EBVS) in 2003. An application for full recognition was submitted in November 2012. The main objective of the EVPC is to “set and maintain professional standards



for veterinarians in Europe specializing in Veterinary Parasitology” (Genchi et al., 2007; EVPC, 2012). This is achieved by advanced post-graduate training of veterinarians, for at least 36 months, preceded by a one-year internship or by equivalent practice experience approved by the individual college. This training enables graduate veterinarians to acquire profound knowledge and skills in general parasitology, clinical veterinary parasitology, laboratory techniques and research. After a successful formal examination diplomas are awarded that give the right to recipients to use the title “DipEVPC” (Diplomate EVPC). EVPC Diplomates are registered in the EBVS as “European Veterinary Specialists in Parasitology”. The development of the EVPC between 2003 and 2012 is a success story as indicated by a current (2012) membership of 195, including 155 active diplomats, the organization of 8 scientific symposia in 6 European countries, an excellent internet performance and the regular publication of Newsletters. Since 2005, the proceedings of the annual meetings are published in “Veterinary Parasitology”, including relevant topics, such as “Application of Molecular Biology to the Diagnosis of Parasitic Diseases” (Anon., 2006), “Food-borne Parasitic Zoonoses” (Anon., 2007) or “Parasite Control and Climate Change” (Anon., 2009). Several presidents and college together with the secretaries Laura Kramer, University of Parma, and Dennis Jacobs , Royal Veterinary College, London, were the main driving forces within the EVPC. The most important achievement of the EVPC is a structured system of intensive training, based on approved standards, for young veterinarians in relevant classical and modern fields of veterinary parasitology resulting in high qualifications for leading positions at universities, in industry, diagnostic laboratories and other institutions. In Europe the recognition as EVPC Diplomate is now an advantage or even a prerequisite for promotion to professorship in Veterinary Parasitology. A “Recognized Speciality in Veterinary Parasitology” – similar to the EVPC – was recently established in the USA. It received provisional recognition in spring 2011 with the prospect to gain permanent status after 4 years (chairman of the organizing committee: Dr. P. Meeus) (Cima, 2011; Meeus, pers. comm., 2012).

3.11. The WAAVP Archive

Thanks to the activities of J. Malone (Louisiana State University), the pervious secretary- treasures A. R. Donoghue and M. Soll and R. Roncalli an archive of WAAVP documents could be established a few years ago at the Library of the Iowa State University (ISU) in Ames, Iowa (USA) (Donoghue, 2010). The ISU Library houses the documents free of charge and provides access through its Document Delivery Service. This is a great achievement as history is not a “pointless subject”, but can teach us valuable lessons for the future (contacts: [http:// www. lib. iastate. edu/spcl/ manuscripts/ MS283.html](http://www.lib.iastate.edu/spcl/manuscripts/MS283.html)).

3. 12. Internationality – a Way to Convergence

Science is universal, and scientific institutions and associations are predestined for disseminating knowledge at a global scale. The UNESCO “Venice Statement”, published in 2009, has defined an individual and collective “right to enjoy the benefits of scientific progress and its applications” (UNESCO, 2009). It should be a general obligation to share the advances of re-search between nations as far as possible and to pay special attention to the needs of disadvantaged countries and groups. In the past the WAAVP has contributed to international understanding and dissemination by various means. However, T. Kennedy, Past President of the WAAVP, has underlined recently that we need more exposure to parasitology from regions currently not well represented in the WAAVP (WAAVP, 2011). In his lecture “Parasitology crossing borders”, delivered 1997 at the WAAVP conference in Sun City, P. Nansen has emphasized the “need for research capacity building in the least developed countries” and expressed some ideas for approaching this goal and for improving the international cooperation (Nansen, 1999).





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3.13. Conclusions

In a historical retrospective the development and the achievements of the WAAVP can be classified as successful. After 50 years of its existence the association does not show any sign of a midlife crisis and has a good basis for future activities. Basically, the prospects for advances in research are favorable, as new research tools are available, international communication is easier than ever, and the political situation in many parts of the world is more favorable for passing borders. However, research funding is generally difficult. Although parasitic diseases are permanent threats to animal and human health, causing enormous socio-economic losses, the support of veterinary parasitology seems to decline in many countries. In this context it has to be underlined that the current problems caused by parasitic diseases and future challenges can only be solved by adequate funding and new research efforts.

4. Future Perspectives

Experts anticipate that the man-made profound transformation, known as “global change”, will influence our planet to an extent as yet unforeseeable (Glaser and Dech, 2012). This change will be associated with an increasing world population approximating 7 to 9 billion in 2050, with declining natural resources, climate change, socio-economic imbalances between various regions and other detrimental factors. In 2010 - 2012 the number of hungry people in the world was estimated to be 870 million, with the vast majority of 850 million living in developing countries (FAO, 2012a). We are aware that hunger and shortage of food for human populations is a multifactorial problem which could only be solved by an array of targeted and decisive public actions (FAO, 2012a), including the promotion of agricultural productivity. Ideally, the food supply should cover the daily energy requirements of 2400/kcal per person and offer simultaneously diversified diets composed of cereals and animal products containing essential micronutrients such as vitamin A, iodine, iron and zinc. Important sources of these micronutrients are meat and meat products, milk, eggs and fish-food.

According to FAO “productivity growth in agriculture is central to economic growth, poverty reduction and food security” (FAO, 2009). In a review presented at the 19th WAAVP conference in New Orleans 2003, Henning Steinfeld, an agricultural economist of the FAO, has discussed the potential role of livestock production for the productivity growth in agriculture under the heading “The livestock revolution – a global veterinary mission” (Steinfeld, 2004).

He pointed out that the demands for animal products in the developing countries are expected to more than double by 2030, driven by rising urbanization and incomes, combined with underlying population growth (Steinfeld, 2004; FAO, 2009). In contrast, slow growth or stagnation of these demands is predicted for industrialized countries (Steinfeld, 2004). The *global* production of meat is projected to rise from 229 million tons in 1991/2001 to 465 million tons in 2050, and that of milk from 580 to 1'043 million tons (Gerber et al. 2010). In crop production a global increase of approximately 50 % is required for providing sufficient food for the population by 2050 (Gruissem, 2012).

However, there are many obstacles for increasing plant and animal production, such as limited agricultural areas, land degradation, water shortage, deforestation, global warming, pollution of soils and water with waste products, including animal manure and effluents, and air pollution. In 2000, about a quarter (26 %) of the world's land area was used as pasture or for fodder crop production (FAO, 2012b). These grasslands are the largest ecosystems of the world which function as an important “sink” in the carbon cycle (Steinfeld, 2004; FAO, 2009). They contribute 30% and 23% to the total beef and mutton production, respectively (Steinfeld,



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2004). Current discussions often neglect the fact that ruminants can convert plants into valuable meat and milk, but stress their role in the production of “greenhouse gases” (GHG). Indeed, livestock contributes about 9% to the anthropogenic emissions of carbon dioxide (CO₂), but 37% of methane (CH₄) and 65% of nitrogen oxide (N₂O) (Gerber et al., 2010). In recent years, this problem has been identified with promising first steps undertaken for limiting agricultural emissions by effective “mitigation” techniques and policies. New Zealand plays a leading role in this respect (Gerber et al., 2010). Experts predict an increasing shift from ruminants to pigs, poultry and fish, driven by the GHG problems and other factors, and growing densities of livestock in peri-urban and urban areas (Gerber et al., 2010; Steinfeld and Geber, 2010). By 2050 approximately 75% of the human population will live in cities, including megacities (Burdett, 2012).

Parasitic and other transmittable diseases of livestock will remain important constraints of animal productivity in many regions (Steinfeld, 2004). Furthermore, climate change, global trade or travel, increasing animal densities within or close to human settlements, poor hygi-enic conditions and insufficient veterinary services can enhance risks for the dissemination or emergence of infectious animal diseases, including parasitic zoonoses. Regarding the latter, food-producing, companion and wild animals have to be considered.

In a network of political, socio-economic and other actions expanded, new research approaches are required to cope with current and future local and global challenges. Such approaches and research needs in veterinary parasitology have been described by Thompson (Thompson, 1999, 2001), Coles (Coles, 2001), Wall (Wall, 2007) and other authors. For example, Coles (2001) has suggested a list of prioritized research requirements, including new drugs, resistance management, vaccines, breeding for resistance, improved diagnostics, zoonoses and the impact of global warming on parasites. Other priorities could be added to this list, such as vector-borne diseases, neglected tropical diseases, or sustainable parasite control strategies.

The 50th anniversary of the WAAVP provides an opportunity for discussing the perspectives and options of the association in view of the current and future challenges. With reference to research options described in the literature (see above), a few general suggestions are presented here, directly related to the WAAVP's competences:

- a) The statement made by Zajac and colleagues (Zajac et al. 2000) should be supported that “veterinary parasitologists must emerge from the classroom and laboratory and become activists in promoting our discipline and bringing it the recognition it merits”. For example, WAAVP could publish an international, well documented plea for defined parasitological institutions or units at veterinary faculties (universities), equipped with a sufficient staff number and financial resources required for teaching veterinary parasitology, research, diagnostics, post-graduate education and potential other tasks.
- b) Stimulation of disciplinary or interdisciplinary, national or international research approaches aimed at the solution of defined problems. The formation and support of parasitology networks (Dupouy-Camet et al., 2009) could be useful in this respect.
- c) More serious attempts should be made to influence targets and structures of large international research programs, as suggested by P. Nansen, without neglecting the support of smaller cooperative projects (Nansen, 1999). Strengthening of official links to international organizations (FAO, WHO, EU etc.) should be classified as a high interest of the WAAVP.
- d) The exposure of the WAAVP to parasitology from regions not well represented in the WAAVP should be increased (WAAVP, 2011), and new members should be recruited from these areas.



e) The preparation of international guidelines should be continued and extended for various applications, such as diagnostic procedures, evaluation of drugs (including “alternative” drugs), epidemiological methods, and sustainable parasite control. Recommendations for parasite control programs should consider aspects of the environment, animal welfare and food-safety.

f) The definition and continuous reconsideration of research requirements is a common procedure in some organizations, for example in the WHO. It could be of interest to establish a list in the internet (only accessible to WAAVP members) to which parasitologists from various parts of the world could add voluntarily local and international research needs. This could be helpful for preparing prioritized lists of research requirements as suggested by Coles (2001).

Hoping that these few suggestions may stimulate a broad discussion I express my best wi-shes for the WAAVP’s future and add sincere thanks for all that the association has given to me.

Table 1

WAAVP Honorary Members

1967	K.I. Skrjabin* (SU)*, B. Schwartz* (USA), W. Stefanski* (Poland)
1975	N.R. Stoll* (USA), R. Wetzel* (Germany), V.S. Ershov* (SU)
1981	M. Abdussalam *(Switzerland), K. Enigk* (Germany), H. McL. Gordon* (Australia)
1983	N.D. Levine*(USA), D.F. Stewart* (Australia)
1985	E.J.L. Soulsby (UK)
1987	J. Euzeby (France)
1993	C. Campbell (USA), B. Bezubik* (Poland), M. Cordero del Campillo (Spain)
1995	J. Armour (UK), J. Eckert (Switzerland), S.M. Gaafar (USA), G. Luffu (France), G.M. Urquhart* (UK)
1997	T. Hiepe (Germany), A. Donald (Australia), J. Boray (Australia), J.O.D. Slocombe (Canada)
1999	T. Kassai (Hungary), C. Himonas* (Greece), W. Mulligan (UK)
2001	J. Duncan (UK), I. G. Horak (Rep. South Africa), P. Nansen* (Denmark), G. Schad* (USA)
2003	J. Williams (USA), M. Eysker (Netherlands)
2005	S. Taylor (UK)
2007	D. Jacobs (UK)
2009	F. Borgsteede (Netherlands), F. Jackson (UK)
2011	I. Beveridge (Australia), K. Fujisaki (Japan) L. Gasbarre (USA)

* Deceased

Table 2

WAAVP Officers, terms of office and congress sites from 2005 to present¹

Officers	2005-2009: Ghent → Calgary	2009-2013: Buenos Aires → Perth
President	Tom Kennedy (USA)	Peter Holdsworth (Australia)
1st Vice President	Thomas Schnieder (Germany)	Doug Colwell (Canada)
2nd Vice President	Stig Thamsborg (Denmark)	Maggie Fischer (UK)
Secretary/Treasurer	Bill Pomroy (New Zealand)	Bill Pomroy (New Zealand)
Directors	Maggie Fisher (UK), Chandrawathani Panchadcharam (Malaysia), Peter Holdsworth (Australia), Sandy Trees (UK)	Chandrawathani Panchadcharam (Malaysia), Thomas Schnieder ² (Germany), Sandy Trees (UK), Barry Hosking (Australia), Carlos Lanusse (Argentina)
Past-President	Jozef Vercruysse (Belgium)	Tom Kennedy (USA)

¹ Data on previous periods from 1963 to 2005 see Malone et al. (2004). ² Deceased on 16th May 2012.

Table 3

WAAVP Conferences (updated and expanded after Malone et al. , 2004)

No.	Date	Site and country (region) ¹	Theme	Attendants	Publication VP: Vet. Parasitol.
01	1963	Hannover*, Germany (E)	The Evaluation of Anthelmintics	~ 40	Soulsby, 1964*
02	1965	Philadelphia, USA (N-A)	The Biology of Parasites of Veterinary Importance	150	Soulsby, 1966*
03	1967	Lyon*, France (E)	Reactions of the Host to Parasitism	160	Soulsby, 1968
04	1969	Glasgow, Scotland, UK (E)	Pathology of Parasitic Diseases		Gaafar, 1971*
05	1971	Mexico City*, Mexico (C-A)	Immunity against Animal Parasites	100	Soulsby, 1972*
06	1973	Vienna, Austria (E)	Parasitic Zoonoses	160	Soulsby, 1974 *
07	1975	Thessaloniki*, Greece (E)	Pathophysiology of Parasitic Infections	110	Soulsby, 1976
08	1977	Sydney, Australia (AUS/NZ)	Epidemiology, Economic Impact and Control of Parasitic Diseases	317	VP 1980: 6 (1-3)*
	1979	Moscow*, SU	WAAVP cancelled, five WVA symposia held	---	---
09	1981	Budapest, Hungary (E)	Ecology of Parasites. Interaction between Parasites and their Enevironments	300	VP 1982: 11 (No. 1)*
10	1983	Perth*, Australia (AUS/NZ)	Tropical Parasitoses of Animals including Zoonoses	~ 300	Dunsmore, 1983*
11	1985	Rio de Janeiro, Brazil (S-A)	Resistance of Parasites to Antiparasitic Drugs and Progress of Research in Veterinary Parasitology	450	VP 1985: 18 (No. 2)*
12	1987	Montreal*, Canada (N-A)	New Approaches in the Diagnosis and Control of Parasitic Diseases	400	VP 1989: 25 (2)
13	1989	Berlin (East), GDR (E)	Ecology and Epidemiology of Internal and External Parasitic Infections	484	VP 1989: 32 (1) vii + 1-100. *
	1991	Rabat, Morocco (AF)	Cancelled, Gulf War		---
14	1993	Cambridge, UK (E)	Understanding and Control of Parasitic Diseases in Animals	555	VP 1994 54 (1-3)*
15	1995	Yokohama*, Japan (AS)	Control of Parasitic Diseases, Food Safety and the Environment	235	VP 1966: 64 (1-2)*



16	1997	Sun City, South Africa (AF)	Veterinary Parasitology into the 21st Century	450	VP 1997: 71 (2-3)
17	1999	Copenhagen, Denmark (E)	Parasites, Production, Environment	738	VP 2000: 88 (1-2)
18	2001	Stresa, Italy (E)	Promoting Advancement- Preserving Tradition	550	VP 2001: 98 (1-3)
19	2003	New Orleans, USA (N-A)	Old Dreams – New Visions	400	VP 2003: 115 (2)*
20	2005	Christchurch, New Zealand (AUS/NZ)	From Science to Solutions	650	VP 2005: 132 (3-4)*
21	2007	Ghent, Belgium (E)	From EPG to Genes	~ 800	VP 2007 148 (1)
22	2009	Calgary, USA (N-A)	One World – One Health: Parasites in a Changing Landscape	677	VP 2009: 163 (3)*
23	2011	Buenos Aires, Argentina (S-A)	Towards Good Management Practices in Parasite Control	827	VP 2011: 180 (1-2)
24	2013	Perth, Australia (AUS/NZ)	Animal Production and Food Security; One World Health; Companion Animals-Challenges for the Future; Prophylactics and Therapeutics – New Approaches		

¹ Abbreviations of regions: AS: Asia, AF: Africa, AUS/NZ: Australia/New Zealand; C- A: Central America, E: Europe, GDR: German Democratic Republic = East Germany; N-A: North America; S-A: South America; SU: Sovjet Union. *: in conjunction with congresses of the World Veterinary Association (WVA)



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Table 4

Recipients of WAAVP awards

Year	Excellence in Research in Veterinary Parasitology ¹ (introduced 1993)	Excellence in Teaching of Veterinary Parasitology or Service (introduced 1993)	Peter Nansen Young Scientist Award (introduced 2001)
1993	James Armour (UK)*	E.J. Lawson Soulsby (UK)*	
1995	Jitender P. Dubey (USA)*	Jacques Euzeby (France)*	
1997	Max Murray (UK)*	Peter Nansen (Denmark)*	
1999	Desmond Hennessy (Australia)*	Johannes Eckert (Switzerland)*	
2001	Roger Prichard (Canda)	Gerhard Schad (USA)	Richard Wall (UK)
2003	Peter Waller (Sweden)**	No award	Samson Mukuratiwa (Zimbabwe)
2005	R.C. Andrew Thompson (Australia)**	No award	Min Hu (Australia)
2007	No award	Peter Holdsworth (Australia)**	Domenica Ontranto (Italy)
2009	Robin Gasser (Australia)**	No award	Aaron Jex (Australia)
2011	Jozef Vercruysee (Belgium)**	Lydden Polley (Canada)**	Laura Rinaldi (Italy)

¹ Alternate denomination: “Outstanding Contributions to Research in Veterinary Parasitology”.

* WAAVP/Pfizer Award, ** WAAVP/Bayer Award.

Tab. 5

WAAVP Guidelines (short titles) with [average number of citations per year]¹

1. Efficacy evaluation of antiparasitic drugs • Ruminants: Anthelmintics (bovine and ovine) (Powers et al., 1982)² [3.29]. Anthelmintics (bovine, ovine, caprine) (2nd ed.) (Wood et al., 1995)³ [11.89]. Ectoparasitocides against biting and nuisance flies (Holdsworth et al., 2006a)⁴[0.14]. Ectoparasitocides against myiasis causing parasites (Holdsworth et al., 2006b)⁵ [0.43]. Acaricides against ticks (Ixodidae) (Holdsworth et al., 2006c)⁶ [1.29]. Biting lice, sucking lice and sheep keds (Holdsworth et al., 2006d)⁷ [0.43]. Acaricides against mange and itch mites (Vercruysse et al., 2006)⁸ [0.29].
• Pigs: Anthelmintics (Düwel et al., 1986) ⁹ [0.78]. Anthelmintics (2 nd ed.) (Hennesy et al., 2006) ¹⁰ [0.14].
• Equines: Anthelmintics (Duncan et. al, 1988) ¹¹ [1.48]. Anthelmintics (2 nd ed.) (Duncan et al., 2002) ¹² [1.91].
• Dogs and cats: Anthelmintics (Jacobs et al., 1994) ¹³ [5.33]. Parasitocides for the treatment, prevention and control of flea and tick infestation on dogs and cats (Marchiondo et al., 2007) ¹⁴ [4.00].
• Poultry: Anthelmintics in chickens and turkeys (Yazwinski et al., 2003) ¹⁵ [2.10]. Anticocci- dial drugs in chickens and turkeys (Holdsworth et al., 2004) ¹⁶ [3.56].
2. Techniques: Methods for the detection of anthelmintic resistance in nematodes (Coles et al., 1992) ¹⁷ [24.76]
3. Nomenclature: Standardized nomenclature of animal parasitic diseases (SNOAPD) (Kassai et al., 1988) ¹⁸ [2.16].

¹ According to Web of Knowledge (status 01.09. 2012). ² Vet. Parasitol. 1982: 10, 265-284. ³ Vet. Parasitol. 1995: 58, 181-213. ⁴ Vet. Parasitol. 2006: 136, 3-13. ⁵ Vet. Parasitol. 2006: 136, 15-28.

⁶ Vet. Parasitol. 2006: 136, 29-43. ⁷ Vet. Parasitol. 2006: 136, 45-54. ⁸ Vet. Parasitol. 2006: 136, 55-66. ⁹ Vet. Parasitol. 1986: 21, 69-82. ¹⁰ Vet. Parasitol. 2006: 141, 138-149. ¹¹ Vet. Parasitol. 1988: 30, 57-72. ¹²Vet. Parasitol. 2002:103, 1-18. ¹³ Vet. Parasitol. 1994: 52, 179-202. ¹⁴ Vet. Parasitol. 2007: 145, 332-344. ¹⁵ Vet. Parasitol. 2003: 116, 159-173. ¹⁶ Vet. Parasitol. 2004: 121, 189-212. ¹⁷ Vet. Parasitol. 1992: 44, 35-44. ¹⁸ Vet. Parasitol. 1988: 29, 299-326.

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Legends to figures

Fig.1: Some attendants of the World Veterinray Congress and the 1st WAAVP conference, August 1963, at the “Westfalenhof”, School of Veterinary Medicine, Hannover, Germany: (right to left): V.S. Ershov (SU), K. Enigk (Germany). K. I. Skrjabin (SU), B. Beneke (Germany), Mrs. Skrjabin (SU), M. Petrovic (former Yugoslavia), K.T. Friedhoff (Germany).

Fig.2: The “Westfalenhof”, School of Veterinary Medicine, Hannover, Germany, in 1963, main building of the Institute of Parasitology and location of the WAAVP “birthday party”.

Fig. 3: WAAVP Presidents 1963 – 2013

Fig. 4: Attendants of the 15th WAAVP Conference in Yokohama, Japan

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Session Details:	8/26/2013 Opening Session 815 - 1000 <i>Riverside Theatre</i>
Oral Presentation Details:	Veterinary Parasitology in Australia – a Short History
Authors:	I. Beveridge ^a, R.B. Besier ^b ^a Department of Veterinary Science, University of Melbourne, Parkville, Victoria 3052 Australia ^b Department of Agriculture and Food Western Australia, 444 Albany Highway, Albany Western Australia 6330 Australia

As an important producer and exporter of livestock products, animal health has always been of major significance to the Australian economy, and research into efficient parasite control has continued since the 1800s. With substantial research achievements also involving parasites of companion animals and wildlife, Australian parasitologists have made numerous contributions of global significance. This summary outlines the development of investigations into parasite biology and parasitic disease in Australia.



Session Details:	8/26/2013 PLENARY SESSION: ONE HEALTH 1030 - 1145 <i>Riverside Theatre</i>
Oral Presentation Details:	One world health: socioeconomic burden and parasitic disease control priorities
Authors:	Paul R. Torgerson Section of Epidemiology, Vetsuisse faculty, University of Zurich, Winterthurestrasse 270, 8057 Zurich, Switzerland email: paul.torgerson@access.uzh.ch

Parasitic diseases present a considerable socio-economic impact to society. Zoonotic parasites can result in a considerable burden of disease in to humans and substantive economic losses to livestock populations. Ameliorating the effects these diseases may consist of attempts at eradicating specific diseases at a global level, eliminating them at a national or local level or controlling the disease to minimise incidence in an endemic disease. Alternatively with some parasitic zoonoses it may only be possible to treat human and animal cases as they arise. The choice of approach will be determined by the potential effectiveness of a disease programme, its cost and the cost effectiveness or cost benefit of undertaking the intervention. Furthermore human disease burden is being increasingly measured by egalitarian non financial measures which do not sit comfortably with measurements of economics costs in livestock. This adds additional challenges to assessing socio-economic burdens of zoonotic diseases. Using examples from the group of neglected zoonotic diseases information regarding the socio-economic effects of these diseases will be reviewed and how this information can be used in decision making with regard to control and treatment of these diseases.

Key words: Parasitic zoonoses, socio economic burden, cost effectiveness

Session Details:	8/26/2013 PLENARY SESSION: ONE HEALTH 1030 - 1145 <i>Riverside Theatre</i>
Oral Presentation Details:	Whose World, Whose Health?
Authors:	Yaowalark Sukthana Assoc. Prof., Dean Faculty of Tropical Medicine Mahidol University Bangkok, Thailand

The world is, nowadays, older, seems smaller but equipped with more advanced technologies. Global warming and climate change cause major disasters such as earthquake, big flooding and sever drought. Those affected environment and ecosystem leading to changing biodiversity of living organisms. Human and animal populations are steadily increasing. Thus normal habitats are facing crisis from deforestation and invasion of wildlife.

Emerging zoonotic infectious diseases due to parasites are not only causing human illness and death annually but also causing economic loss in the past 20 years. Human knowlesi malaria is a classic example of vector-borne parasitic zoonosis occurring due to expansion of human-wildlife interface. California sea otters death by toxoplasmosis indicated a close relationship of land and marine mammal link by runoff effect of contaminated environment by infective oocysts from land to sea. Steady prevalence of trichinellosis, a meat-borne parasitic infection, is transmitted from both domestic and wild pigs. Giardia and Cryptosporidium are two water-borne protozoa that resist harsh environment with low infective dose, thus causing diarrheal outbreaks in recreation and drinking waters. Extracellular multiplication of Cryptosporidium in biofilms could be responsible for outbreaks or spreading of cryptosporidiosis. Whether Blastocystis is a pathogen remains controversial, though, genotypic study strongly shows zoonotic potential in various domestic animals and wildlife.

Thus the world does not belong to only human but also to other living organisms as well as the environment. Human and animal face health hazards if the environment is poor. “One Health” approach which is multisectoral collaboration, including: physicians, veterinarians, public health scientists, ecologists, economists and others, together with advance technologies are necessary for effective management in term of surveillance, treatment, prevention and control in making all sectors-human, animal, environment-healthy.



Session Details:	8/26/2013 PLATINUM SPONSOR SESSION: BAYER 1700 - 1800 <i>Riverside Theatre</i>
Oral Presentation Details:	Long-term efficacy of an imidacloprid 10 % / flumethrin 4.5 % polymer matrix collar (Seresto®, Bayer) in dogs and its potential to prevent canine leishmaniasis in a hyper-endemic area
Authors:	Domenico Otranto ^{1*} , Filipe Dantas-Torres ^{1, 2} ¹ Università degli Studi di Bari, Valenzano, Italy ² Centro de Pesquisas Aggeu Magalhães, Recife, Brazil

Canine leishmaniasis (CanL) caused by *Leishmania infantum* is one of the most important vector-borne diseases affecting dogs worldwide. Due to its zoonotic potential, the prevention of CanL infection is a must for both dog and human health and requires a holistic approach on animals (at individual and population level) and in the environment.

Over the last decades, considerable efforts have been directed towards developing novel and cost-effective control strategies against this disease. However, due to the complexities involved in the transmission of *L. infantum* by the phlebotomine sand flies, the control of CanL has proven challenging. Control measures by application of insecticides in the environment may have momentary effect but it is usually unsustainable in the long term for technical and economic reasons. Recently, a polymer matrix collar containing a combination of imidacloprid 10 % and flumethrin 4.5 % (Seresto®, Bayer Animal Health, Germany), with a high repellent and insecticidal efficacy against fleas and ticks was tested as a novel prophylactic measure to prevent *L. infantum* infections in young dogs from a hyper-endemic area of southern Italy. The study was carried out on 124 young dogs of which, 63 were collar treated (group A) at study start (March – April 2011) until March 2012, whereas 61 were left untreated (group B). Blood and skin samples were collected at baseline (March – April 2011) and at the first, second, third and fourth follow-up time points (July, September 2011 and November 2011, March 2012, respectively). At the end of the trial, no dog from group A was positive for *L. infantum* at any follow-up, whereas 22 dogs from group B were infected (incidence density rate (IDR) = 45.13 %). Therefore, the use of collars containing 10 % imidacloprid and 4.5 % flumethrin conferred long-term protection against *L. infantum* infection in dogs located in a hyper-endemic area, thus representing a reliable and sustainable tool against CanL.



Session Details:	8/26/2013 PLATINUM SPONSOR SESSION: BAYER 1700 - 1800 <i>Riverside Theatre</i>
Oral Presentation Details:	Prevention of tick-borne diseases in dogs using an imidacloprid / flumethrin collar
Authors:	Filipe Dantas-Torres ^{1, 2*} , Domenico Otranto ¹ ¹ Università degli Studi di Bari, Valenzano, Italy ² Centro de Pesquisas Aggeu Magalhães, Recife, Brazil

Abstract: Tick-borne diseases are a group of maladies of great medical and veterinary significance. A range of tick-borne pathogens, including species of bacteria and protozoa, can affect dogs, and some of these are of zoonotic concern. The control of tick infestations is pivotal towards the prevention of tick-borne pathogen transmission. In this perspective, different insecticidal and repellent products have been developed in recent years for use on dogs. A collar containing a combination of imidacloprid 10 % and flumethrin 4.5 % has been proven effective against tick and flea infestations in dogs. From March 2011 to October 2012, a field study was conducted in southern Italy to assess the efficacy of this collar in the prevention of dogs against tick infestation and tick-borne pathogen transmission in young dogs. A total of 122 animals were enrolled in the study and randomly assigned to group A (n = 64), which were collared, and group B (n = 58), left as untreated controls. Dogs were monthly examined for ticks and systematically tested for selected tick-borne pathogens. An overall efficacy against tick infestation of 99.7 % was recorded with an overall efficacy of 90.9 % against tick-borne pathogen infections in dogs from group A (i.e., from 91.1 % for *Anaplasma platys* to 100 % for *Babesia vogeli*). This study demonstrates that the imidacloprid / flumethrin collar is an effective preventive against ticks and tick-borne pathogens in dogs.



Session Details:	8/27/2013 PLENARY SESSION: COMPANION ANIMALS 0830 - 0945 <i>Riverside Theatre</i>
Oral Presentation Details:	Future challenges for parasitology: vector control and one health in the Americas
Authors:	Susan E. Little*, DVM, PhD, DACVM-Parasit. Center for Veterinary Health Sciences, Oklahoma State University, Stillwater, OK USA

‘One Health’ is a term that encapsulates and underscores the inherent interrelatedness of the health of people, animals, and the environment. Vector-borne infections are central in one health. Many arthropod vectors readily feed on humans and other animals, serving as an ideal conduit to move pathogens between a wide spectrum of potential hosts. As ecological niches flux, opportunities arise for vectors to interact with novel species, allowing infectious agents to broaden both geographic and host ranges. Habitat change has been linked to the emergence of novel human and veterinary disease agents, and can dramatically facilitate expansion opportunities by allowing existing vector populations to flourish and by supporting the establishment of new pathogen maintenance systems. At the same time, control efforts can be hindered by the development of parasiticide and pesticide resistance, foiling efforts to meet these challenges. Using examples drawn from representative diseases important in one health in the Americas, including rickettsial infections, Lyme borreliosis, Chagas disease, and West Nile virus, this paper reviews key aspects of vector-borne disease maintenance cycles that present challenges for one health in the Americas, including emergence of vector-borne disease agents, the impact of habitat change on vector-borne disease transmission, and the complexities faced in developing effective control programs. Novel strategies will be required to effectively combat these infections in the future if we are to succeed in the goal of fostering an environment which supports healthy animals and healthy people.



Session Details:	8/27/2013 NOVARTIS SPONSORED SESSION 1630 - 1730 Riverside Theatre
Oral Presentation Details:	Effecting cestode impacts on human and veterinary patients
Authors:	Susan E. Little, DVM, PhD, Dipl. ACVM Calum N. L. Macpherson, PhD, FRSPH

Join us for this one-hour symposium showcasing a one-health view of parasitology. We'll be exploring the impact cestodes have on both human and animal health, as well as the importance of controlling cestodes as part of protecting human and animal health. The results of this focused discussion on tapeworms should help increase our understanding of the significant impact cestodes have on both animals and people and the complex host, intermediate host and parasite interactions involved.

The session will be moderated by Dr. Arthur Redpath from Novartis Animal Health and features two dynamic speakers:

Susan E. Little, DVM, PhD, DACVM-Parasit., Regents Professor and Krull-Ewing Endowed Chair in Veterinary Parasitology, Department of Veterinary Pathobiology, Center for Veterinary Health Sciences, Oklahoma State University and Calum N.L. Macpherson, PhD, Vice Provost, International Program Development Professor & Dean, Graduate Studies, Director of Research, St. George's University.



Session Details:	8/27/2013 PLENARY SESSION: COMPANION ANIMALS 0830 - 0945 <i>Riverside Theatre</i>
Oral Presentation Details:	Future challenges for parasitology: Vector control and ‘One health’ in Europe.
Authors:	Norbert Mencke, Bayer Animal Health GmbH, Kaiser-Wilhelm-Allee 50, 51373 Leverkusen, Germany

The medical as well as the veterinary importance of parasitic arthropods or ectoparasites in general terms, is characterized by the primary or secondary impact on the health of humans and companion animals alike. The parasitic arthropods addressed here are those ectoparasites belong to the class of insects, such as fleas and sand flies, or the subclass of acarids, such as ticks. These parasitic arthropods interact intensively with their hosts by blood feeding. Fleas, sand flies and ticks hold the vector capacity to transmit pathogens such as virus, bacteria or protozoa to cats, dogs and humans. The diseases caused by these pathogens are summarized under the terms canine vector-borne diseases (CVBD), feline vector-borne diseases (FVBD) or metazoonoses. In small animal practice, it is important to understand that the transmitted pathogen may either lead to a disease with clinical signs, or more often to asymptomatic, clinically healthy, or silent infections. Blocking of the vector–host interactions, the blood feeding and subsequently the transmission of pathogens during blood feeding is a key element of CVBD control. The focus of this review is on the current knowledge of the epidemiology of parasitic vectors and three important CVBDs they transmit; rickettsiosis, tick borreliosis and canine leishmaniosis from a European perspective, and how veterinary medicine may contribute to the challenges of CVBDs and their control. Prevention of CVBDs is fundamentally based on ectoparasite control. Ectoparasite management in cats and dogs is important not only for the health and well-being of the individual companion animal but for public health in general and is therefore a perfect example of the ‘One health’ approach.

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Session Details:	8/27/2013 NOVARTIS SPONSORED SESSION 1630 - 1730 <i>Riverside Theatre</i>
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Session Details:	8/27/2013 PLENARY SESSION: PROPHYLACTICS AND THERAPEUTICS 0830 - 0945 <i>Riverside Theatre</i>
Oral Presentation Details:	Immunomodulatory Molecules of <i>F. hepatica</i>: Candidates for Both Vaccine and Immunotherapeutic Development
Authors:	Prof. John P. Dalton <i>Institute of Parasitology McGill University</i>

The liver fluke, *Fasciola hepatica*, causes fascioliasis in domestic animals (sheep, cattle) and humans. The parasite rapidly invades the gut wall of its host and quickly influences the function of various host immune cells (e.g. dendritic cells, macrophages and mast cells). The parasite secretes a myriad of molecules that direct the immune response towards a favourable non-protective Th2-mediate/regulatory environment. Cysteine peptidases such as cathepsins L (FhCL1) and cathepsins B (FhCB), are amongst the major molecules secreted by the invading parasites and most certainly are involved in modulating the host immune response. Thus these molecules are under development as the first generation of fluke vaccines. However, other secreted immunomodulatory molecules, such as peroxiredoxin (FhPrx) and helminth defence molecule (FhHDM-1) are also prime vaccine targets that should be considered worthwhile vaccine candidates, alone or in combination with other molecules. Furthermore, because of the ability to modulate host immune cell function these molecules could be harnessed to help treat immune-related conditions in humans and animals.



Session Details:	8/28/2013 ASP/ELSEVIER SESSION 1115 - 1315 Riverside Theatre
Oral Presentation Details:	Filling the gaps: expression profiling of zoonotic Apicomplexa in definitive hosts
Authors:	Adrian Hehl University of Zurich

The intestinal development of the zoonotic Apicomplexa *Toxoplasma gondii* and *Cryptosporidium parvum* has remained understudied because of the highly limited access to these stages within infected animals and the difficulties of establishing in vitro culture systems. To date *Cryptosporidium* can be maintained in animals only, primarily because all stages of the life cycle are entirely restricted to the intestine of a single host and cannot be fully replicated in cell culture. Similarly, the coccidial life cycle of *Toxoplasma* is confined to intestinal epithelial cells of felids, but asexually proliferating stages also establish systemic infections in cats and in a wide range of intermediate hosts including humans. These extraintestinal stages of *Toxoplasma* are easily cultivated in vitro and amenable to a vast range of experimentation including forward and reverse genetics. During the past two decades this provided an exceptional opportunity to discover many aspects of the Apicomplexa-specific molecular machinery responsible for host –parasite interaction. Because of the recent massive increase in sequencing and computing power the hitherto hidden enteroepithelial stages are now also becoming accessible to molecular analysis. Filling the vast knowledge gaps to draft a new chapter in research on coccidia and other Apicomplexa is within reach. These new opportunities to unlock the hidden biology of enteroepithelial stages are based on complete interdisciplinary pipelines for gene expression profiling of parasites isolated from experimentally infected animals. Although almost all knowledge about Apicomplexa biology is currently about cultivatable extraintestinal stages, this information now proves invaluable by providing a multitude of biological reference points for the interpretation of new gene expression data and a scaffold for the rapid construction of a molecular road map of enteroepithelial development.



Session Details:	8/28/2013 ASP/ELSEVIER SESSION 1115 - 1315 Riverside Theatre
Oral Presentation Details:	Specific and/or unspecific mechanisms of anthelmintic resistance: How could we tackle this conundrum?
Authors:	Georg von Samson-Himmelstjerna, Jürgen Krücken, Janina Demeler

Anthelmintic resistance is progressively spreading both in terms of spatial distribution as well as concerning occurrence in different parasite species. Recent examples include reports on increased prevalence of benzimidazole resistance in equine cyathostomins or cases of macrocyclic lactone resistance in cattle trichostrongyles or *Parascaris equorum* in horses. Numerous scientific studies have contributed to our understanding of the mechanism of anthelmintic resistance in parasitic nematodes. Both specific, i.e. drug target associated, as well as unspecific, that is drug efflux or metabolism associated processes have been shown to be involved in resistance directed towards for example benzimidazoles as well as macrocyclic lactones. To our best current knowledge it seems that in both, experimentally as well as field selected benzimidazole resistant populations, a few specific changes in the β -tubulin coding sequence, leading to single amino acid exchanges, result in reduced drug susceptibility. Thus for benzimidazole resistance a clear correlation with specific resistance mechanisms is evident. Nevertheless, there is also compelling evidence for drug efflux mediated, namely P-glycoprotein associated, mechanisms of benzimidazole resistance in nematodes. In addition to drug efflux, drug metabolism, for example mediated by increased of enzymes belonging to the broad family of cytochrome P450 oxidases, was found to potentially contribute to anthelmintic resistance in fluke and trichostrongyles. Albendazol biotransformation has been demonstrated in *Caenorhabditis elegans* which upregulate cytochrome P450 monooxygenases and UDP-glycuronosyl transferases and produce glycosylated albendazol metabolites. Accordingly, at least two principally unrelated processes may lead to benzimidazole resistance and it has thus far often been ignored to systematically examine these different resistance pathways simultaneously while characterizing worm populations showing reduced drug susceptibility. The practical consequences of these findings still remain more or less unclear as long as we do not know if both routes of resistance frequently occur simultaneously in the field and if this occurs which effect this will have on levels of resistance? Also it has not been established how to best detect the presence of the two resistance mechanisms in field populations. This paper will highlight our current knowledge concerning the specific and unspecific mechanisms of resistance and discuss approaches to study potential interdependencies.



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Session Details:	8/28/2013 ASP/ELSEVIER SESSION 1115 - 1315 Riverside Theatre
Oral Presentation Details:	Wildlife Parasitism in a Changing Climate: Shifting boundaries, barriers, and paradigms
Authors:	Dr Susan Kutz ¹ ¹ University of Calgary

Parasites play multiple roles in host populations on evolutionary and ecological timescales, simultaneously driving diversity and affecting population dynamics. Climate is a major factor influencing host-parasite interactions and may manifest in many ways. Much effort has been focused on examining the direct effects of temperature on pathogen and vector development, survival, and transmission, and recent approaches that apply the metabolic theory of ecology to pathogens hold promise for developing broader generalizations of host-parasite interactions under climate change. Climate change is also influencing wildlife ecology, food-web structure, animal behavior and movement patterns, habitat quality and quantity, and increasing or decreasing barriers to animal and pathogen movement. Many of these processes are being played out in real time at high latitudes, leading to changes in host-pathogen communities and interactions. In this presentation we explore new insights gained from studies on the ecology of parasites in caribou and muskoxen in a rapidly warming Arctic.





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Session Details:	8/29/2013 PLENARY SESSION: ANIMAL PRODUCTION AND FOOD SECURITY 0830 - 1000 <i>Riverside Theatre</i>
Oral Presentation Details:	Parasitology in a Hungrier, Warmer, Riskier World
Authors:	Dr G Douglas Gray ACIAR, South Australia

Parasitologists live in the changing world. Implementation of our parasitological knowledge needs to reflect these changes: in the rise and fall of livestock and aquaculture practices, the emergence of new drugs and vaccines and their limitations, and of the ethical and economic standards to which we are held. Research however, must do more than reflect today’s world and needs to predict possible future scenarios in which to remain relevant. Scientific gatherings provide one opportunity to scope the future of livestock production and its role in food security, ask hard questions to prompt new parasitological research and the training of young researchers needs which in 10, 20, 30 years time will be capable of being applied. In this paper I would like to ask some of these questions against the backdrop of predicted supply and demand for food, climate change associated with global warming, and the risks generated by poor access to food and water. All of these present challenges for veterinary parasitology in 2050 and steps might be taken now in preparation. Some key questions are:

- What will be the role of livestock in global agricultural production?
- Is livestock production a threat or opportunity to food security
- How will disease occurrences and impacts be report, by whom and to what institutions?
- Who will be responsible for solving parasite problems and will they be seen as problems as we now see them?
- How best can a new generation of livestock parasitologists be trained to meet these challenges?

The current trends to intensified and industrialised production of pigs and poultry is at risk of the subsidy policies of major governments and competing demands for input feeds of soy and maize. There is a strengthening movement to localise production of minor essential food components and highly innovative approaches to food production based on solar energy, sea water, algal and bacterial inputs. Conventional disease reporting is being challenged by public reporting and analysis of internet data, There is resistance, especially among emerging economies, to the reporting, surveillance and control approaches developed last century by the industrialised economies. Parasitology has always been an integrative science. Research on Individual organisms will continue to be essential, with the solutions to the real world problem of 2050 likely to require even more integration with other disease disciplines and with the sciences of animal production, socioeconomics and the environment.



Session Details:	8/29/2013 PLENARY SESSION: ANIMAL PRODUCTION AND FOOD SECURITY 0830 - 1000 <i>Riverside Theatre</i>
Oral Presentation Details:	Global Food Security - Reducing the Impact of Livestock Endemic Disease
Authors:	Julie Fitzpatrick Moredun Research Institute

Global food security will require the production of more food using resources, including land, more efficiently, and with less waste. This goal must be achieved within the context of climate change and while ensuring minimal adverse environmental impact from both crop and livestock production. Disease, especially infectious disease, is a main constraint of biologically efficient livestock production and both endemic and exotic disease results in mortality and morbidity and hence less food than should ideally be available in current farming systems. A significant proportion of diseases affect the safety of food supplies, in addition to or instead of, their effect on volume and quality of food products. Parasitological diseases including those caused by nematodes, trematodes, protozoa and ectoparasites, have widely differing effects on meat, milk and fibre production and many new technologies have been developed in order to prevent or treat them. Approaches to developing better control of parasites have included livestock breeding strategies, improved nutrition and management, and the development of new drugs, diagnostic tests and vaccines. Some of the most important examples include both the development of new anthelmintic products, and better means of using existing drugs in order to maximise their effectiveness in the face of rapidly increasing parasite resistance; diagnostic tests which are able to detect low levels of nucleic acids or proteins from infectious agents rapidly; and vaccines derived from either native or recombinant proteins and designed to stimulate the most appropriate protective response from livestock species. Some of the parasitic diseases affect restricted regions around the world, however most affect very large global populations. The development of technologies of suitable and affordable livestock products for use in developing countries where most pressure on increased production for food will occur, provides a particular challenge. Most if not all new technologies form part of integrated management schemes on farms and these vary hugely in differing systems and geographical regions of the world. If the benefit of improved technologies for optimal health, welfare and biological efficiency of livestock is to be realised, then the veterinary, farming, commercial animal health and public service communities need to learn lessons from past successes and failures in the delivery of newly developed technologies to the farmer. The combination of technology and rural development in the veterinary parasitological field has played a key role in current food production and is well placed to continue this trend to help in ensuring future food requirements for the world.



Session Details:	8/29/2013 PLATINUM SPONSOR SESSION: ZOETIS 1630 - 1730 <i>Riverside Theatre</i>
Oral Presentation Details:	The Evolutionary Biology of Pesticide Resistance
Authors:	Jeffrey G. Scott Cornell University, Ithaca NY USA

Pesticide resistance continues to be a vexing problem in all areas of pest control. Early researchers used bioassays to define resistance and lay the foundation for our understanding of the basic principles of this specific example of evolutionary biology. For the last 20 years, molecular studies have added tremendous detail to our understanding of the changes that occur in response to the strong selective forces in a pesticide treated environment. Newer technologies, such as high throughput sequencing, offer (potentially) even greater insights into resistance. The basic principles of pesticide resistance will be reviewed and examples of the molecular basis for changes that result in resistance will be presented.



Session Details:	8/29/2013 PLATINUM SPONSOR SESSION: ZOETIS 1630 - 1730 Riverside Theatre
Oral Presentation Details:	Lessons from agriculture on adaptive resistance management
Authors:	Tom Walsh CSIRO

Parallels likely exist between the management of resistance by key pests in agriculture and antimicrobial agents in human or veterinary medicine. Cotton expressing proteins from the soil bacteria *Bacillus thuringiensis* (Bt) has been gradually released and adopted by Australian growers since 1996. It was initially deployed primarily to control the polyphagous pest *Helicoverpa armigera* (Hübner) which in the 1990's became increasingly difficult to control due to widespread resistance to synthetic chemical insecticides. Since then, experts worldwide have considered the Australian Cotton Industry to be leading the way in pre-emptive resistance management of insecticidal transgenic crops. This talk aims to outline the strategies adopted by the industry to control resistance by its recidivist pest nemesis. The primary tactic is based on the "high-dose plus refuge" strategy which takes advantage of the likely recessive nature of resistance to Bt toxins. Killing potentially resistant pupae during winter aestivation is another critical component of the resistance management plan, as is restricting opportunities for selection by limiting exposure. An integral component of the plan is monitoring populations of this pest to warn of impending resistance that may be prolonged by altering components of the resistance management plan.

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Achieving veterinary guided parasite control for sustainable veterinary practice. Rob Churchill <i>Crookwell Veterinary Hospital</i>	Echinococcus spp. in northern North America Emily Jenkins <i>University of Saskatchewan</i>	Age-related patterns of infection for an invasive fluke in free-ranging wapiti (Cervus canadensis) in Alberta, Canada Melissa Beck <i>University of Lethbridge</i>	Somethin's happenin' here: Apparent precocious excystation of Dicrocoelium dendriticum metacercariae in their ant intermediate host Doug Colwell <i>Agriculture and Agri-Food Canada</i>
Gastrointestinal nematodes and the technical efficiency of dairy farms Mariska Van Der Voort <i>Institute for Agricultural and Fisheries Research</i>	Lungworms in muskoxen in Norway - a potential threat with warmer climate? Inger Hamnes <i>Norwegian Veterinary Institute</i>	Of macropods and nematodes: A novel technique for investigating host-parasite population dynamics Matthew Lott <i>Macquarie Univeristy</i>	The Angiostrongylus vasorum transcriptome provides deep insights into theparasite's biology and immunobiology, and prospects for new interventions Brendan Ansell <i>University of Melbourne</i>
An investigation into the current transmission pathway of Taenia ovis in Australia David Jenkins <i>Charles Sturt University</i>	Exploiting parallels between livestock and wildlife systems Hannah Rose <i>University of Bristol</i>	Behaviour, bettongs and blood-suckers: using social network models to understand parasite transmission in wildlife populations Stephanie Godfrey <i>Murdoch University</i>	Cytokine expression in the placenta of cattle following inoculation withNeospora caninum throughout gestation Germán Cantón <i>Moredun Research Institute</i>
Helminth neurobiology: Identifying the moving targets of cholinergic anthelmintics Richard Martin <i>Iowa State University</i>	Toxoplasma gondii in Scandinavian brown bears Krista Jones <i>Hedmark University College</i>	Trypanosomes and their ectoparasitic vectors on a translocated population of Australian marsupials Judy Dunlop <i>Murdoch University</i>	How does galectin-11 mediate gastrointestinal nematode resistance in sheep? Sarah Preston <i>Monash University</i>
Gastrointestinal helminths of camels (Camelus dromedarius) in center of Iran Alireza Sazmand <i>Institute of Applied-Scientific Education of Jihad-E-Agriculture, MolaSadra Cent</i>	(IWAAPV Session) Accounting for detection probability improves Toxoplasma gondiiseroprevalence estimates in arctic foxes Emily Jenkins <i>University of Saskatchewan</i>	Blastocystis in West Australian Wildlife Unaiza Parkar <i>Murdoch University</i>	Neonatal porcine isosporosis does humoral immune response confer protection Anja Joachim <i>Vetmeduni Vienna</i>

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Organisation of cathepsin cysteine proteases within the Fasciola hepatica genome Krystyna Cwiklinski <i>University of Liverpool</i>	Different exposure indicators to pasture-borne nematodes as tools for selectiveanthelmintic treatment in adult dairy cattle Nadine Ravinet <i>IDELE, French Livestock Institute</i>	Efficacy of ivermectin, pyrantel and fenbendazole treatments against Parascaris equorum infection in foals in southern Australia Kristopher Hughes <i>Charles Sturt University</i>	Zoonotic Enterocytozoon in Thailand: surveillance in humans, domestic animals, and wildlife Hirotake Mori <i>Mahidol University</i>
Proteomics of the moulting process in Oesophagostomum dentatum Martina Ondrovics <i>University of Veterinary Medicine Vienna</i>	Can easy-to-measure indicators predict production responses to anthelmintictreatment in dairy cattle? Johannes Charlier <i>Ghent University</i>	Macrocytic lactone resistance in cyathostomins and Parascaris equorum on Australian horse farms Anne Beasley <i>University of Queensland</i>	Echinococcus control requires dog population management David Heath <i>DNA Investments Ltd</i>
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Functional characterisation of S. mansoni egg-secreted proteins usinglentivirus-delivered microRNAs Bernd Kalinna <i>The University of Melbourne</i>	Use of a persistent anthelmintic injection to promote stimulation of a host response to intestinal nematodes in calves Peter Pulford <i>Virbac New Zealand Ltd</i>	Equine parasites commonly anthelmintic resistant in Finland Antti Oksanen <i>Finnish Food Safety Authority Evira</i>	Differences in in vitro sensitivity and accumulation of anthelmintics in Trichuris suis and Oesophagostomum dentatum A/Prof Peter Nejsum <i>University of Copehagen</i>

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Helminth control in Malaysia: Dealing with anthelmintic resistance Chandrawathani Panchadcharam <i>Ipoh Malaysia</i>	Effects of climate change regarding survival and selection pressure of cattle parasites on pasture Friederike Knapp-Lawitzke <i>Freie Universität Berlin</i>	Assessing calves as carriers of Cryptosporidium and Giardia with zoonotic potential on dairy and beef farms within a water catchment area by mutation scanning Harshanie Abeywardena <i>University of Melbourne</i>	Assessing risk: Spatial trends and environmental risk factors for an emerging liver fluke of sympatric host species in Alberta, Canada Melissa Beck <i>University of Lethbridge</i>
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One health in action: parasites transmitted among people, pets, wildlife, and the environment in remote and rural communities in Saskatchewan, Canada Emily Jenkins <i>University of Saskatchewan</i>	Vaccination of pigs and lambs against Toxoplasma gondii reduces tissue cyst formation; safer meat for human consumption. Alison Burrells <i>Moredun Research Institute</i>	Babesia lengau possibly incriminated in causing feline babesiosis in South Africa Banie Penzhorn <i>University of Pretoria</i>	Iron deposits in spleens and livers of malaria and schistosoma infected mice Tim St Pierre <i>The University of Western Australia</i>
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Research experience on the practical approach to parasite control in livestock in parts of Southern Africa, a changing scenario Dr Tom Strydom <i>Director, MSD Research Unit, Malelane, South Africa</i>	Biochemical characterisation of serine protease inhibitors from <i>Schistosoma japonicum</i> Adebayo Molehin <i>Queensland Institute of Medical Research</i>	Morphological features and molecular characteristics of piroplasms infecting the Platypus (<i>Ornithorhynchus anatinus</i>) Andrea Paparini <i>Murdoch University</i>	A high-throughput diagnostic platform for gastrointestinal nematode infections in small ruminants Florian Roeber <i>AusDiagnostics Pty Ltd</i>
	RNAi-Based Screening for Vaccine Targets Identification of <i>Schistosoma mansoni</i> Tegument Proteins Yee Leow <i>Queensland Institute of Medical Research</i>	Novel parabasalid flagellates endosymbiotic in native Australian subterranean termites Linda Ly <i>University of Queensland</i>	Molecular diagnosis and therapeutic trials on fasciolosis in sheep Khalid Mehmood <i>Slamia University of Baha</i>
	Immunomics-based identification of schistosomiasis vaccine antigens: an integrated discovery and validation approach Mark Pearson <i>James Cook University</i>	The micromorphological specializations of the sucking louse <i>Linognathus setosus</i> from the Springbok <i>Antidorcas marsupialis</i> . Edward Green <i>University of Limpopo</i>	High prevalence of <i>Taenia saginata</i> cysticercus infection in slaughtered dairy cows in Central Europe: a multi-test analysis Ramon Marc Eichenberger <i>University of Zurich</i>
	Molecular Characterization of Annexin (Anx) and Tetraspanin (TSP) Gene Families from <i>Fasciola hepatica</i> Vignesh Rathinasamy <i>Latrobe University</i>	A novel <i>Babesia</i> spp. associated with morbidity and mortality in eastern grey kangaroos. Christopher Peacock <i>University of Western Australia</i>	Genetic characterization of selected parasites from people with histories of gastrointestinal disorders Anson Koehler <i>University of Melbourne</i>
	Field Trial in Commercial Irish Farms with Experimental Vaccine Using Recombinant Mutant <i>Fasciola hepatica</i> Cathepsin L1 in Cattle Andreas Chrysafidis <i>University College Dublin</i>	Presence of cryptic species within the nematode genus <i>Cloacina</i> Mary Shuttleworth <i>The University of Melbourne</i>	No more confusion: it is <i>Tritrichomonas foetus</i> based on comparative analysis of <i>Tritrichomonas foetus</i> cat and cattle genotype, and <i>Tritrichomonas suis</i> at ten DNA loci Jan Slapeta <i>University of Sydney</i>

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Do gastro-intestinal nematode infections induce pain in their sheep hosts? Caroline Chylinski <i>INRA</i>	Using next generation sequencing to identify ivermectin resistance loci in <i>Haemonchus contortus</i> . Peter Hunt <i>CSIRO</i>	Effects Of Protein Supplementation On Gastrointestinal Nematode Infestation InLambs Farhana Chaudhry <i>University</i>	<i>Echinococcus canadensis</i> in slaughtered farmed elk in Southern Alberta, Canada Brenda Ralston <i>Alberta Agriculture and Rural Development</i>
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Scabies mites give bacteria a helping hand - <i>Staphylococcus aureus</i> co-infections of mite infected skin are promoted by mite complement inhibitors Pearl Swe <i>Queensland Institute of Medical Research</i>	Whole genome analysis for macrocyclic lactone resistance markers in <i>Dirofilaria imitis</i> Catherine Bourguinat <i>McGill University</i>	Assessment of monepantel and monepantel sulphone gastrointestinal concentrationprofiles in sheep:-relevance of the kinetics/ efficacy relationship- Adrian Lifschitz <i>Centro de Estudios Veterinarios (CONICET) Facultad Cs. Veterinary</i>	Oxfendazole treatment trial to control porcine cysticercosis in AngóniaDistrict, Mozambique Stig Milan Thamsborg <i>University of Copenhagen</i>
<i>Eimeria bovis</i> modulates endothelial host cell cholesterol metabolism Carlos Hermosilla <i>Justus Liebig University Giessen</i>	Drug-efflux and target-site gene expression patterns in levamisole-resistant <i>Haemonchus contortus</i> . Ranbir Sarai <i>CSIRO Animal, Food and Health Sciences</i>	Ewe but not lamb worm control increases weaning weight of prime lambs Michelle Dever <i>University of New England</i>	Control of <i>Taenia solium</i> : calculation of the minimum number ofvaccination/chemotherapy interventions required in pigs per year to achievecontrol Marshall Lightowlers <i>University of Melbourne</i>



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Gastrointestinal nematode control in sheep under three grazing management systems and factors influencing faecal worm egg count Stephen Walkden-Brown University of New England	To serve or to protect? Functional analysis of Fasciola hepatica type 2cystatin. Sasa Stefanic Institute of Parasitology
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Evaluation of resistance in a selected field strain of Haemonchus contortus to ivermectin and moxidectin using the Larval Migration on Agar Test Marcelo Molento Universidade Federal Do Parana	Treatment and control of bovine mange infestation with ivermectin long-acting injection (IVOMEC® GOLD) Dietmar Hamel Merial GmbH
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Transcriptome of Cryptosporidium parvum (bovine genotype) in vitro and in vivostages: New insights into the biology of an intestinal parasite Christoph Lippuner <i>University of Zurich</i>	The use of a stochastic model to predict the role of monepantel in combination anthelmintics Barry Hosking <i>Novartis Animal Health</i>	A Humanized Mouse Model for Transmission Blocking Antimalarial Assessment andDiscovery. Alice Butterworth <i>Queensland Institute of Medical Research</i>	
In silico analysis of Dermanyssus gallinae transmembrane and excretory/secretory proteins Sabine Schicht <i>University of Veterinary Medicine Hannover</i>	Monepantel resistance selection studies in Teladorsagia circumcincta David Bartley <i>Moredun Research Institute</i>	In vitro and in vivo studies of fenofibric acid-based drug combinations fortreatment of malaria Rina Wong <i>University of Western Australia</i>	
Proteins of the Toxoplasma secretome influence the host epigenome: an in-silicoapproach Genevieve Syn <i>Telethon Institute for Child Health Research</i>	Molecular genetic analysis of interspecies hybridization between Haemonchuscontortus and Haemonchus placei and its implications for the spread ofbenzimidazole resistance mutations Umer Chaudhry <i>University of Calgary</i>	Potent ex vivo activity of pyronaridine, naphthoquine and methylene blue againstchloroquine resistant field isolates of Plasmodium falciparum and P. vivax Jutta Marfurt <i>Menzies School of Health Research</i>	

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Session Details:	8/26/2013 COMMERCIAL LIVESTOCK - GENERAL 1145 - 1300 Riverside Theatre
Oral Presentation Details:	Achieving veterinary guided parasite control for sustainable sheep production
Presentation Time:	1145 -1200
Authors:	Windsor P ¹ , Kozaruk M ¹ , Churchill R ² ¹ Faculty of Veterinary Science, University of Sydney, ² Crookwell Veterinary Hospital

Parasitism by gastrointestinal nematodes and anthelmintic resistance present an increasing threat to the profitability of the Australian sheep industry.^{1,2} However there is declining use of rural veterinary practitioners by livestock producers,³ with the majority of parasitological advice provided to farmers from non-veterinary sources such as rural produce stores retailing anthelmintic products. With parasites and their control constituting the most significant financial constraint of all pathogens on ruminant production¹, provision of farm-specific parasite management advice within a whole farm animal health plan is increasingly desirable.

We examined the effectiveness of a parasitological monitoring and anthelmintic retailing service provided by a rural veterinary practice in south-eastern Australia from 2003 to 2012. Practice records of sheep producers utilising gastrointestinal parasite management were examined with results from pre and post-treatment faecal egg counts used to identify factors influencing anthelmintic effectiveness, calculated as faecal egg count reduction percentage (FECR%), via linear mixed model analyses. Further, trends in anthelmintic merchandising and uptake of veterinary services for ovine parasite management were determined via logistic regression analyses.

Results indicated that FECR% varied according to type of treatment group used ($P<0.001$), with decreasing effectiveness of the macrocyclic lactone group ($P=0.008$), increased use of 4-way combination anthelmintic treatments ($P<0.001$) and declines in other treatments ($P<0.05$). There was an increasing proportion of properties performing post-treatment faecal egg counts over the study period ($P=0.001$). The study concluded that veterinary guided gastrointestinal parasite management in sheep has mutual benefits for sheep producers and rural veterinary practices, including: appropriate advice on parasitological management; observations on trends in regional anthelmintic usage and early indication of anthelmintic resistance. This service provides a strategic approach that can significantly increase the proportion of sheep properties checking for drench effectiveness and applying appropriate parasitic management. Importantly it enables increased veterinary involvement in livestock disease surveillance through improved communication between private rural veterinarians and livestock producers³ and wider adoption of this approach is encouraged.



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¹Sackett D, Holmes P, Abbott K, Jephcott S, Barber M. Assessing the economic cost of endemic disease on the profitability of Australian beef cattle and sheep producers. *Final Report of Project AHW087*. MLA Australia, Sydney, 2006.

²Besier RB, Love SCJ. Anthelmintic resistance in sheep nematodes in Australia: the need for new approaches. *Aust J Exp Agr* 2003;43:1383-1391.

³Frawley PT. Review of rural veterinary services. DAFF Australia. <http://www.ava.com.au/sites/default/files/documents/Other/Frawley%20report.pdf>. 2003. Accessed 30 July 2011.



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Session Details:	8/26/2013 COMMERCIAL LIVESTOCK - GENERAL 1145 - 1300 Riverside Theatre
Oral Presentation Details:	Gastrointestinal nematodes and the technical efficiency of dairy farms
Presentation Time:	1200 -1215
Authors:	Van Der Voort M ¹²³ , Van Meensel J ¹ , Lauwers L ¹ , Vercruysse J ² , Van Huylenbroeck G ³ , Charlier J ² ¹ Institute For Agricultural And Fisheries Research, ² Department of Virology, Parasitology and Immunology, Faculty of Veterinary Medicine, ³ Department of Agricultural Economics, Faculty of Bio-Engineering

Parasitic helminth infections affect the productivity of livestock farms. The aim of this study was to analyse the relation between gastrointestinal nematode (GI) infections and the overall productive efficiency of dairy farms. Previous studies mostly focused on the impact on technical key performance indicators, like daily growth or milk production per cow. However, the impact on the whole farm performance remains unclear. Using production efficiency analysis it becomes possible to analyse the effect on the overall transformation of inputs (e.g. feed, materials, labour) into outputs (e.g. milk). While efficiency analysis is frequently used in management sciences, it has not often been applied in animal health sciences and is new in parasitology.

This study links parasitic data (bulk tank milk *Ostertagia ostertagi* ELISA results, expressed as ODR), from a monitoring study with farm accountancy data from the Belgian Farm Accountancy Data Network (FADN) and the accounting system of Boerenbond (Flemish farmers union). Two unbalanced panels are constructed for the period 2006-2010, consisting of 48 FADN farms and 152 Boerenbond farms, respectively. To calculate the efficiency scores, milk production serves as the output while concentrate use, roughage use, pasture, number of dairy cows, health costs and replacement rate are inputs. Stochastic frontier analysis is used to analyse the relation between the GI nematode *O. ostertagi* and technical efficiency (TE).

Results show that *O. ostertagi* has a significant (P<0.05) effect on TE in both datasets. Farms reporting a high level of infection were less efficient in production. An increase in *O. ostertagi* infection level with 1 was associated with a reduction in the TE of 2.2%. These results will contribute to the development of a farm-specific optimisation model for the economic farm performance and the helminth infection status.

Acknowledgements:

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Oral presentation

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Session Details:	8/26/2013 COMMERCIAL LIVESTOCK - GENERAL 1145 - 1300 Riverside Theatre
Oral Presentation Details:	An investigation into the current transmission pathway of <i>Taenia ovis</i> in Australia
Presentation Time:	1445 -1500
Authors:	Jenkins D ¹ ¹ Charles Sturt University, ² School of Medicine, Australian National University

Recent abattoir data show *Taenia ovis* infection in sheep is common and widespread, especially in Western Australia and Australian meat processors are complaining that the presence of *Taenia ovis* cysts in sheep meat is causing them considerable financial losses. During the last 18 months a study funded by Meat and Livestock Australia has re-visited potential on-farm risk factors associated with transmission of *T. ovis*. *Taenia* species infecting wild carnivores, foxes (*Vulpes vulpes*) and wild dogs (dingoes (*Canis lupus dingo*) and its hybrids (*C. lupus dingo* X *Canis familiaris*)) caught or shot in sheep rearing areas are being identified using molecular methods. In addition, a study of the financial impact of *T. ovis* is being undertaken in five Australian abattoirs, one in Western Australia, one in Tasmania and three in New South Wales. One hundred and one farmers have been recruited into the study (NSW 50; Tasmania 31: WA 20), each completing a questionnaire. The faeces of 229 dogs belonging to these farmers have been examined for the eggs of intestinal helminths. The intestines of 450 foxes have been examined, tapeworms of the genus *Taenia*, identified morphologically, have been collected and identified to species using molecular methods. We will present the data from our studies and discuss the implications of our findings.



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Session Details:	8/26/2013 COMMERCIAL LIVESTOCK - GENERAL 1145 - 1300 Riverside Theatre
Oral Presentation Details:	Helminth Neurobiology: Identifying the moving targets of cholinergic anthelmintics
Presentation Time:	1230 -1245
Authors:	Martin R ¹ , Beethamn J ² , Romine N ¹ , Robertson A ¹ , Buxton S ¹ , Dong L ³ , Charvet C ⁴ , Neveu C ⁴ , Cabaret J ⁴ ¹ Biomedical Sciences, Iowa State University, Ames, IA 50011, USA,, ² Veterinary Pathology, Iowa State University, Ames, IA 50011, USA, ³ Electrical and Computer Engineering, Iowa State University, Ames, IA 50011, USA, ⁴ NRA, Infectiologie et Santé Publique, Tours, 37380 Nouzilly, FRANCE

We are seeking new ways to study how anthelmintics act and to study mechanisms of resistance. We will describe the application of recently introduced techniques to study modes of action and mechanisms of resistance. We use levamisole-sensitive and -resistant isolates of the pig nematode, *Oesophagostomum dentatum* and apply: microfluidics techniques on L₃ larvae; transcriptomic techniques on adults; *in vivo* electrophysiology on muscle preparations of adults and; cloning & expression of nicotinic acetylcholine receptor in *Xenopus* oocytes to examine effects of different cholinergic anthelmintics.

The new microfluidic techniques allow very high-resolution concentration-response phenotyping of anthelmintic-sensitive and -resistant isolates using measurements of velocity and muscle force produced by single larvae. The transcriptomic techniques allow expression levels of signaling pathway genes to be studied. The *in vitro* expression techniques have allowed separation and molecular characterization of different subtypes of cholinergic receptors. It is now possible to study actions of different cholinergic anthelmintics at whole-worm levels and at single-channel levels in sensitive and resistant worms.

The intact worm studies show that resistance is associated with a reduction in the number of active receptors and changes in their pharmacological properties; the microfluidic techniques show that the larvae are less sensitive to levamisole and, actually, can swim faster; the transcriptomic approach suggests that a number of pathway genes are involved, rather than a single gene. Our current understanding suggests that the development of resistance is polygenic, allowing a less anthelmintic sensitive phenotype to appear which retains fitness for survival.

Acknowledgements:

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Oral Presentation Details:	Gastrointestinal helminths of camels (<i>Camelus dromedarius</i>) in center of Iran
Presentation Time:	1245 -1300
Authors:	Sazmand A ¹, Anvari Tafti M ², Hekmatimoghaddam S ³, Moobedi I ⁴ ¹ Institute Of Applied-Scientific Education Of Jihad-E-Agriculture, MolaSadra Center, University Of Applied Science And Technology, Yazd, Iran, ² Department of Pathobiology, School of Medicine, Shahid Sadoughi University of Medical Sciences, Yazd, Iran, ³ Department of Laboratory Sciences, School of Paramedicine, Shahid Sadoughi University of Medical Sciences, Yazd, Iran, ⁴ Department of Medical Parasitology & Mycology, School of Public Health & Institute of Public Health Research, Tehran University of Medical Sciences, Iran

Camels are multipurpose animals in Iran. As parasitic diseases are the major cause of impaired meat and milk production in this animal, the present study aimed at determining gastrointestinal helminthic infections of Iranian camels in center of the country. Gastrointestinal tract of 144 carcasses of one-humped camels slaughtered in Yazd, Esfahan and Kerman provinces’ abattoirs were examined for adult helminths. Camels were from both sexes and different ages. Recovered parasites were identified according to described keys by light microscope. Of 144 tested camels 117 were infected with at least one helminth species (81.3%). Totally 28 worm species from 14 genera were identified in digestive tract of infected animals, including 26 species of nematodes and two species of cestodes. The infection rates in compartment 3 of stomach, small intestine, and cecum/large intestine were 86.3%, 91.5% and 11.1%, respectively. However, no worm was found in esophagus. The recovered worms with decreasing infection rate were: *Camelostrongylus mentulatus* 41.7%, *Stilesia globipunctata* 38.9%, *Trichostrongylus probolurus* 37.5%, *Parabronema skrjabini* 34.7%, *Haemonchus contortus* 15.3%, *Haemonchus longistipes* 14.6%, *Trichostrongylus colubriformis* 14.6%, *Physocephalus sexalatus* 13.9%, *Nematodirus spathiger* 6.9%, *Nematodirella cameli* 6.3%, *Nematodirus mauritanicus* 4.9%, *Trichuris globulosa* 4.9%, *Nematodirella longissimespiculata* 4.2%, *Moniezia expansa* 4.2%, *Trichuris lani* 3.5%, *Trichostrongylus vitrinus* 3.5%, *Nematodirus dromedarii* 3.5%, *Cooperia pectinata* 2.8%, *Impalaia tuberculata* 2.1%, *Nematodirus abnormalis* 2.1%, *Trichuris skrjabini* 1.4%, *Haemonchus tataricus* 0.7%, *Marshallagia marshalli* 0.7%, *Nematodirus helvetianus* 0.7%, *Oesophagostomum radiatum* 0.7%, *Oesophagostomum venulosum* 0.7%, *Trichostrongylus hamatus* 0.7%, and *Trichuris fundibulus* 0.7%. In the present study *Haemonchus tataricus*, *Trichostrongylus hamatus* and *Trichuris fundibulus* were reported from Iranian dromedaries for the first time. Regarding high prevalence of infection, using anthelmintic drugs seems necessary to increase the health and productivity of camels. On the other hand, the high rate of zoonotic species indicates that camels have important role in maintaining and transmitting infection to humans related to them.

Acknowledgements:

The authors would like to thank Tehran University of Medical Sciences for financial supports



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Session Details:	8/26/2013 IWAAP5 - Fifth international workshop on Arctic and Antarctic parasites 1145 - 1300 Meeting Room 1
Oral Presentation Details:	Echinococcus spp. in northern North America
Presentation Time:	1145 -1200
Authors:	Emily J. Jenkins ^{1*} , Karen M. Gesy ¹ , Janna M. Schurer ¹ , Michael Pawlik ¹ , Janet E. Hill ¹ , Andrew Peregrine ² , R.C. Andrew Thompson ³ , Chris Somers ⁴ , Brett Elkin ⁵ , Helen Schwantje ⁶ ¹ University of Saskatchewan, Saskatoon, Saskatchewan (SK), CANADA ² University of Guelph, Guelph, Ontario, CANADA ³ Murdoch University, Murdoch, WA, AUSTRALIA ⁴ University of Regina, Regina, SK, CANADA ⁵ Government of the Northwest Territories, Yellowknife, Northwest Territories, CANADA ⁶ Government of British Columbia, Victoria, British Columbia, Canada

Echinococcus spp. cestodes are emerging and re-emerging as animal and public health concerns across the circumpolar North. In northern North America, *E. multilocularis* and *E. canadensis* (previously the cervid genotype in the *E. granulosus* species complex) circulate in sylvatic carnivore definitive hosts and herbivore intermediate hosts, and occasionally spill over into people and domestic dogs. In northwestern Canada, we recently detected European-type strains of *E. multilocularis*, including adult cestodes in the intestines of wild coyotes (prevalence 27% of 26) and alveolar hydatid cysts in 2 clinically affected dogs. In rodent intermediate hosts in the Central North American region, 6% of 783 deer mice harbored alveolar hydatid cysts that, upon characterization at multiple mitochondrial loci, displayed unexpectedly high genetic diversity. This suggests that this region represents a highly endemic, well-established focus of *E. multilocularis* and not, as previously suggested, a recent introduction from the Arctic. Adult cestodes of *Echinococcus* spp. were detected in 37 of 93 wolves (40%) from northwestern Canada. Upon molecular characterization, these proved to be (in decreasing order) *E. canadensis* G10, *E. multilocularis*, and *E. canadensis* G8. Mixed infections of G8/G10, *E. canadensis*/*E. multilocularis*, and *Echinococcus*/*Taenia* spp. were observed. Taeniid eggs were detected in rectal feces in only half of the wolves harboring adult *Echinococcus* cestodes in the intestine. Wolves were previously thought to be natural definitive hosts for *E. canadensis*, but not *E. multilocularis*, in North America. Hydatid cysts from moose, elk, and caribou intermediate hosts from northwestern Canada proved to be the G10 genotype, while only the G8 genotype was detected in a muskox and cervids from northeastern North America. These studies identify vulnerable areas and range expansion of endemic and introduced strains of *Echinococcus* in North America, as well as highlight the importance of recognizing genetic diversity with significance for zoonotic potential and pathogenicity.

Submitted for consideration for oral presentation in the International Workshop on Arctic and Antarctic Parasitology, special session at the WAAVP conference.



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Session Details:	8/26/2013 IWAAP5 - Fifth international workshop on Arctic and Antarctic parasites 1145 - 1300 <i>Meeting Room 1</i>
Oral Presentation Details:	Lungworms in muskoxen in Norway – a potential threat with warmer climate?
Presentation Time:	1200 -1215
Authors:	Rebecca K. Davidson ¹ , Guilherme G. Verocai ² , Hanne Amundsen ³ , Nora Oftenes-Lie ³ , Inger S. Hammes ¹ , Susan J. Kutz ^{2*} and Bjørnar Ytrehus ¹ ¹ Norwegian Veterinary Institute, Oslo, Norway ² Faculty of Veterinary Medicine, University of Calgary and Canadian Cooperative Wildlife Health Centre, Calgary, Canada ³ Norwegian School of Veterinary Science, Oslo, Norway

Introduced muskoxen in the Norwegian mountains live at the southern edge of their thermal tolerance zone and are extremely vulnerable to climate change. Climate change has altered lungworm infection pressure in other muskox populations¹ but little was known about lungworms in muskoxen in Norway. Field faecal samples were collected in June (N=96) and in August (N=71). Dorsal spine protostrongylid larvae (DSL) were detected in 82% (136/165) whilst *Dictyocaulus* larvae were detected in 76% (126/165). Significant differences in prevalence and intensity were seen between age groups and month of sampling. DSL larvae were not detected in June calf samples, just one had *Dictyocaulus* larvae. In August, more than half the calves had DSL and *Dictyocaulus* larvae. The opposite trend was seen for *Dictyocaulus* prevalence in adults. The highest mean DSL larval burdens were seen in adults whilst the highest mean *Dictyocaulus* LPG was found in yearlings with a decreasing trend with increasing age. Larval counts in June, excepting the calves, were higher than in August. Molecular analysis of the larvae is on-going. *Dictyocaulus eckerti* has previously been identified in muskoxen from this region and our preliminary results indicate that *Muellerius capillaris* is also present.

Lungworms were extremely widespread with calves becoming infected during their first summer. High intensity of *Dictyocaulus* sp. infections in yearlings is consistent with findings in other muskox populations where it's been associated with mortality events in this age group². The field study revealed that a number of the animals observed were coughing suggesting that perhaps lungworms are already a significant problem for this population.

This baseline data can be used in future studies to assess the impact of global warming-related increases in parasite abundance and diversity on a vulnerable species. The cold-adapted muskoxen may function as a sentinel species for such changes, a veritable hairy canary.

Acknowledgements:

Thanks to Tord Bretten, at the Norwegian Directorate for Nature Management, for his advice and help with the fieldwork and to the Norwegian University of Science and Technology for the loan of the biological field station at Kongsvoll.



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Session Details:	8/26/2013 IWAAP5 - Fifth international workshop on Arctic and Antarctic parasites 1145 - 1300 Meeting Room 1
Oral Presentation Details:	Exploiting parallels between livestock and wildlife systems
Presentation Time:	1215 -1230
Authors:	Rose H ¹ , Hoar B ² , Kutz S ² , Morgan E ¹ ¹ University Of Bristol, ² University of Calgary

Models aimed at predicting the seasonal dynamics of helminth infections in livestock are useful when experiments or observations are difficult, such as projecting onto future climate scenarios. However, such models are often developed to address specific research questions, with parameters fitted to specific parasite and livestock species, limiting their transferability to free-living ruminant systems.

The model presented here is under development as part of the EU FP7 project “GLOWORM”, which aims to predict the impact that global change may have on helminth challenge in livestock in Europe. The model integrates environmental factors and host-parasite dynamics within a framework which allows parameterisation for multiple host and parasite species and application to a range of research questions. By exploiting the many parallels that exist between farmed and free-living ruminants, including their parasite fauna, physiology, grazing behaviour, and movements (pasture rotation *cf.* migration), it is possible to apply this model to free-living systems. Preliminary results are presented for the gastrointestinal nematode *Ostertagia gruehneri* infecting caribou (*Rangifer tarandus*) with vital parameters derived from previous experiments on the free-living stages of *O. gruehneri* and related species. The aim was to assess likely impacts of environmental change, including altered migration patterns, on parasite transmission in Arctic Canada.

Within GLOWORM, further research on key life-history traits of gastrointestinal nematode species infecting sheep and cattle in Europe, including *Haemonchus contortus*, *Teladorsagia circumcincta* and *O. ostertagi*, is guided by the evaluation of model uncertainty and successive rounds of parameter refinement and model validation. Since these species and closely related species are present in free-living ruminants, the impact and potential application of research emerging from GLOWORM extends beyond livestock systems.

Acknowledgements:

The study received funding from FP7 GLOWORM project – Grant agreement N° 288975CP-TP-KBBE.2011.1.3-04)

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Session Details:	8/26/2013 IWAAP5 - Fifth international workshop on Arctic and Antarctic parasites 1145 - 1300 Meeting Room 1
Oral Presentation Details:	Toxoplasma gondii in Scandinavian brown bears
Presentation Time:	1230 -1245
Authors:	Jones K ¹ , Godfroid J ² , Evans A ¹ , Swenson J ³ , Arnemo J ¹ ¹ Hedmark University College, ² Norwegian School of Veterinary Science, ³ Norwegian University of Life Sciences

Toxoplasma gondii is a ubiquitous parasite with serious implications for public health and conservation. ¹ Human infection typically occurs via ingestion of oocysts shed in felid feces or consumption of undercooked meat of an intermediate host; the relative paucity of domestic cats and higher rate of game consumption, compared to the U.S., makes human exposure via the latter a proportionally greater concern in Scandinavia. While not well studied, exposure may affect bear fitness as well. To better understand the public health risk and explore possible population effects, this study used an ELISA to investigate exposure of brown bears (*Ursus arctos*) to *T. gondii*. 1172 serum samples collected in Sweden from 1995 to 2012 were tested; a variety of ecological data, including demographic and fitness factors, were also available. Logistic regression and generalized linear mixed models were used to assess risk factors and attributes associated with exposure, employing backwards stepwise model selection. Overall seroprevalence was 25% (133/541 individuals); there were 55 incidences of seroconversion and three of seroreversion. Only 2% (9/371) of yearlings were seropositive, with limited evidence of vertical transmission. The preferred logistic regression model (n=541, df=526, AIC=392.67) showed significant interactive effects between age and both sex (p=0.0018) and study site (p=0.02). Risk of exposure increased with age, with the effect more dramatic in males; prevalence was higher at the southern site. Differing dietary preferences and domestic cat densities likely contributed to these effects. Possible associations between exposure and body condition, reproductive success, and survivorship were also explored.[†] The results of this study assess the potential impact of this zoonosis on bear fitness and highlight the need for hunter awareness. Further research is needed to investigate possible effects on bear movements and diet, as research in people and other species increasingly demonstrates behavioral effects of exposure, even in immunocompetent individuals.

Acknowledgements: The authors would like to thank everyone involved with the Scandinavian Bear Project since its inception for making this project possible. Funding was provided by the American-Scandinavian Foundation and the US-Norway Fulbright Foundation.

References: ¹Dubey, J.P., J.L. Jones. 2008. *Toxoplasma gondii* infection in humans and animals in the United States. Int J Parasitol 38: 1257-1278.

[†]Results of these analyses are still pending.



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Session Details:	8/26/2013 IWAAP5 - Fifth international workshop on Arctic and Antarctic parasites 1145 - 1300 Meeting Room 1
Oral Presentation Details:	(IWAAP Session) Accounting for detection probability improves <i>Toxoplasma gondii</i> seroprevalence estimates in arctic foxes
Presentation Time:	1245 -1300
Authors:	Elmore S ¹ , Al-Adhami B ² , Samelius G ³ , Huyvaert K ⁴ , Bailey L ⁴ , Alisauskas R ⁵ , Gajadhar A ² , Jenkins E ¹ ¹ University Of Saskatchewan, ² Canadian Food Inspection Agency, ³ Swedish University of Agricultural Science, ⁴ Colorado State University, ⁵ Environment Canada

The full suite of hosts and transmission routes of *Toxoplasma gondii* is not perfectly elucidated in arctic regions, where human seroprevalence can be high and toxoplasmosis-associated mortality has been recognized in arctic foxes. To understand *T. gondii* ecology in the central Canadian Arctic, we investigated its occurrence in the Karrak Lake goose colony, Queen Maud Gulf Migratory Bird Sanctuary, Nunavut. This terrestrial arctic ecosystem supports high breeding densities of snow geese (*Chen caerulescens*), Ross's geese (*Chen rossii*) and arctic foxes (*Vulpes lagopus*). Foxes feed primarily on birds, eggs, and small mammals, but also scavenge carcasses of larger animals, such as caribou. In this study, we compare the detection of *T. gondii* antibodies in arctic foxes measured by direct agglutination test, an indirect fluorescent assay, and an indirect enzyme-linked immunosorbent assay, allowing for a comparison among these antibody detection methods. These assays remain unvalidated in arctic foxes, contributing to uncertainty and potential bias in prevalence estimates. To address imperfect detection by the three tests, our laboratory approach followed an occupancy modelling framework, using replicates of tests to create a detection history, which is then analysed to produce estimates of the probability of antibody detection for each of the tests, as a metric of test performance. We also estimated the probability that a fox within the Karrak Lake ecosystem is seropositive, which is related to seroprevalence (preliminary estimate: 0.584 (0.421, 0.730)). This study documents a new geographical record of *T. gondii* exposure in arctic foxes and demonstrates an emerging application of ecological modelling techniques to account for the use of imperfect diagnostic tests in wildlife species.

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Session Details:	8/26/2013 CONSERVATION AND WILDLIFE ECOLOGY 1145 - 1300 Meeting Room 2
Oral Presentation Details:	Age-related patterns of infection for an invasive fluke in free-ranging wapiti (<i>Cervus canadensis</i>) in Alberta, Canada
Presentation Time:	1145 -1200
Authors:	Beck M ¹ , Goater C ¹ , Colwell D ¹ University of Lethbridge, ² Agriculture and Agri-Food Canada

Determining the host specific characteristics that affect the survival, development and fecundity of macroparasites is a key challenge in parasite epidemiology^{1,2}. Variation in exposure and/or susceptibility has been documented in numerous empirical studies involving domestic hosts², but there is little data available on infections within populations of large wildlife species exposed to emerging parasites². Our study aimed to assess the role of intrinsic host factors in determining variation in mean worm counts of an invasive liver fluke (*Dicrocoelium dendriticum*) in a free-ranging, hunter-harvested wapiti population. We evaluated data on the prevalence and intensity of adult worms from intact wapiti livers collected between 1997-2011. Hosts were sexed in the field, livers weighed at time of dissection and accurate ages were based upon cementum analyses of lower incisor teeth³. The frequency distribution of *D. dendriticum* was aggregated ($k = 0.199$), with more than two thirds of hosts containing less than 100 worms, and a small proportion (~5%) containing greater than 1000 worms. Host gender and liver size were not significant determinates of this pattern. Mean worm intensities peaked in hosts between the ages of 0.5 to 24 months, followed by a gradual decline in older wapiti. The fit of our age-infection profile to a negative binomial distribution using maximum likelihood methods⁴ was significant and there was a linear decrease in variance-to-mean ratios with age. These results provide strong evidence that the decline in fluke intensity was age-dependant^{4,5}. This infection profile is best explained by age-dependent acquired immunity resulting from continual exposure to metacercariae from ingested lock-jaw ants on grazing pasture each summer, as has been documented through the detection of humoral immune responses (IgG1 and IgM) to *D.dendriticum* in co-grazing domestic livestock⁶. Direct evidence for the role of acquired immunity in wild hosts such as wapiti requires follow-up experimentation.

Acknowledgements:

We appreciate the generous cooperation of the local big-game hunters, ranchers, Parks personnel, and Provincial wildlife authorities of Cypress Hills Provincial Park, Alberta, Canada without which this project would not have been possible. This research was supported by grants from the Alberta Conservation Association.



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Session Details:	8/26/2013 CONSERVATION AND WILDLIFE ECOLOGY 1145 - 1300 Meeting Room 2
Oral Presentation Details:	Of macropods and nematodes: A novel technique for investigating host-parasite population dynamics
Presentation Time:	1200 -1215
Authors:	Matthew Lott ^{*1} , Grant Hose ¹ , Michelle Power ¹ ¹ Macquarie University, Sydney, Australia

Contemporary species management practices may alter existing host-parasite dynamics. Potential consequences include the reduced productivity of animal-based primary industries and less effective wildlife conservation efforts. The control of problematic taxa is dependent on the development of techniques which are non-invasive for the host yet facilitate the rapid and accurate discrimination of individual parasites, as well as the capacity to monitor entire parasite communities across time and space. To this end, we have developed and evaluated a rapid fluorescence-based method, terminal restriction fragment length polymorphism (T-RFLP) analysis, for the characterisation of parasitic nematode assemblages in macropodid marsupials. Sequence data from two genetic loci (ITS+ and CO1) were used to map the position of restriction enzyme binding sites across 20 species of nematode (suborder Strongylida) to determine the level of accuracy with which T-RFLP was capable of distinguishing between the taxa which constitute a given parasite community. Our results demonstrate that with fluorescent labelling of both the forward and reverse terminal restriction fragments (T-RFs) of the ITS+ region, the restriction enzyme *Hinf1* was capable of generating species specific T-RFLP profiles. A notable exception was the genus *Cloacina*, in which closely related species often shared identical T-RFs. This may be a consequence of the group’s comparatively recent evolutionary radiation. Additionally, while the CO1 displayed higher sequence diversity than the ITS+, the subsequent T-RFLP profiles were taxonomically inconsistent and could not be used to further differentiate species within *Cloacina*. These data suggest that the question of T-RFLPs utility in monitoring parasite communities cannot be addressed without considering the ecology and unique evolutionary history of the constituent taxa.

Acknowledgements:

Special thanks to Professor Ian Beveridge of Melbourne University for his assistance in procuring and identifying macropodid nematode specimens.



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Session Details:	8/26/2013 CONSERVATION AND WILDLIFE ECOLOGY 1145 - 1300 <i>Meeting Room 2</i>
Oral Presentation Details:	Behaviour, bettongs and blood-suckers: using social network models to understand parasite transmission in wildlife populations
Presentation Time:	1215 - 1230
Authors:	Stephanie Godfrey¹ , Alexander Kabat ² , R. C. Andrew Thompson ¹ ¹ Murdoch University, Western Australia, AUSTRALIA ² Australian Wildlife Conservancy, AUSTRALIA;

Understanding how different parasites spread through wildlife populations is essential to conservation management. Host behaviour and patterns of space use can influence the transmission of a range of parasites, including those requiring host contact for transmission (contagious parasites), and those transferred by overlap in space use (parasites with infectious stages in the off-host environment). Social network models provide a framework for tracing the transmission pathways of parasites in host populations and understanding how animal behaviour influences parasite transmission. We asked whether parasite infection patterns of the critically endangered brush-tailed bettong (*Bettongia penicillata*) are influenced by behaviour, using social network models. We used micro-GPS loggers to track the movement of bettongs within a population in SW Western Australia. Specifically, we tracked behaviours and movement patterns that might influence parasite transmission. We developed separate alternative social network models to represent the transmission pathways of parasites with different methods of transmission, including those influenced by direct contact (contagious parasites, such as lice), asynchronous nest sharing (fleas and nidiculous ticks) and overlap in space use (ticks and nematodes). We compared these models with empirical measures of parasite infection dynamics to deduce which networks best predicted infection dynamics. This study will provide insights into the aspects of host behaviour that are most important to parasite transmission, and will more specifically improve our understanding of how brush-tailed bettong parasites are transmitted.

Acknowledgements:

We would like to acknowledge the Australian Research Council for funding the project, and the Australian Wildlife Conservancy and the Western Australian Department of Environment and Conservation for their support.



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Session Details:	8/26/2013 CONSERVATION AND WILDLIFE ECOLOGY 1145 - 1300 Meeting Room 2
Oral Presentation Details:	Trypanosomes and their ectoparasitic vectors on a translocated population of Australian marsupials
Presentation Time:	1230 -1245
Authors:	Dunlop J ^{1,2} , Morris K ² , Thompson A ¹ ¹ Murdoch University, ² Department of Environment and Conservation

Abstract:
As part of many threatened species conservation programs, wildlife are often relocated from one area to another in order to enhance conservation status, remove human-animal conflicts or as part of captive breeding programs. One impact associated with these relocations is the effect that these movements have on the host, its associated parasites and the environment. Although health checks are often discussed in relocation programs, longitudinal monitoring following release is rare. We examined two native Australian marsupial species, *Bettongia lesueur* and *Isodon auratus*, their ectoparasites and trypanosomes at the time of their relocation and intensively for 18 months afterwards. Half of the mammal population was treated regularly with an antiparasitic, with the goal to disrupt the ectoparasite and trypanosome life cycles. This did not appear to have an impact on the presence of ectoparasites or trypanosomes, but may have been partially responsible for the disappearance of some tick species from the system. Boodies from different source populations were found to have different species of trypanosomes, and to have transmitted these 6 months after they were released. Factors correlating to trypanosome infection and ectoparasite presence on the population are discussed, as well as identification of the likely trypanosome vector present in the ecosystem.



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Session Details:	8/26/2013 CONSERVATION AND WILDLIFE ECOLOGY 1145 - 1300 Meeting Room 2
Oral Presentation Details:	Blastocystis in West Australian Wildlife
Presentation Time:	1245 -1300
Authors:	Unaiza P ¹ , Wayne A ² , Elliot A ¹ , Lymbery A ¹ , Traub R ³ , Morris K ⁴ , Thompson A ¹ ¹ Murdoch University, Perth, AUSTRALIA, ² Department of Environment and Conservation, Manjimup, AUSTRALIA, ³ University of Queensland, Gatton, AUSTRALIA, ⁴ Department of Environment and Conservation, Perth, AUSTRALIA

Blastocystis is an enteric parasite found in various hosts worldwide. It has been detected previously in Australian wildlife. This study focuses upon the prevalence and characterization of *Blastocystis* isolates from four species of Australian native wildlife. A multiplex PCR was also developed to screen various hosts for *Blastocystis*, *Cryptosporidium* sp. and *Giardia duodenalis*. The sensitivity and specificity of this multiplex PCR is also evaluated against methods routinely used for the detection of these parasites.



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Session Details:	8/26/2013 HOST PARASITE RELATIONSHIPS 1 1145 - 1300 Meeting Room 3
Oral Presentation Details:	Somethin’s happenin’ here: Apparent precocious excystation of <i>Dicrocoelium dendriticum</i> metacercariae in their ant intermediate host.
Presentation Time:	1145 -1200
Authors:	Colwell D ¹ , Goater C ² , Leggett F ¹ , Ivarson A ¹ , Gray D ¹ ¹ Agriculture And Agri-Food Canada, ² Department of Biological Sciences, University of Lethbridge

Encysted metacercariae of the lancet liver fluke float freely in the haemocoel of their ant intermediate host where the cyst protects the fluke from attack by the ant’s innate immune response. Exit from the cyst by the metacercariae usually takes place in the gut of the final host where it is stimulated by increased temperature as well as the presence of host digestive enzymes and bile salts. During studies of the biology and ecology of *D. dendriticum* in the Cypress Hills region of southeastern Alberta, Canada initial observations with confocal laser scanning and scanning electron microscopy of ants collected as they were clinging onto plants noted the presence of flukes emerging from cysts within the haemocoel. Subsequently, dissections of ants collected at several times between early June through the end of August revealed that between 4.4% to 7.6% of the ants had empty cysts and free metacercariae in their haemocoel. The proportion of excysted metacercariae in each ant varied from 1.6% to 21.3%. This phenomenon was noted in ants that had been held overnight at 4°C as well as in ants that were flash frozen in the field, establishing that the cool temperature storage was not a contributing factor. The adaptive nature, if any, of these paradoxical observations are unclear. One possibility is that precocious excystation is engendered in a proportion of the metacercariae as a response to conditions within the ant that cue impending ingestion by a potential final host. The ants, restrained on a plant potentially exhibit stress responses; e.g. increased levels of octopamine^{1,2} which are detected by metacercariae, a portion of which excyst showing a state dependent response in the sense proposed by Thomas et al.³

Acknowledgements:

We thank the Cypress Hills Provincial Park authorities for permission to conduct the field research. We also thank Melissa Beck and Brad van Paridon for their spirited help in the field and in the laboratory

References:

1. Adamo, S.A. 2012. The effects of the stress response on immune function in invertebrates: An evolutionary perspective on an ancient connection. *Hormones and Behavior*, 62, 324-330.

2. Adamo, S.A. and Parsons, N.M. 2006. The emergency life-history stage and immunity in the cricket, *Gryllus texensis*. *Animal Behavior*, 72, 235-244.

3. Thomas, F., Brown, S.P., Sukhdeo, M., Renaud, F. 2002. Understanding parasite strategies: a state-dependent approach. *Trends in Parasitology*, 18, 387-390.



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Session Details:	8/26/2013 HOST PARASITE RELATIONSHIPS 1 1145 - 1300 Meeting Room 3
Oral Presentation Details:	The <i>Angiostrongylus vasorum</i> transcriptome provides deep insights into the parasite's biology and immunobiology, and prospects for new interventions
Presentation Time:	1200 -1215
Authors:	Ansell B University Of Melbourne

Angiostrongylus vasorum is a metastrongyloid nematode of dogs and other canids, of major clinical importance in many countries. In order to gain first insights into the molecular biology of this worm, we conducted the first large-scale exploration of its transcriptome, and predicted essential molecules linked to metabolic and biological processes and host immune responses. We also predicted and prioritized drug targets and drug candidates. Following Illumina sequencing (RNA-seq), 52.3 million sequence reads representing adult *A. vasorum* were assembled and annotated. The assembly yielded 20,033 contigs, which encoded proteins with 11,505 homologues in *C. elegans*, and additional 1,933 homologues in various other parasitic helminths for which curated datasets were publicly available. Functional annotation was achieved for 11,752 (58.6%) proteins predicted for *A. vasorum*, including peptidases (4.5%) and peptidase inhibitors (1.6%), protein kinases (1.7%), G protein-coupled receptors (GPCRs) (1.5%) and phosphatases (1.2%). Contigs encoding excretory/secretory and immuno-modulatory proteins represented some of the most highly transcribed molecules, and encoded enzyme that digest haemoglobin were conserved between *A. vasorum* and other blood-feeding nematodes. Using an essentiality-based approach, drug targets, including neurotransmitter receptors, an important chemosensory ion channel, and cysteine proteinase-3 were predicted in *A. vasorum*, as were associated small molecular inhibitors. Future transcriptomic analyses of all developmental stages of *A. vasorum* should facilitate deep explorations of the molecular biology of this important parasitic nematode and support the sequencing of its genome. These advances will provide a foundation for exploring immuno-molecular aspects of angiostrongylosis and have the potential to underpin the discovery of new methods of intervention.

Acknowledgements:
This project was funded by the Australian Research Council and National Health and Medical Research Council (NHMRC) (R.B.G.), Howard Hughes Medical Institute (HHMI) and the National Institutes of Health (NIH) (P.W.S.). This project was also supported by a Victorian Life Sciences Computation Initiative (VLSCI) grant number VR0007 on its Peak Computing Facility at the University of Melbourne, an initiative of the Victorian Government. Other support from the Australian Academy of Science, the Australian-American Fulbright Commission, Alexander von Humboldt Foundation, Melbourne Water Corporation and the IBM Research Collaboratory for Life Sciences – Melbourne is gratefully acknowledged (R.B.G). N.D.Y is an NHMRC Early Career Research (ECR) Fellow. We also acknowledge the continued contributions of all staff at WormBase (www.wormbase.org).



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Session Details:	8/26/2013 HOST PARASITE RELATIONSHIPS 1 1145 - 1300 Meeting Room 3
Oral Presentation Details:	Cytokine expression in the placenta of cattle following inoculation with Neospora caninum throughout gestation
Presentation Time:	1215 -1230
Authors:	Cantón G ^{1, 2} , Katzer F ¹ , Maley S ¹ , Bartley P ¹ , Benavides-Silván J ^{1, 3} , Palarea-Albaladejo J ⁴ , Pang Y ¹ , Rocchi M ¹ , Buxton D ¹ , Innes E ¹ , Chianini F ¹ ¹ Moredun Research Institute, ² Instituto Nacional de Tecnología Agropecuaria (INTA), Balcarce, Argentina, ³ Instituto de Ganadería de Montaña (CSIC-ULE), León, Spain, ⁴ Biomathematics & Statistics Scotland (BioSS), Edinburgh, United Kingdom

Despite *N. caninum* being recognized as a major cause of bovine abortion, its pathogenesis is only partially understood. Evidence of immune mediated placental pathology has been reported as being responsible for compromising pregnancy probably due to the adverse effect of an exacerbated Th1 cytokine production at the maternal-foetal interface. Different clinical outcomes are known to follow experimental infections at different stages of gestation, with foetal death being the most common finding during early gestation infections, and the birth of live congenitally infected calves upon infection at mid or late gestation. The aim of the current study was to characterize Th1 cytokine expression (IL-12, IFN-γ and TNF-α) by *in situ* hybridization using placental tissue sections, which were collected from cattle experimentally inoculated with the tachyzoites of the Nc-1 strain of *Neospora* during early, mid and late gestation. A moderate to severe infiltration of IL-12, IFN-γ and TNF-α expressing cells was observed in the placentas collected at early gestation and this infiltration was more pronounced in the samples of placentome collected from dams carrying a dead foetus or one that had aborted, compared with the mothers carrying live foetuses at the moment of sampling. Contrastingly, the infiltration of Th1 cytokine expressing-cells was milder following *N. caninum* infection at mid gestation and scarce during infection at late gestation. The presence of a milder Th1 cytokine expression following Nc-1 infection during the second and third trimesters of gestation could partially explain the less severe clinical outcome observed when animals are infected at this gestational stage.

Acknowledgements:

We wish to acknowledge Helen Todd for her assistance in the production of the cytokine probes.

References:

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Session Details:	8/26/2013 HOST PARASITE RELATIONSHIPS 1 1145 - 1300 Meeting Room 3
Oral Presentation Details:	How does galectin-11 mediate gastrointestinal nematode resistance in sheep?
Presentation Time:	1230 -1245
Authors:	Sarah Preston ^{1,2*} , Els Meeusen ¹ , Stephen Walkden-Brown ² and David Piedrafita ¹ . ¹ Biotechnology Research Laboratories, Monash University, Clayton Victoria, 3800, Australia ² Cooperative Research Centre for Sheep Industry Innovation, CJ Hawkins Homestead, University of New England, Armidale NSW, 2800, Australia

Due to widespread anthelmintic resistance, alternative methods to control gastrointestinal nematodes (GIN) are required. Breeding GIN resistant sheep is a sustainable alternative form of control. As the immune response is responsible for resistance, understanding mechanisms mediating resistance would aid such selection. Galectin-11 is a protein secreted from host epithelial cells into the mucus during GIN infections and its function is unknown. Previous literature has supported the role for galectin-11 in resistance against GIN, *Haemonchus contortus* (*H. contortus*) (Robinson et al., 2011). Therefore the overall aim of this project was to investigate the interaction between galectin-11 and *H. contortus* in order to define a function. Firstly, immunofluorescent studies were employed to determine if galectin-11 bound to *H. contortus*. Results showed that recombinant galectin-11 binds to the surface of *H. contortus* L4 but not L3. Additionally, native galectin-11 was found to bind the surface of *H. contortus* adults which were directly collected from an infected animal. To explore the possible effect of galectin-11 binding to *H. contortus* L4, an *in vitro* assay which monitors the exsheathment of L3 to L4 was developed. Interestingly, recombinant galectin-11 was found to significantly inhibit the exsheathment of L3 to L4 by approximately 50% compared to control treatments (29.4±7.8 cf 73±3.7, p=0.001, respectively). Preliminary research is also indicating a detrimental effect of recombinant galectin-11 on L4 growth *in vitro*. In summary, we have shown that galectin-11 binds to the surface of L4 and adult *H. contortus* and can interfere with the development of L3 to L4 *in vitro*. Future studies aim to identify the native ligand of galectin-11. It is anticipated that further understanding of the interaction between galectin-11 and *H. contortus* will be important to comprehend the mechanisms associated with GIN immunity and support future investigation of galectin-11 as a potential genetic marker of GIN resistance.

Acknowledgements:

SheepCRC, (Cooperative Research Centre for Sheep Industry Innovation) for my PhD scholarship funding.

References:

ROBINSON, N., PLEASANCE, J., PIEDRAFITA, D. & MEEUSEN, E. N. 2011. The kinetics of local cytokine and galectin expression after challenge infection with the gastrointestinal nematode, *Haemonchus contortus*. *International Journal for Parasitology*, 41, 487-493.



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Session Details:	8/26/2013 HOST PARASITE RELATIONSHIPS 1 1145 - 1300 <i>Meeting Room 3</i>
Oral Presentation Details:	Neonatal porcine isosporosis does humoral immune response confer protection
Presentation Time:	1245 -1300
Authors:	Joachim A, Schwarz L, Worliczek H Vetmeduni Vienna

Neonatal porcine isosporosis is characterised by watery diarrhoea and poor weight gain in suckling piglets during their first weeks of life. Currently the disease can solely be controlled by the application of anticoccidial drugs during the prepatent stage of infection. Vaccination to reduce clinical symptoms and / or oocyst excretion would provide an alternative to chemotherapy. Since direct vaccination of piglets would not provide protection in the first days of life when the impact on piglet health and growth performance is strongest, the protective potential of maternal immunisation against *I. suis* was investigated. Specific IgG, IgA, and IgM against in the blood of sows, antibody contents in the colostrum/milk, the antibody uptake by the piglets, and the course of disease in experimentally infected piglets were investigated. In experiment 1 infected and non-infected piglets of non-naïve sows were compared. In experiment 2 infected piglets from sows after repeated superinfections ante partum were compared with piglets from sows without superinfections. Transfer of specific antibodies from non-naïve sows to their piglets and a correlation between higher IgA titres in piglet sera and a firmer faecal consistency could be shown. In the second study piglets from superinfected sows showed a longer prepatency and a significantly firmer faecal consistency compared to piglets from the controls. Most prominently, there was a significant correlation between a milder course of the disease and increased IgA titres in milk. The results lead to the conclusion that ante partum superinfections of sows with *I. suis* have a positive influence on the severity of neonatal piglet isosporosis. Whether this effect is based only on antibodies or also on the colostral transfer of specific lymphocytes still needs to be elucidated.



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Session Details:	8/26/2013 FUNCTIONAL GENOMICS 1 1145 - 1300 Meeting Room 5
Oral Presentation Details:	HelmDB - getting more out of helminth transcriptomes
Presentation Time:	1145 -1200
Authors:	Mangiola S ¹ , Young N ¹ , Korhonen P ¹ , Mondal A ¹ , Scheerlinck J ¹ , Sternberg P ² , Hall R ¹ , Jex A ¹ , Gasser R ¹ ¹ Faculty of Veterinary Science, The University of Melbourne, ² Biology Division, California Institute of Technology

Parasitic worms of humans and other animals cause diseases of major socio-economic importance worldwide. Investigating the molecular biology of such worms could underpin the design of new and improved interventions against them. Currently, the functional annotation of genomic and transcriptomic sequence data relies almost exclusively on comparative bioinformatic analyses using model organism- and other databases. However, many genes and gene products of parasitic worms (often > 50%) cannot be annotated using this approach, as they do not have identifiable homologues in other organisms for which sequence data are available. The inability to fully annotate transcriptomes and predicted proteomes is a major challenge, and limits our understanding of parasites at the molecular level. Here, we compiled transcriptomic data sets of some important parasitic worms, and constructed and validated a curated database, called HelmDB (www.helmdb.org). We show how this database can be used for improved functional annotation employing data integration and clustering. HelmDB provides a toolkit for sequence browsing and comparative analyses, and should be applicable to a range of other organisms.



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Session Details:	8/26/2013 FUNCTIONAL GENOMICS 1 1145 - 1300 <i>Meeting Room 5</i>
Oral Presentation Details:	The draft Trichuris suis genome
Presentation Time:	1200 -1215
Authors:	Jex A ¹ , Young N ¹ , Nejsum P ² , Korhonen P ¹ , Hall R ¹ , Li B ³ , Fang X ³ , Li L ³ , Sternberg P ⁴ , Wang J ³ , Wang J ³ , Gasser R ¹ ¹ The University Of Melbourne, ² The University of Copenhagen, ³ BGI-Shenzhen, ⁴ California Institute of Technology

Parasitic worms have a substantial, long-term impact on health and welfare worldwide. More than 2 billion people are infected with soil-transmitted helminths (STHs), including the whipworm (*Trichuris trichiura*), hookworms (*Necator* and *Ancylostoma*) and giant roundworm (*Ascaris*), predominantly in impoverished nations of Africa, Asia and Latin America. In people, the burden of disease caused by these STHs is comparable with that of tuberculosis and malaria in disability-adjusted life years (DALY) and is reported to result in more than 100,000 deaths per year. *Trichuris* alone infects 1 billion humans and, in children, chronic and high intensity infections cause typhlitis and/or colitis (trichuriasis) and reduced physical and cognitive development. The *Trichuris suis*-pig model is used to investigate trichuriasis at the immuno-molecular level and to produce *Trichuris* eggs for the treatment of inflammatory bowel disease (IBD) and other immunological disorders in humans. To support fundamental and biotechnological research areas, we report here the 80 megabase (Mb) draft genome of *Trichuris suis* and compare it with those of other nematodes. This genome has a high repeat content (32%) and encodes 15,500 protein-coding genes. Notably, the *T. suis* secretome predicted to represent < 700 proteins is rich in peptidases linked to the degradation and penetration of host tissues, and molecules likely to be involved in evading or modulating immune responses. This genome and associated transcriptomes provides a basis for fundamental explorations of *Trichuris*, for developing new interventions and diagnostic tests for trichuriasis and might provide prospects for better insights into the components that are curative in humans affected by immunological disorders, such IBD.



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Session Details:	8/26/2013 FUNCTIONAL GENOMICS 1 1145 - 1300 Meeting Room 5
Oral Presentation Details:	Organisation of cathepsin cysteine proteases within the Fasciola hepatica genome
Presentation Time:	1215 -1230
Authors:	Cwiklinski K ¹ , Paterson S ¹ , Dalton J ² , Williams D ¹ , Hodgkinson J ¹ ¹ University Of Liverpool, ² Queen's University, Belfast

The liver fluke, *Fasciola hepatica* is an economically important pathogen of sheep and cattle. It has been recently described as a re-emerging zoonosis and is a major focus of anthelmintic resistance and vaccine development research. Excretory-secretory proteins, in particular the proteolytic cathepsin cysteine proteases, act at the host-parasite interface and aid survival of the migratory stages, the newly excysted juveniles (NEJ) and adults. These important proteases can be subdivided into several clades/subtypes of cathepsin L and B cysteine proteases. To increase our understanding of these proteases and how they can be manipulated for vaccine and diagnostic tools, it is important to analyse the genomic organisation and differential transcription of these proteases. Recently we have generated an 897 Mb *F. hepatica* draft genome from a single adult fluke (Shrewsbury isolate, Ridgeway Research) by a combination of Roche 454 and Illumina sequencing. The data was assembled into contigs and scaffolds and annotation is underway, using automated pipelines to generate gene models based on *F. hepatica* transcriptome and Schistosoma protein sequence. This study reports mining of the *F. hepatica* genome to determine the genomic organisation of the cathepsin L and B genes, which has clarified the organisation of this protein family. Comparative transcriptomics was performed for the egg, metacercariae, NEJ, juvenile and adult fluke lifecycle stages to determine the relative transcription of the cathepsin protease family, using counts for the cathepsin transcripts compared with MAKER gene model transcripts from the *F. hepatica* genome. Cathepsin L clade proteases are transcribed by both the NEJ and the juvenile flukes at significantly higher levels than the other lifecycle stages, whereas the cathepsin B proteases are primarily transcribed by the NEJ. This study highlights the potential of the cathepsin proteases for the continued development of early diagnostic tools and vaccines.



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Session Details:	8/26/2013 FUNCTIONAL GENOMICS 1 1145 - 1300 Meeting Room 5
Oral Presentation Details:	Proteomics of the moulting process in Oesophagostomum dentatum
Presentation Time:	1230 -1245
Authors:	Ondrovics M ¹ , Silbermayr K ¹ , Gasser R ² , Mitreva M ^{3,4} , Joachim A ¹ ¹ Institute Of Parasitology, University Of Veterinary Medicine Vienna, ² Faculty of Veterinary Science, The University of Melbourne, ³ Genome Institute, Washington University School of Medicine, ⁴ Division of Infectious Diseases, Department of Internal Medicine, Washington University School of Medicine

Exsheatment of infective larvae of nematodes constitutes a crucial step in the transition from a free-living to a parasitic stage. To unravel proteins involved in this process, we established a method to explore the exsheatment process at the protein level. Proteomic profiles displayed using differential in-gel electrophoresis (DIGE) identified 20 protein spots that are over-expressed in this transition, but not before or after exsheathment. Using MALDI-TOF mass spectrometry, 17 of the 20 spots were annotated and represented 11 different proteins, including phosphoenolpyruvate carboxykinase, cuticlin-1 and transthyretin-like protein 5. In this study, we provide first insights into the molecular biology of the moulting process in *O. dentatum*, a useful model for parasitic nematodes, which might also provide prospects for drug target discovery.



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Session Details:	8/26/2013 FUNCTIONAL GENOMICS 1 1145 - 1300 <i>Meeting Room 5</i>
Oral Presentation Details:	RIO kinases of parasitic nematodes
Presentation Time:	1245 -1300
Authors:	Breugelmans B ¹ , Mondal A ¹ , Boag P ² , Hofmann A ³ , Jex A ¹ , Gasser R ¹ ¹ The University Of Melbourne, ² Monash University, ³ Griffith University

Protein kinases are enzymes that catalyze the transfer of phosphate groups to specific amino acid residues of their target proteins. Based on their structure, protein kinases are classified as eukaryotic protein kinases (ePKs) and atypical protein kinases (aPKs). RIO (*right open reading frame*) kinases are members of the latter group because they lack the substrate-binding site and the activation loop present in eukaryote protein kinases, and possess an additional, flexible loop, which is believed to contain the autophosphorylation site. Very little is known about the RIO kinases in multicellular organisms, including helminths. Supported by information and data available for the free-living nematode, *Caenorhabditis elegans*, and other eukaryotes, we the three RIO kinase genes from *Haemonchus contortus* and other important nematodes. Analyses of these genes and their products predict that they each play critical roles in the developmental pathways of parasitic nematodes. These findings indicate prospects for functional studies of these genes in *C. elegans* (as a surrogate) and opportunities for the design of a novel class of nematode-specific inhibitors of RIO kinases. The latter aspect is of importance, given the serious problems linked to anthelmintic resistance in parasitic nematode populations of livestock.



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Session Details:	8/26/2013 FUNCTIONAL GENOMICS 1 1145 - 1300 Meeting Room 5
Oral Presentation Details:	Functional characterisation of <i>S. mansoni</i> egg-secreted proteins using lentivirus-delivered microRNAs
Presentation Time:	1300 -1315
Authors:	Hagen J, Every A, Gasser R, Kalinna B Faculty of Veterinary Science, The University of Melbourne, Parkville, Victoria 3052, AUSTRALIA

Waterborne schistosomiasis plagues tropical regions of the world and it is estimated that currently 800 million people at risk of infection, with 200 million infected. Chronic morbidity during infection with *S. mansoni* develops as a result of schistosome eggs that lodge in the liver, gut and other organs causing extensive tissue damage. An immuno-competent host mounts a T-cell dependent immunological response to parasite eggs with the development of a vigorous collagen-rich granulomatous reaction around the eggs and skewing of the immune response to TH2. This response eventually sequesters egg products but can also lead to severe hepatic fibrosis and portal hypertension.

The ability of egg-secreted proteins (ESP) to skew immune responses has been studied in a well-established *in vitro* model of DC/T cell co-culture [1,2] and it has been shown that *S. mansoni*-derived ESP, and the single molecule omega-1 are strong inducers of TH2 [3].

Extending and improving on our earlier use of Mouse Moloney Leukaemia Virus to deliver silencing constructs into the parasites [4] we have now produced lentiviral vectors that express artificial microRNAs in the context of human miR-30 [5, 6] to induce specific and stable silencing of the gene expression of the ESPs omega-1, IPSE and kappa-5 which has enabled us to examine their role in granuloma formation *in vivo*

In *in vitro* lentivirus-transduced eggs the transcription levels of omega-1, IPSE/alpha-1 and kappa-5 were down-regulated by 50-80% and the effect lasted at least for 10 days. In BALB/c mice, injected with transduced eggs, the silencing of omega-1 resulted in the reduction of the numbers of tissue-infiltrating CD4+ T cells, DCs, B cells and interstitial macrophages and in a significant reduction of granuloma size. These results demonstrate, for the first time, the fundamental role of omega-1 in schistosome immunopathology in an *in vivo* setting.

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Session Details:	8/26/2013 DRUG TARGETED SELECTIVE TREATMENT 1145 - 1300 Meeting Room 6
Oral Presentation Details:	The repeatability of FEC of horses and the implications for targeted selective treatment
Presentation Time:	1145 -1200
Authors:	Scheuerle M¹, Honeder A¹, Becher A¹, Stear M², Pfister K¹ ¹ Comparative Tropical Medicine And Parasitology, Ludwig-Maximilians-Universität München, Germany, ²Institute of Infection, Immunity and Inflammation, University of Glasgow, United Kingdom

The selective treatment of horses is an important method to decrease the number of treatments per horse and year and to thereby slow down the development of anthelmintic resistance. The method tries to identify low and high egg-shedders, respectively, using faecal egg counts (FEC). However, the value of this method depends upon the stability of faecal egg counts over time. One way to assess the stability of animal ranking is the repeatability which is defined as the variance between horses divided by the total variance. The repeatability varies between 0 (no consistency in the values) to 1 (perfect consistency). To determine the repeatability of FEC in naturally infected horses over time, 2637 FEC from 303 horses were collected and analysed with SAS 9.3.

The distribution of FEC was overdispersed with an excess of zeros. Therefore, a zero-inflated negative binomial model in the GENMOD procedure was used. The within-horse-repeatability was approx. 32.4% of the total variance, with covariance parameter estimates for horse: 0.1050 and for residuals: 0.2190. The model estimated that 12% of horse FEC belonged to the zero distribution. In a second analysis, we excluded horses that were treated during the study period by dropping all FEC values within the respective egg reappearance period. In this analysis, 3% of horse FEC belonged to the zero distribution and the within-horse-repeatability was even stronger with approx. 51.0% of the total variance (covariance parameter estimates for horse: 0.5117, residuals: 0.4918). The analysed data show that FEC of individual horses stay fairly consistent over time and support the idea that FEC can be used as a reliable basis for treatment decisions in the context of targeted selective treatment.



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Session Details:	8/26/2013 DRUG TARGETED SELECTIVE TREATMENT 1145 - 1300 <i>Meeting Room 6</i>
Oral Presentation Details:	Genetic evaluation of lambs subjected to a targeted selective treatment anthelmintic regime
Presentation Time:	1200 - 1215
Authors:	Andrew Greer¹, Chris Logan¹ ¹ Lincoln University, Christchurch, NEW ZEALAND

Targeted selective anthelmintic treatments (TSTs) allow for the identification of individuals less reliant on anthelmintic. However, the impact of genetic selection of those with a low anthelmintic requirement on the productive potential is not known. Breeding values (BVs) for production traits and associated indexes for 214 female lambs and 158 male Coopworth lambs were compared with their requirement for anthelmintic treatment following exposure to a liveweight gain-based TST regime. Mean liveweight gain for both sexes was reduced with increasing anthelmintic requirement ($P<0.001$). Favourable increases in BVs with decreasing anthelmintic requirement were observed for fecundity for both sexes ($P=0.003$) and for survival for females only ($P=0.028$). No effect was observed for BVs for maternal survival, weaning weight, maternal weaning weight, live weight at 8-months, live weight at 12-months or fleece weight at 12-months ($P>0.05$ for all). Index values for resilience increased with decreasing anthelmintic requirement ($P<0.001$) while dual purpose meat index and overall productivity were not affected ($P>0.05$ for both). Given the low heritability estimates for resilience traits, it is concluded that modest improvements in the requirement for anthelmintic can be made through selecting animals that required fewer treatments with no apparent disadvantage in the genetic potential for other production traits.



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Session Details:	8/26/2013 DRUG TARGETED SELECTIVE TREATMENT 1145 - 1300 <i>Meeting Room 6</i>
Oral Presentation Details:	Different exposure indicators to pasture-borne nematodes as tools for selective anthelmintic treatment in adult dairy cattle
Presentation Time:	1215 -1230
Authors:	Ravinet N^{1, 2}, Lehebel A^{3, 2}, Ponnau A², Chartier C^{2, 3}, Bareille N^{2, 3}, Chauvin A^{2, 3} ¹ IDELE, French Livestock Institute, UMT Cattle Herd Health Management, ² LUNAM Université, Oniris, Nantes-Atlantic College of Veterinary Medicine and Food sciences and Engineering, UMR BioEpAR, ³ INRA, UMR1300 Biology, Epidemiology and Risk Analysis in animal health

To investigate future tools for selective treatment for gastrointestinal nematodes (GIN) in adult dairy cows, we evaluated herd and individual variation factors of the evolution of milk production (MP) after treatment. A field trial involving 20 pastured dairy herds in Western France was conducted in autumn 2010 and autumn 2011. In each herd, lactating cows were randomly allocated to a treatment group (fenbendazole) (533 cows), or a control group (544 cows). Daily cow MP was recorded from 2 weeks before until 14 weeks after treatment. Individual serum anti-Ostertagia antibody levels (expressed as ODR), pepsinogen levels, egg output, and bulk tank milk ODR were measured at time of treatment. Moreover, in each herd, information regarding heifers' grazing history was collected to assess the time of effective contact (TEC, expressed in months) with GIN larvae before the first calving. TCE was expected to reflect the development of immunity against GIN. MP data were analyzed using linear mixed models (herd and cow as random effects). The overall treatment effect was significant but slight (maximum=+0.86 Kg/d on week 6 after treatment). Cows from low-TEC *versus* high-TEC (>8 months) herds, particularly when the bulk tank milk ODR was high, showed the best response to treatment; however, bulk tank milk ODR taken into account alone did not appear as a significant variation factor. Cows from herd where the percentage of positive egg count was >22.6% responded better than those from herd where it was lower. Primiparous cows, cows with days in milk (DIM)<200 at time of treatment, and cows with low individual ODR (<0.38) responded better than multiparous cows, cows with DIM>200, and cows with higher ODR respectively. These results highlight promising key criteria for selective treatment for GIN in dairy cows, particularly those reflecting a low level of immunity against GIN.

Acknowledgements:

The authors thank all the farmers for their participation, Jean-Yves Audiart, Nadine Brisseau, Françoise Leray, Emmanuelle Blandin, Marie-Astrid Malard, Didier Billon (ONIRIS) for technical assistance and the CASDAR project N°1127 (Ministère de l'Agriculture, de l'Agroalimentaire et de la Forêt) for financial support.



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Session Details:	8/26/2013 DRUG TARGETED SELECTIVE TREATMENT 1145 - 1300 Meeting Room 6
Oral Presentation Details:	Can easy-to-measure indicators predict production responses to anthelmintic treatment in dairy cattle?
Presentation Time:	1230 - 1245
Authors:	Johannes Charlier¹, Sien Verschave¹, Jozef Verschave¹, Andy Forbes², Geert Opsomer¹, Luc Duchateau¹, ¹Ghent University, Merelbeke, BELGIUM ²Merial SAS, Lyon, FRANCE

Gastrointestinal nematodes are an important cause of reduced performance in cattle. Previous studies showed that after anthelmintic treatment an average effect on milk production of around 1 kg per day can be expected. However, little is known of cow factors affecting this treatment response. A better knowledge of such factors, could help to select animals that benefit most from treatment and thus lead to a more rational use of anthelmintics. Therefore, a randomized, controlled clinical trial was performed on 11 commercial dairy farms (477 animals) in Belgium, aiming (1) to study the effect of eprinomectin treatment (0.1ml/kg body weight) at calving on milk production and fertility and (2) to investigate whether production responses were related to easy-to-measure parameters. Analyses show that eprinomectin treatment resulted in an average ($\pm$ standard error) increase of 0.97 ($\pm$ 0.41) kg in daily milk yield. Milk yield responses were higher in multiparous compared to primiparous cows and in cows with a lower body condition score. In addition, treatment responses were associated with higher fecal egg counts at calving and higher *O. ostertagi* antibody level from a milk sample in the previous lactation. Nonetheless, high responses were also seen in animals with a low *O. ostertagi* antibody level. For the fertility parameters evaluated (i.e. number of inseminations, interval calving to first insemination and interval calving to last insemination) no overall treatment effect was found. However, significant interactions were found between the effect of anthelmintic treatment and the *O. ostertagi* ELISA results of the previous lactation. After treatment, animals with high antibody levels (>0.6 ODR) required fewer inseminations and had a shorter interval calving to last insemination compared to untreated controls. To conclude, our results confirm previously reported production effects after anthelmintic treatment of dairy cows and identify several indicators of interest to enable targeted selective treatment.

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Session Details:	8/26/2013 DRUG TARGETED SELECTIVE TREATMENT 1145 - 1300 <i>Meeting Room 6</i>
Oral Presentation Details:	A performance-based targeted selective anthelmintic treatment regime for grazing dairy calves
Presentation Time:	1245 -1300
Authors:	McAnulty R , Greer A, Gibbs J Lincoln University

Abstract:
Recent studies have highlighted the risk of anthelmintic resistance due to use of neo suppressive drenching regimes in dairy heifer’s. Effective parasite control and reduced anthelmintic usage can be achieved through targeted selective treatment (TST) anthelmintic regimes. However, recent investigations in sheep and cattle suggest that FEC is a poor indicator of which individuals are likely to benefit from treatment. This investigation sought to determine if a production based TST was an effective option for dairy calves.

Studies over three years, across a number of farms evaluated the performance of various groups of Friesian and Friesian x Jersey calves (n=100+) in two different grazing systems. In system 1 calves were grazed in front of the main milking herd whereas in system 2 where calves were sent for grazing off farm. Within each grazing system calves were allocated into two groups (n=50) with one group treated on a monthly basis, a neo suppressive treatment, (NST) and the second group were treated on individual basis by their failure to reach a production target (TST). Calves were monitored at monthly intervals for individual FEC and live weights (LW) from around 4 months of age until 10 months of age.

Results confirm initial trial findings with substantial reductions (p=0.001) in drench usage in TST treated groups, ranging from 57% to 73%. By year 3 there was no significant difference seen between LWG of NST and TST calves, on three of the four farms. This supports earlier findings which suggested that as you approach a 50% treatment frequency, differences in LWG between NST and TST groups were eliminated. The adoption of a production based TST appears to reduce drench usage without compromising calf production and would tie in nicely with industry recommendations to frequently monitor calf liveweights during their first grazing season.



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Session Details:	8/26/2013 DRUG TARGETED SELECTIVE TREATMENT 1145 - 1300 Meeting Room 6
Oral Presentation Details:	Use of a persistent anthelmintic injection to promote stimulation of the immune response to intestinal nematodes in calves
Presentation Time:	1300 -1315
Authors:	Pulford P Virbac New Zealand Ltd

The immune system of cattle becomes fully competent during the latter stages of pregnancy. Despite this, parasitic nematodes appear to be able to evade the immune response often for the duration of the first season at grass. The challenge of the naïve host with the burden of parasitic worm larvae often experienced under intensive grazing conditions appears to either overwhelm the innate immune response or modulate the acquired immune response so that survival, growth and reproduction of the parasite can occur.

Many helminth parasites are able to evade the immune system of their hosts and recent research interest has been focussed on determining the mechanisms involved. The modulation of the immune system by parasites may also increase the susceptibility of the host to other parasite species and pathogens or even alter the response of the host to vaccines.

This study involved the use of a moderately persistent macrocyclic lactone injectable anthelmintic in a group of calves that eliminated the resident susceptible nematode population and prevented re-establishment for sufficient time to allow the host to mount an immune response. Once the persistent action of the anthelmintic ceased, the nematodes were first observed to begin to re-establish followed by a period when the host appeared to control the nematode burden in the absence of any anthelmintic activity. The observed period of natural control by the host would allow for an increase in the duration of the standard inter-dose interval between anthelmintic administrations, reducing dependency on anthelmintics, providing refugia for anthelmintic susceptible parasites and a mechanism to slow the development of anthelmintic resistance.

Acknowledgements:

Dr. Mark Vickers



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Session Details:	8/26/2013 HORSE PARASITES 1145 - 1300 Meeting Room 7
Oral Presentation Details:	Prevalent gastrointestinal parasites and most efficient deworming protocols in horses under hot dry climates
Presentation Time:	1145 -1200
Authors:	Al-Ghamdi G ¹ , Al-Qudari A, Al-Jabr O ¹ AlBaha University, ² King Faisal University

The impact of gastrointestinal parasites on the health of the horse as well as the finance of horses owners is devastating. Little information is available on the prevalence of these parasites in horses and the efficacy of deworming protocols utilized by horse owners in the hot dry climates of Saudi Arabia. The goal of this study was to document the prevalence of gastrointestinal parasites among horses residing farms in the eastern province of Saudi Arabia, a hot dry area. In the meantime, we wanted to determine the most efficient drugs being used under field conditions. During this study, 302 horses residing horse farms in the Eastern Province of Saudi Arabia were tested. Fecal samples were examined using three approaches; direct smear, flotation, and sedimentation techniques. In the meantime three drugs; the ivermectin, praziquantel, and fenbendazole that were most commonly used were examined. *Tritrichomonas equi*, *Parascaris equorum*, *Dictyocaulus arnfieldi*, *Strongyle-type ova*, *Oxyuris equi* and *Eimeria leukarti* were detected. Ivermectin cleared the strongyles and effectively reduced *Oxyuris* and *Dictyocaulus* while the reduction of *Parascaris* was low. Praziquantel cleared the strongyles and *Oxyuris* while *Dictyocaulus* and *Parascaris* were less effectively reduced. Fenbendazole cleared the strongyles, *Dictyocaulus* and *Oxyuris* and less effectively reduced *Parascaris*. Seasonal prevalence as well as the associated clinical manifestation were observed. In addition variation in drug efficacy under field conditions was evident.

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Session Details:	8/26/2013 HORSE PARASITES 1145 - 1300 Meeting Room 7
Oral Presentation Details:	Treatment of equine gastric habronemosis with moxidectin
Presentation Time:	1200 -1215
Authors:	Rolf K. Schuster*, Saritha Sivakumar ¹ Central Veterinary Research Laboratory, Dubai, UAE

Habronematosis is a vector borne parasitic disease of equines and camels caused by spiruroid nematodes of the family Habronematidae with 3 species occurring in horses. The adult dioecious nematodes (*Habronema muscae*, *H. microstoma* and *Drascheia megastoma*) live in the stomach of the horse and produce eggs/larvae that are passed with the faeces.

Cases of cutaneous habronematosis (summer sores) drew our attention to a hors stable in Dubai. A fly survey on the farm in the 1st quarter of 2012 revealed the presence of *Musca domestica* and *Stomoxys calcitrans* with habronematid larvae being present only in the first species. *H. muscae* was detected in 131 out of 522 examined house flies in numbers between 1 and 35. In 18 out of 49 tested horses patent habronematid infections were diagnosed using a xenodiagnostic method with *M. domestica* grown on individual equine faecal samples. All horses were treated with a moxidectin gel in a dosage of 400 mg/ kg b.w. in late April at a time when temperature conditions for *M. domestica* change from optimum to pessimum. Examination of faecal samples 7 days after treatment showed that egg excretion stoped in all but one horse. The only still positive horse was re-examined 3 weeks later with negative results.

Examination of 644 *M. domestica* and 117 *S. calcitrans* caught in the barns between May 2012 and January 2013 gave negative results and proved that a single treatment of horses with moxidectin at a strategically favourable moment can lead to a complete devastation of gastric habronemosis.



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Session Details:	8/26/2013 HORSE PARASITES 1145 - 1300 Meeting Room 7
Oral Presentation Details:	Efficacy of ivermectin, pyrantel and fenbendazole treatments against <i>Parascaris equorum</i> infection in foals in southern Australia
Presentation Time:	1215 -1230
Authors:	Hughes K , Armstrong S, Woodhouse R, Gough S, Sangster N Charles Sturt University

Aim: to determine the efficacy of ivermectin, pyrantel and fenbendazole against *P. equorum* infection in foals in southern Australia. **Methods:** Foals aged >3 months on 5 stud farms in southern NSW which were naturally infected with *Parascaris equorum* were used. Faecal samples were collected from each foal 2 days pre-treatment and foals with a *P. equorum* faecal egg count (FEC) of >100 eggs per gram (EPG) were used to measure anthelmintic efficacy using the FEC reduction (FECR) test. After recruitment, foals on each farm were allocated randomly to a control or ivermectin, pyrantel pamoate or fenbendazole treatment group. Treatment was administered on day 0 and a FEC was performed on day 14 post-treatment. All FECs were performed using a modified McMaster technique (detection limit: 10 EPG). Anthelmintic efficacy was determined using FECR methods where (1) changes in the control group are considered¹ and (2) each animal serves as its own control². Treatment was considered effective (susceptible parasites), equivocal (suspect resistance) or ineffective (resistance) when the FECR was >90%, 80-90%, and < 80%, respectively. Conservative cut-off values were selected to reduce the likelihood of over-estimating anthelmintic resistance. **Results:** Prevalence of patent *P. equorum* infection was 58.3% (147/252 foals) and 91 foals on 5 farms with >100 EPG were included in the FECR study. Resistance of *P. equorum* to ≥1 anthelmintic, assessed by at least one of the FECR methods used, was present on each farm. Four farms had evidence of multiple drug resistance. Ivermectin was effective on 1, equivocal on 1 and ineffective on 3 farms. Fenbendazole was ineffective on 2 farms and equivocal on 2 farms. Pyrantel was effective on 2, equivocal on 1 and ineffective on 1 farm. **Conclusions:** This study indicates that anthelmintic-resistant *P. equorum* populations are present in southern Australia and multiple drug resistance may occur.

Acknowledgements: The Faculty of Science, Charles Sturt University for funding and staff of the Veterinary Diagnostic Laboratory, CSU for laboratory assistance throughout this study.

References:

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Session Details:	8/26/2013 HORSE PARASITES 1145 - 1300 Meeting Room 7
Oral Presentation Details:	Macrocyclic Lactone resistance in cyathostomins and <i>Parascaris equorum</i> on Australian horse farms
Presentation Time:	1230 -1245
Authors:	Beasley A¹, Coleman G¹, Kotze A² ¹ University Of Queensland, ² CSIRO Livestock Industries

Cyathostomins are of major importance to the equine industry as agents of clinical disease (e.g. larval cyathostomiasis, colic). The ascarid worm, *Parascaris equorum*, is common in young horses and it too is associated with disease but more commonly impacts on growth during the critical first 12 months of life. Anthelmintic resistance is already common in the cyathostomins, particularly with regard to benzimidazole compounds. Resistance to Macrocyclic Lactone (ML) drugs has been documented in *P. equorum* populations on European, Canadian and American horse farms and is likely a result of their frequent and often exclusive use in interval treatment regimes. ML-resistance is also an emerging issue in cyathostomin control, however, data on surveillance of drug efficacy on Australian horse farms is lacking. With no new drug class expected on the equine market in the near future, it is crucial that the horse industry adopts more sustainable worm control practices in order to preserve this drug class for use into the future.

We are currently investigating the efficacy of ML's against *P. equorum* and cyathostomins using faecal egg count reduction tests (FECRT), on farms from several states. Preliminary results indicate that resistance is present in *P. equorum*. No evidence of cyathostomin resistance has been found, however, isolated cases of a shortened egg reappearance period following ML treatment have been observed.

Whilst the FECRT is the “gold standard” technique for detection of resistance, it has well-recognised limitations and consequently there is a need to develop cost-effective and reliable tools to assist early detection of resistance. This project also aims to develop and/or evaluate a number of *in vitro* assays to identify differences in susceptibility of equine worm populations to ML anthelmintics. Of primary importance is the development of an assay for use in determining ML-resistance within *P. equorum* isolates.

Acknowledgements:

Acknowledgement goes to the RIRDC for funding the project, and to the many horse owners and breeders who have contributed in kind by collecting and submitting samples for the study.

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Session Details:	8/26/2013 HORSE PARASITES 1145 - 1300 <i>Meeting Room 7</i>
Oral Presentation Details:	Equine strongylid egg re-appearance period after ivermectin or moxidectin treatment in Italy, the Netherlands and Belgium
Presentation Time:	1245 -1300
Authors:	Donato Traversa^{1,*} , Deborah van Doorn ² , Edwin Claerebout ³ , Frans Kooyman ² , Antonio Frangipane di Regalbano ⁴ , Nathalie De Wilde ³ , Paola Beraldo ⁵ , Angela Di Cesare ¹ , Jozef Vercruysse ³ , Sofie De Keersmaecker ⁶ , Bruno Besognet ⁶ , Thomas Geurden ⁶ ¹ Department of Comparative Biomedical Sciences, University of Teramo, Italy ² Department of Infectious Diseases and Immunology, Utrecht University, The Netherlands ³ Laboratory for Parasitology, Ghent University, Belgium ⁴ Department of Veterinary Medicine, Production and Health, University of Padua, Italy ⁵ Department of Food Science, Division of Veterinary Pathology, University of Udine, Italy ⁶ Zoetis

The efficacy and egg reappearance period (ERP) after treatment with ivermectin (IVM) and moxidectin (MOX) was evaluated in Italy, the Netherlands and Belgium on farms with a history of frequent use of macrocyclic lactones. In total, 362 horses on 32 study sites were examined, with a minimum of 10 sites per country. Horses were naturally infected with intestinal nematodes. The animals were randomly allocated to one of two treatment groups (minimum 4 horses per treatment group) based on the pre-treatment FEC and treated either with IVM or MOX. FEC were performed in at least fortnightly intervals until Day 56 for the IVM treated animals or Day 84 for the MOX treated animals. All faecal samples were examined using a modified McMaster technique, with a sensitivity of 25 eggs per gram of faeces. The efficacy was defined as the % reduction in arithmetic mean egg counts at D14, while the ERP was defined as the time between treatment and the first breaching of a 90% efficacy threshold. The efficacy at D14 was 92-100% for IVM and 100% for MOX. For IVM, the ERP was shorter than expected (56 days) in 3 study sites in Italy, 5 sites in The Netherlands and 4 sites in Belgium. For MOX, the ERP was shortened on 2 sites in Italy, 5 in The Netherlands and 6 in Belgium. This study demonstrates that, despite a high efficacy 14 days after treatment, the ERP of IVM and MOX was decreased, especially on farms with a history of intensive use of macrocyclic lactones.

Acknowledgements:

The help of all the assisting veterinarians, horse farmers and owners is acknowledged.

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Session Details:	8/26/2013 HORSE PARASITES 1145 - 1300 Meeting Room 7
Oral Presentation Details:	Equine Parasites Commonly Anthelmintic Resistant in Finland
Presentation Time:	1300 -1315
Authors:	Näreaho A ¹ , Vainio K ¹ , Oksanen A ² ¹ Department of Veterinary Biosciences, Faculty of Veterinary Medicine (FINPAR), ² Finnish Food Safety Authority Evira, Production Animal And Wildlife Health Research Unit (FINPAR)

We assessed the resistance against macrocyclic lactones in the roundworm *Parascaris equorum* and against tetrahydropyrimidine derivatives in strongyles (no species or genus identification) in Finnish trotter foals. On 18 training farms, we examined 112 foals, mostly 1 year old, for these parasites with a modified McMaster egg count method. Foals positive for *P. equorum* (n=24) were given ivermectin orally at a dose of 200 µg/kg b.w., and strongyle positive but *P. equorum* negative foals (n=38) received pyrantel embonate orally at a dose of 19 mg/kg. Sixteen ivermectin treated foals also harboured strongyles. The farms were visited three times; first to screen all the foals to identify the ones to be treated. Second; to anthelmintic treat foals and collect, Faecal Egg Count Reduction Test (FECRT) reference (first) samples. Third; fourteen days later was the time for the second sampling (reduction samples). The FECR was calculated for each foal/parasite combination. The reduction efficacies of ivermectin against *P. equorum* (mean 52 %) and pyrantel against strongyles (43 %) were strongly suggestive of widespread resistance. We also found indication of ivermectin resistance among strongyles. The widespread use of anthelmintics for Finnish horses obviously has led to resistance buildup. Partly the results stimulated Finnish equine veterinary practitioners to reconsider equine deworming practices in order to slow down the development of resistance.



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Session Details:	8/26/2013 ONE HEALTH 1 1145 - 1300 Meeting Room 8
Oral Presentation Details:	Investigating the suitability of dogs and pigs as animal models for <i>blastocystosis</i>
Presentation Time:	1145 -1200
Authors:	Wenqi Wang^{1*} , Leigh Cuttell ¹ , Helen Owen ¹ , Helle Bielefeldt-Ohmann ^{1, 2} , Rebecca J Traub ^{1, 2} ¹ School of Veterinary Science, University of Queensland, Australia ² Australian Infectious Disease Centre, University of Queensland, Australia

Blastocystis is a ubiquitous, globally distributed intestinal protist infecting humans and a wide range of animals. Recently there has been emerging evidence of a role in human Irritable Bowel Syndrome (IBS). The proposed mode of transmission is the faecal-oral route by direct contact or food and water-borne transmission and *Blastocystis* has been shown to be a potential zoonosis. Animal models for blastocystosis are essential for investigating the significance and pathogenesis of the organism in gastrointestinal disease. We aimed to investigate whether dogs and/or pigs could be suitable animal models for blastocystosis.

To date, we have tested 240 dog faecal samples from three different environments (the Queensland and Northern Territory states of Australia and India) to estimate *Blastocystis* prevalence using microscopic and molecular methods and characterise subtypes (ST) using genetic data. Our results showed that dogs are not natural hosts for *Blastocystis* but rather are transiently and opportunistically infected and therefore not suitable animal models for blastocystosis (Wang et al., manuscript submitted).

In the porcine study, we tested faeces from 250 pigs from 17 different piggeries in Southeast Queensland, Australia. Approximately 70% were positive by PCR for *Blastocystis* with a predominance of ST5. A minority of these pigs harboured ST1 or ST3, which are the two most common STs found in humans. Piggery staff were also shown to harbour a high prevalence of *Blastocystis* (16/21, 76%) with 3/21 carrying ST5 and the remainder carrying ST1 and/or ST3. Our results suggest that pigs are likely to be natural hosts of *Blastocystis* as indicated by a high *Blastocystis* prevalence (70%) and a host adapted ST (ST5) which reflects host-parasite co-adaptation. Natural hosts such as pigs may therefore represent a suitable animal model for blastocystosis. In addition, our results also indicated that blastocystosis is a zoonosis (ST5) and a reverse zoonosis (ST1 and ST3).

Acknowledgements: The University of Queensland, School of Veterinary Science; William Peter Richards Trust Award Grant;Piggeries and piggery staff; Logan City Council; Vets Beyond Borders, Jeevasharam, Krishanasharam and In Defence of Animals, India.



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Session Details:	8/26/2013 ONE HEALTH 1 1145 - 1300 Meeting Room 8
Oral Presentation Details:	Parasite contamination of sandpits in public parks and playgrounds in Korea
Presentation Time:	1200 -1215
Authors:	Yong Suk Lim1, Kyong Hee Kim, Hee-Jeong Youn, Joon-Seok Chae College of Veterinary Medicine, Seoul National University, Seoul, 151-742, Korea

In order to examine the contamination of playgrounds with parasite eggs in Korea, five hundreds and sixteen samples of sand were collected from a surface of sandpits in across the country’s playground from 2005 to 2010. The samples were investigated by the sedimentation and floatation technique by use of sugar solution. The eggs of *Toxocara cati* (0.97%) and *Toxocara canis* (0.19%), unidentified nematode larva (5.04%) and eggs (0.39%), unidentified mite (1.74%) and it’s eggs (0.78%) and coccidia oocysts (0.19%) were detected from sand samples. The eggs of *Toxocara cati* (7.22%), *Toxocara canis* (5.50%), *Toxascaris leonina* (0.34%) and *Ophiosthorchis* spp (2.75%), unidentified nematode larva (8.25%) and egg (1.03%), unidentified mite (5.16%) and it’s egg (5.50%), and oocysts of *Coccidia* (0.34%) were also detected from 291 sand samples from the playground at 2011. The eggs of *Toxocara cati* (3.72%), *Toxocara canis* (0.21%) and *Toxascaris leonina* (0.41%), unidentified nematode larva (6.41%) and egg (0.83%), unidentified mite (1.24%) and it’s egg (0.41%), cyst of ciliate (1.03%), and oocysts of *Coccidia* (0.21%) were also detected from 484 sand samples from the playground at 2012. *Trichuris vulpis* (34.50%), *Toxocara canis* (5.00%) and *Coccidia* (14.16%) were detected from 86 feces samples of shelter dogs.

Keywords : Soil contamination; Parasite eggs; Playgrounds; Sandpits; *Toxocara* spp

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Session Details:	8/26/2013 ONE HEALTH 1 1145 - 1300 <i>Meeting Room 8</i>
Oral Presentation Details:	Zoonotic <i>Enterocytozoon</i> in Thailand: surveillance in humans, domestic animals, and wildlife
Presentation Time:	1215 -1230
Authors:	Hirotake Mori^{1*} , Aongart Mahittikorn ¹ , Nathamon Kosoltanapiwat ² , Saengduen Moonsom ¹ , Supaluk Popruk ¹ , Wichit Rojekittikhun ³ , Marnoch Yindee ⁴ , Yaowalark Sukthana ¹ ¹ Department of Protozoology, ² Department of Microbiology and Immunology, ³ Department of Helminthology, Faculty of Tropical Medicine, Mahidol University, Bangkok, Thailand ⁴ Faculty of Veterinary Science, Mahidol University Salaya Campus, Nakhonpathom, Thailand

Enterocytozoon bieneusi is a common opportunistic intestinal organism of humans and animals. Recent developments in molecular epidemiology have shown that zoonotic genotypes are responsible for gastrointestinal symptoms, especially among immunocompromised patients. However, the extent of animal involvement and the transmission routes of the organism have not been fully elucidated.

Therefore, we conducted molecular epidemiological surveillance of *Enterocytozoon* among humans and animals in Thailand. We investigated 180 healthy children in communities in northern and western Thailand. The prevalence of *E. bieneusi* was 3.8% and 2.9% by nested PCR, respectively, and genotypic analysis identified zoonotic *Enterocytozoon* genotype D to be predominant in both communities. Furthermore, we conducted surveillance of *E. bieneusi* in animals, both domestic animals and wildlife. We investigated dogs and cats in Thai temples, known endemic places for parasitic infections, where we identified a high prevalence (31.3%) of *E. bieneusi* genotype D in cats. We also investigated forest wildlife in western Thailand; genotype D was identified in deer.

Zoonotic *E. bieneusi* is prevalent in both humans and animals in Thailand. The host specificity of genotype D is low, so that the *Enterocytozoon* zoonotic genotype may be transmitted among humans and a variety of domestic animals and wildlife. In this presentation, we discuss the zoonotic significance of *Enterocytozoon* in humans and animals, both within and outside Thailand, their potential transmission routes, and the further investigations that are required.





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Session Details:	8/26/2013 ONE HEALTH 1 1145 - 1300 <i>Meeting Room 8</i>
Oral Presentation Details:	Echinococcus control requires dog population management
Presentation Time:	1230 -1245
Authors:	Heath D¹, Kachani M², MacMorran D³ ¹ DNA Investments Ltd, ² Western University of Health Sciences, California, USA, ³ Connovation Ltd., Auckland, New Zealand

Cystic echinococcosis in humans is caused by *Echinococcus granulosus* and alveolar echinococcosis is caused by *E. multilocularis*. Both species can be acquired by humans from ingestion of the eggs of *Echinococcus spp.* worms living in the dog intestine. The carnivore is the definitive host. Dog population management is an essential component in the control of dog transmitted zoonotic diseases, especially in developing countries. The degree of transmission of zoonoses is a function of the infected biomass, and reduction in the biomass, especially of unowned dogs, not only reduces the risk of transmission but also makes disease control more practical. The biomass of owned infected dogs can also play a significant role in human echinococcosis.

Euthanasia is likely to be the most effective procedure in developing countries where resources are scarce. Both euthanasia and fertility control are ongoing events, with no predictable end point. If no fostering/rehoming facilities are available, humane euthanasia may be preferable to long-term kennelling, for reasons of animal welfare. An important part of *Echinococcus* spp. control can be most effectively managed by cost-effective humane euthanasia of unwanted dogs, combined with keeping less female dogs so that replacements keep pace with requirements. Cost-effective humane euthanasia can now be achieved using the correct formulation of PAPP (para-aminopropiophenone) . PAPP is registered in New Zealand for the control of stoats and feral cats, and registration is proceeding in Australia for foxes and wild dogs.

PAPP acts by rapidly forming methaemoglobin (the ferric state of haemoglobin) which is unable to release bound oxygen. This creates a lethal deficit of oxygen in cardiac muscle and the brain. Death in stoats and feral cats usually occurs within 2 hours after eating a lethal dose. The animals become lethargic and sleepy before they die. Death in dogs takes 2-4 hours.

References:

OIE Terrestrial Animal Health Code 2010 (chapter 7.7 Stray dog population Control)

Murphy E.C., Eason C.T., Hix S., MacMorran D. (2007) Developing a new toxin for potential control of feral cats, stoats and wild dogs in New Zealand. *Managing Vertebrate Invasive Species*, Paper 33.

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Session Details:	8/26/2013 ONE HEALTH 1 1145 - 1300 <i>Meeting Room 8</i>
Oral Presentation Details:	A cryptosporidiosis swimming pool associated outbreak in Kimberley, Western Australia
Presentation Time:	1245 -1300
Authors:	Josephine S. Y. Ng-Hublin^{a*} , Dimity Hargrave ^b , Barry Combs ^c , Una Ryan ^a ^a School of Veterinary and Life Sciences, Murdoch University, South Street, Murdoch, WA, 6150, Australia ^b Environmental Health Services, Shire of Broome, Broome, Western Australia, 6725, Australia ^c OzFoodNet Communicable Disease Control Directorate, Perth, Western Australia, Australia

Cryptosporidium, a protozoan parasite which causes gastroenteric disease in humans and animals, is transmitted via the fecal oral route through ingestion of water, food or fomites contaminated with its infective oocyst stage. The disease, cryptosporidiosis, manifests primarily as watery diarrhea with varying chronicity and severity, dependent on host age and immune status, among various other factors. In the months of November and December of 2012, the Kimberley Population Health Unit (KPHU) observed the notification rate of cryptosporidiosis was 6-times higher than the average number of notifications for the same period in the last 5 years. Interviews carried out by KPHU on 18 notified cases revealed that all cases have been swimming at the Broome Recreational and Aquatic Centre. Genotyping at the *Cryptosporidium* gp60 gene locus carried out on both human faecal DNA samples collected from the interviewed cases as well as water samples from three different locations detected the *C. hominis* IbA10G2 subtype in both human and water samples. The investigation into this outbreak will be presented.



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Session Details:	8/26/2013 ONE HEALTH 1 1145 - 1300 Meeting Room 8
Oral Presentation Details:	Differences in <i>in vitro</i> sensitivity and accumulation of anthelmintics in <i>Trichuris suis</i> and <i>Oesophagostomum dentatum</i>
Presentation Time:	1300 -1315
Authors:	A/Prof Peter Nejsum University Of Copenhagen

Background: The current strategy in control programs targeting the whipworm of man (*Trichuris trichiura*) is administration of a single-dose of albendazole (ALB, 400 mg) or mebendazole (MBD, 500 mg)¹. Both reported as having non-satisfactory efficacy against *T. trichiura*²⁻⁵.

Trichuris suis and *Oesophagostomum dentatum* are both found in the large intestine of pigs^{6,7}, but in contrast to *T. suis*, *O. dentatum* is highly sensitive towards benzimidazoles (BZs).

Objective: We used *T. suis* as a model for *T. trichiura*, to evaluate whether the purported difference in sensitivity towards BZs could be related to different levels of accumulation of BZs within the two parasitic species.

Method: A motility assay was used to evaluate the efficacy of fenbendazole (FBZ), ALB and levamisole (LEV) *in vitro* on adult *T. suis* and *O. dentatum*. High performance liquid chromatography (HPLC) was used to measure the concentrations of FBZ, ALB and LEV within dead and alive worms and to estimate the maximum binding of FBZ and ALB within the two species.

Results: The motility of *T. suis* was less affected by increasing concentrations of FBZ (*P* < 0.028) and ALB (*P*<0.0001) than *O. dentatum*, whereas LEV decreased the motility of *T. suis* more than *O. dentatum* (*P* < 0.0002). The concentration of ALB and LEV was significantly lower in *T. suis* than in *O. dentatum* when adults of both were alive (ALB: *P*=0.003, LEV: *P*=0.02) and dead (ALB: *P*=0.002, LEV: *P*=0.008), but the concentration of FBZ was only lower in *T. suis* when worms were dead (*P*=0.003). Maximum binding of FBZ and ALB was significantly lower in *T. suis* than *O. dentatum* (*P* < 0.0001, *P* =0.002 respectively).

Conclusion: Our data suggests that differences in efficacy of FBZ and ALB against *T. suis* and *O. dentatum* *in vitro* can be related to differences in the uptake of drugs.

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Session Details:	8/26/2013 ACIAR - Parasite control and livestock production in SE Asia 1400 - 1515 Riverside Theatre
Oral Presentation Details:	Epidemiology, impact and benefits of control, and vectors of surra affecting livestock in Mindanao, Philippines
Presentation Time:	1400 - 1415
Authors:	Alan Dargantes ^{1,2} , Robert Dobson ² , Linda McInnes ² , Ian Robertson ² and Simon Reid ^{2,3} ¹ Central Mindanao University, Philippines, ² Murdoch University, Australia, ³ University of Queensland, Australia

There is insufficient information on *Trypanosoma evansi* (surra), a serious disease of livestock in Mindanao. This project mainly financed by ACIAR was conducted to determine the epidemiology and impact of surra in livestock, evaluate losses and the economic benefits of surra control options, and determine tabanid vectors. Approximately 5,000 buffaloes, horses, cattle, pigs and goats were sampled from >100 villages in Mindanao and tested for *T. evansi* using various diagnostic techniques. A bio-economic surra model was developed to estimate losses and benefits of control. Tabanids were trapped from selected villages to determine the local tabanid fauna and their abundance, and detect trypanosomes and tabanid hosts using genetic markers.

Surra seroprevalence estimates were 59%, 41%, 41%, 35% and 25% amongst buffaloes, cattle, horses, goats and pigs, respectively. Surra caused significant negative impact on buffalo populations with high mortality and reproductive losses, and high estimated financial losses. However, regular targeted treatment of all sick animals using a highly effective drug would have substantial benefits. All five species of trapped tabanids were more abundant in low-altitude areas and abundance was significantly associated with high rainfall. *Trypanosoma evansi* and *T. theileri* were detected from all trapped tabanid species, and buffaloes, pigs, goats, humans and chickens were identified as tabanid hosts.

It is concluded that *T. evansi* infection is highly prevalent amongst livestock in Mindanao and causes significant economic losses but its effective control would provide substantial financial benefits, and tabanids identified in Mindanao are potential transmitters of *T. evansi*. A more effective and sustainable surra control and surveillance programme amongst livestock is needed in Mindanao.



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Session Details:	8/26/2013 ACIAR - Parasite control and livestock production in SE Asia 1400 - 1515 Riverside Theatre
Oral Presentation Details:	Helminth Control In Malaysia: Dealing With Anthelmintic Resistance
Presentation Time:	1415 -1430
Authors:	¹ Chandrawathani P., ² Khadijah S., ¹ Prema B., ¹ Jamnah O., ¹ Zaini CM., ¹ Adnan M., ¹ Nurul Aini R., & ¹ Ramlan M. ¹ Veterinary Research Institute, Ipoh Malaysia ² Universiti Malaysia Terengganu, Kuala Terengganu, Malaysia Corresponding author: chandra1959@gmail.com

The ACIAR programme in Malaysia for worm control in small ruminants in the 1990’s and early 2000’s has led to several offshoot projects such as sustainable worm control programmes for government farms using rotational grazing, cut and carry feeding, anthelmintic resistance testing, nutritional interventions in smallholder farms with urea mollasses blocks as well as training and capacity building for field personnel to ensure parasitic diseases are professionally handled. These have further evolved to include the use of herbal remedies such as neem (*Azadirachta indica*), cassava (*Manihot esculenta*) and other indigenous plants. The use of FAMACHA is also becoming popular among farmers. Due to the escalating anthelmintic resistance status in local Malaysian farms, a survey was conducted in major small ruminant farming areas. Results indicated more than 80% of the farms had strongyle populations resistant to two or more anthelmintics. The techniques such as larval development assay and egg hatch assay were studied, as well as the traditional faecal egg count reduction test was instituted as the method of choice to determine anthelmintic resistance status in farms. In the process of worm control, the McMaster egg count and faecal larval cultures were instated as critical parasitological techniques that were standardized in all regional veterinary laboratories. The Veterinary Research Institute is regularly training field and laboratory staff and is at the forefront of innovating sustainable methods for worm control for small ruminants.



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Session Details:	8/26/2013 ACIAR - Parasite control and livestock production in SE Asia 1400 - 1515 Riverside Theatre
Oral Presentation Details:	Epidemiology of strongyle infections in small ruminants in three management systems in Malaysia
Presentation Time:	1430 -1445
Authors:	¹ Sani R.A., ² Sam-Mohan A. and ² Chandrawathani P. ¹ Faculty of Veterinary Medicine, Universiti Putra Malaysia, Serdang, Malaysia ² Veterinary Research Institute, Ipoh, Malaysia Corresponding author : rehana@vet.upm.edu.my

One of the main thrusts of the ACIAR program in Malaysia in the nineties was to investigate the epidemiology of strongyle infections of small ruminants. Previous to this, there were a few reports on prevalences of strongyles in small ruminants but where concerning epidemiology there was only one or two studies reported. Knowledge on epidemiology is crucial to formulate control measures for grazing animals. Three grazing systems were monitored; namely in open pasture, on vegetation under rubber trees and under oil palm. Lambs were naturally infected upon grazing and monitored from birth till around 12 months of age to determine when they acquire immunity to trichostrongyles as shown by a drop in FEC. This occurred after 8 months old in all three systems. Ewes were also monitored for periparturient rise in FEC and this happened 4-6 weeks before and 6-8 weeks after parturition. The bionomics of the free living stages of trichostrongyles was also investigated. The knowledge on epidemiology of trichostrongyle infection led to testing of various grazing patterns. The use of the medicated feed block was introduced in this program. The findings of the ACIAR program as well as that of other projects formed the base for the investigation of other non-chemical control options when the extent of anthelmintic resistance was realised. Presently work on parasite control focuses on testing of herbal remedies and manipulations of the animal husbandry system.



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Session Details:	8/26/2013 ACIAR - Parasite control and livestock production in SE Asia 1400 - 1515 Riverside Theatre
Oral Presentation Details:	Trichinellosis in pigs and humans in northern Laos
Presentation Time:	1445 -1500
Authors:	James Conlan¹, Khamphouth Vongxay², Boualam Khamlome³, Stuart Blacksell^{1,4,5}, Stanley Fenwick¹ & R.C. Andrew Thompson¹ ¹ School of Veterinary and Life Sciences, Murdoch University, Murdoch, AUSTRALIA ² National Animal Health Centre, Department of Livestock and Fisheries, Vientiane, LAOS ³ Department of Hygiene and Prevention, Ministry of Health, Vientiane, LAOS ⁴ Mahidol-Oxford Tropical Medicine Research Unit, Mahidol University, Bangkok, THAILAND ⁵ Centre for Tropical Medicine, Nuffield Department of Clinical Medicine, Oxford, UK.

Trichinellosis is endemic throughout Southeast Asia in domestic pigs and wildlife, causing sporadic outbreaks and cases of human disease. Several outbreaks and sporadic cases of trichinellosis have occurred in Laos over the past five years with the majority of the reported cases being associated with consumption of raw pork. Little is known of the risk factors of exposure and the meat consumption habits of people living in the ethnically diverse regions of northern Laos. Similarly, relatively little is known about the prevalence of *Trichinella* infection in pigs and the species circulating in the domestic pig population. We conducted a survey of domestic pigs using muscle digestion and a cross-sectional serological survey of the human population in four provinces of northern Laos. Prevalence of reactive serum in the ES ELISA was 19.1% and prevalence of strongly reactive serum was 7.5%. We observed significant differences in prevalence for ethnicity, province, wealth status, age, gender and consumption of uncooked beef, uncooked pork and uncooked fermented pork sausage for ES ELISA reactive serum. Significant differences in prevalence were observed for ethnicity, province, wealth status, age and consumption of uncooked beef and uncooked fermented pork sausage for ES ELISA strongly reactive serum. *Trichinella* larvae were isolated from 2% of pigs surveyed and prevalence varied significantly by province. All larvae from which DNA could be amplified by PCR (13/15) were identified as *T. spiralis*. This study confirms endemicity of *T. spiralis* in the pig population of Laos and the consumption of uncooked meat places Lao people at considerable risk of infection.

Acknowledgements:

Australian Centre for International Agricultural Development (ACIAR) for providing funding for this research.



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Session Details:	8/26/2013 ACIAR - Parasite control and livestock production in SE Asia 1400 - 1515 Riverside Theatre
Oral Presentation Details:	Zoonotic parasite transmission within a remote northern Laos village – implications for control and the one health concept.
Presentation Time:	1500 -1515
Authors:	Amanda Ash^{1*}, Anna O’kello², John Allen², Andrew Thompson¹ ¹Murdoch University, Perth, AUSTRALIA ²Australian Animal Health Laboratory, Geelong, AUSTRALIA

Zoonotic transmission of parasites is significantly dependent on the level of interaction between humans and animals. These interactions can include physical contact between hosts, faecal contamination of the environment, hygiene practices and the food chain.

A parasitological survey was conducted in a remote northern Lao village where the level of interaction between humans and domestic animals is substantial. Open defecation is common among the human population, domestic animals are able to roam freely, dogs inhabit the same living spaces as people and the consumption of pork is a significant proportion of the village diet.

Faecal samples were acquired from a proportion of the villagers and the resident pigs and dog population. The prevalence and diversity of parasitism was ascertained for all host species through a combination of traditional microscopy techniques and molecular characterisation. The results obtained indicate parasite transmission is occurring between these three host species in a variety of modes, including human to human, pig and dog to human and vice versa.

The human health implications within this village are of significant concern and a control strategy to be implemented will require both veterinary and human health professionals. This approach will provide an example of how the 'one health' concept can be employed to treat a complex multi-host disease challenge.



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Session Details:	8/26/2013 PARASITES AND CLIMATE CHANGE 1400 - 1515 <i>Meeting Room 1</i>
Oral Presentation Details:	More rapid and severe disease outbreaks for aquaculture at the tropics: implications for food security
Presentation Time:	1400 -1415
Authors:	Tommy L. F. Leung^{1*} and Amanda E. Bates ^{2,3} ¹ University of New England, Armidale, NSW, 2351, AUSTRALIA ² Deakin University, PO Box 432, Warrnambool, Vic., 3280, AUSTRALIA ³ University of Tasmania, PO Box 49, Taroona, TAS, 7001, AUSTRALIA

Aquaculture is replacing capture fisheries in supplying the world with dietary protein and although disease is a major threat to aquaculture production, the underlying global epidemiological patterns are unknown. For this study, we analysed severity of disease outbreak (measured in terms of cumulative mortality) across different latitudes in a diverse range of aquaculture systems including both finfishes and invertebrates. Our analyses include a wide range of factors including latitude, governance efficiency, taxon of the cultured species, whether the cultured species were native to the range where the outbreak occurred, and the type of disease agent (bacterial, viral or parasitic) which caused the outbreak. We found that disease outbreaks at lower latitudes progresses more rapidly and results in higher cumulative mortality. We also found that invertebrates and juveniles stages of finfish are particularly vulnerable and suffer greater losses. Overall, tropical countries suffer proportionally greater losses in aquaculture during disease outbreaks and have less time to take actions to mitigate losses. Disease can present a major problem for food production and security in equatorial regions where fish and shellfish provide a major source of dietary protein. As the incidences of some infectious diseases may increase with climate change, adaptation strategies must consider global patterns in disease vulnerability of aquaculture and develop options to minimize impacts on food production.

Acknowledgements:

Sarah Herbert, Robert Poulin, and David Thieltges for helpful comments. Mike Melnychuk for advice on modelling approaches.



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Session Details:	8/26/2013 PARASITES AND CLIMATE CHANGE 1400 - 1515 <i>Meeting Room 1</i>
Oral Presentation Details:	Effects of climate change regarding survival and selection pressure of cattle parasites on pasture
Presentation Time:	1415 -1430
Authors:	Knapp-Lawitzke F, Deme J Freie Universität Berlin

The IPPC (2007) predicts that the most likely climate scenario (A1B) will lead to warmer and drier conditions in Lower Saxony. It is assumed that drought and high temperatures shorten the lifespan of infective third stage larvae (L3) in the environment, leading to a reduced refugium and therefore higher selection pressure. Within a regional research project (KLIFF) possible influences of climatic changes on survival and therefore development of resistance in L3 are investigated using different experimental designs:

1a) semi-controlled glass-house-experiment with 10 different pasture compositions (grass/herbage without clover, with 40% or 50-60% clover), inoculated with *Cooperia oncophora* L3 and kept under drought-stress versus an adequately watered control (n=4 per group). Harvest of herbage and recovery of larvae were performed after 1, 4 and 6 weeks, recovery from soil after 6 weeks.

Statistical analysis revealed that clover content leads to significantly higher numbers of L3 recovered from herbage (p<0.0001) and soil (p=0.0018). Additionally drought-stress and sampling time were identified as important variables leading to no statistical differences after one week, whereas after four and six weeks the p-values (p=0.003 and p=0.0001) indicate that there were more L3 on adequately watered herbage than on drought-stressed plants.

1b) controlled incubator-experiment with *C. oncophora* L3 on *Lolium perenne* using two different temperature profiles (spring and summer day conditions in Lower Saxony), drought stress management and larval recovery similar to the glass house–experiment. Preliminary results indicate that drought stress negatively affects larval fitness which is even intensified by warm temperatures.

These experiments show that long-lasting drought significantly impairs survival of L3. In order to investigate the impact of frequent treatment and reduced refugium on selection for resistance a field experiment currently uses pyrosequencing to quantify resistance associated alleles in the β -tubulin in a partly benzimidazole resistant *Ostertagia ostertagi* population under subsequent anthelmintic treatment.

Acknowledgements:

We gratefully acknowledge the Ministry of Lower Saxony for Science and Culture for financial support of KLIFF (Research association for the effects of climate change in Lower Saxony) and

Frank and Kai Küchenmeister (Georg-August-University Göttingen) for enabling of the glass-house experiment and scientific support.



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Intergovernmental panel on climate change (www.ipcc.ch)

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Session Details:	8/26/2013 PARASITES AND CLIMATE CHANGE 1400 - 1515 Meeting Room 1
Oral Presentation Details:	Reduction in greenhouse gas emissions associated with sustainable worm control in lambs
Presentation Time:	1430 -1445
Authors:	Skuce P¹, Dick J², Coulter D², Smith R², McBean D¹, Kenyon F¹ ¹ Moredun Research Institute, ² SEE-360

Efficient ruminant livestock production is constrained globally by endemic, production-limiting disease, most notably gastrointestinal nematode parasitism. To compound this, sustainable parasite control is compromised by the emergence and spread of anthelmintic resistant nematode populations. In this study, we have used an IPCC Tier 2-compliant model to calculate the greenhouse gas (GHG) emissions from naturally grazing lambs under 4 different anthelmintic treatment regimes over a 5-year study period. Treatments were either ‘monthly’, ‘strategic’ or based on ‘clinical signs’ and administered to the whole flock or ‘targeted’ to selected individual animals based on a calculated need to treat. Commercial sheep farming practices were simulated, with lambs reaching a pre-determined target market weight (38kg) removed from the analysis as they would no longer contribute to the GHG budget of the flock. Results revealed a significant treatment effect over all years, with lambs in the ‘clinical signs’ group consistently taking longer to reach market weight, with an extra 10% emission of CO₂e/kg of weight gain over all other treatments. There were no statistically significant differences between the other three treatment strategies in terms of production efficiency or cumulated GHG emissions over the study period, but we have shown that ‘monthly’ treatment selects strongly for anthelmintic resistance, hence, ‘strategic’ or ‘targeted’ treatments would be the preferred options for sustainable worm control. This study has shown that endemic disease control can contribute to a reduction in GHG emissions from animal agriculture and help reduce the carbon footprint of livestock farming.

Acknowledgements:

This study received financial support from the Scottish Government Strategic Research Programme, Quality Meat Scotland (QMS) and the EU-FP7 GLOWORM project



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Session Details:	8/26/2013 PARASITES AND CLIMATE CHANGE 1400 - 1515 Meeting Room 1
Oral Presentation Details:	Review of geo-spatial sampling methods for parasite ecology and epidemiology studies
Presentation Time:	1445 -1500
Authors:	Mintiens K¹, Rinaldi L², Catelan D³, Ducheyne E¹, Lagazio C³, Cringoli G², Musella V², Biggeri A³, Hendrickx G¹ ¹ Avia-GIS, Zoersel, Belgium, ² University of Naples Federico II, Naples, Italy, ³ E&P, Milan, Italy, ⁵ ,

Survey methodology (Foreman, 1991) is used in many disciplines to obtain information of interest from study populations by estimation from a number of sampled population units. The main principle for obtaining unbiased estimates is providing each individual of the population an equal probability for being sampled, which is not always easy to achieve. Parasite ecology and epidemiology studies (see e.g. Rinaldi et al 2010) tend to add spatial and also temporal dimensions to study populations which are expected to require specific considerations when conducting survey sampling. Defining the optimal geo-spatial sampling design should consider following issues:

- Multi-level sampling;
- Evaluating sampling costs against geographical variability;
- Stratified sampling according to influential geographical features and barriers related to the host or the parasite;
- Sequential geographical rotation of the sampling units when producing time-series;
- Spatial autocorrelation.

Different alternatives to simple random sampling, such as systematic sampling, proportional allocation, grid sampling, transect sampling and geographical capture/re-capture are used in parasite ecology and epidemiology studies to address the specific requirements of geo-spatial sampling.

This paper will review and illustrate the different alternatives for geo-spatial sampling for parasite ecology and epidemiology studies and will assess the alternatives’ capacity of obtaining accurate sample estimates in terms of bias and precision. Based on the review results, guidelines for geo-spatial sampling design for parasite ecology and epidemiology studies will be proposed.

Acknowledgements:

The studies received funding form FP7 GLOWORM project – Grant agreement N° 288975CP-TP-KBBE.2011.1.3-04.

References:

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Session Details:	8/26/2013 PARASITES AND CLIMATE CHANGE 1400 - 1515 <i>Meeting Room 1</i>
Oral Presentation Details:	Integrating host, parasite, climate, and management: global change and gastrointestinal nematodes
Presentation Time:	1500 -1515
Authors:	Rose H¹, Verschave S², Charlier J², Phelan P³, O’Kiely P³, Vercruysse J², van Dijk J⁴, Morgan E¹ ¹ University of Bristol, ² Ghent University, ³ Teagasc, ⁴ University of Liverpool

Global change is likely to alter the dynamics of gastrointestinal nematode (GIN) infections in livestock, rendering current management practices unsustainable in the long-term. Predicting the impact this may have on the seasonal risk of infection will contribute to the future sustainability of the European livestock industry by providing a foundation for the development of strategic management practices which mitigate or enable adaptation to the altered risk. However, predictions are not straightforward due to the complexity of the system. Climate-driven changes to husbandry and land use may affect host availability and pasture contamination through changes in grazing management, lambing/calving patterns and treatment strategies. Increasing temperatures may increase or decrease over-winter survival of larvae on pasture, and affect developmental success in a non-linear way through increased development and mortality rates. However, the expected impact of increased temperatures may be confounded by changes to the amount and distribution of rainfall, affecting the migration of larvae between faeces, soil and herbage.

Here we present a flexible mechanistic model framework which integrates climate, parasite, host and farm management factors to simulate seasonal and inter-annual variation in GIN population dynamics under different scenarios of climate change and farm management strategies. Traditional models considering the impact of temperature on the availability of infective larvae on pasture are extended to explicitly incorporate migratory behaviour and moisture availability. The model will be parameterised for four GINs infecting sheep and cattle in Europe (*Ostertagia ostertagi*, *Cooperia oncophora*, *Haemonchus contortus* and *Teladorsagia circumcincta*) and replicated for target regions throughout Europe. Once validated, the model will be projected onto future climate predictions and scenario-based simulations will be used to evaluate a range of strategic management practices for nematode control against the backdrop of climate and land-use change.

Acknowledgements:

The study received funding from FP7 GLOWORM project – Grant agreement N° 288975CP-TP-KBBE.2011.1.3-04)



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Session Details:	8/26/2013 FUNCTIONAL GENOMICS 1 1145 - 1300 <i>Meeting Room 5</i>
Oral Presentation Details:	The draft Trichuris suis genome
Presentation Time:	1200 -1215
Authors:	Jex A ¹ , Young N ¹ , Nejsum P ² , Korhonen P ¹ , Hall R ¹ , Li B ³ , Fang X ³ , Li L ³ , Sternberg P ⁴ , Wang J ³ , Wang J ³ , Gasser R ¹ ¹ The University Of Melbourne, ² The University of Copenhagen, ³ BGI-Shenzhen, ⁴ California Institute of Technology

Parasitic worms have a substantial, long-term impact on health and welfare worldwide. More than 2 billion people are infected with soil-transmitted helminths (STHs), including the whipworm (*Trichuris trichiura*), hookworms (*Necator* and *Ancylostoma*) and giant roundworm (*Ascaris*), predominantly in impoverished nations of Africa, Asia and Latin America. In people, the burden of disease caused by these STHs is comparable with that of tuberculosis and malaria in disability-adjusted life years (DALY) and is reported to result in more than 100,000 deaths per year. *Trichuris* alone infects 1 billion humans and, in children, chronic and high intensity infections cause typhlitis and/or colitis (trichuriasis) and reduced physical and cognitive development. The *Trichuris suis*-pig model is used to investigate trichuriasis at the immuno-molecular level and to produce *Trichuris* eggs for the treatment of inflammatory bowel disease (IBD) and other immunological disorders in humans. To support fundamental and biotechnological research areas, we report here the 80 megabase (Mb) draft genome of *Trichuris suis* and compare it with those of other nematodes. This genome has a high repeat content (32%) and encodes 15,500 protein-coding genes. Notably, the *T. suis* secretome predicted to represent < 700 proteins is rich in peptidases linked to the degradation and penetration of host tissues, and molecules likely to be involved in evading or modulating immune responses. This genome and associated transcriptomes provides a basis for fundamental explorations of *Trichuris*, for developing new interventions and diagnostic tests for trichuriasis and might provide prospects for better insights into the components that are curative in humans affected by immunological disorders, such IBD.



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Session Details:	8/26/2013 ONE HEALTH - CRYPTOSPORIDIUM AND GIARDIA 1400 - 1515 <i>Meeting Room 2</i>
Oral Presentation Details:	Assessing calves as carriers of <i>Cryptosporidium</i> and <i>Giardia</i> with zoonotic potential on dairy and beef farms within a water catchment area by mutation scanning
Presentation Time:	1415 -1430
Authors:	Abeywardena H¹, Jx A¹, Firestone S¹, McPhee S², Driessen N², Koehler A¹, Haydon S², Stevens M², Gasser R¹ ¹ University Of Melbourne, ² Melbourne Water Corporation

We undertook a molecular epidemiological survey of *Cryptosporidium* and *Giardia* in calves on three dairy and two beef farms within an open drinking water catchment area (Melbourne, Australia). A total of 474 faecal samples were collected from three dairy and two beef farms at two time points (five months apart) and tested for *Cryptosporidium* and *Giardia* employing regions within the genes of small subunit of ribosomal RNA, 60 kDa glycoprotein and triose phosphate isomerase (designated pSSU, *pgp60* and *ptpi*, respectively). The pSSU, *pgp60* and *ptpi* regions were specifically amplified from 155 (32.7%), 29 (6.1%) and 140 (29.5%) of the 474 individual faecal samples, respectively. A mutation scanning-coupled sequencing approach was used for specific and genotypic identification. The sequences were aligned with homologous reference sequences and subjected to phylogenetic analysis by Bayesian inference. Using pSSU, the *C. bovis*, *C. parvum*, *C. ryanae* and a new genotype of *Cryptosporidium* were identified in totals of 74 (15.6%), 35 (7.3%), 37 (7.8%), 9 (1.9%) samples, respectively. Using *pgp60*, *C. parvum* genotype IIa subgenotype A18G3R1 was detected in 29 samples. Using *ptpi*, *G. duodenalis* assemblage A and E were detected in totals of 10 (2.1%) and 130 (27.4%) samples, respectively. This study shows that a significant proportion of dairy and beef calves in this open water catchment region harboured *Cryptosporidium* (i.e. subgenotype IIaA18G3R1) and *Giardia* (e.g. assemblage A) that are consistent with those infecting humans, inferring that they are of zoonotic importance.



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Session Details:	8/26/2013 ONE HEALTH - CRYPTOSPORIDIUM AND GIARDIA 1400 - 1515 Meeting Room 2
Oral Presentation Details:	One Health, wildlife and parasites
Presentation Time:	1430 -1445
Authors:	Ryan U, Paparini A, Yang R, Ng-Hublin J, McInnes L, Irwin P Murdoch University

People, animals and the environment are all connected, including the sharing of disease-causing organisms. Insufficient attention has been given to the impact of infectious diseases on the health of wildlife. For example, urban encroachment and translocation expose wildlife to novel pathogens, which may impact on their health or even establish new reservoirs for human disease (Thompson et al., 2009). Protozoan parasites are the most commonly encountered parasitic pathogens for both humans and animals. Currently there is a lack of fundamental knowledge on protozoan parasite prevalence in marsupials, their zoonotic potential and their impact on marsupial populations. Therefore the collection and analysis of data on the diversity and ecology of protozoan parasites and the nature of the host/parasite relationships are very important in terms of conservation.

Trypanosomes and piroplasms (*Babesia* and *Theileria*) are blood borne protozoa, requiring arthropod vectors for transmission. Little is known about their prevalence and clinical impacts on marsupials. Recent studies have identified three species of trypanosome (*T. irwini*, *T. gilletti* and *T. copemani*) infecting koalas, which appear to be having a negative clinical impact on koala health and survival. Both *Babesia* and *Theileria* spp. have been identified in endangered native marsupials. Similarly, few studies have been conducted on the prevalence and zoonotic potential of the enteric parasites *Giardia* and *Cryptosporidium* in native marsupials. To date, a range of zoonotic and non-zoonotic *Cryptosporidium* sp. have been identified in Australian marsupial species and a high prevalence of zoonotic genotypes of *Giardia* in both captive and wild marsupials has also been identified which warrants further investigation. We will discuss the zoonotic potential and clinical impact of blood-borne and enteric protozoan parasites in native Australian marsupials.

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Session Details:	8/26/2013 ONE HEALTH - CRYPTOSPORIDIUM AND GIARDIA 1400 - 1515 Meeting Room 2
Oral Presentation Details:	Molecular prevalence of <i>Cryptosporidium</i> infection in Graded Murrah buffalo calves in Andhra Pradesh state, India
Presentation Time:	1445 -1500
Authors:	R. Venu ^{1*} , B. R. Latha ² , G. Dhinakar Raj ² , C. Sreekumar ² , M. Raman ² ¹ College of Veterinary Science, S. V. Veterinary University, Tirupati – 517 502, A. P. India ² Madras Veterinary College, Chennai-600 007, Tamil Nadu, India

Molecular prevalence of *Cryptosporidium* infection in Graded Murrah buffalo calves in Andhra Pradesh state, India was reported. Ninety four dung samples were randomly collected from Graded Murrah buffalo calves of less than 3 months of age belonging to 5 dairy farms in Andhra Pradesh state, India during the period 2009-10. All the dung samples were screened by nested PCR using 18S rRNA *Cryptosporidium* gene specific primers. Among the dung samples screened, 28 (29.78 %) samples were found positive for *Cryptosporidium* infection. All the *Cryptosporidium* positive samples by nested PCR were subjected to speciation by PCR-RFLP using SspI, VspI and MboII restriction enzymes. Based on the banding pattern obtained by PCR-RFLP, the *Cryptosporidium* species identified as *Cryptosporidium ryanae* and *Cryptosporidium parvum* in 24 (85.71 %) and 4 (14.29 %) dung samples, respectively. The prevalence range of *Cryptosporidium* infection among the 5 dairy farms was 4.65 % to 85.0 %. In conclusion, all the 5 dairy farms were showed the *Cryptosporidium* infection. *Cryptosporidium ryanae* was the major species identified in 4 farms and in only one farm the zoonotic species, *Cryptosporidium parvum* was reported. No mixed infection was observed. Based on the availability of the literature this is the first report from this state regarding the *Cryptosporidium* infection in Graded Murrah buffalo calves.



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Session Details:	8/26/2013 ONE HEALTH - CRYPTOSPORIDIUM AND GIARDIA 1400 - 1515 <i>Meeting Room 2</i>
Oral Presentation Details:	Presence and molecular characterization of <i>Giardia</i> and <i>Cryptosporidium</i> in sheep, goats and horses in Greece
Presentation Time:	1500 -1515
Authors:	Tzanidakis N¹ , Kostopoulou D ¹ , Voutzourakis N ¹ , Ehsan M ² , Claerebout E ² , Sotiraki S ¹ , Geurden T ² ¹ Laboratory of Parasitology, Veterinary Research Institute, Hellenic Agricultural Organization Demeter, ² Laboratory of Parasitology, Faculty of Veterinary Medicine, Ghent University

Giardia spp. and *Cryptosporidium* spp. are important intestinal parasites in animals and humans. Both host-specific and zoonotic *Giardia* and *Cryptosporidium* species exist. The aim of this study was to investigate the presence of *Giardia* and *Cryptosporidium* in sheep, goats and horses in Greece and to investigate their zoonotic potential. In a nationwide cross-sectional study, faecal samples were collected from 429 lambs and 255 goat kids from 21 flocks and from 190 foals. The number of *Giardia* cysts (cpg) and *Cryptosporidium* oocysts (opg) per gram of faeces was assessed with a direct immunofluorescence assay. Positive samples were genotyped for β -giardin and TPI genes of *Giardia* spp. and 18S rDNA, gp60 and HSP70 genes of *Cryptosporidium* spp. *Giardia* positive samples were detected in more than 90% of sheep and goat flocks, while *Cryptosporidium* positive samples were detected in 57% and 50% of sheep and goat flocks, respectively. More than one third of lambs and kids (37.8% and 40.4%, respectively) were excreting *Giardia* cysts, while *Cryptosporidium* infection rates did not exceed 8% for both host species. In foals, 11% and 3% of the samples were positive for *Giardia* and *Cryptosporidium*, respectively. Molecular characterization of *Giardia* spp showed that the livestock-specific assemblage E was the predominant genotype in lambs and goat kids (>89%), while the zoonotic assemblage A was detected in only a limited number of samples. *Giardia* zoonotic assemblages A and B were identified in 2 and 6 foal samples, respectively. The *Cryptosporidium* species identified in lambs and goat kids were *C. xiaoi* (56%), *C. ubiquitum* (16%) and *C. parvum* subtype IId (28%) while for horses the genotyping is still ongoing. In conclusion, both protozoa were detected in the three animal species examined, with *Giardia* exhibiting the highest infection rates. Host-specific and zoonotic *Giardia* assemblages were predominant in small ruminants and foals, respectively.

Acknowledgements:

We would like to express our deep appreciation to the vets Eirini Fragkiadaki, Eleni Malama, Amalia Mitsoura, Konstantinos Okkas and Alexandros Stefanakis and also to Stijn Casaert, Katerina Saratsi and Anastasios Saratsis for their laboratory work.



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Session Details:	8/26/2013 ECOLOGY AND EPIDEMIOLOGY- LIVESTOCK 1400 - 1515 Meeting Room 3
Oral Presentation Details:	Application of a Geographical Information System to assess the spatial distribution of <i>Fasciola hepatica</i> infection in dairy cattle herds in Ireland
Presentation Time:	1400 -1415
Authors:	Selemetas N ¹ , Phelan P ² , O' Kiely P ² , de Waal T ¹ ¹ University College Dublin, Dublin, IRELAND, ² Teagasc, Grange, IRELAND

Liver fluke caused by *Fasciola hepatica* is typically a subclinical infection in dairy cattle and may reduce significantly the economic production in dairy cattle farms. This study investigates the prevalence of fasciolosis in 1470 dairy cattle herds from 18 counties in Ireland during autumn 2012, using an in-house antibody-detection ELISA applied to bulk tank milk samples. Using a cut-off value of 15 per cent positivity (PP), the analysis of milk samples shows that 66.3% (n=975) of the dairy herds had been exposed to liver fluke, confirming the high prevalence of fasciolosis in Irish dairy herds. The infection level of liver fluke, expressed as the mean PP values of each county's milk samples, is higher in the west and north-west counties, whereas south-east counties present considerably lower exposure to the disease. The meteorological data from 25 synoptic stations were collected and the correlation of the infection level of each county with various climate variables (rainfall, air temperature, soil temperature and global solar radiation) was determined. The Pearson correlation coefficient was calculated to evaluate the strength of association between variables - p values <0.01 were considered statistically significant. The statistical analysis indicates that there is a strong correlation of autumn infection levels with the February solar radiation (r=-0.737), September rainfall (r=0.654) and November solar radiation (r=-0.621). Also, there is a moderately strong correlation of autumn infection levels with the February (r=0.592) and January (r=0.57) rainfall; the January (r=-0.555) and September (r=-0.555) solar radiation; the July (r=-0.515) and summer (r=-0.507) temperature. This study represents the first attempt to construct a geospatial map of fasciolosis in dairy cattle herds in Ireland that will contribute to a better understanding of the disease epidemiology and distribution, and help inform control options.

Acknowledgements:

The research leading to these results has received funding from the European Community's Seventh Framework Programme (FP7/2007-2013) under grant agreement n° 288975.



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Session Details:	8/26/2013 ECOLOGY AND EPIDEMIOLOGY- LIVESTOCK 1400 - 1515 Meeting Room 3
Oral Presentation Details:	Assessing risk: Spatial trends and environmental risk factors for an emerging liver fluke of sympatric host species in Alberta, Canada
Presentation Time:	1415 -1430
Authors:	Beck M ¹ , Goater C ¹ , Colwell D ² ¹ University of Lethbridge, ² Agriculture and Agri-Food Canada

The development of accurate spatial predictions for invasive parasites that incorporate environmental risk factors is important for understanding transmission heterogeneity and directing mitigation efforts¹. An understanding of the epidemiological dynamics within multi-host systems is limited by current broad-scale (100's to 1000's of km²) models, as well as by our limited understanding of the optimal environmental conditions for transmission. A model system for a fine-scale GIS-based risk assessment involves the invasive trematode *Dicrocoelium dendriticum*, in the island-like Cypress Hills Interprovincial Park (CHP) in southwestern Canada. Absent in CHP prior to the 1990's³, the parasite is now present in 40-80% of elk, deer, and cattle. Standard GIS methods and spatial statistic models^{1,4} were used to evaluate associations between the presence and density of infected ants (*Formica* spp., second intermediate host) with ecological predictors using data collected at over 100 randomly-selected sites. Results indicate that the presence of pure or mixed stands of aspen (*Populus tremuloides*) was most important in predicting further "hotspots" for ant-to-ungulate transmission, with infected intermediates not present under other canopy types. These aspen dominated hotspots of transmission were typically associated with moderately graded, south facing slopes and all sites were associated with intermediate levels of incident solar radiation. Finally, a predictive map was generated by projecting model outputs to geographically unsampled regions within and outside CHP, ranking ideal habitat for transmission according to the presence of the above ecological covariates. These results provide one of the first fine-scale (1-30m² resolution) GIS-based risk maps for an emerging parasite in North America. The approach presented here allows for the quantification and visualization of transmission risk to both domestic and wildlife hosts. These methods will be instrumental in determining the underlying processes directing the distribution and potential spread of this and other emerging parasites.

Acknowledgements:

We thank the Cypress Hills Provincial Park authorities for permission to conduct the field research. We are also grateful to SRD Lethbridge who generously provided the base aerial photographs of the Park. This project was supported by grants from the Agriculture Funding Consortium, Alberta Conservation Association and the Beef Cattle Research Council.



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2. Goater, C. P., and D.D. Colwell. 2007. Epidemiological characteristics of an invading parasite: *Dicrocoelium dendriticum* in sympatric wapiti and beef cattle in southern Alberta, Canada. *Journal of Parasitology* **93**:491-494.

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Session Details:	8/26/2013 ECOLOGY AND EPIDEMIOLOGY- LIVESTOCK 1400 - 1515 <i>Meeting Room 3</i>
Oral Presentation Details:	Prevalence and transmission of <i>Theileria</i> species in dairy cattle in Gippsland, Australia.
Presentation Time:	1430 -1445
Authors:	Elizabeth Read¹, Terry Spithill¹ and Grant Rawlin² ¹ Department of Agricultural Sciences and Centre for AgriBioscience, La Trobe University, Bundoora, AUSTRALIA; ² Department of Primary Industries, Centre for AgriBioscience, Bundoora, AUSTRALIA.

Theileria is a major disease-causing protozoan parasite of ruminants. In Africa *Theileria parva* and *Theileria annulata* cause East Coast Fever and Tropical Theileriosis, respectively, resulting in major economic losses. These losses include costs relating to treatment and vaccination as well as production losses from sick animals and death of livestock. A seemingly benign species of *Theileria*, *Theileria orientalis*, is present on the East Coast of Australia and throughout Europe, Asia and America. While benign *Theileria* has been present for a long time, the recent emergence of disease- causing *T. orientalis* genotypes in Australia and overseas has prompted investigation of the parasite’s prevalence and transmission. *T. orientalis* has been implicated in a number of cases of mild to severe anaemia, jaundice, abortions and death in cattle. Transmission of *T. orientalis* overseas is via ticks (*Haemaphysalis spp*) but studies have yet to confirm that this is the vector transmitting Theileriosis in Australia.

In this paper we will sample several healthy and infected dairy cattle from a single farm in Maffra, Victoria, to determine the disease prevalence. Blood samples will be tested for Hb levels, serum biochemistry and specific antibody responses. Blood smears stained with Giemsa will provide visual proof of the parasite. Tick sampling will also be conducted and PCR used to detect *Theileria* infection to determine whether ticks are the transmission vector.



Session Details:	8/26/2013 ECOLOGY AND EPIDEMIOLOGY- LIVESTOCK 1400 - 1515 Meeting Room 3
Oral Presentation Details:	The occurrence of <i>Haemonchus placei</i> in cattle in southern Western Australia – an unexpected finding
Presentation Time:	1445 -1500
Authors:	Jabbar A ¹ , Cotter J, Lyon J, Koehler A, Gasser R, Besier B ¹ The Unievrsity Of Melbourne, ² The Unievrsity Of Melbourne, ³ Department of Agriculture and Food, Albany, Western Australia

Haemonchus placei is generally regarded as an abomasal parasite of cattle, primarily in tropical and subtropical areas of the world. In Western Australia (WA), this nematode is commonly found in the hot semi-tropical Kimberley region, in the far north of the state. Although cattle are occasionally transferred to southern parts of WA, it was believed that *H. placei* would not occur in southern regions, as it is less cold-adapted than *H. contortus*, and the free-living stages would not develop during the cold winters and dry summer periods. Here, we show that although *H. contortus* is occasionally found in cattle in the temperate southwest region of WA, it appears that *H. placei* also occurs in this region. While investigating the prevalence of anthelmintic resistance in young cattle in WA, the existence of *H. placei* was suspected on a range of participating farms, following the morphological examination of third-stage larvae cultured from faeces, and of adult worms recovered from experimental infections with these larvae in sheep. Genomic DNAs from individual worms as well as from eggs from pooled faecal samples from seven farms in southern WA were subjected to PCR-based mutation scanning and sequence analyses of the second internal transcribed spacer (ITS-2) of the nuclear ribosomal DNA. The results showed that both *H. contortus* and *H. placei* were present in cattle. This is the first record of *H. placei* in cattle in southern WA, and raises questions as to the prevalence and distribution in other temperate and cool climatic regions of Australia. Although clinical disease due to *H. placei* has never been seen in southern WA, global climatic trends suggest that where environments become warmer, there is the potential for an increased importance of such parasites in the longer term.

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Session Details:	8/26/2013 ECOLOGY AND EPIDEMIOLOGY- LIVESTOCK 1400 - 1515 Meeting Room 3
Oral Presentation Details:	The Importance of Soil as a Reservoir of Gastrointestinal Nematode Larvae of Sheep
Presentation Time:	1500 -1515
Authors:	Sarah Groat ¹ , Steve Walkden-Brown ¹ , Sara Bowers ¹ , Michael Raue ¹ ¹ University of New England, Armidale, AUSTRALIA

Several studies have shown that a significant proportion of infective L3 of *Trichostrongylus colubriformis* (Tc) and *Haemonchus contortus* (Hc) are found in soil (Rees 1950; Silangwa and Todd 1964; Rose and Small 1985; Stromberg 1997). We aimed to determine whether such larvae migrate on to pasture and thus form a true reservoir. A 2 x 3 x 2 x 6 factorial experiment with two replicates was conducted over a five-week period using 120 pots growing Italian rye grass (*Lolium multiflorum*) in climate chambers. Pots contained either previously autoclaved or non-autoclaved soil and were inoculated with a solution containing 10,000 L3, of 50:50 Tc and Hc. Larvae were deposited on the soil surface or 0.5cm and 2.5cm below it at 10 sites in a volume of 0.1ml per site using a 23-gauge needle. Total recovery of Tc and Hc L3 from pasture, the top 5cm of soil and the soil below 5cm was determined weekly.

L3 migrated effectively from all soil depths onto pasture. There was no significant effect of L3 inoculation depth on larval recovery (P = 0.9). Significantly higher numbers of L3 were recovered from normal than from autoclaved soil (10.8% and 4.1% respectively, P ≤ 0.0001). The highest recoveries overall were from the top 5cm of the soil, and significantly higher numbers of Tc were recovered than Hc (13.5% and 1.4% respectively, P ≤ 0.0001). More L3 were recovered from the entire soil strata than those recovered from pasture over the duration of the experiment, which supports previous findings that suggest that the L3 utilise a sit-and-wait migration strategy, utilising a soil phase(Rose and Small 1985; Lettini and Sukhdeo 2006; Amaradasa, Lane et al. 2010).



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Session Details:	8/26/2013 PARASITE ZONOOSES AND TROPICAL MEDICINE 1400 - 1515 <i>Meeting Room 5</i>
Oral Presentation Details:	Dogs, Zoonoses and Tropical Beaches
Presentation Time:	1400 -1415
Authors:	Calum M St. George's University

It is estimated that in 2013 more than a billion tourists will fly to foreign destinations. Many seek sunshine and for some, sandy beaches. In countries with poor garbage collection and dog population control programs can result in large free roaming dog populations. This study examined the potential for the transmission of zoonotic helminths on the Caribbean island of Grenada. Grand Anse, a 1.36 mile long beach has numerous 5 star hotels along its shores in addition to some private houses. A questionnaire on dog ownership and knowledge of Cutaneous Larva Migrans (CLM) was administered to people living close to the beach and to staff at two local health clinics. The ownership pattern and behaviour of the free roaming beach dogs was recorded by direct observation. Dog faeces seen being deposited on the beach was collected and later examined microscopically. Surface temperatures of the sand were recorded at different times of the day and year.

Results: Dogs were observed for 10,410 minutes over a period of a year and a half. *Cryptosporidium* spp. were found in 45%, *Toxocara canis* eggs in 5% and *Ancylostoma* spp eggs in 95% out of 20 dog faecal samples examined. The mean midday sand temperatures were 38.8°C (dry season) and 37.7°C (wet season). No cases of CLM were seen at the clinics and 95% (n=51) of people interviewed were unable to identify CLM. The dogs on the beach were loosely “owned” but they were not de-wormed by the “owners”.

Conclusions: Helminth eggs from dogs deposited on the beach are exposed to surface temperatures which are inimical to egg or larval survival. The potential for human exposure to infection, through walking barefoot on the beach etc, appears to rarely result into CLM cases. A government led garbage clean up program reduced dog scavenging opportunities and numbers of dogs on the beach. Overall benefits of dog and garbage control measures will be presented.

Acknowledgements:

Thanks to the Clinic Staff, people who participated in the project, the IRB and IACUC committees and funding support from the SGU Small Research Grants Initiative.



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Session Details:	8/26/2013 PARASITE ZONOSSES AND TROPICAL MEDICINE 1400 - 1515 <i>Meeting Room 5</i>
Oral Presentation Details:	Climate and Global Change Impacts on Vector-Borne Zoonotic Diseases in Europe
Presentation Time:	1415 -1430
Authors:	Mas-Coma S Universidad De Valencia

Climate change may be expected to have an important impact on the diseases parasites cause. Climate variables are able to affect prevalences, intensities and geographical distribution of parasites both directly influencing on free-living larval stages, as well as indirectly influencing on mainly invertebrate but also vertebrate hosts. Additionally, monoxenous parasites (one-host life-cycle parasites) are not those presenting bigger health control problems within this context. Zoonotic parasitoses and, among them, those having less definitive host specificity and transmitted by a non-strictly specific vector (or intermediate host) show higher introduction, spreading and emergence capacities. In Europe, climate and global changes represent potential risks for several zoonotic parasitoses. Several diseases illustrate good examples. In leishmaniasis, intra-European transport of domestic dogs (reservoir) with northern tourists visiting southern countries and a global warming inducing a northward spread of phlebotomine vectors imply a possible northward spread from its original south-European distribution. Similar arguments may be highlighted for dirofilariasis, which is showing an evident increase of human cases in Europe, mainly in its eastern part. Recent human fascioliasis outbreaks in France were related to the unexpected contamination of commercially grown watercress in its turn due to the adaptation of the parasite to the nutria, a sylvatic rodent recently introduced from South America. Cercarial dermatitis and eosinophilic meningoencephalitis are other emerging problems. The emergence of Chagas disease in Europe is a completely different situation. Thousands of patients have been diagnosed among Southamerican immigrants, mainly in Spain but also in France, Portugal, Switzerland and Italy. This disease cannot be established in Europe due to the absence of triatomine vectors, but its pathogenic sequelae, mother transmission to newborns, and direct transmission capacity through infected blood donors illustrate large health problematics Europe never expected to face.

Acknowledgements:

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Oral Presentation Details:	Polyparasitism - the ecological complexities and impact of mixed infections
Presentation Time:	1430 -1445
Authors:	RC Andrew Thompson School of Veterinary and Life Sciences, Murdoch University, WA 6150, Australia

The term polyparasitism refers to concurrent/concomitant/co-/mixed infections of either different species and/or intraspecific variants of parasites. It is a phenomenon that has been recognised for many years but only recently has it been ‘re-discovered’ with increasing interest from ecologists and epidemiologists. This is due to greater awareness of the complexities of mixed parasite infections, reliance on, and limitations of the DALY system to determine the impact on human health of parasitic diseases, and the application of molecular tools to accurately characterise the components of parasite infections. Awareness of the significance of polyparasitism in terms of malaria, schistosomes and more recently gastrointestinal helminths, is now well established whereas much less is known about the occurrence and impact of genetically mixed infections of enteric and systemic protozoan infections. For example, the prevalence of mixed infections with enteric protozoa in developing countries show that they are the rule rather than the exception, with children most at risk usually harbouring at least two species of protozoan.

It is now clear that the clinical impact of mixed infections may be greater than single infections, that mixed infections confound accurate diagnosis and will influence the outcome of prophylactic and chemotherapeutic interventions. These scenarios are of most significance in developing regions of the world, particularly in children, and in ecosystems where the frequency of parasite transmission is high. A number of examples will be discussed of enteric and systemic parasitic infections in humans and other animals.



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Oral Presentation Details:	Zoonotic Primate Malarias in Peninsular Malaysia: Identifying Hotspots of Infection
Presentation Time:	1445 -1500
Authors:	Lee CL ¹ , Anna LJ ¹ , Priya M ¹ , Japning JRR ² , Sitam F ² , Divis PCS ³ , Singh B ³ , Sharma RSK ^{1,4 *} ¹ Faculty of Veterinary Medicine, University Putra Malaysia, 43400 UPM, Serdang, Selangor, MALAYSIA ² Department of Wildlife and National Parks Peninsular Malaysia, Km 10 Jalan Cheras, 56100 Kuala Lumpur, MALAYSIA ³ Malaria Research Centre, Faculty of Medicine and Health Sciences, University Malaysia Sarawak, 93150 Kuching, Sarawak, MALAYSIA ⁴ Wildlife Research and Conservation Centre, University Putra Malaysia, 43400 UPM, Serdang, Selangor, MALAYSIA

Malaria is a major health problem in many tropical countries and rapid diagnosis, elimination of vectors and identification of reservoir hosts are vital in controlling the spread of the disease. Molecular diagnostics has shown that zoonotic malaria caused by *Plasmodium knowlesi* is widespread in Southeast Asia. The long-tailed Macaque (*Macaca fascicularis*), a common primate species in Malaysia and its neighbouring countries, appears to be a major reservoir host. With the rapid conversion of forested land for urbanization, these macaques are driven out of their natural habitat and have established many urban populations throughout the country. It is therefore pivotal to screen these macaques in order to determine their carrier status for *P. knowlesi* and other potentially zoonotic malaria species. The present study employed nested PCR to detect *Plasmodium* in the blood of 719 *M. fascicularis* in five west coast states in peninsular Malaysia, in order to determine the prevalence of the parasite and to identify hotspots of infection. Five species of *Plasmodium* were detected with the following mean prevalence: *P. inui* (19.7%), *P. knowlesi* (15.2%), *P. cynomolgi* (12.9%), *P. coatneyi* (10.7%), and *P. fieldi* (8.3%). Two states recorded the highest prevalences for *P. knowlesi*, in which 30.4% and 27.9% of the macaques tested positive for the parasite. These states also recorded the highest infection rates for *P. inui* and *P. cynomolgi*. Confirmed cases of human infection with *P. knowlesi* have been reported in Malaysia, while *P. inui* and *P. cynomolgi* have high zoonotic potential. This study is the first attempt to concurrently detect the five primate *Plasmodium* in peninsular Malaysia, and has established that these zoonotic parasites occur at a high prevalence in certain areas. This is of public health concern and important for both veterinarians and medical personnel involved in the control of zoonotic malaria.



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Session Details:	8/26/2013 PARASITE ZONOSSES AND TROPICAL MEDICINE 1400 - 1515 Meeting Room 5
Oral Presentation Details:	Iron Metabolism in Schistosomes: Insights for novel methods for diagnosis
Presentation Time:	1500 -1515
Authors:	Jones M ¹ , Karl S ² , Gutierrez L ² , Candido R ³ , Lucyk-Maurer R ³ , Toh S ¹ , Woodward R ² , Graeff Teixeira C ³ , St Pierre T ¹ University Of Queensland, ² University of Western Australia, ³ Pontificia Universidade Católica do Rio Grande do Sul, Brazil

There is a great need for reliable and sensitive diagnostic tests for schistosomiasis that are affordable and able to be applied in field and laboratory settings. We have shown that magnetic beads bind strongly to schistosome eggs and can be used to manipulate and purify the eggs. The interaction between the beads and eggs is intriguing and of potential value in diagnosis.

Adult schistosomes live in the vasculature of their human host, where they feed extensively on blood. Females are adapted to process large quantities of blood cells, which are digested using extracellular and epicellular digestive strategies. In addition to their requirements for catabolic products of haemoglobin, schistosomes also have nutritional dependence on many other metabolites and trace elements, notably iron (Fe). A number of pathways for Fe and haem uptake, transmembrane transport and storage have been identified for schistosomes. Schistosomes store abundant quantities of iron in vitelline glands, a follicular network of cells that synthesise precursors for eggshell formation. We have shown that this Fe store is most likely used during eggshell formation, becoming incorporated into the matrix and as iron-phosphate particles within pores of the shell.

In this presentation, we will outline our studies on Fe and haem metabolism in schistosomes, focusing specifically on fate of Fe in embryogenesis. We will then discuss possible mechanisms for the strong interactions between magnetic beads and schistosome eggs and how this may be exploited for future diagnostic developments.



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Session Details:	8/26/2013 SCYNEXIS- The innovative solutions for parasiticide drug discovery 1400 - 1515 Meeting Room 6
Oral Presentation Details:	Carbonic Anhydrase inhibitors as Antimalarials
Presentation Time:	1400 -1415
Authors:	Fisher G ^{1,2} , Sumanadasa D ^{1,2} , Moeker J ¹ , Andrews K ^{1,2} , Poulsen S ¹ ¹ Griffith University, ² Queensland Institute of Medical research

Malaria is a significant global infectious disease, resulting in ~1 million deaths annually. There is currently no vaccine and many of the available drugs are becoming less effective due to parasite resistance. This means that we need to identify new drugs, preferably those with novel modes of action, to help prevent issues of cross-resistance. Carbonic anhydrase inhibitors have been used clinically for over fifty years and have recently been identified as a possible new antimalarial drug class. In this study a panel of clinically used carbonic anhydrase inhibitors were first screened for *in vitro* activity against *P. falciparum* 3D7 parasites. Poor activity (IC₅₀ >12 µM) was observed for these compounds. In contrast, when the antimalarial activity of a panel of novel synthetic primary sulphonamide carbonic anhydrase inhibitors was tested, five compounds were found to have IC_{50s} between 0.9 - 4 µM, and good selectivity for *P. falciparum* versus mammalian cells (SI >50-100). Analogues of these compounds lacking the primary sulfonamide group were then synthesised to allow the impact of the primary sulfonamide functional group on antimalarial activity to be evaluated. These analogues displayed decreased activity against *P. falciparum*, providing evidence that the primary sulfonamide may be responsible for the antimalarial activity of these compounds. This study has identified novel primary sulfonamide compounds as hits for development of new antimalarial drug leads. These compounds may allow the investigation of *P. falciparum* carbonic anhydrase as a potential new antimalarial drug target.



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Session Details:	8/26/2013 SCYNEXIS- The innovative solutions for parasiticide drug discovery 1400 - 1515 Meeting Room 6
Oral Presentation Details:	In vitro effects of novel ruthenium complexes in Neospora caninum and Toxoplasma gondii tachyzoites
Presentation Time:	1415 -1430
Authors:	Hemphill A ¹ , Barna F ¹ , Debache K ¹ , Vock C ² , Küster T ¹ ¹ Institute Of Parasitology, University Of Bern, ² Institute of Biochemistry, University of Greifswald

A panel of 16 compounds with anti-proliferative properties in cancer cells were investigated in *Toxoplasma gondii* and *Neospora caninum* infected human foreskin fibroblasts (HFF). The panel included 8 ruthenium complexes, several pyridine-based CYP inhibitors, and a lipophilic imidazolium salt, 1,3-bis(2,4,6-trimethylphenyl)imidazolium chloride. Only three compounds (16-18) belonging to the group of hydrolytically stable ruthenium complexes exhibited varying degrees of activity against both parasites, with compounds 16 and 18 showing IC₅₀ values in *N. caninum* of 6.7 and 11.3 nM and in *T. gondii* of 18.7 and 41.1 nM, respectively. IC₅₀ values in HFF monolayers were 2.4 and 6.95 µM, respectively. Compound 16 and 18 both severely affected the viability and infectivity of extracellular *N. caninum* tachyzoites, while in *T. gondii* tachyzoites this was observed only for compound 16. Treatments with both drugs for 3 days at concentrations up to 500 nM did not exert parasitocidal activity *in vitro*. *T. gondii* and *N. caninum* tachyzoites could both adapt to increasing concentrations of compound 18 during long term treatments (up to 45 days with step-wise increase of drug pressure). However, treatments with compound 16 at 160 nM after 27 days led to complete loss of viable *T. gondii* and *N. caninum* tachyzoites were non-viable after 22 days and at a concentration of 80 nM. TEM confirmed that compound 16 had a rapid impact and induced morphological and ultrastructural alterations in both parasites. Ruthenium-based compounds could thus represent an interesting option that should be for further pursued in studies involving animal experimentation.

Acknowledgements:

This work was financed through the National Science Foundation (grant No. 31-127374).



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Oral Presentation Details:	The effect of genetic and phenotypic diversity on the control of <i>T.cruzi</i> infection using drug interventions
Presentation Time:	1430 -1445
Authors:	Perez C, Thompson A, Lymbery A Murdoch University

Trypanosoma cruzi is a flagellated protozoan that is the known causative agent of Chagas Disease (CD). CD is a neglected tropical disease that has the potential to cause debilitating chronic damage to the gastrointestinal tract and/or heart of humans.

To date, education and vector eradication programs have proven integral to the reduction of human infection via the insect vector, however drug discovery efforts remain the only curative hope for the 7 to 8 million people worldwide infected with CD. Phenotypic variability has been observed across *T.cruzi* strains with regard to parasite virulence, growth pattern, infectivity and drug susceptibility and these differences have to some degree been correlated with genetic differences.

The circulation of *T.cruzi* in the wild involves transmission between a wide range of insect vectors and mammalian hosts and results in a constantly evolving parasite system.

With drug discovery efforts so heavily dependent on the reproducibility of assays and the constant culture of *T.cruzi* parasites in either *in vitro* or *in vivo* cultures, investigations into drug development have the potential to be dramatically affected by this variability. This study aims to examine how the control of *T.cruzi* infection through drug interventions can be affected by the genetic and phenotypic diversity of the parasite.



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Session Details:	8/26/2013 SCYNEXIS- The innovative solutions for parasiticide drug discovery 1400 - 1515 <i>Meeting Room 6</i>
Oral Presentation Details:	Innovative Solutions for Parasiticide Drug Discovery
Presentation Time:	1445 - 1415
Authors:	Kerrie Powell ¹ ¹ SCYNEXIS Inc, Durham, UNITED STATES OF AMERICA

Repurposing drugs currently used for the treatment of human diseases for use in animal health is a strategy of many companies. One facet of human health drug discovery with synergies to the animal health market, that is often overlooked, is the development of drugs for neglected tropical diseases. The causative parasites of human neglected diseases are related to parasite species that target animals. Further, targeting improved quality of production animals for those in developing countries is known to improve the quality of life of those most in need. While many of the target product profiles for the animal health and human health drugs differ, there is an opportunity to develop and optimize compounds for the appropriate indication early in the discovery phase of drug development. SCYNEXIS has established a state-of-the-art platform for the evaluation of compound collections from the Biotech industry for antiparasitic activity. The Integrated Parasitology screening platform allows for the assessment of compound collections against over thirty parasite species relevant to Global Health and aligns chemistries with the optimal Target Product Profile and animal and human health partners. A case study will be presented highlighting this research and business model.



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Session Details:	8/26/2013 COMMERCIAL LIVESTOCK - CATTLE 1400 - 1515 Meeting Room 7
Oral Presentation Details:	Dictyocaulus viviparus infection in adult dairy cows in France: abattoir survey and monitoring of faecal larval excretion and individual/tank milk MSP-ELISA in a high risk dairy farm
Presentation Time:	1400 -1415
Authors:	CHARTIER C ¹ , MURIGNEUX G ¹ , PELLERIN M ¹ , STRUBE C ² , PLOEGER H ³ , CAMUSET P ⁴ ¹ ONIRIS, Nantes-Atlantic College Of Veterinary Medicine, Food Sciences And Engineering, Nantes, France, ² Institute for Parasitology, University of Veterinary Medicine, Hannover, Germany, ³ Department of Infectious Diseases and Immunology, Veterinary Faculty, Utrecht, The Netherlands, ⁴ Commission Parasitologie SNGTV, Clinique Vétérinaire, Yvetot, France

Dairy cows can suffer *Dictyocaulus viviparus* infection if previous contacts were absent or long ago since protective immunity lasts for 6-12 months only. This survey was two-fold. Firstly, an abattoir survey was conducted from March to October 2011 using 100 lungs of adult dairy cows in western France. Pulmonary arteries of lungs were perfused according to the Inderbitzin's method and worms were recovered on a 45µm sieve. Apparent prevalence was 13.0±6.7% and mean worm burden was 5.8±7.6 (worm size ≥1.5mm). Secondly, in a high risk dairy herd located in Normandy, 50 lactating cows (½ primiparous) were sampled fortnightly for coproscopy. At the same time, possible clinical signs were recorded. Individual and tank milk were monthly collected from 2 weeks before turnout in March until occurrence of clinical disease in early July for subsequent examination with the recombinant MSP ELISA. Until June, adult cows were excreting larvae at low prevalence (2 to 6%) and low intensity (1 to 2 L1/30 g faeces). From mid-June, 2 weeks before clinical signs, prevalence raised to 27.1% and excretion intensity to 11.3 L1/30 g, with primiparous cows having significantly higher figures for both. On the whole period, 40.4% of cows excreted at least once. Average individual and tank MSP ELISA's ODR values were stable in March, April and May (0.108 to 0.140). In early July, a 3-fold increase was recorded for primiparous milk (0.384; range: 0.018-0.741) as well as for tank milk (0.301). In early July, about 20% of cows were coughing and an anthelmintic treatment on the whole adult flock was realized afterwards. This work gives valuable data on subclinical *Dictyocaulus* infection of dairy cows for western France. It confirms the validity of MSP ELISA for the lungworm surveillance and the benefit of targeting faecal and milk sampling to primiparous cows.

Acknowledgements:

The authors thank Charal SAS (Cholet, France) for allowing us to work in their abattoir, LSI laboratory (Life Technologies Santé Animale, Lyon, France) for performing MSP ELISA tests and Merial SAS (Lyon, France) for financial support. This study was performed in the UMT "Cattle Herd Health Management" framework.



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Session Details:	8/26/2013 COMMERCIAL LIVESTOCK - CATTLE 1400 - 1515 Meeting Room 7
Oral Presentation Details:	Evaluating the presence of an emerging parasite, <i>Toxocara vitulorum</i> , in bison in western Canada.
Presentation Time:	1415 -1430
Authors:	Wagner B ¹ , Ben Ezra E ² , Wilkins W ³ , Douma D ⁴ , Woodbury M ² ¹ Department Of Veterinary Microbiology, University Of Saskatchewan, Saskatoon, SK. CA, ² Department of Large Animal Clinical Sciences, University of Saskatchewan, Saskatoon, SK. CA, ³ 3Disease Surveillance Veterinarian, Animal Health Unit, Ministry of Agriculture, Regina, SK, CA, ⁴ 4Animal Health and Welfare, Manitoba Agriculture, Food and Rural Initiatives, Winnipeg, MB. CA

Toxocara vitulorum is a common parasite of water buffalo and cattle in tropical and subtropical regions of the world. This large roundworm was found for the first time in Canada in the spring of 2011 in ranched bison calves from Manitoba. Numerous calves from the index farm were ill and 3 infected animals died. A fecal survey of commercial bison in 2 provinces, Manitoba and Saskatchewan, was conducted in the summer of 2012 to investigate the prevalence and distribution of this and other gastrointestinal parasites. Samples were collected by provincial livestock inspectors, study personnel, or the producer from adult bison (n=1109) on 34 and 64 farms, and from calves of about 3 weeks of age and older (n=1211) on 33 and 63 farms, in Manitoba and Saskatchewan, respectively. Fecal samples (pooled calf or individual adult) were examined for helminth and coccidian parasites using a quantitative Wisconsin double centrifuge technique. *Toxocara vitulorum* eggs were found in calves from 4 farms in Manitoba, but were not detected in Saskatchewan. All four of the positive farms had a history of recent animal acquisition. In fecal samples collected from adult bison, eggs of trichostrongyle type nematodes, *Capillaria* sp., *Nematodirus* sp., *Trichuris* sp., and *Moniezia* sp. were detected. As well there was a high prevalence (69.2% n=821) of *Eimeria* sp. oocysts in adult bison. 100 randomly selected samples (calf and adult) were examined for *Giardia* and *Cryptosporidium* spp. using a commercial immunofluorescent antibody test. *Giardia* sp. cysts were detected infrequently in adult animals (5% n=20) but commonly in the calf pools (61.3% n=80). It is not known how *T. vitulorum* arrived in Canada. Further studies are needed to evaluate the threat that the roundworm may pose to domestic cattle and Canadian wildlife.



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Session Details:	8/26/2013 COMMERCIAL LIVESTOCK - CATTLE 1400 - 1515 Meeting Room 7
Oral Presentation Details:	Epidemiology of <i>Babesia ovata</i> and clinical significance of coinfection with <i>Theileria orientalis</i> in cattle
Presentation Time:	1430 -1445
Authors:	Thillaiampalam Sivakumar ^{1*} , Naoaki Yokoyama ¹ , Ikuo Igarashi ¹ ¹ National Research Center for Protozoan Diseases, Obihiro University of Agriculture and Veterinary Medicine, Obihiro, Hokkaido, Japan

Babesia ovata is a benign bovine hemoprotozoan parasite that is endemic in Japan. In this study, a PCR assay specific for *B. ovata* was developed based on apical membrane antigen-1 (AMA-1) gene and evaluated using bovine blood DNA samples prepared from 10 different countries. *B. ovata* was detected from cattle populations not only in Japan but also in Mongolia and Thailand. The partial *B. ovata* AMA-1 sequences formed a monophyletic clade closer to *B. bigemina* in the phylogram. Subsequently, grazing cattle in a dairy farm in Hokkaido, Japan, were screened for *B. ovata* and *Theileria orientalis* using parasite-specific PCR assays. When blood samples were analysed to measure the red blood cell (RBC) count, hemoglobin concentration (Hb), and hematocrit value (HCT), anemia was found in a proportion of animals that were infected with both of the parasites and only with *T. orientalis*. Interestingly, the anemia rate was higher in the coinfectd animals (42.9%) than the animals infected only with *T. orientalis* (18.2%). The animals infected only with *B. ovata* showed mean values similar to those of non-infected animals for RBC count, Hb, and HCT. However, lower mean RBC numbers were observed for the animals solely infected with *T. orientalis* or co-infected with both parasites. In contrast, only the coinfectd animals showed lower mean values for Hb and HCT values than those of non-infected group. These findings indicate that the AMA-1-PCR is a useful assay for the specific detection of *B. ovata* in cattle, and that although *B. ovata* might not cause anemia in endemic areas as a sole agent, the parasite may contribute to the anemia development when coinfectd with *T. orientalis*. Therefore the control measures for hemoprotozoan parasites of cattle should also include the strategies to minimize the prevalence of *B. ovata* in the endemic countries.

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- Sivakumar et al. 2012. PCR detection of *Babesia ovata* from cattle reared in Japan and significance of coinfection with *Theileria orientalis*. J. Clin. Microbiol. 50:2111–2113.
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Session Details:	8/26/2013 COMMERCIAL LIVESTOCK - CATTLE 1400 - 1515 <i>Meeting Room 7</i>
Oral Presentation Details:	A hitherto undetected biosecurity breach leads to a <i>Taenia saginata</i> “cysticercosis storm” in a New South Wales feedlot
Presentation Time:	1445 -1500
Authors:	Jenkins D ¹ ¹ Charles Sturt University, ² School of Medicine, Australian National University

Survey data collected in 2008 from almost half a million slaughtered cattle concluded that *Taenia saginata* infection in Australian cattle is “extremely rare”. This is a reasonable conclusion since Australian cattle rarely have the opportunity to be in contact with pasture contaminated with human faeces. However, infection in Australian cattle is still detected periodically, despite the low sensitivity of standard abattoir meat inspection procedures with detection rates being rarely better than 30%. A recently investigated cysticercosis storm in a feedlot in NSW led to the total condemnation of 26 beasts and down grading of the rest of the mob. Apart from the direct financial loss to the producer, this outbreak lead to the loss of a contract to supply meat to a national supermarket chain and the loss of producer’s reputation as a producer of high grade beef. By a process of elimination, the cause of this outbreak of bovine cysticercosis was determined to be from human faeces-contaminated feed supplement imported into Australia from Papua New Guinea.



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Session Details:	8/26/2013 COMMERCIAL LIVESTOCK - CATTLE 1400 - 1515 Meeting Room 7
Oral Presentation Details:	The challenge of achieving <i>Toxocara vitulorum</i> and <i>Fasciola gigantica</i> control in developing tropical smallholder large ruminant farming systems: a case study from Laos
Presentation Time:	1500 -1515
Authors:	Rast L ¹ , Windsor P ¹ , Toribio J ¹ , Khounsy S ² ¹ University Of Sydney, ² Department of livestock And Fisheries Lao PDR

T.vitulorum and *F.gigantica* infection in large ruminants are endemic in south-east Asia and despite investments in research, sustained control is still largely absent. For example, recent surveys in northern Laos identified prevalence for *T. vitulorum* in calves of 22.6 % and *F. gigantica* in adults of 17.2% (field) and 34.1% (slaughterhouse), with 76.8% and 73.3% of sampled villages having at least one animal positive for each parasite respectively. As calf morbidity (42.6%) and mortality (37.3%) were high, economic analysis showed a very positive net benefit of 6-23USD per calf if treated for *T.vitulorum*.

Two surveys examined the knowledge, attitudes and treatment practices (KAP) of smallholder farmers of *T.vitulorum* and *F.gigantica* using face-to-face interviews with farmers (n=273 and 306). Interviewed farmers had either no (80.6%) or minimal (19.4%) knowledge of *T. vitulorum* with only 3.6% of the farmers treating their calves with the recommended regime, despite widespread anecdotal reports that this intervention is highly valued by farmers. Although 20.6% of farmers reported having seen *F.gigantica* in livers of slaughtered cattle or buffalo, they had either no (93.1%) or minimal (6.9%) knowledge of *F.gigantica* lifecycle and impacts, although, 95.4% of farmers indicated a desire to learn more about the disease.

These surveys were conducted in villages where government livestock extension staff have worked with farmers for several years to implement interventions aimed at increasing livestock productivity. However despite training in large ruminant health and production plus extension, their ability to transfer effective KAP improvements on parasitism to farmers needs further attention, particularly given current focus on endemic infectious and transboundary diseases. With declining populations of large ruminants due to increasing regional red meat demand and evidence that control of *T.vitulorum* calves is a very cost-effective strategy to increase calf survival and performance, increased efforts to strengthen the ‘parasitism extension’ capacity in northern Laos is required to ensure that smallholder farmers can optimise their potential contribution to regional food security.



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Session Details:	8/26/2013 INTERNATIONAL COMMISSION ON TRICHINELLOSIS 1400 - 1515 Meeting Room 8
Oral Presentation Details:	Assessment of freezing and other sample conditions on the performance of digestion assay for the recovery of <i>Trichinella</i> larvae
Presentation Time:	1400 -1415
Authors:	Gajadhar A, Konecsni K, Scheller C, Scandrett B, Ostrander R, Renneberg L Canadian Food Inspection Agency

Trichinella continues to garner attention globally as a cause of foodborne disease outbreaks, and much effort and resources have been devoted to its control and to documenting negligible risk in the production of pork and other meats. Effective practices for the detection and control of *Trichinella* infection in susceptible food animals and game are essential for achieving these goals. The digestion method can consistently detect *Trichinella* larvae in meat at the level of sensitivity necessary to prevent human disease and control animal infection. However, reliable performance of the assay can only be assured when validated parameters of samples and test method are used. Validation data for this assay have been based exclusively on the use of muscle samples which have not been previously frozen. The present study was conducted to help define suitable sample parameters when using frozen meat. Various sample conditions were assessed by a previously validated digestion assay using meat from a horse and pig naturally infected with *T. murrelli* and *T. spiralis*, respectively. Sample variables included storage temperature (4, -10, -20°C), storage period (0, 2, 4, 6, 8, 12 wks), sampling site (7 different muscles), and sample weight (1, 5, 10, 20, 100 g). Some of the larvae recovered were assessed for motility or infectivity. A limited number of samples were used to evaluate the performance of trichinelloscopy relative to digestion assay. The study defined a range of freezing and storage conditions for samples from various muscle sites which required little or no modification of the standard digestion assay to achieve the necessary level of sensitivity when testing pork or horsemeat for *Trichinella* spp. This should increase flexibility in the storage and treatment of samples in the field and laboratory and thus facilitate the management and control of *Trichinella* infection in the food supply chain.



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Session Details:	8/26/2013 INTERNATIONAL COMMISSION ON TRICHINELLOSIS 1400 - 1515 Meeting Room 8
Oral Presentation Details:	Distribution patterns and predilection muscles of <i>Trichinella zimbabwensis</i> larvae in experimentally infected Nile crocodiles (<i>Crocodylus niloticus</i>)
Presentation Time:	1415 -1430
Authors:	Louis J. La Grange, ^{1,2*} ; Samson Mukaratirwa ¹ ¹ School of Life Sciences, University of KwaZulu-Natal, Westville Campus, Durban, South Africa. ² Chief Directorate Veterinary Services, Department of Agriculture, Rural Development and Land Administration, Nelspruit, Mpumalanga, South Africa.

To determine the distribution patterns of *T. zimbabwensis* larvae and predilection muscles, fifteen crocodiles (*Crocodylus niloticus*) were randomly divided into three cohorts of five animals each representing high infection (640larvae/kg of bodyweight), medium infection (415larvae/kg of bodyweight) and low infection (135larvae/kg of bodyweight) cohorts. In the high infection cohort, high percentages of larvae were observed in the tricep muscles (26%) and hind limb muscles (13%). In the medium infection cohort, high percentages of larvae were found in the tricep muscles (50%), sternomastoid (18%) and hind limb muscles (13%). For the low infection cohort, larvae were mainly found in the intercostal muscles (36%), longissimus complex (27%), forelimb muscles (20%), and hind limb muscles (10%). Predilection muscles in the high and medium infection cohorts were similar to those reported in naturally infected crocodiles despite changes in infection intensity. The high infection cohort had significantly higher numbers of larvae in the intercostal, longissimus complex, external tibial flexor, longissimus caudalis and caudal femoral muscles ($P < 0.05$) compared to the medium infection cohort. In comparison to the low infection cohort, the high infection cohort harboured significantly higher numbers of larvae in all muscles ($P < 0.05$) except for the tongue and pterygoid. The high infection cohort harboured significantly higher numbers of larvae ($P < 0.05$) in the sternomastoid, tricep, intercostal, longissimus complex, external tibial flexor, longissimus caudalis and caudal femoral muscles compared to naturally infected crocodiles. Results from this study show that, in Nile crocodiles, larvae of *T. zimbabwensis* appear first to invade predilection muscles closest to their release site in the small intestine before occupying those muscles situated further away. The recommendation for the use of masseter, pterygoid and intercostal muscles as sampling sites for the detection of *T. zimbabwensis* in crocodiles (European Commission, 2005) is in contrast to the results from this study where the fore- and hind limb muscles had the highest number of larvae.



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Session Details:	8/26/2013 INTERNATIONAL COMMISSION ON TRICHINELLOSIS 1400 - 1515 Meeting Room 8
Oral Presentation Details:	Evaluation of ELISA coupled with confirmatory testing as a surveillance tool for <i>Trichinella</i> infection in Australian wild boar
Presentation Time:	1430 -1445
Authors:	Leigh Cuttell ^{1*} , Maria Angeles Gomez Morales ² , Beth Cookson ³ , Peter J. Adams ⁴ , Simon Reid ¹ , Paul B. Vanderlinde ³ , Louise A. Jackson ⁵ , Rebecca J. Traub ¹ (presenting author asterisked) ¹ The University of Queensland, Gatton, AUSTRALIA ² Istituto Superiore di Sanita, Rome, ITALY ³ Department of Agriculture, Fisheries and Forestry, Hamilton, AUSTRALIA ⁴ Murdoch University, Perth, AUSTRALIA ⁵ Biosecurity Queensland, Archerfield, AUSTRALIA

Trichinella surveillance in wildlife currently relies on muscle digestion although serological methods such as ELISA could offer surveillance alternatives. ELISA should be coupled with confirmatory tests however because of high false positive rates encountered in wildlife. We investigated the utility of ELISA coupled with Western Blot (WB) or real-time PCR (Cuttell et al., 2012b) in *Trichinella* diagnosis of Australian wild boar. Sera were collected from 673 wild boars from a high- and low-risk region for *Trichinella* introduction within mainland Australia which is considered *Trichinella*-free. Sera were examined using an in-house and commercially available indirect-ELISA that used excretory-secretory (E/S) antigens and the cut-off values determined using sera from the low-risk population. High-risk wild boars had previously been examined by muscle digestion and 139/321 (43.3%) of the wild boar from the low-risk region were examined by digestion here. WB also using E/S antigen and real-time PCR using 10 g of muscle for the detection of *Trichinella* larvae *in situ* was carried out on all ELISA-positive samples. The ELISAs correctly classified all positive controls as well as a naturally infected wild boar from Gabba Island, Torres Strait originally described in Cuttell et al. (2012a). In both populations, the ELISA results showed substantial agreement (κ -value= 0.66) that increased to very good (κ -value= 0.82) when WB-confirmed only samples were compared. In the high-risk mainland population, there was a two to four-fold higher seroprevalence estimate by ELISA compared to the muscle prevalence estimate of 0.0% (95% C.I. 0.0-1.1). Real-time PCR in seropositive samples did not detect muscle larvae in any mainland wild boar, but did detect a second larvae-positive animal on Gabba Island, supporting its utility as an alternative, sensitive method in muscle examination. The serology results suggest Australian wildlife may already be exposed to *Trichinella* parasites, but because of the likelihood of non-specific reactions with other parasitic infections, more work using well-defined cohorts of positive and negative samples is required.

Acknowledgements:

Funding for this work was provided by the Australian Biosecurity Cooperative Research Centre for Emerging Infectious Diseases (AB-CRC).



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Cuttell, L., Corley, S.W., Gray, C.P., Vanderlinde, P.B., Jackson, L.A., Traub, R.J., 2012b, Real-time PCR as a surveillance tool for the detection of *Trichinella* infection in muscle samples from wildlife. *Vet Parasitol* 188, 285-293.



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Session Details:	8/26/2013 INTERNATIONAL COMMISSION ON TRICHINELLOSIS 1400 - 1515 Meeting Room 8
Oral Presentation Details:	Detection of <i>Trichinella murrelli</i> in an imported horse in Canada during routine certified testing of meat for export
Presentation Time:	1445 -1500
Authors:	Scandrett B, Gajadhar A, Lalonde L, Konecsni K, Ostrander R, Renneberg L Canadian Food Inspection Agency

Trichinella murrelli (T5) is a zoonotic nematode which has been found in mammalian wildlife in temperate areas of North America, and has been implicated in outbreaks of human trichinellosis. In Canada, only one occurrence of this parasite has been documented, in a wild cougar from Vancouver Island, BC, Canada. There has previously been only indirect evidence of natural infection with *T. murrelli* in a domestic livestock host, in a horse originating from Connecticut, USA and implicated in an outbreak of trichinellosis in France. We report the recent detection of *T. murrelli* infection in a horse imported from the USA to Canada for slaughter and requisite testing for freedom from *Trichinella* prior to export to the European Union (EU). Sampling and testing were performed by an abattoir laboratory certified under a CFIA lab certification program which incorporates appropriate international guidelines including those of the OIE, ISO, ICT and EU. Using the artificial digestion assay for routine certified testing, and for confirmatory testing conducted by the national reference laboratory (NRL), a mean of 5 *Trichinella* larvae per gram were consistently recovered from multiple samples of tongue and diaphragm from the infected horse. Multiplex PCR performed by the NRL identified the larvae as *T. murrelli*. This is the first direct evidence of naturally acquired *T. murrelli* infection in a horse, and reaffirms the potential food safety risk posed by this species in meat derived from horses and other susceptible hosts from areas of North America where this parasite exists. To our knowledge, this is the first time that routine screening for any *Trichinella* species in horse meat has prevented its entry into the food chain, exemplifying the importance of quality assured food safety testing programs in mitigating the risk of trichinellosis to consumers.



Session Details:	8/26/2013 INTERNATIONAL COMMISSION ON TRICHINELLOSIS 1400 - 1515 Meeting Room 8
Oral Presentation Details:	Study on the prevalence of <i>Trichinella</i> spp. in the red fox population in Germany, 2011
Presentation Time:	1500 -1515
Authors:	Noeckler K, Reckinger S, Kaesbohrer A, Mayer-Scholl A Federal Institute For Risk Assessment

Trichinellosis is an important meat borne disease in humans caused by the larval stage 1 of the genus *Trichinella*. *T. spiralis*, *T. pseudospiralis*, *T. britovi* and *T. nativa* can occur in the domestic and/or sylvatic cycle in European countries, whilst wild animals such as foxes and raccoon dogs are considered the main reservoir for this parasite (Gottstein et al., 2009).

To assess the current situation in the red fox population, 3154 foxes from 9 Federal States in Germany were examined for *Trichinella* larvae in 2011. From each fox, about 10 g of tongue and/or forearm musculature were examined in a pool of 100 g by artificial digestion (magnetic stirrer method). Muscle samples from positive foxes and isolated *Trichinella* larvae were obtained for the calculation of the larval burden per g of muscle (lpg) and the identification of *Trichinella* species by multiplex PCR.

Trichinella larvae were found in 10 out of 3154 foxes examined (0.3%) while regional prevalence among the Federal States varied between 0% and 1.4%. The highest *Trichinella* prevalence in foxes was detected in Mecklenburg-Western Pomerania and Saxony, which are located in Eastern Germany at the border to Poland. The 10 *Trichinella* isolates from foxes were mostly identified as *T. spiralis* (60%), followed by *T. britovi* (30%) and mixed infections with *T. spiralis*/*T. britovi* (10%). The larval burden could be calculated for 8 *Trichinella* positive foxes with a median of 1.85 lpg, while the maximum larval burden was 8.4 and 216 lpg for *T. spiralis* and *T. britovi*, respectively.

Trichinella spp. is present in the red fox population in the majority of German Federal States which participated in the study. The high *Trichinella* occurrence in foxes found in Mecklenburg-Western Pomerania corresponds to the high *Trichinella* prevalence in wild boars and raccoon dogs reported in the region (Pannwitz et al., 2010).

Acknowledgements:

We thank the competent authorities of the participating Federal States for the provision of data and the local laboratories for the muscle samples from positive foxes and *Trichinella* isolates.

References:

Gottstein, B., Pozio, E., Nöckler, K., 2009. Epidemiology, diagnosis, treatment, and control of trichinellosis. Clin. Microbiol. Rev. 22, 127-145.

Pannwitz, G., Mayer-Scholl, A., Balicka-Ramisz, A., Nöckler, K., 2010. Increased prevalence of *Trichinella* spp., Northeastern Germany, 2008. Emerg. Inf. Dis. 16, 936-942.

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Session Details:	8/26/2013 AQUACULTURE ANIMAL HEALTH - Novartis session 1545 - 1700 <i>Riverside Theatre</i>
Oral Presentation Details:	Parasitic Diseases in South East Asian Aquaculture
Presentation Time:	1600 - 1615
Authors:	Supranee Chinabut ¹ , Worawit Maneepitaksanti ¹ , Varinee Panyawachira ¹ ¹ Inland Aquatic Animal Health Research Institute, Department of Fisheries, Bangkok, THAILAND

Aquaculture continues to be the fastest growing animal food-producing sector that provides source of aquatic protein for global population. However, world aquaculture is dominated by the Asia-Pacific regions, which account 90 percent of production in terms of quantity and 77 percent in terms of value. Global production from aquaculture has grown substantially, culture system has developed to super-super intensive culture system for the maximize production. Importation of live aquatic animal or products and domestic movements of live aquatic animals is also increasing. Then health issue becomes one of the constraints in aquaculture. A wide variety of parasitic diseases have been reported as causing significant losses in aquaculture. Major parasitic diseases that cause serious damage in aquaculture are as follow: protozoan (*Trichodinids*, *Amyloodinium*, *Cryptocaryon/Ichthyophthirius*, *Tetrahymena*), monogenean (*Benedenia*, *Diplectanum*), digenean (*Didymozoid*), branchiopod (*Argulus*), copepod (*Caligus*), and isopod (*Alitropus*) infestation.



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Session Details:	8/26/2013 AQUACULTURE ANIMAL HEALTH - Novartis session 1545 - 1700 Riverside Theatre
Oral Presentation Details:	The Potential Impact Of Alien Invasive Parasites On Economic Important Freshwater Fish Species In The Eastern Cape, South Africa
Presentation Time:	1600 -1615
Authors:	K.J. McHugh¹, Olaf L.F. Weyl² & Nico J Smit¹ ¹Water Research Group (Ecology), Unit for Environmental Sciences and Management, Potchefstroom Campus, North West University, Private Bag X6001, Potchefstroom, 2520, South Africa. ²South African Institute for Aquatic Biodiversity, Private Bag 1015, Grahamstown, 6140 South Africa

The impacts of alien fish species on indigenous fish species include the transfer of associated parasites, direct predation on indigenous fish and ecosystem effects resulting from changing invertebrate community structure. As a result alien invasive fishes are considered the primary threat to the native fish fauna in South Africa. However, the effect of alien parasites on economic fish species are not directly known, therefore the aim of the study was to determine the effects of alien parasites on economic important fish species from various impoundments. The study took place in the Amatola region of the Eastern Cape. The three dams were Binfield Park Dam, a 260ha dam used both by subsistence anglers from a local community and occasionally by recreational bass anglers, Sandile Dam, used by recreational bass anglers and rural subsistence fishers and Wriggleswade Dam, a 1000ha impoundment used extensively by recreational bass and carp anglers. The fish sampled for parasites were *Labeo umbratus* and *Labeobarbus aeneus*. No alien parasites were found in Binfield park Dam but the anchor worm, *Lernaea cyprinacea* was found on *Labeo umbratus* from Sandile Dam and both *L. cyprinacea* and the tapeworm, *Bothriocephalus acheilognathi* was found infecting *Labeobarbus aeneus* from Wriggleswade Dam. *Bothriocephalus acheilognathi* was not found in *Cyprinus carpio* from Wriggleswade dam. *Cyprinus carpio* was not found in Binfield Park or Sandile Dam however its associated parasite *L cyprinacea* was found in Sandile Dam. Anchor worm *L cyprinacea* can cause high mortalities in freshwater cultured fish stocks, the adult parasites are extremely harmful to young fish because of their relative large size and their mode of attachment and feeding. It is also responsible for secondary infections, as well as the transmission of viruses and bacteria can also be transmitted by infection.



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Session Details:	8/26/2013 AQUACULTURE ANIMAL HEALTH - Novartis session 1545 - 1700 Riverside Theatre
Oral Presentation Details:	Comparison Study of <i>Clinostomum complanatum</i> (Digenea: Clinostomatidae) in Fresh Water Fish from Riau and Yogyakarta, Indonesia
Presentation Time:	1615 -1630
Authors:	Riauwaty, Windarti and S. Tato* Riau University, Riau, Indonesia Gadjah Mada University, Yogyakarta, Indonesia

Clinostomiasis is one of diseases caused by digenea trematoda *Clinostomum complanatum*, known well as “yellow grubs”. This is a zoonotic parasite and causes the “laryngo-pharyngitis”, and death caused by asphyxia in humans. *Clinostomum complanatum* infection of freshwater fish in Indonesia causes high fish mortality and economic losses. The objectives of research were a) to identify and to compare the morphological and molecular characteristic of *C. complanatum* (Digenea: Clinostomidae) infecting freshwater fishes in Riau and Yogyakarta, and b) to find out their strain variation of DNA in ITS region. Climbing perch (*Trichogaster trichopterus*) infected by *Clinostomum* sp. were caught from Kali Progo, Yogyakarta. Excysted *Clinostomum* sp. was found in the body cavity and visceral organ, were aseptically taken using needle, preserved in 10% formalin and absolute ethanol solution. Morphological examination was done with *Semichon’s acetocarmine* staining and *Scanning Electron Microscope* (SEM). Molecular examination consisted of extraction, amplification in the ITS region, and sequencing. Sequencing results were analysed by maximum parsimony and neighbour-joining methods. Genetic distance were calculated using Kimura parameter model. The worm from Riau was categorized as a new species, whereas worm from Yogyakarta was identified as *Clinostomum complanatum* based on SEM. The PCR rDNA product of *Clinostomum* sp. at ITS Region had a clear band of 1300 bp. Product of RFLP using *Pst*I and *Alu*I restriction enzyme showed different restriction site among the five worms. There was intraspecific variation in *Clinostomum* sp. of metacercariae in Riau and Yogyakarta. Phylogenetic analysis showed that *Clinostomum* sp. from Yogyakarta identic to *Clinostomum complanatum*, whereas *Clinostomum* sp. from Riau were suspected as a new species (difference > 2%) which is included in one cluster with *Clinostomum phalacrocorasis*.

Keyword: *Clinostomum complanatum*, fresh water fish, climbing perch



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Oral Presentation Details:	Recent investigations into the aetiology of winter mortality disease in Sydney rock oysters (<i>Saccostrea glomerata</i>)
Presentation Time:	1630 -1645
Authors:	Spiers Z¹, Gabor M¹, Fell S¹, Dove M², O'Connor W², Jenkins C¹ ¹ NSW Department of Primary Industries State Veterinary Diagnostic Laboratory, ² NSW Department of Primary Industries, Port Stephens Fisheries Institute

Winter Mortality is a poorly understood, yet significant disease affecting Sydney rock oysters (*Saccostrea glomerata*) in New South Wales. Commercial losses due to winter mortality affect mature oysters (> 3 years old), in cool temperatures (July to September in the Southern half of NSW) and high salinities (30-35ppt). While the clinical syndrome is well recognised by oyster growers from affected areas, the histopathology and aetiology described in previous studies does not reflect the complexity of the disease in local conditions. The Haplosporidia parasite *Bonamia roughleyi* has been reported to cause the disease, however this organism is rarely seen in clinical cases of winter mortality and evidence linking clinical signs and histopathology to molecular data identifying a bonamiasis is lacking. Recent longitudinal studies and diagnostic cases submitted to the Elizabeth Macarthur Agricultural Institute are reviewed for this presentation. These include histopathology and transmission electron microscopy results from diagnostic submissions, and a longitudinal study conducted from February to November 2010 comparing the clinical syndrome, histopathology, molecular investigations and associated environmental data from affected estuaries. Characteristic gross and histopathology changes were prevalent in the studied oysters and intralesional microcell-like structures were sometimes noted. PCR testing for *Bonamia* spp. revealed the presence of an organism belonging to the *Bonamia exitiosa*-*B.roughleyi* clade in these samples; however the very low prevalence of this organism relative to histological changes and the lack of reactivity of affected oysters in subsequent *in situ* hybridization experiments led us to conclude that the *Bonamia* sp. is not responsible for winter mortality. Another aetiological agent and/or a confluence of environmental factors are a more likely explanation for the disease.

Acknowledgements:

The oyster growers who participated in the studies and diagnostic submissions, the Histology and EM units at the Elizabeth Macarthur Agricultural Institute, support from the Hermon Slade Foundation for the longitudinal study and Ryan B. Carnegie for providing reference material.



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Session Details:	8/26/2013 DIAGNOSTICS - FLUKES 1545 - 1700 Meeting Room 1
Oral Presentation Details:	Development of recombinant antigen-based serological diagnosis for the detection of <i>Schistosoma japonicum</i> infection in water buffaloes
Presentation Time:	1545 -1600
Authors:	Angeles J¹, Goto Y², Kirinoki M³, Leonardo L⁴, Asada M¹, Rivera P⁴, Villacorte E⁴, Inoue N¹, Chigusa Y³, Kawazu S¹ ¹ National Research Center For Protozoan Diseases, Obihiro University Of Agriculture And Veterinary Medicine, Obihiro, Hokkaido, Japan, ² Laboratory of Molecular Immunology, Department of Animal Resource Sciences, Graduate School of Agricultural and Life Sciences, The University of Tokyo, Tokyo, Japan, ³ Laboratory of Tropical Medicine and Parasitology, Dokkyo Medical University, Tochigi, Japan, ⁴ Department of Parasitology, College of Public Health, University of the Philippines, Manila, Philippines

Schistosoma japonicum is known to infect humans and other mammalian hosts. Inclusion of animal surveillance in existing schistosomiasis control programs should therefore be done in strengthening the capabilities of current serological tests. Thioredoxin peroxidase-1 (SjTPx-1) and four tandem repeat proteins (Sj1TR, Sj2TR, Sj4TR, Sj7TR) were initially evaluated against human sera showing SjTPx-1 and Sj7TR with high sensitivity and specificity. In this study, these recombinant proteins were further evaluated using ELISA on water buffalo serum samples collected from Gonzaga, Cagayan, the Philippines as compared with the soluble egg antigen (SEA). For specificity, 3 goat serum samples positive with *Fasciola hepatica* were used and among the antigens used, only SEA showed cross-reaction. Stool PCR targeting the *S. japonicum* 82-bp mitochondrial NAD-1 gene served as the standard test. SjTPx-1 and Sj1TR gave the highest sensitivity among the recombinant proteins which were higher than that of SEA. These results prove that SjTPx-1 is a good candidate antigen both for human and zoonotic diagnosis whereas Sj1TR showed good results for water buffaloes. Furthermore, SjTPx-1 and Sj1TR were used to assess the prevalence rate among water buffaloes in another endemic area namely Calatrava, Negros Occidental, the Philippines as compared to other coprological, serological and molecular techniques. Stool microscopy only captured 1 positive sample whereas stool PCR detected the highest number of positive samples. Among the serological techniques, Sj1TR-ELISA showed good detection capabilities almost comparable with stool PCR. Moreover, SjTPx-1 showed lower sensitivity in the Calatrava samples than the Gonzaga samples possibly due to antigenic polymorphisms which needs further investigations. Although stool PCR might be more sensitive than the use of recombinant proteins, it is more costly requiring expensive equipment and reagents. The use of recombinant antigens like Sj1TR therefore might be more significant in the field purposes such as zoonotic epidemiological studies and disease surveillance.



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This study was funded by a grant from Global COE Program from the Japanese Ministry of Education, Science, Sports, Culture and Technology; Grant H23-Shinkosaiko-014 for research on emerging and re-emerging infectious diseases from the Ministry of Health, Labour and Welfare of Japan; a Grant-in-Aid for Scientific Research from the Japan Society for the Promotion of Science; and A-STEP Grant from the Japan Science and Technology Agency.

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1. Angeles JM, Goto Y, Kirinoki M, Leonardo L, Tongol-Rivera P, Villacorte E, Inoue N, Chigusa Y, Kawazu S. Human antibody response to thioredoxin peroxidase-1 and tandem repeat proteins as immunodiagnostic antigen candidates for *Schistosoma japonicum* infection. American Journal of Tropical Medicine and Hygiene; 85(4), 2011: 674–679.

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Session Details:	8/26/2013 DIAGNOSTICS - FLUKES 1545 - 1700 Meeting Room 1
Oral Presentation Details:	Characterisation of IgE antibody responses to <i>Anoplocephala perfoliata</i> infection in horses.
Presentation Time:	1600 -1615
Authors:	April Lawson, Charles Pittaway, Gerald Coles* and Doug Wilson School of Veterinary Sciences, University of Bristol, Langford House, Bristol BS40 5DU UK.

Introduction: *Anoplocephala perfoliata* is the most common intestinal tapeworm of horses. Infected horses have IgG antibodies specific for *Anoplocephala* excretory secretory (ES) antigens but the role of IgE antibody is unknown.

Methods: Blood, tissue samples and worms were collected from a licenced horse abattoir. Anti-IgE monoclonal antibody had been produced at the vet school.

Results: Serum samples collected from horses with a post mortem diagnosis of *A.perfoliata* infection had IgG(T), IgA and IgE antibodies to E/S antigens measured by ELISA, although the OD values for IgE were very low. Some horses showed strong IgE antibody binding to the surface layers of the proglottids by immunohistology, while IgG gave only a marginal signal suggesting a novel antigenic target of IgE on the worm surface. Parasite surface carbohydrate exhibited strong binding of the lectin *Ulex europaeus* agglutinin (fucose) and to a lesser extent peanut agglutinin (galactose). Dual staining showed that IgE and lectin binding co-localized and pre-incubation with IgE antibody completely blocked lectin binding implying the IgE antibodies are directed at a carbohydrate epitope. Immunohistology of colon sections revealed large numbers of IgE+ve cells in the lamina propria along with mast cells and eosinophils. Increased numbers of lymphoid follicles containing IgE+ve cells were also seen at the site of *A.perfoliata* attachment and QRT-PCR confirmed active IgE transcription at these locations. Furthermore *A.perfoliata* specific IgE was detected in the supernatant of gut explant cultures indicating that local IgE synthesis and the accumulation of IgE mediated effector cells are characteristic of the immune response to *A.perfoliata* infection in horses.

Discussion: The horse mounts IgE responses against the tapeworms but this is very localised and serum IgE cannot be used for diagnosis of the infection.



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Session Details:	8/26/2013 DIAGNOSTICS - FLUKES 1545 - 1700 Meeting Room 1
Oral Presentation Details:	The identification of the rumen fluke, <i>Calicophoron daubneyi</i> , in livestock from the British Isles: Implications for epidemiology and diagnosis of liver fluke
Presentation Time:	1615 -1630
Authors:	Skuce P¹, Gordon D², Sargison N², Zadoks R³ ¹ Moredun Research Institute, Edinburgh UK, ² Royal (Dick) School of Veterinary Studies, University of Edinburgh, UK, ³ Institute for Biodiversity, Animal Health and Comparative Medicine, University of Glasgow, UK

Rumen fluke (paramphistomes) have been increasingly diagnosed in home-bred livestock from the British Isles in recent years and have been responsible for clinical disease and deaths in young stock, both sheep and cattle. The commonly held belief is that these belong to the species *Paramphistomum cervi* and may have entered livestock over time via the deer population. Their presence, often as co-infections with liver fluke, *Fasciola hepatica*, may mask liver fluke diagnosis because their eggs are morphologically similar, also, persistence of rumen fluke eggs following treatment for liver fluke may lead to erroneous declarations of treatment failure. As part of an evaluation of the commercial Bio-X *F. hepatica* coproantigen ELISA, we tested the cross-reactivity of the MM3 monoclonal antibody with rumen fluke using immunohistochemistry on paraffin wax sections and found it to be specific for liver fluke, with intense staining of the gastrodermis of *F. hepatica* and none in equivalent rumen fluke sections. We subsequently PCR amplified and sequenced the ITS-2 region from the same batch of fixed rumen fluke specimens, collected from home-bred Scottish cattle. GenBank database searching and DNA sequence alignment revealed these to be *Calicophoron daubneyi*, the predominant rumen fluke species in mainland Europe, and not *P. cervi*. Results have been confirmed by inclusion of reference *C. daubneyi* and *P. cervi* specimens from Europe and extended by inclusion of rumen fluke specimens from home-bred sheep and cattle sourced from Scotland, England, Wales and Ireland, including both asymptomatic and clinical cases. These findings would suggest that *C. daubneyi* is endemic in the British Isles and may have implications for the epidemiology of rumen fluke, because *C. daubneyi* is known to utilise *Galba truncatula*, (Mage *et al*, 2002), the same mud snail intermediate host as liver fluke, rather than the planorbid water snails favoured by paramphistome species.

Acknowledgements:

This study received financial support from the Scottish Government Strategic Research Programme and Quality Meat Scotland (QMS)

References:

Mage C, Bourgne H, Touillieu JM, Rondelaud D and Dreyfuss G, 2002. Fasciola hepatica and Paramphistomum daubneyi: changes in prevalences of natural infections in cattle and in Lymnaea truncatula from central France over the past 12 years. Veterinary Research 33(5):439-447



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Session Details:	8/26/2013 DIAGNOSTICS - FLUKES 1545 - 1700 Meeting Room 1
Oral Presentation Details:	Development of a quantitative DNA diagnostic test for liver fluke in sheep
Presentation Time:	1630 -1645
Authors:	Jody McNally^{1*}, M. Knox¹ and Peter W Hunt¹ ¹Commonwealth (of Australia) Scientific and Industrial Research Organisation (CSIRO) Armidale, NSW, AUSTRALIA

Methodology has been developed to measure liver fluke (*Fasciola hepatica*) infection using DNA extracted directly from sheep faeces and a modified version of a published qPCR protocol (Alasaad, et al., 2011). Liver fluke eggs are relatively tough to break and we thus developed a disruption method combining ‘dry’ bead beating with silicon carbide beads and chrome steel balls followed by further ‘wet’ bead beating in lysis buffer. This method combined with magnetic bead DNA extraction allowed the complete extraction of good quality liver fluke egg DNA. A specific TaqMan based qPCR assay was used to detect DNA from multiple stages of the liver fluke lifecycle including adult liver fluke, the infective larval stage, metacercariae and from eggs. Standard curves were developed by adding known quantities of liver fluke eggs into helminth naive faeces. The relationship between qPCR result (Cq) and egg number per gram was very good (r²=0.988) allowing this standard curve to be used to calculate the quantity of liver fluke eggs in faecal samples from grazing sheep. 51 faecal samples were collected from artificially infected sheep housed under controlled conditions in the CSIRO animal house as well as from farms throughout the New England area of NSW. Most samples had known infections from either bulk or individual fluke egg counts using a microscope-based method (Palmer and Lyon, 2011). The correlation between these two methodologies will be presented.

Acknowledgements:

This work was funded through a Science and Innovation Award 2012 from the Australian Government Department of Agriculture, Fisheries and Forestry, sponsored by Meat and Livestock Australia. Thanks to Jane Lamb, Rad Neilson and the diagnostic lab staff at Veterinary Health Research, Armidale for providing the infective larvae, advice and some infected faecal samples.

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Palmer D. and Lyon J. (2011) Detection of Trematode eggs and Eimeria leuckarti – sedimentation method – faecal samples. PAM-26 Department of Agriculture and Food, Western Australia.

Alasaad S., Soriguer R.C., Abu-Madi M., El Behairy A, jowers M.J., Díez Baños P, Píriz A, Fickel J., Zhu X. (2011) A TaqMan real-time PCR-based assay for the identification of Fasciola spp. Veterinary Parasitology 179:266-271.



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Session Details:	8/26/2013 DIAGNOSTICS - FLUKES 1545 - 1700 Meeting Room 1
Oral Presentation Details:	Liver fluke: Evaluating coprological diagnostics in sheep
Presentation Time:	1645 -1700
Authors:	Danielle Gordon^{1,2*}, Matthew Denwood³, Neil Sargison², Ruth Zadoks^{1,3} and Philip Skuce¹ ¹Moredun Research Institute, Edinburgh, UK ²R(D)SVS, University of Edinburgh, UK ³Glasgow University, UK

Fasciolosis, a production limiting disease caused by the liver fluke *Fasciola hepatica*, is the cause of substantial losses to the UK ruminant livestock industry. Whilst coprological testing is non-invasive, unlike blood based diagnostic testing, it is currently only used in the form of a faecal egg count (FEC). FEC cannot detect the potentially fatal pre-patent infection and can lack sensitivity in low patent infections. It can also lack specificity post effective treatment, due to egg sequestration. A coproantigen ELISA (cELISA) has the potential to detect pre-patent infection and to be specific to live infection (Mezo et al., 2004, Flanagan et al., 2011). Both FEC and cELISA were evaluated using over 2000 British sheep samples including pre-patent and patent infections and pre- and post-treatment samples (Gordon et al., 2012, 2013). In addition the potential of composite sample testing was investigated. The results were analysed using a latent class model. Initial analysis indicates that the cELISA lacks sensitivity in pre-patent infections where there is a low burden, but shows potential as a diagnostic tool for determining treatment outcome 7 days post treatment. Initial analysis also indicates that both FEC and cELISA composite testing have low sensitivity in flocks where there is a low prevalence of fluke infection. An incidental finding in this study was numerous triclabendazole (TCBZ) treatment failures, one of which was confirmed as being due to TCBZ resistance by dose and slaughter, yielding the first confirmed TCBZ resistant isolate from the UK.

Acknowledgements:

Danielle Gordon is in receipt of the Moredun Foundation Doherty Scholarship. We would also like to thank Quality Meat Scotland for additional funding. Thanks to Scottish Agricultural College Consulting Veterinary Services, Participating Farmers and Veterinarians for the provision of samples.

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Flanagan, A.M., Edgar, H.W.J., Forster, F., Gordon, A., Hanna, R.E.B., McCoy, M., Brennan, G.P., Fairweather, I., 2011. Standardisation of a coproantigen reduction test (CRT) protocol for the diagnosis of resistance to triclabendazole in *Fasciola hepatica*. *Veterinary Parasitology* 176, 34–42.

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Session Details:	8/26/2013 DRUGS AND DRUG RESISTANCE - CATTLE 1545 - 1700 <i>Meeting Room 2</i>
Oral Presentation Details:	Farmers’ Dilemma - Which “Experts” to Believe Concerning Drug Resistance
Presentation Time:	1545 -1600
Authors:	J.A. van Wyk* Faculty of Veterinary Science, University of Pretoria, South Africa

Globally, poor farmer uptake of well validated, effective methodology for reducing selection for anthelmintic resistance (AR), is leading to unabated escalation thereof. Despite vigorous propagation by strong extension teams over two decades for farmers to have anthelmintic efficacy testing done regularly, only 31% of farmers in New Zealand had ever complied by 2006 (Rhodes *et al.*, 2006), and estimates for both New Zealand and Australia were that only 10% of farmers were testing (respectively Leathwick, 2011 and Le Feuvre, 2011). And the problem goes much wider; similar imploring of strict quarantining of incumbent animals on farms to prevent introduction of economically crippling animal health conditions, have failed to convince many farmers to quarantine even animals of unknown background, purchased at auctions.

Farmers commonly voice confusion from clashes in the recommendations from different scientific disciplines as a reason for non-compliance, and this should be investigated. Many different disciplines face similar problems of resistance, yet function almost completely compartmentalised, with serious clashes as a result. For instance, compulsory macrocyclic lactone (ML) sheep scab treatment at short intervals of 9-12 days (O’Brien, 1999) in winter in a resource-poor farming region of South Africa has led to serious ML resistance in *Haemonchus contortus* (Van Wyk, unpublished observations, 2009), where financial constraints on communal pasture preclude private blanket treatments. Furthermore, frequent short interval ML treatments for ticks in cattle seriously select for *H. contortus* resistance, and repeated nation-wide blanket treatment recommended by medical helminthologists for river blindness in humans is done (Basáñez *et al.*, 2006.) despite veterinary nematodes having shown propensity for development of resistance to the drug concerned.

Finally it is suggested that comprehensive, possibly automated, electronic feedback to farmers in relation to sample/data evaluation results, combined with periodic pop-up messaging may hold the potential to improved training and farmer uptake of recommendations.

Acknowledgments:

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Session Details:	8/26/2013 DRUGS AND DRUG RESISTANCE - CATTLE 1545 - 1700 Meeting Room 2
Oral Presentation Details:	Anthelmintic resistance of cattle gastro-intestinal nematodes in 4 European countries
Presentation Time:	1600 -1615
Authors:	Thomas Geurden¹, Christophe Chartier², Antonio Frangipane di Regalbono⁷,Donato Traversa³, Georg von Samson-Himmelstjerna⁶, Domenico Otranto⁴, Alain Chauvin², Janina Demeler⁶, Marie-Astrid Malard², Filipe Dantas-Torres^{4,5}, Jane Fanke⁶, Riccardo Paolo Lia⁴, David Bartram¹ ¹ Zoetis ² Ecole Nationale Vétérinaire, Agroalimentaire et de l'Alimentation Nantes Atlantique – ONIRIS, UMR BioEpAR France ³ University of Teramo, Department of Comparative Biomedical Sciences, Italy ⁴ Dipartimento di Medicina Veterinaria, University of Bari, Italy ⁵ Centro de Pesquisas Aggeu Magalhães, Recife, BRAZIL ⁶ Institute for Parasitology and Tropical Veterinary Medicine; Freie Universität Berlin, Germany ⁷ University of Padua, Department of Animal Medicine Production and Health, Italy

Anthelmintic resistance in bovine gastro-intestinal nematodes is emerging worldwide. This study aimed to evaluate the efficacy of injectable formulations of moxidectin (MOX) and ivermectin (IVM) in first grazing season calves naturally infected with gastro-intestinal nematodes. The study was conducted in the UK, France, Germany and Italy, with 8 to 12 study sites per country. The selection of study sites was based on a history of frequent use of anthelmintics or or prior concerns of anthelmintic resistance on the farm. Animals were allocated into 2 treatment groups based on the individual pre-treatment faecal egg counts (FEC). A modified McMaster technique with a sensitivity of 12.5 to 15 eggs per gram of faeces (epg) was used to monitor faecal egg excretion before and after treatment. Assessment of efficacy was based on the difference between the arithmetic mean FEC prior to treatment and 14 days post treatment, for each treatment group, separately. The results illustrate differences in anthelmintic efficacy between countries. In Italy, both MOX and IVM were highly effective. In the 3 other countries suspected or confirmed anthelmintic resistance was observed both for IVM and MOX on several of the farms, although high efficacy of both molecules was also identified in other farms. The pre-treatment larval identification showed a range of parasites on these farms, with *Ostertagia* and *Cooperia* being the most prevalent nematodes before treatment. On farms with reduced efficacy, *Cooperia* larvae were most frequently identified. *Ostertagia* larvae were also identified after treatment, comprising up to 38% of the larval population. On one farm in the UK, 94-100% of the larvae post-treatment were identified as *Ostertagia*. The results of this study indicate that on farms with a high usage of MOX or IVM, the efficacy of treatment can be reduced mainly for *Cooperia* spp. and, to a lesser extent, *Ostertagia* spp.



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Session Details:	8/26/2013 DRUGS AND DRUG RESISTANCE - CATTLE 1545 - 1700 <i>Meeting Room 2</i>
Oral Presentation Details:	Anthelmintic resistance in nematodes of beef cattle– results from a survey of Western Australian farms.
Presentation Time:	1615 -1630
Authors:	Cotter J , Besier B, Van Burgel A Department Of Agriculture And Food WA

Tests for anthelmintic resistance were conducted on nineteen randomly-selected beef cattle farms in the south west of Western Australia between 2010 and 2011. The anthelmintics tested were ivermectin (injectable), fenbendazole (oral) and levamisole (oral), with comparisons of worm egg counts with those of an untreated control group before treatment and 10 -14 days later. A topical ivermectin ‘pour-on’ formulation was also tested on 9 farms, with cattle in this treatment separated from others over the sampling period. Resistance was defined as less than a 95% reduction in worm egg count for a particular worm species.

Resistance to ivermectin (injectable) in *Cooperia oncophora* was detected on 66% of farms, but this was fully effective against *Ostertagia ostertagi*. Conversely, fenbendazole and levamisole were fully effective against *Cooperia oncophora* on all farms, but resistance in *Ostertagia ostertagi* was present on 43% and 53% of farms, respectively. Although similar results against *Cooperia oncophora* were found with ivermectin by both injectable and the ‘pour on’ formulations, resistance to *Ostertagia ostertagi* was found on 37% of farms.

Despite evidence of widespread ivermectin resistance in *Cooperia oncophora*, production losses or clinical parasitism were not observed on farms where macrocyclic lactones were routinely used, presumably due to the relatively mild pathogenicity associated with this species. However, the detection of resistance in the more pathogenic *Ostertagia ostertagi* to the pour-on ivermectin formulation suggests that a potentially more serious problem may be emerging.



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Session Details:	8/26/2013 DRUGS AND DRUG RESISTANCE - CATTLE 1545 - 1700 Meeting Room 2
Oral Presentation Details:	Effects of Ivermectin Long-acting Injection (IVOMEC® GOLD) on Nematode Parasitism and Weight Gain in First-season Grazing Cattle in Bavaria, Germany
Presentation Time:	1630 -1645
Authors:	Knaus M¹, Visser M¹, Winter R¹, Yoon S², Cramer L², Rehbein S¹ ¹ Merial GmbH, Kathrinenhof Research Center, Rohrdorf, Germany, ² MERIAL Limited, Duluth, GA, USA

Anthelmintic efficacy and bodyweight gain of cattle after a single treatment with ivermectin long-acting injection (IVM LAI; IVOMEC® GOLD, Merial; 3.15% ivermectin w/v) was evaluated in two studies conducted at different locations in Bavaria. Cattle were exposed to natural nematode infection for 84 days under continuous stocking conditions. Each study involved 68 male Brown Swiss cattle. Animals weighed 100-188 kg prior to treatment and were 4 to 6 months old. Studies were conducted under a randomized block design. Pre-treatment bodyweights were used to form replicates of four animals each. Animals within a replicate were randomly assigned to treatments, one to saline (control) and three to IVM LAI. Treatments were administered at 1 mL/50 kg once subcutaneously anterior to the shoulder. Animals in each study were grazed on one pasture throughout the study period. Cattle were weighed and fecal samples were collected pre-treatment and at 28, 56, 70, and 84 days after treatment for fecal egg and lungworm larval counts.

Pre-treatment fecal examination and culture indicated the presence of the genera *Cooperia* (dominating), *Haemonchus*, *Nematodirus*, *Ostertagia*, *Trichostrongylus*, and *Dictyocaulus* in the cattle. Following treatment, IVM LAI-treated cattle did not shed any *Dictyocaulus* larvae while controls continued passing larvae. Compared to saline-treated controls, IVM LAI-treated cattle had significantly (p<0.01) lower strongylid egg counts with ≥94% reductions from 28 to 70 days following treatment in both studies; at 84 days, reductions were 89.9% or 83.9%, respectively. Over the study period, IVM LAI-treated cattle gained significantly more weight than controls: 50.1 kg and 40.6 kg vs. 27.4 kg and 30.6 kg.

The two studies demonstrated a high efficacy of IVOMEC GOLD against bovine gastrointestinal and pulmonary nematode infections under field conditions in Germany which was associated with improved weight gain.

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Session Details:	8/26/2013 DRUG EFFICACY - GENERAL 1545 - 1700 <i>Meeting Room 3</i>
Oral Presentation Details:	Considerable heterogeneity of the Ca²⁺-activated and voltage-gated K⁺-channel SLO-1 between different clades of nematodes and the potential impact on the interaction of SLO-1 and emodepside
Presentation Time:	1545 - 1600
Authors:	Kulke D¹⁺², von Samson Himmelstjerna G¹, Miltsch S³, Wolstenholme A⁴, Townson S⁵, Ballesteros C⁶, Geary T⁶, Keiser J⁷, Krücken J¹ ¹ Freie Universität Berlin, ² Bayer Animal Health, ³ Max Planck Institute of Colloids and Interfaces, ⁴ University of Georgia, ⁵ Northwick Park Institute for Medical Research, ⁶ McGill University, ⁷ Swiss Tropical and Public Health Institute

The mode of action of emodepside is not completely understood (Krücken *et al.*, 2012). In *Caenorhabditis elegans*, SLO-1 was described to be essential for emodepside activity (Guest *et al.*, 2007). SLO-1 channels of *Ancylostoma caninum* and *Cooperia oncophora* reconstitute emodepside sensitivity in *C. elegans slo-1* loss-of-function mutants (Welz and Krüger *et al.*, 2012). In *Ascaris suum* muscle flaps, emodepside causes slow activation of SLO-1-like K⁺-channels (Buxton *et al.*, 2012). However, SLO-1 and its role in emodepside action have only been investigated in clade V nematodes and the clade III ascarid *A. suum* within the very heterogeneous phylum Nematoda. Therefore it was investigated whether SLO-1 is also present in *Trichuris muris* (clade I) and the filariae *Brugia malayi*, *Dirofilaria immitis* and *Onchocerca gutturosa* (clade III).

In *B. malayi*, *D. immitis* and *O. gutturosa* a single slo-1 cDNA was obtained. However, two slo-1 paralogs (slo-1.1 and slo-1.2) were identified in *T. muris*. This is the first evidence for the presence of multiple SLO-1 homologs in a nematode genome. In addition, alternative splicing of *D. immitis* slo-1 and *T. muris* slo-1.1 was demonstrated. A high degree of sequence identity within conserved domains among SLO-1 proteins of different nematodes suggests functional conservation. But extensive variation in the variable domains might result in functional differences, potentially including emodepside susceptibility.

Currently, physiological characterisation of SLO-1 channels is performed in *Xenopus laevis* oocytes using a two-electrode voltage clamp technique.

Acknowledgements:

Thanks to Thomas Duguet, Vanessa Dufour and Robin Beech (McGill University) for introducing me to *Xenopus laevis* oocytes as heterologous expression system.



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Session Details:	8/26/2013 DRUG EFFICACY - GENERAL 1545 - 1700 <i>Meeting Room 3</i>
Oral Presentation Details:	Xenobiotic-metabolizing system in flukes with focus on phase 1 in <i>Opisthorchis felineus</i> (Trematoda, Platyhelminthes).
Presentation Time:	1600 -1615
Authors:	Pakharukova M¹, Ershov N¹, Vavilin V², Zadesenets K¹, Katokhin A¹, Duzhak T³, Merkulova T¹, Mordvinov V¹ ¹ Institute Of Cytology And Genetics, Novosibirsk, RUSSIA, ² Institute of Molecular Biology and Biophysics, Novosibirsk, RUSSIA, ³ International Tomography Center, Novosibirsk, RUSSIA

Anthelmintics are the primary tools used to control helminth parasites, which cause significant morbidity and mortality in man and animals. The treatment of helminthic infections has become problematic because of frequent drug resistance of helminth parasites especially of livestock [1]. In spite of its increasing importance, there is still a poor understanding of the molecular basis of resistance.

Xenobiotic metabolizing enzymes (XME) protect the body against the potential harmful exposure to xenobiotics in diverse organisms, and the development of drug resistance can be facilitated by the action of XME enzymes [2, 3], especially CYPs, belonging to the cytochrome P450 superfamily.

Aims of this study were (1) to identify XME coding genes in *O. felineus* and (2) to test CYP activity in liver fluke *Opisthorchis felineus*.

We have identified CYPs, ABC-transporters and other XME genes of *O. felineus*.

The only one cytochrome P450 has been identified in various species of parasitic flatworms including Trematoda (Opisthorchiidae, Schistosomatidae, Fasciolidae), Cestoda (Taeniidae).

We have cloned and sequenced CYP450 mRNA in *O. felineus*. Predicted secondary structure of CYP showed high level of similarity with the mammalian CYP2 proteins. The observed conformational similarity between proteins indicates a high probability of coincidence of their functions. Indeed, we have demonstrated a monooxygenase CYP activity in maritae tissues *in vivo*. It was similar to the mammalian CYP2E1 (HPLC) and CYP2B (MS) and was almost fully inhibited by ketoconazole.

The level of CYP mRNA expression in maritae was constitutive and significantly higher than in other life stages. So we have shown highly expressed functional monooxygenase system with broad substrate specificity and with conservative organization that seems to play an important role in parasite metabolic system.



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This work is supported in part by RFBR grant N 13-04-00662a and SB RAS Research Partnership grant N 19.

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Session Details:	8/26/2013 DRUG EFFICACY - GENERAL 1545 - 1700 Meeting Room 3
Oral Presentation Details:	The Varroa Gate – a novel Approach to protect Honeybee Colonies from <i>Varroa destructor</i>
Presentation Time:	1615 -1630
Authors:	Krieger K¹, Loehr R¹, Jiritschka W¹, Koeniger G², Koeniger N² ¹ Bayer Health Care, Leverkusen, Germany, ² Honeybee Research Center Oberursel, Goethe-University, Frankfurt, GERMANY

Apis mellifera, the Western honeybee, is the predominant species in managed honeybee colonies and the most economically valuable pollinator for crop cultures worldwide. Significant decline of honeybee populations has been reported from North America and Europe and is subject to controversial discussions about the cause. The external parasitic mite, *Varroa destructor*, is considered the most serious threat to *Apis mellifera*. Being a natural parasite of the Asian honeybee, *Apis cerana*, it has invaded into *Apis mellifera* colonies during the last century, where it reproduces more successfully and transmits pathogenic viruses and bacteria. If left uncontrolled, varroosis will almost certainly lead to the premature death of infested colonies.

Varroa mites have spread nearly worldwide except Australia. Efforts to breed varroosis resistant *A. mellifera* bees have not succeeded so far. Varroa control basically depends on treatment of honeybee colonies with acaricides, organic acids and essential oils. Only a few acaricides have been developed and approved for varroa control: amitraz, coumaphos, flumethrin and tau-fluvalinate. Repetitive and unprofessional use of these chemicals has led to resistance development in some varroa populations and to accumulation of residues in beeswax. For this reason the implementation of integrated pest management (IPM) principles has been proposed, using biotechnological methods and rotation of treatment with regulatory approved acaricides with different mode of action.

Novel, polymer-matrix acaricide carriers have been designed as a gate for the beehive entrance in order to protect honeybee colonies from horizontal infection. While passing this varroa gate, infested honeybees contact active ingredient from the surface of the carriers which kills the varroa mites before reproduction. Varroa efficacy of >90% and safety for treated honeybee colonies have been demonstrated during a three months treatment period with coumaphos and flumethrin varroa gate formulations starting after honey extraction.

Acknowledgements:

Bernd Grünewald and his team, Honeybee Research Center Oberursel, Goethe-University, Frankfurt
Annette Schuermann, Bayer Bee Care Center, Monheim, Germany

References:

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Varroosis Position Paper. *Working Group* German *Bee Research Institutes*. Celle 2011



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Session Details:	8/26/2013 DRUG EFFICACY - GENERAL 1545 - 1700 Meeting Room 3
Oral Presentation Details:	Efficacy of dinotefuran, permethrin and pyriproxyfen combination spot-on on dogs against <i>Culex pipiens</i>
Presentation Time:	1630 -1645
Authors:	Franc M.^{1*}, Lienard E.¹, Jacquet P.¹, S. Warin², Bouhsira E.¹, 1: Université de Toulouse, INP-ENVT, UMR 1225, Ecole Nationale Vétérinaire de Toulouse, 23 Chemin des Capelles, F-31076 Toulouse cedex 3, France 2: Ceva Santé Animale, F-33500 Libourne, France

This study was conducted to evaluate the efficacy of a topical spot-on containing dinotefuran 4.95 %, permethrin 36.08 %, and pyriproxyfen 0.44 % (w/w) (*Vectra® 3D* - Ceva) against *Culex pipiens*. The trial was performed according to Animal Welfare and Good Clinical Practice. Twelve dogs (six males and six females, >4 years old, weighing 10.7-12.5 kg) were randomly allocated to treatment groups on pre-treatment mosquito counts: six served as untreated control, and six dogs were treated with the formulation. Treatment administered on day 0 delivered topically at least 46.6 mg.kg⁻¹ permethrin, 6.4 mg.kg⁻¹ dinotefuran and 0.57 mg.kg⁻¹ pyriproxyfen: a combination designed to control fleas, ticks, sandflies and mosquitoes. Clinical observations were performed 2 and 4 hours after treatment. Each dog was infested with 100 (±2) adult unfed *Culex* female, once before treatment (Day-9) and at 1, 7, 14, 21, and 28 days post treatment. Counts and engorgement determination of dead and alive mosquitoes were performed after 1 hour of exposure period. All live mosquitoes recovered from individual animals at the end of the exposure period were placed in separate individual nets and incubated for 1 day before viability assessment. In the treated group, more than 98.3% of mosquitoes were repelled based on engorgement status, at 1, 7, 14, 21 and 28 days post treatment. Insecticidal efficacy (or mortality effect) after 24 hours incubation post-exposure was 50.3% on Day 2, 68.6% on Day 8, 54.7% on Day 15, 38.7% on Day 22 and 18.9% on Day 29 post treatment. The difference between the two groups are statistically significant for the mortality effect and anti-feeding effect at each challenge point (p<0.05 from Day 1 until Day 28). No adverse event was observed following treatment. The administration of the combinaison could be recommended monthly for the prevention of dogs against *Culex pipiens* bites.



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Session Details:	8/26/2013 DRUG EFFICACY - GENERAL 1545 - 1700 Meeting Room 3
Oral Presentation Details:	Efficacy of a 10% imidacloprid / 4.5% flumethrin collar for preventing the transmission of <i>Cytauxzoon felis</i> by <i>Amblyomma americanum</i> to domestic cats
Presentation Time:	1645 -1700
Authors:	Arther B ¹ , Thomas J, Hostetler J, Little S, Meinkoth J, Reichard M ¹ Bayer HealthCare, Animal Health, ² Oklahoma State University, ³ Bayer HealthCare, Animal Health, ⁴ Oklahoma State University, ⁵ Oklahoma State University, ⁶ Oklahoma State University

Infection of *Cytauxzoon felis* in domestic cats produces a severe disease characterized by fever, lethargy, inappetence, anorexia, depression, dehydration, icterus, and often death. Transmission of *C. felis* to cats is dependent on being fed upon by an infected *Amblyomma americanum* (lone star tick). The purpose of the present study was to determine if application of a 10% imidacloprid / 4.5% flumethrin collar to cats (Seresto™) prevents transmission of *C. felis* by repelling ticks. Twenty cats were randomized to either a treated (n = 10) or non-treated control group (n = 10) based on their susceptibility to ticks. Cats of high, medium, and low tick susceptibility were represented in both groups. Treated cats were fitted with 10% imidacloprid / 4.5% flumethrin collars on study day 0 and then both groups were infested with *C. felis*-infected *A. americanum* on study day 30. Tick thumb counts were performed at 24 and 48 hours post-infestation. Transmission of *C. felis* was determined by examining blood of cats by DNA extraction followed by PCR amplification with piroplasm-specific primers. Ticks did not attach to any of the 10% imidacloprid / 4.5% flumethrin treated cats. However, ticks attached and fed on all the untreated control cats. The geometric mean number of ticks attached to the non-treated control cats at 24 and 48 hours was 15.3 and 14.2, respectively. *Cytauxzoon felis* was transmitted to 9 of 10 (90%) non-treated control cats; *C. felis* was not transmitted to any of the treated cats. Transmission of *C. felis* to the non-treated cats occurred between 8 and 16 days post-infestation. Our results indicate that application of the 10% imidacloprid / 4.5% flumethrin collar to cats prevented ticks from attaching, feeding and transmitting *C.felis*.



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Session Details:	8/26/2013 ONE HEALTH 2 1545 - 1700 <i>Meeting Room 5</i>
Oral Presentation Details:	Novel and zoonotic <i>Cryptosporidium</i> species/genotypes identified in fish and goats Papua New Guinea.
Presentation Time:	1545 -1600
Authors:	Koinari M¹, Karl S², Ng J¹, Lymbery A¹, Ryan U¹ ¹ Murdoch University, ² The University of Western Australia

Very little is known about the prevalence of the enteric parasite *Cryptosporidium* in humans, domesticated animals or wildlife in Papua New Guinea (PNG). In order to better understand the epidemiology of *Cryptosporidium* in PNG, a total of 504 faecal samples were randomly collected from goats (*n*=193) and sheep (*n*=311) in village and institutional farms and a total of 614 fish were collected from freshwater aquacultures and rivers and saltwater off the coastal shores of Madang and Rabaul. All samples were screened for the presence of *Cryptosporidium* using PCR at the 18S locus and the positive isolates were sequenced and phylogenetic analyses were conducted. The overall prevalences were 5.2% (10/193) for goats, 1.9% for sheep (6/311) and 1.14% (7/614) for fish. The species/genotypes identified were *C. hominis* (*n*=6, only in goats), *C. parvum* (*n*=11, sheep, goats and fish), *C. andersoni* (*n*=1, in sheep), *C. bovis* (*n*=1, in a goat), and *C. scrofarum* (*n*=1, in a sheep), rat genotype II (*n*=1, in a goat) and a novel piscine genotype (*n*=2, in fish). This is the first report of *Cryptosporidium* spp. identified in sheep, goats and fish in PNG. The detection of *Cryptosporidium hominis* in goats suggests these animals may serve as reservoir for human infection. Genetic sequence analysis at the GP60 locus will also be presented.

Acknowledgements:

We are grateful to the owners of the herds and the staff of National Agriculture Research Institute and Eastern Highlands Province Department of Livestock in Papua New Guinea for their support during sampling.

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Session Details:	8/26/2013 ONE HEALTH 2 1545 - 1700 <i>Meeting Room 5</i>
Oral Presentation Details:	Blastocystis subtype distribution from a variety of animals including Australian native animals
Presentation Time:	1600 -1615
Authors:	Roberts T ¹ , Stark D ¹ , Harkness J ¹ , Ellis J ² ¹ Department of Microbiology, SydPath, St. Vincent's Hospital, N.S.W, Australia, ² i3 Institute, School of Medical and Molecular Sciences, University of Technology, Sydney, N.S.W, Australia

Blastocystis is a single celled enteric parasite that is commonly found in humans and a number of different animal species. In humans, gastrointestinal symptoms are common but it is still unclear as to what impact *Blastocystis* has on animal health. *Blastocystis* has shown to exhibit extensive genetic diversity and through many recent studies on the small subunit (SSU) ribosomal (r)RNA gene, 14 subtypes (ST) have been identified from humans and a variety of animals. There are a number of subtypes which appear to show low host specificity and not one subtype is specific to humans, which raises the possibility of zoonotic transmission. A higher incidence of infection rates has been reported in zoo keepers who come in close contact with animal enclosures which also supports this role of zoonotic transmission.

A total of 438 stool samples from 38 different species of animal from seven different locations within New South Wales, Australia, were studied for the presence of *Blastocystis*. PCR analysis was completed on all samples and DNA sequence data from the rDNA were submitted to subtype allocation. A total of 80 (18%) sequences from 18 species, and nine different subtypes were identified- ST1, ST2, ST3, ST4, ST5, ST7, ST11, ST12 and ST13. This is the first report of *Blastocystis* from the eastern grey kangaroo, red kangaroo, wallaroo, snow leopard and ostrich. This study highlights the genetic variability within the subtypes and shows the possibility for zoonotic transmission.



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Session Details:	8/26/2013 ONE HEALTH 2 1545 - 1700 Meeting Room 5
Oral Presentation Details:	Lethal <i>Encephalitozoon cuniculi</i> (genotype III) infection in Steppe lemmings (<i>Lagurus lagurus</i>)
Presentation Time:	1615 -1630
Authors:	Hofmannová L ¹, Jekl V ², Mináriková A ², Sak B ³, Kváè M ^{3, 4} ¹ Department of Pathological Morphology and Parasitology, University Of Veterinary And Pharmaceutical Sciences Brno, Czech Republic, ² Avian & Exotic Animal Clinic, University Of Veterinary And Pharmaceutical Sciences Brno, Czech Republic, ³ Institute of Parasitology, Biology Centre of the Academy of Sciences of the Czech Republic, v.v.i., Èeské Budijovice, Czech Republic, ⁴ Faculty of Agriculture, University of South Bohemia in Èeské Budijovice, Czech Republic

Microsporidia are ubiquitous, spore-forming, intracellular parasites infecting vertebrates. Some of them are important opportunistic pathogens in humans, including three species of genus *Encephalitozoon*. Intraspecies genetic variation with a different range of hosts is known in *E. cuniculi*: genotype I (rabbit), II (mouse), III (dog). Recently, *E. cuniculi* is often observed in pet animals. This study described the first report of encephalitozoonosis caused by *E. cuniculi* genotype III in a group of arvicolid rodents Steppe lemming (*Lagurus lagurus*) kept as pets by a private owner. Adult lemmings showed symptoms as progressive weight lost, aggression and cannibalism. Purulent conjunctivitis and hind limb paresis were noted 24-48 hours before death. In a period of three months, whole pet breeding colony comprised of 15 animals was affected and died.

Organs (heart, lungs, liver, kidney, spleen, muscle and brain) of two diseased adults were processed for histopathological examination, which reveal microsporidial vacuoles with typical spores (~ 2 x 1µm) in brain tissue and kidneys. A total DNA of the organs was isolated for PCR diagnostic of *E. cuniculi* and the internal transcribed spacer region (ITS) of rDNA was amplified and sequenced (Katzwinkel-Wladarsch et al., 1996; Hester et al., 2002). All organs examined by PCR were positive. The alignment of the obtained sequences with reference ITS sequences showed 100% homology with *E. cuniculi* genotype III (dog strain). This genotype was previously identified in dogs, in tamarin colonies from zoos, in birds and in humans (Mathis et al., 2005; Kašičková et al., 2009). The present study displayed that *E. cuniculi* genotype III can cause lethal infection in rodents, which can represent a potential source of the infection for immunocompromised humans or animals (dogs). Moreover, the Steppe lemmings can be a new useful laboratory model for this microsporidial infection.

Acknowledgements:

This work was supported by the project “CEITEC-Central European Institute of Technology” from European Regional Development Fund (CZ.1.05/1.1.00/02.0068) and grant of the Czech Science Foundation (P505/11/1163).



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Session Details:	8/26/2013 ONE HEALTH 2 1545 - 1700 <i>Meeting Room 5</i>
Oral Presentation Details:	One health in action: parasites transmitted among people, pets, wildlife, and the environment in remote and rural communities in Saskatchewan, Canada
Presentation Time:	1630 -1645
Authors:	Emily J. Jenkins^{1*} , Janna M. Schurer ¹ , Janet E. Hill ¹ , Momar Ndao ² , Stuart Skinner ¹ , James Irvine ¹ , Stacey A. Elmore ¹ , Tasha Epp ¹ ¹ University of Saskatchewan, Saskatoon, Saskatchewan, CANADA ² National Reference Centre for Parasitology, Montreal, Quebec, CANADA

Some parasitic zoonoses have a high prevalence in people in remote and rural communities in Canada due to a complex array of ecological, cultural, and socioeconomic determinants of health. Dogs can serve as sentinels and sources of zoonotic parasites in these communities. At least one intestinal protozoan or helminth parasite species was present in 20-83% of fecal samples environmentally or rectally collected from dogs in 7 remote and rural communities in Saskatchewan, 5-20 times higher than in dogs in a nearby urban centre. We detected parasites of public health concern, including *Toxocara canis*, *Baylisascaris* spp., *Diphyllbothrium* spp., *Echinococcus canadensis*, *Alaria* spp., *Cryptosporidium* spp., and *Giardia* spp. (zoonotic genotype A). In addition, other zoonotic parasites of concern in remote communities include *Toxoplasma gondii* and *Trichinella nativa*/T6. We report the results of a joint human-animal health investigation in a community in northern Saskatchewan, where residents harvest wildlife, live in close contact with free roaming dogs, and lack access to permanent veterinary services. Using enzyme-linked immunosorbent assay (ELISA), sero-prevalence rates in 201 human volunteers were as follows: *Echinococcus* spp. (48%), *Trichinella* spp. (16%), *Toxoplasma gondii* (14%), and *Toxocara canis* (13%). These rates were higher than those reported in most other remote communities in Canada. Administration of pyrantel pamoate to a subset of dogs (N = 122) in the community in the first year was followed by reduced shedding of *T. canis* and other roundworms in the second year, demonstrating the potential utility of canine de-worming as a public health intervention. Reducing human risks associated with zoonotic parasites in remote and rural regions in Canada requires a One Health approach that acknowledges the value of wildlife for subsistence and cultural practices, dogs for security and companionship, and a need to better deliver veterinary public health services in these under-served populations.

Submitted for oral presentation in the One World Health theme (sub-theme zoonoses)



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Session Details:	8/26/2013 ONE HEALTH 2 1545 - 1700 Meeting Room 5
Oral Presentation Details:	Endoparasites in Eastern European stray dogs imported to Norway
Presentation Time:	1645 -1700
Authors:	Inger Sofie Hamnes^{1*}, Siv Klevar¹, Rebecca K Davidson¹, Felix Grimm², Helga Høgåsen¹ and Arve Lund¹ ¹Norwegian Veterinary Institute, P.O. Box 750 Sentrum, 0106 Oslo, Norway ²University of Zürich, Switzerland

Harmonization of regulations in the European Union (EU) and European Economic Area (EEA), as of 1st January 2012, has led to an increase in the number of stray dogs imported to Norway from Eastern European countries, notably Romania. The entry requirements for dogs entering Norway are rabies vaccination and prophylactic *Echinococcus multilocularis* treatment. The criteria for inclusion in the study were that the dog was considered a stray animal in its country of origin, and had arrived from Romania, Hungary, the Balkan and Baltic countries during 2012. Blood samples from 75 and fecal samples from 68 dogs were submitted to the Norwegian Veterinary Institute. Faeces were examined by McMaster’s method, direct smears and Baermann’s method for parasite eggs, oocysts and larvae. Blood samples were examined for *Dirofilaria immitis* surface antigens using a *D. immitis* Ag-ELISA, while IFAT was used to detect antibodies against *Babesia canis*.

Eggs of *Uncinaria stenocephala* (5.9%), *Trichuris* spp. (11.8 %), *Giardia* spp. (15.8%), *Isospora* sp. (2.9%), *Toxocara canis* (1.5%) and *Toxascaris leonina* (2.9 %) were identified in faecal samples (the percentage of positive dogs shown in brackets). Antibodies against *Babesia canis* were detected in 9.6 % of the blood samples. Antigens from adult female *Dirofilaria immitis* worms were detected in 8.2 % of the examined dogs.

The parasites detected only occur at a very low to low prevalence (*Babesia*, *Uncinaria* , *Trichuris*, *Toxascaris*, *Toxocara*, *Isospora*) or not at all (*Dirofilaria immitis*) in native Norwegian dogs. We conclude that the import of stray dogs represents a real risk of spreading pathogens across borders. This risk should not be neglected; several of the parasites in question, once introduced, may become endemic and pose a threat to both animal and human health. Education of dog owners about the risks involved with import and about risk reducing measures is essential.



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Session Details:	8/26/2013 VACCINES - GENERAL 1 1545 - 1700 Meeting Room 6
Oral Presentation Details:	Is antigenicity of bovine lungworm vaccine candidates predictable by <i>in vitro</i> immune cell assays?
Presentation Time:	1545 -1600
Authors:	Joekel D¹, Bäumer W², Werling D³, Schnieder T¹, Strube C¹ ¹ Institute For Parasitology, University Of Veterinary Medicine Hannover, ² College of Veterinary Medicine, North Carolina State University, ³ Department of Pathology and Infectious Diseases, The Royal Veterinary College

The bovine lungworm *Dictyocaulus viviparus* is one of the most important parasites in grazing cattle leading to considerable economic losses. Although an attenuated live vaccine based on irradiated L3 is available in several European countries, the typical disadvantages of a live vaccine result in limited acceptance of veterinarians and farmers. The development of a recombinant subunit vaccine would overcome the drawbacks of a live vaccine and could prevent dictyocaulosis without the use of anthelmintics.

In the context of recombinant vaccine development, the antigenic potential of the recombinant lungworm proteins paramyosin (Pmy), cathepsin-L (Cat-L), cathepsin-B3 (Cat-B3) and legumain-1 (Leg-1) was evaluated in terms of unspecific stimulation of a multiple lymphocyte population (peripheral blood mononuclear cells, PBMC). Preliminary experiments indicate that the antigens induce a slight increase of PBMC proliferation in naïve animals compared to an unstimulated control. Marked increases of proliferation were detected only when cells were harvested from cattle currently faced with the antigen.

Besides PBMCs, in vitro generated naïve dendritic cells (DC) were stimulated with the recombinant vaccine candidates and expression of cell surface receptors essential for antigen presentation (MHC II and CD86) was measured via FACS analysis. Furthermore, the ability of stimulated DCs to induce a specific T-cell (TC) proliferation was examined. However, the vaccine candidates do not induce specific TC proliferation compared to an unstimulated control. Further experiments with DCs generated from cells harvested from cattle currently facing the respective bovine lungworm antigens are planned. Overall, preliminary results indicate that immune cell assays might not be suitable as a tool for evaluation of bovine lungworm vaccine candidates.

Acknowledgements:

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Session Details:	8/26/2013 VACCINES - GENERAL 1 1545 - 1700 Meeting Room 6
Oral Presentation Details:	A proposed <i>in silico</i> vaccine discovery pipeline for <i>Neospora caninum</i>
Presentation Time:	1600 -1615
Authors:	Goodswen S , Kennedy P, Ellis J University Of Technology Sydney

Neospora caninum is a protozoan parasite of the phylum Apicomplexa that can cause the clinical disease neosporosis, which most notably is associated with abortion in cattle. The worldwide economic loss to cattle industries due to these abortions is estimated to exceed US\$1 billion annually [1]. From economic analyses [2], a vaccine is the most cost-effective approach to control neosporosis. The increasing volume of *N. caninum* –omics data is now providing an opportunity for an *in silico* approach to the discovery of a protein-based vaccine. Effectively the wet laboratory in the traditional culture-based approach to cultivate, dissect, and identify antigens is replaced by a computer. As yet there are no *in silico* derived subunit vaccines against eukaryotic pathogens. We have conducted a feasibility study of a proposed high-throughput *in silico* vaccine discovery pipeline. The pipeline is based on the principle of reverse vaccinology and is constructed from freely available high-throughput prediction programs. These programs are used to gather computational evidence that allows a researcher to make an informed decision as to which proteins, among potentially thousands constituting the *N. caninum* parasite, are promising vaccine candidates worthy of laboratory validation. We present an overview of the pipeline and discuss the challenges and pitfalls. The primary challenge is that the evidence is mainly in different independent formats, contradicting, and inaccurate. This considerable uncertainty in the reliability of the evidence arises because it is well acknowledged that an unknown percentage of the ingredients to the pipeline (e.g. protein sequences, database annotations, and predicted evidence itself) are incorrect. We illustrate, using proteins experimentally shown to be potential vaccine candidates, how supervised machine learning algorithms can detect hidden patterns within contradicting and inaccurate evidence that can effectively distinguish true from false vaccine candidates with a sensitivity and specificity of 74% and 83% respectively.

Acknowledgements:

SJG gratefully acknowledges receipt of a PhD scholarship from Pfizer Animal Health

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Session Details:	8/26/2013 VACCINES - GENERAL 1 1545 - 1700 <i>Meeting Room 6</i>
Oral Presentation Details:	Investigations into cestode development and antigens that form the basis of recombinant vaccines in animal hosts
Presentation Time:	1615 -1630
Authors:	Charles Gauci* , Abdul Jabbar, Marshall Lightowlers University of Melbourne, Australia

Highly effective recombinant vaccines have been developed against taeniid cestode parasites. The defined antigens are derived from the larval oncosphere stage, providing protective immunity to the establishment of infection in animal intermediate hosts. Vaccine-induced protective immunity in the host appears to be associated with antibody dependent complement mediated lysis of the developing parasite.

Studies have been undertaken that have investigated expression of the vaccine antigens in different developmental stages of the parasites. These investigations utilized reverse transcription-PCR on samples from *in vitro* cultured parasites and identified the activated oncosphere as the stage of development in which the antigens are maximally produced. More recently, the precise locations of the host protective antigens have been investigated in *in vitro* cultured oncospheres. The antigens were localized within secretory structures and in the cytoplasm of distinct cells in oncospheres. Although the antigen localization studies demonstrated that the antigens are secreted by newly activated oncospheres within membrane-enclosed cytoplasmic blebs, there was no evidence to indicate that any of the protective antigens is present on the surface of the invading oncosphere. This interesting outcome indicates that invading oncospheres do not appear to be susceptible to vaccine-induced antibody and complement-mediated attack. Such studies provide novel insights into parasite development and vaccine-induced immunity.



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Session Details:	8/26/2013 VACCINES - GENERAL 1 1545 - 1700 Meeting Room 6
Oral Presentation Details:	Vaccination of pigs and lambs against <i>Toxoplasma gondii</i> reduces tissue cyst formation; safer meat for human consumption
Presentation Time:	1630 -1645
Authors:	Alison Burrells^{1*}, Germán Cantón^{1,2}, Julio Benavides^{1,3}, Jackie Thomson¹, Paul Bartley¹, Yvonne Pang¹, Callum Harvey^{1,4}, Francesca Chianini¹, Elisabeth Innes¹, Frank Katzer¹ ¹Moredun Research Institute, Edinburgh, Scotland, UNITED KINGDOM ²Instituto Nacional de Tecnología, Agropecuaria (INTA), Balcarce, ARGENTINA ³Instituto de Ganadería de Montana (CSIC-ULE), León, SPAIN ⁴Glasgow University, Faculty of Veterinary Medicine, Glasgow, Scotland, UNITED KINGDOM

The protozoan parasite *Toxoplasma gondii* (*T. gondii*) is a zoonotic pathogen that has the ability to infect all warm blooded animals including humans (Tenter *et al* 2000). Toxoplasmosis is a major opportunistic disease of immunocompromised patients. It also represents a serious threat during pregnancy, causing severe foetal abnormalities or potentially leads to problems in childhood or later adult life (Koppe *et al* 1986). Undercooked or raw meat containing infective tissue cysts are a significant source of human infection (Cook *et al* 2000). The production of *T. gondii* tissue cyst free meat could reduce the risk of human exposure to *T. gondii*.

In two different animal studies a group of 23 pigs and 32 lambs were used to determine the efficacy of a commercially available vaccine that protects sheep from abortions caused by *T. gondii*, with an aim to reduce tissue cyst formation. Following vaccination, animals were challenged with oocysts. Subsequently a mouse bioassay, using a variety of porcine tissues, resulted in a 100% survival of mice that received tissues from vaccinated/challenged pigs. While bioassays of tissues from non-vaccinated pigs resulted in a survival rate of 51%. Parasite DNA was also identified in the homogenate used in bioassays from the non-vaccinated/ challenged group but not in the vaccinated/challenged pigs. In a similar experiment, *T. gondii* DNA was tested for in the tissues of lambs. Following vaccination and challenge with 100,000 oocysts of the Moredun M4 strain, the parasite was detected at significantly lower levels in heart and skeletal muscle samples from the vaccinated/challenged group (0% and 5.9% respectively), when compared to the non-vaccinated/challenged animals (75% heart, 87.9% skeletal muscle).

The results demonstrate that vaccination of pigs and lambs with the S48 attenuated *T. gondii* strain can reduce the formation of tissue cysts, resulting in potentially safer meat for human consumption.

Acknowledgements:

The Scottish Government, Rural and Environmental Sciences and Analytical Services (RESAS), European Union Seventh Framework Network of Animal Disease Infectiology Research Facilities (NADIR; reference number FP7-228394)



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Session Details:	8/26/2013 VACCINES - GENERAL 1 1545 - 1700 Meeting Room 6
Oral Presentation Details:	Neutrophil extracellular traps as innate immune reaction against the emerging apicomplexan parasite <i>Besnoitia besnoiti</i>
Presentation Time:	1645 -1700
Authors:	Hermosilla C¹, Munoz Caro T¹, Silva L², Cortes H¹, Taubert A¹ ¹ Institute of Parasitology, Justus Liebig University Giessen, Germany, ² Institute of Parasitology, University of Evora, Portugal

Besnoitia besnoiti infection in cattle is an important emerging protozoan disease in Europe, causing economic losses and severe clinical signs, such as generalized dermatitis, orchitis and vulvitis in affected animals. Neutrophil extracellular trap (NET) formation was recently demonstrated as an important effector mechanism of PMN acting against several invading pathogens. In the present study, interactions of bovine PMN with tachyzoites of *B. besnoiti* were investigated in this respect *in vitro*. For the demonstration and quantification of NETs, extracellular DNA was stained by Sytox Orange or Pico Green. Fluorescent illustrations as well as scanning microscopy analyses (SEM) showed PMN-promoted NET formation rapidly being induced upon contact with *B. besnoiti* tachyzoites. Simultaneous staining of extracellular DNA and histones confirmed the NET nature of parasite entrapment structures. Exposure of PMN to viable and dead tachyzoites both induced strong NET formation, but even UV-attenuated tachyzoites as well as tachyzoite homogenates and soluble factors (*in vitro* supernatants) significantly promoted NETs when compared to negative controls. NETs were abolished by DNase treatment and were reduced by diphenylene iodonium, a potent NADPH oxidase inhibitor. Tachyzoite-triggered NET formation led to parasite entrapment as quantitative assays indicated that 28% of tachyzoites were immobilized in NETs. In consequence, tachyzoites were hampered from active invasion of host cells. Thus, transfer of tachyzoites, previously being confronted with PMN, to adequate host cells resulted in significantly reduced infection rates (40% reduction) when compared to PMN-free controls.

To our knowledge, we here report for the first time *B. besnoiti*-induced NET formation. Our results indicate that PMN-triggered Etosis may represent an important effector mechanism of the host early innate immune response against *B. besnoiti* which may lead to diminishment of initial parasite infection rates.



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Session Details:	8/26/2013 VECTOR BORNE DISEASES - PIROPLASMS 1545 - 1700 Meeting Room 7
Oral Presentation Details:	Investigating the possible presence of <i>Theileria parva</i> carrier cattle in Mnisi area
Presentation Time:	1545 -1600
Authors:	Choopa C¹, Collins N², Geysen D³, Knobel D⁴, Oosthuizen M⁵ ¹ Department Of Veterinary Tropical Diseases,Faculty Of Veterinary Science, University Of Pretoria, ² Department Of Veterinary Tropical Diseases,Faculty Of Veterinary Science, University Of Pretoria, ³ Institue of Tropical Medicine, Antwerp, Belgium, ⁴ Department Of Veterinary Tropical Diseases,Faculty Of Veterinary Science, University Of Pretoria, ⁵ Department Of Veterinary Tropical Diseases,Faculty Of Veterinary Science, University Of Pretoria

Corridor disease (buffalo-derived *Theileria parva*) caused by *Theileria parva lawrencei* is the most important *Theileria* sp. posing a threat to the cattle farming industry in South Africa. The African buffalo (*Syncerus caffer*) is the reservoir host for this protozoan parasite which is transmitted by the three host ticks *Rhipicephalus appendiculatus* and *Rhipicephalus zambeziensis*. Although it is considered self-limiting because most cattle die before the parasites develop to the tick-infective stage, recent experimental studies have shown that a carrier state can be produced in infected cattle that survive the disease. A study to identify *T. parva* carrier cattle in Mnisi area was conducted. Records from Hluvukani Animal Health Centre and Bushbuckridge State Veterinary office were scrutinized and plain blood samples were collected from herds that recorded Corridor disease cases in the past three years. Additionally, herds that grazed in areas where buffaloes grazed when they broke from the Kruger National Park or private game reserves in the past three years were sampled. The indirect fluorescent antibody test was used to check for *T. parva* antibodies. DNA was extracted from EDTA blood samples collected from sero-positive herds and screened for the presence of piroplasm parasite DNA using a *T. parva*-specific quantitative real-time PCR (qPCR). The full-length parasite 18S rRNA gene of selected positive samples will be amplified, cloned and sequenced. The sequences will be compared with those found in clinical Corridor disease cases in Mnisi area as well as with isolates from buffalo.

Acknowledgements:

I would like to thank the Department of Veterinary Tropical Diseases and Institute for Tropical Medicine (DVTD-ITM Collaborative initiative) for financing the project. Gratitude also goes to my supervisors for the much needed guidance they provided for the work to get to this stage.



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Session Details:	8/26/2013 VECTOR BORNE DISEASES - PIROPLASMS 1545 - 1700 Meeting Room 7
Oral Presentation Details:	Epidemiological survey of <i>Theileria orientalis</i> in cattle following theileriosis outbreaks in Victoria
Presentation Time:	1600 -1615
Authors:	Perera P ¹ , Gasser R ¹ , Bell C ² , Koehler A ¹ , Jabbar A ¹ ¹ Faculty of Veterinary Science, The University of Melbourne, Parkville, Victoria, AUSTRALIA, ² Animal Biosecurity & Welfare Branch, Department of Primary Industries, Bendigo, Victoria, AUSTRALIA

This study investigated *Theileria orientalis* following outbreaks of oriental theileriosis in cattle in the state of Victoria, Australia, from Sept. 2010 to Jan. 2012, using traditional and molecular methods of diagnosis. Blood samples (n = 301) were collected from symptomatic and asymptomatic cattle from 19 cattle farms. Individual blood samples were examined for the presence of *Theileria* on stained smears and tested using a PCR-based approach, employing the major piroplasm surface protein gene (*mpsp*) as a marker. The microscopic examination of stained smears detected stages consistent with theilerial piroplasms in 28.1% (79/281) of the blood samples. PCR products were amplified from 70.8% (213/301) of the samples. Mutation scanning analysis of all amplicons displayed seven distinct profiles. Following direct sequencing of representative amplicons, genotypes *ikedai*, *chitose*, *buffeli* and *type 5* were detected in 91.1%, 32.9%, 2.35% and 1.4% of 213 blood samples, respectively. The distribution of these four genotypes varied among the 19 farms; genotype *ikedai* was detected on all farms, whereas genotypes *chitose*, *buffeli* and *type 5* were detected on 14, 3 and 2 farms, respectively. Mixed infections with genotypes *ikedai* and *chitose* (21.6%) were common. Future investigations will focus on developing improved tools for investigating and managing oriental theileriosis.



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Session Details:	8/26/2013 VECTOR BORNE DISEASES – PIROPLASMS 1545 - 1700 Meeting Room 7
Oral Presentation Details:	Genetic diversity and host specificity of Theileria equi and Babesia caballi in rural areas of eastern Romania
Presentation Time:	1615 - 1630
Authors:	Martina Gallusová^{1*}, Moneeb A. Qablan¹, Andrei Mihalca³, Gianluca D´Amico³, David Modrý^{1,2} ¹Department of Pathological Morphology and Parasitology, University of Veterinary and Pharmaceutical Sciences Brno, CZECH REPUBLIC ²Institute of Parasitology, Biology Centre, and Faculty of Sciences, University of South Bohemia, České Budějovice (Budweis), CZECH REPUBLIC ³Department of Parasitology and Parasitic Diseases, University of Agricultural Sciences and Veterinary Medicine, Cluj-Napoca, ROMANIA

Piroplasmids are tick-transmitted intracellular protozoan parasites responsible for causing diseases of livestock with an economic impact, mainly in tropics and subtropics. *Theileria equi* and *Babesia caballi* are species responsible for equine piroplasmosis. Recent Romanian research had focused on piroplasmids in domestic animals and stray dogs, however, no data is available regarding prevalence in semi-feral and feral horse population. Study indicates a cross-transmission of equine piroplasms to canids which is confirmed by studies from Jordan, Spain, France and Croatia. This study aimed to (i) investigate the infraspecific diversity of *T. equi* and *B. caballi* and (ii) provide an insight into host specificity of equine piroplasms and to trace their possible exchange between horses and dogs in shared habitats. Research covered 17 localities inside and outside Danube delta. A total 176 horses, 15 donkeys and 190 rural dogs from the same localities were sampled. Screening followed for the presence of *T. equi*, *B. caballi*, along with canine piroplasmids using PCR methods targeting part of 18S rRNA gene. Apparently, the infections with *T. equi* and *B. caballi* are enzootic in all localities included in the present study. PCR results showed 68 horses positive for *T. equi* (38,6 %), 7 horses for *B. caballi* (4 %) and 5 donkeys for *T. equi* (33,3 %) and this was confirmed by bidirectional sequencing of the PCR amplicons. 5 horses were mix infected, which makes 2,8 % of prevalence. Phylogenetic analysis revealed the occurrence of four *T. equi* (A, B, C, E) and one *B. caballi* genotype (A). Concerning dogs, one came out positive for *Babesia canis*, and, interestingly, one infected with *Theileria equi* (genotype C). In areas, where equines share habitats (and ticks) with stray or domestic dogs, they apparently share also piroplasmid pathogens, though the epidemiological consequences of this fact are not clear.

Acknowledgements:

The present study was supported by the Grant Agency of the Czech Republic (523/09/1972) and also funded by “CEITEC – Central European Institute of Technology” (CZ.1.05/1.1.00/02.0068) from European Regional Development Fund.



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Session Details:	8/26/2013 VECTOR BORNE DISEASES - PIROPLASMS 1545 - 1700 Meeting Room 7
Oral Presentation Details:	Babesia lengau possibly incriminated in causing feline babesiosis in South Africa
Presentation Time:	1630 -1645
Authors:	Bosman A ¹ , Ooshhuizen M ¹ , Venter E ¹ , Steyl J ² , Gous T ³ , Penzhorn B ¹ Department Of Veterinary Tropical Diseases, ² Department Of Paraclinical Sciences, ³ Specialist Veterinary Pathologist

Although reported sporadically from various countries, feline babesiosis appears to be a significant clinical entity only in South Africa, where *Babesia felis* is usually incriminated as the causative agent. It is mainly confined to the eastern and southern seaboard (KwaZulu-Natal, Eastern and Western Cape provinces) with foci of infection along the eastern escarpment of Mpumalanga Province. Other inland cases are usually in cats taken along on vacation to the coast. *Babesia lengau*, recently described from asymptomatic cheetahs, has now possibly been incriminated as the causative agent in two severe clinical cases in domestic cats, one of which resided far inland. Both cats were euthanised in extremis. While typical feline babesiosis in South Africa is an afebrile disease with a chronic manifestation, there was acute onset of severe clinical signs in both cats and their body temperatures were above the normal range when they were presented for treatment. Haemolytic anaemia was confirmed in one case. To our knowledge, this is the first report of cerebral babesiosis in cats. On reverse line blot DNA extracted from both cats showed positive hybridisation profiles with the *B. lengau* species-specific probe. The two sequences obtained were virtually identical and showed a high similarity (99,9 %) with *B. lengau*. In a representative tree constructed by the neighbor-joining method using the two-parameter model of Kimura the two specimens and *B. lengau* formed a monophyletic group with *B. conradae* and sequences previously isolated from humans and wildlife in the western USA. *Babesia lengau* could possibly account for the rare clinical cases in resident inland cats not visiting *B. felis*-endemic areas.

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Session Details:	8/26/2013 VECTOR BORNE DISEASES - PIROPLASMS 1545 - 1700 Meeting Room 7
Oral Presentation Details:	Detection of vector-borne pathogens by molecular methods in ticks and fleas infesting dogs in Albania
Presentation Time:	1645 -1700
Authors:	Silaghi C¹, Knaus M², Hamel D², Rapti D³, Pfister K¹, Rehbein S² ¹ LMU Munich, ² Merial, Rohrdorf, ³ Agricultural University Tirana

This study aimed to add knowledge to the occurrence of vector-borne pathogens in this Mediterranean country. Ticks and fleas were collected from 68 dogs in Tirana, Albania during 2009/10. DNA was extracted, and screening with PCR or real-time PCR was carried out for *Rickettsia* spp. and filariids (ticks and fleas); *Bartonella* spp. and *Mycoplasma* spp. (fleas only); *Anaplasma platys*, *Ehrlichia canis*, *Hepatozoon canis* and *Babesia* spp. (ticks only).

Total 1,503 fleas (1,470 *Ctenocephalides canis*, 31 *C. felis*, 2 *Pulex irritans*) and 358 *Rhipicephalus sanguineus* ticks were collected. *Ctenocephalides canis*, *C. felis* and *P. irritans* were recovered from 94.1%, 26.5% and 2.9% of the dogs. *Rickettsia felis* was detected in 3.2% of the *C. felis* fleas while all *C. canis* were negative for *Rickettsia* spp. *Mycoplasma*-DNA was detected in nine *C. canis* flea pools (7x *M. haemocanis*, 2x Candidatus *M. turicensis*); and in four *C. canis* flea pools, DNA of the filariid *Acantocheilonema reconditum* was found. No fleas were positive for *Bartonella* spp.

Rhipicephalus sanguineus ticks were collected from 25% of the dogs, predominantly during summer. Nine ticks were positive for *R. conorii* or *Rickettsia* spp.; *A. platys* was recorded in 6 nymphs and 79 ticks tested positive for *E. canis*. The screening of the ticks for the presence of DNA of *H. canis*, *Babesia* spp. and filariids is in progress.

The results of this study demonstrated a high diversity of vector-borne pathogens in both fleas and ticks parasitizing dogs in Albania. Their impact on public and veterinary health should be the focus of future studies in the Balkans. In addition, *C. canis* was found to be predominating on dogs in Albania, which is in contrast to Central Europe where *C. felis* is the dominating species of flea on dogs.

Acknowledgements:

Enstela Shukullari for assistance in the flea and tick collection, Martin Visser for flea identification, Tim Tiedemann and Claudia Thiel for technical assistance.



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Session Details:	8/26/2013 APICOMPLEXAN BIOLOGY 1 1545 - 1700 Meeting Room 8
Oral Presentation Details:	Role of T Regulatory and Th17 Cell during Lethal <i>Plasmodium berghei</i> ANKA and Non-Lethal <i>Plasmodium yoelii</i> infection
Presentation Time:	1545 -1600
Authors:	Keswani T University Of Calcutta

The outcome of malaria infection is determined, in part, by the balance of pro-inflammatory and regulatory immune responses. Failure to develop an effective balance of pro-inflammatory and regulatory immune responses can lead to unrestricted parasite replication and severe immunopathology Host immune responses in disease including malaria are finely regulated by the opposing effects of Th17 and T regulatory (Treg) cells. Here we have examined the role of Treg cells and Th17 cells during malaria infection and find that low levels of Treg cells influence the outcome of *Plasmodium berghei* ANKA (*PbA*). In contrast, we observed that possibly high level of Treg cells influencing the outcome of non lethal *Plasmodium yoelii* (*P. yoelii*) infections. We observed decreased expressions of TGF-β, CD4IL-2 and IL-10 during *PbA* infection, whereas expression remains high during *P. yoelii* infection. On the other hand TNF-α, IL-6, IFN-γ and IL-23 expression is high during *PbA* infection and lower during *P. yoelii* infection. In combination with functional studies, we posit that Treg may convert to Th17 during *PbA* infection whereas; Th17 initially high during *P. yoelii* infection possibly converts to Treg cells. Thus, results from this study suggest that the critical balance between Treg and Th17 might have a key role on host pathogenesis during malaria infection.



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Session Details:	8/26/2013 APICOMPLEXAN BIOLOGY 1 1545 - 1700 <i>Meeting Room 8</i>
Oral Presentation Details:	<i>Plasmodium falciparum</i> gametocytes: hiding out and growing up
Presentation Time:	1600 -1615
Authors:	Katharine R Trenholme* and Donald L Gardiner Queensland Institute of Medical Research, Brisbane, AUSTRALIA

Gametocytes are the only stage of the malaria parasite life cycle able to mediate transmission from the human host to the mosquito vector. The development of asexual blood stage parasites into gametocytes represents a transition period during which the parasite differentiates morphologically and biochemically from a life of asexual reproduction within the human host to one of sexual development within the mosquito vector. In the case of *Plasmodium falciparum*, gametocytes require 10 -12 days to complete this transition and reach maturity. During their development, immature gametocytes are known to sequester in host tissue yet to date no gametocyte ligand for this interaction has been identified raising the question of where and how they sequester. It has been postulated that they utilise areas of reduced circulatory flow such as the extracellular spaces of the bone marrow which may provide protection from the host immune system despite the lack of the cytoadherence complex. Our data indicate that gametocytogenesis is enhanced in the presence of erythroid progenitors found within the bone marrow. Furthermore our atomic force microscopy studies indicate that developing gametocytes undergo remarkable shifts in their erythrocyte membrane elasticity which may allow them to be retained safely within the bone marrow until maturation. At this point they return to the peripheral circulation where they remain for extended periods and only undergo further development when taken up by the mosquito vector.

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Session Details:	8/26/2013 APICOMPLEXAN BIOLOGY 1 1545 - 1700 Meeting Room 8
Oral Presentation Details:	Plasmodium Falciparum And Plasmodium Vivax Gametocyte Clearance In Melanesian Children Determined By Magnetic Fractionation Illustrates Species Specific Differences In Malaria Transmission
Presentation Time:	1615 -1630
Authors:	St. Pierre T ¹ , Karl S ¹ , Koleala T ² , Laman M ² , Moore B ¹ , Woodward R ¹ , Betuela I ² , Siba P ² , Mueller I ³ , Manning L ¹ , Davis T ¹ ¹ The University Of Western Australia, ² Papua New Guinea Institute of Medical Research, ³ Walter and Eliza Hall Institute of Medical Research

Gametocytes are the blood stages of malaria parasites which transmit the disease to the mosquito vector. They naturally contain high quantities of hemozoin. Gametocytes in both, *P. falciparum* and *P. vivax* species occur at very low frequencies, making it difficult to investigate their production and clearance kinetics. We have previously described a method of high field gradient magnetic fractionation to simultaneously and quantitatively detect *P.falciparum* and *P. vivax* gametocytes in peripheral blood with very high sensitivity.

In the present study we investigated *Plasmodium falciparum* and *Plasmodium vivax* gametocyte clearance in a cohort of Melanesian children when treated with either one of two Artemisinin Combination Therapies for treatment of malaria infection.

We show that *P. falciparum* and *P. vivax* gametocytes are cleared at very different rates, presumably due to different adaptation of these parasite species to survive prolonged periods of low transmission. Whereas *P. falciparum* relies on long-living, metabolically inactive gametocytes resistant to drug action, *P. vivax* produces dormant liver stages – hypnozoites and thus its gametocyte forms are short lived and rapidly cleared.

In the present study, magnetic fractionation identified 82% of children with *P. falciparum* malaria and all children infected with *P. vivax* as gametocyte carriers. *P. falciparum* gametocytes were present in 51% of children two weeks after treatment. while all children with *P. vivax* were gametocyte free at 48h after treatment. In contrast, six weeks after treatment about 40% of children had *P. vivax* gametocytes, whereas only 7% has *P. falciparum* gametocytes suggesting frequent relapse of *P. vivax* from dormant liver stages.

Magnetic fractionation is a convenient and sensitive method for simultaneous detection of *P. falciparum* and *P. vivax* gametocytes in peripheral blood. In addition, the present study illustrates the different strategies these two malaria parasite species have adapted to overcome periods of low or absent transmission.

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Oral Presentation Details:	Iron deposits in spleens and livers of malaria and schistosoma infected mice
Presentation Time:	1630 -1645
Authors:	St. Pierre T ¹ , Karl S ¹ , Gutierrez L ¹ , Wong R ¹ , Toh S ² , Lucyk-Maurer R ³ , Candido R ³ , Boyd A ¹ , Woodward R ¹ , Graeff-Teixera C ³ , Jones M ² , Davis T ¹ ¹ The University Of Western Australia, ² Queensland Institute of Medical Research and University of Queensland, ³ Pontificia Universidade Católica do Rio Grande do Sul

Malaria and schistosomiasis are two common and debilitating human parasitic diseases. Current WHO estimates of global infections range from 200-500 million new malaria cases each year and approximately 200 million chronic schistosomal infections.

When within the human host, both parasites catabolize hemoglobin. To counteract the accumulation of toxic free heme, both parasites have evolved a specific pathway converting free heme to polymeric hemozoin material. It is known that hemozoin accumulates in host tissues during malaria infection and it is likely that the same happens during infections with Schistosomes. Available evidence indicates that hemozoin can persist for many years post-infection. We hypothesise that its accumulation over a lifetime represents a potentially quantifiable integrated record of an individual’s history of malaria and/or schistosomal infection.

In addition to hemozoin, iron-containing ferritin granules are also deposited in tissues during malaria infection. It is not known whether the same occurs in schistosomiasis.

In the present study we investigated livers and spleens of mice infected with *Plasmodium berghei* ANKA and *Schistosoma mansoni*, by transmission electron microscopic elemental mapping, nuclear magnetic resonance and superconducting interference device magnetometry. We show that hemozoin and ferritin colocalize in the spleens and livers of malaria and schistosoma infected mice resulting in unique magnetic signals which are clearly distinct from uninfected controls. This study illustrates that it may be possible to differentiate past episodes of malaria and schistosomiasis via measurement of potentially non-invasive, disease-specific magnetic signals.



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Session Details:	8/26/2013 APICOMPLEXAN BIOLOGY 1 1545 - 1700 Meeting Room 8
Oral Presentation Details:	It's easy being green: carbon utilization in a photosynthetic sister of the apicomplexan parasites
Presentation Time:	1645 -1700
Authors:	Foster C ¹ , Portman N ¹ , Chen M ² , Slapeta J ¹ ¹ Faculty of Veterinary Science, The University Of Sydney, NSW, Australia, ² School of Biological Sciences, Faculty of Science, The University Of Sydney, NSW, Australia

Chromera velia is a photosynthetic, coral-associated microalga that is phylogenetically placed as a sister organism to the apicomplexan parasites, which include the causative agents of malaria and toxoplasmosis. As *C. velia* shares many molecular and morphological features in common with the Apicomplexa, it has the potential to serve as a model organism for the study of the evolution and physiology of these parasites. To facilitate such studies, it is important to optimise the laboratory cultivation of *C. velia* to best support its growth and investigate aspects of its physiology and metabolism. The nutritional modes of *C. velia*'s relatives within the alveolate protist lineage are very diverse, including phototrophy, predatory or parasitic heterotrophy, and a combination of these systems termed 'mixotrophy'. Phylogenetic analyses of character state distributions suggest that the common alveolate ancestor was mixotrophic, with multiple losses of photosynthesis occurring amongst its descendents. The present study investigates the utilization by *C. velia* of a range of exogenously supplied organic carbon sources, including sugars, sugar-alcohols, amino acids and organic acids. Here we present the analysis of *C. velia* culture growth and photosynthetic pigment production under these mixotrophic conditions. Further, we discuss the implications of these findings in terms of *C. velia* cultivation, ecology, and the study of carotenoid and essential tetrapyrrole (haem, chlorophyll) biosynthesis in this organism.



Session Details:	8/27/2013 GENETIC IMMUNITY 1015 - 1130 <i>Riverside Theatre</i>
Oral Presentation Details:	Gastro-Intestinal parasite species change in response to selection in the Rylington Merino Flock
Presentation Time:	1015 -1030
Authors:	John Karlsson^{1*} , Shimin Liu ² , Dieter Palmer ¹ & Johan Greeff ¹ ¹ Department of Agriculture & Food, Western Australia ² CSIRO, Perth.

The long-term selection line for resistance to the common G-I Nematodes 'Rylington Merino' was established in 1987 (Karlsson *et al.* 1995). In the environment where this flock has been kept in the south west of WA the two main G-I genera are *Trichostrongylus* and *Teladorsagia*, in the early stages on larval culture and differentiation typically in the proportion of 70% and 20% respectively. Now some 25 years later *Teladorsagia* dominates typically representing over 90% of the total population.

Since the establishment and up to 2012 anthelmintic treatments have included the Macrocyclic Lactone group. This would offer a selective advantage to *Teladorsagia* as it is the dose limiting species for this anthelmintic group.

In 2003 & 2004 hogget and weaner age sheep from the unselected control and the parasite resistant lines of the Rylington Merino Flock were used in a collaborative pen trial with CSIRO Floreat Park WA. Briefly, worm free sheep were artificially infected weekly with 10,000 larvae each of *Tri. colubriformis* & *Tel. circumcincta* for 12 and 18 weeks in two trials, respectively Liu *et al.*, (2005):

Based on weekly worm egg counts hogget age animals of the resistant line excreted only 18% of the eggs compared to the control line. In the selected line about half of the animals had zero egg counts throughout this monitoring. At necropsy resistant animals had 93% fewer adult *Tri. colubriformis*, 44% fewer adult *Tel. circumcincta* with a 40% reduction of fertility indicators (worm length and number of eggs *in utero*). In the resistant sheep there was an 11% increase in the proportion of early 4th stage *Tel. circumcincta* larvae.

Our results suggest that worm resistant sheep can regulate *Tri. colubriformis* by rejecting adult worms but *Tel. circumcincta* is regulated by a combination of suppressed development and reduced female fecundity.

The increase in relative proportion of *Tel. circumcincta* in this flock is probably due to the combined effect of anthelmintic selection advantage and a genetically determined differential capacity of the host immune response.

Acknowledgements:

The Australian Merino Sheep Industry support for Rylington Merino.



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Session Details:	8/27/2013 GENETIC IMMUNITY 1015 - 1130 <i>Riverside Theatre</i>
Oral Presentation Details:	Variation and High Linkage Disequilibrium among OVAR-DRB1, DQA1 and DQB1 loci in Scottish Blackface
Presentation Time:	1030 -1045
Authors:	Md Isa N^{1,2}, Stear M¹ ¹ University Of Glasgow, ² Universiti Putra Malaysia

Genes within the Major Histocompatibility Complex (MHC) are strong candidates for disease resistance. In sheep, the Ovar-DQ and Ovar-DR loci, in the Class IIa sub-region, show extensive polymorphism and have been associated with resistance to nematode infection. The current study determined gene frequencies at the antigen-presenting Class IIa genes and estimated linkage disequilibrium among the alleles by direct sequencing in Scottish Blackface sheep. This information is needed to plan powerful disease studies.

All sheep were from a commercial upland farm in Southwest Strathclyde, central Scotland. All lambs were kept on the same field after weaning at three or four months of age until the grazing season. There were 5 consecutive cohorts of 200 lambs and DNA was extracted from the buffy coat. Six locus-specific PCR primers were used to amplify the second exon of ovine DRB1, DQA1 and DQB1 loci. PCR products were directly sequenced from genomic DNA. Sequence alignment, translations and comparisons were carried out using CLC Genomic Workbench version 6.1 (CLC bio, Denmark). The ALLELE and HAPLOTYPE procedures on the SAS suite of statistical programs version 9.3 (SAS Institute, Carolina) were used to estimate allele frequencies and to determine linkage disequilibrium.

DRB1 is the most polymorphic locus followed by DQB1 and DQA1. Moreover, several new DR and DQ sequences were identified in this population. Linkage disequilibrium (LD) was very strong among DRB1, DQA1 and DQB1 loci.

To sum up, there is diversity of alleles and high linkage disequilibrium at MHC Class II DRB1, DQB1 and DQA1 in Scottish Blackface population. We now plan to estimate the association of individual loci with resistance to nematode infection and fine-map the causative mutations.

Acknowledgements:

We thank McComb for technical assistance. This research was supported by BBSRC, Universiti Putra Malaysia and Higher Education Malaysia.

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Session Details:	8/27/2013 GENETIC IMMUNITY 1015 - 1130 Riverside Theatre
Oral Presentation Details:	Functional investigation of a QTL region affecting resistance to <i>Haemonchus contortus</i> in sheep
Presentation Time:	1045 -1100
Authors:	Jacquet P ¹ , Salle G ^{1,2,3} , Moreno C ³ , Ruesche J ³ , Lienard E ^{1,2} , Weisbecker J ⁴ , Bouvier F ⁵ , Prevot F ^{1, 2} , Trumel C ² , Grisez C ^{1,2} , Francois D ³ , Legarra A ³ ¹ Veterinary School, ² University of Toulouse, ³ INRA UR 631, SAGA, Castanet-Tolosan, ⁴ INRA, UE Domaine de Langlade, Pompertuzat, ⁵ INRA UE Domaine de la Sapinière, Osmoy

Gastro-intestinal nematodes such as *Haemonchus contortus* are of major concern to sheep health worldwide. Selectively breeding sheep for increased resistance could help sustain production targets in the face of increasing anthelmintic resistance. This study reports a functional characterization of a chromosome segment associated with resistance to *H.contortus* infection.

Following analysis of a dense SNP map and a thousand fecal egg count (FEC) records from *H.contortus* challenged back-cross (BC) lambs (Sallé et al., 2012)a genome scan was carried out using 1,275 Romane × Martinik Black Belly backcross lambs. The entire population was challenged with *Haemonchus contortus* in 2 consecutive experimental infections, and fecal egg counts (FEC, a segment of chromosome 12 explained 4% of the observed variation in resistance of both immune-naïve and primed BC lambs. Based on the linkage analysis results, BC sheep were selected for a 20-Mbp-wide QTL region, and mated together to produce BCxBC progenies carrying two favorable or unfavorable QTL alleles. Subsequent to this marker-assisted mating, an association analysis pinpointed a 4-SNP haplotype that was used to predict the resistance of 61 BCxBC sheep. Sheep were experimentally infected with 10,000 *H.contortus* larvae. FEC were determined every three days from 18 days post-infection (dpi) and haematological parameters were determined at 0, 14 and 27 dpi. After one month, sheep were sacrificed to determine worm burden and worm fertility and to sample tissues for gene expression analysis.

Significant differences in FEC and packed cell volume drop were found between the 4-SNP based groups of sheep. In addition, the female worms recovered in predicted resistant sheep were less fecund. A gene expression analysis was performed between carriers of two 4-SNP alleles with opposite effects. A 4-fold over-expression was found for IL4 and IL13 genes in the abomasal mucosa of the sheep carrying the favorable QTL allele, indicating a higher Th2-biased cytokinic environment. Still, no functional candidate gene underlying the QTL region has been validated so far.

The dissection of this region should contribute to predict the intrinsic resistance level of sheep.

Acknowledgements:

This project was funded by Apisgene and the ANR (SheepSNPQTL project) and the European Union (3SR project, www.3srbreeding.eu). G. Sallé was granted by the INRA Animal Health and Animal Genetics departments.

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Sallé, G., P. Jacquet, L. Gruner, J. Cortet, C. Sauvé, F. Prévot, C. Grisez, J.P. Bergeaud, L. Schibler, A. Tircazes, et al. 2012. A genome scan for QTL affecting resistance to *Haemonchus contortus* in sheep. *Journal of animal science*. 90:p.4690–4705.



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Session Details:	8/27/2013 GENETIC IMMUNITY 1015 - 1130 <i>Riverside Theatre</i>
Oral Presentation Details:	Comparison of tick resistance of cross-breed Senepol x Limousin with pure-breed Limousin
Presentation Time:	1100 -1115
Authors:	Hüe T¹, Hurlin J¹, Teurlai M², Naves M³ ¹ Institut Agronomique Néo-Calédonien, ² Institut de Recherche pour le Développement, ³ Institut National de Recherche Agronomique

The cattle tick *Rhipicephalus microplus* is responsible for heavy production losses in the cattle industry worldwide. The development of resistance against acaricides requires using other methods to control this parasite, such as the use of genetically resistant cattle. Some cattle breeds are known to be more resistant to tick infestation and among them, Senepol cattle are the most recently developed. The Senepol breed is a cross of N'Dama and Red Poll breeds, and it is considered as '*Bos taurus* adapted to tropical conditions'. Despite its *Bos taurus* genetics, it is believed to have a good tick resistance, but this resistance has never been assessed.

Historically, Limousin cattle have been widely bred in New-Caledonia for their carcass conformation but are highly susceptible to tick infestation. In this French Pacific territory, tropical conditions are favourable to this parasite's development and expansion of acaricide resistant tick strains requires breeders to investigate different resistant cattle breeds.

In this study, we compared the resistance to natural tick infestation by *Rhipicephalus microplus* (Canestrini, 1887) of cross-breed Senepol (Senepol x Limousin) and purebred Limousin cattle. Tick counts on 76 animals, under natural infestation, were carried in three farms, three to four times during the wet season. Mixed-effect models were used to assess the effect of the breed on the number of ticks. Results show that Senepol x Limousin on average carry five time fewer ticks than purebred Limousin. These results underline the opportunity to use Senepol for crossing with *Bos taurus* in tick infested areas to combine tick resistance and carcass conformation.

Session Details:	8/27/2013 GENETIC IMMUNITY 1015 - 1130 <i>Riverside Theatre</i>
Oral Presentation Details:	Breeding for breech strike resistance in Merino sheep
Presentation Time:	1115 - 1130
Authors:	Johan Greeff ¹ , John Karlsson ¹ , Anthony Schlink ¹ ¹ Department of Agriculture & Food, Western Australia, AUSTRALIA

Breec strike is a serious condition in wool sheep, caused mainly by *Lucilia cuprina*. Animals are currently protected by mulesing, crutching and jetting sheep with an effective insecticide at strategic times. These management strategies are expensive but susceptible animals are being protected. However, this also implies that susceptible genes for breec strike are being maintained in the population. If there is a positive relationship between susceptibility to breec strike and wool production, then this may result in an increase in the frequency of breec strike as genetic progress is being made to increase wool production. Reducing the proportion of susceptible animals in sheep flocks should therefore be an important selection strategy to reduce breec strike in commercial flocks.

An experiment was initiated in 2005, funded by Australian Wool Innovations Ltd to determine whether breech strike is a heritable trait and to identify indicator traits for breech strike that could be used by breeders to breed for breech strike resistance without the need to expose animals to the blowfly.

The results (Greeff *et al.* 2009, 2010, 2013) showed that large phenotypic differences exist between sire progeny groups in susceptibility/resistance to breech strike. The most susceptible sire's progeny was 25 times more likely to be struck than the most resistant sire's progeny. These large differences were also expressed at the genetic level which show that breech strike has a heritability of 0.51. This indicates that breeding is possible. Dags (faecal soiling), skin wrinkles and urine stain have been identified as the most important indicator traits for breech strike and breeding values have been developed for these traits. Breeders can use these indicator traits with confidence to breed indirectly for breech strike resistance without sacrificing genetic gain in other traits.

Acknowledgement:

Australian Wool Innovations Ltd.

References:

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GREEFF JC and KARLSSON LJE 2009. Opportunities to breed for resistance to breech strike in Merino sheep in a Mediterranean environment. *Proc. Assoc. Advmt. Anim. Breed. Genet* 18:272-278. Held in South Australia, 28 September to 1st October 2009.

Session Details:	8/27/2013 VECTOR BORNE DISEASE - TRYPANOSOMES 1015 - 1130 <i>Meeting Room 1</i>
Oral Presentation Details:	The Resilience of the African Grasscutter (<i>Thryonomys swinderianus</i>) to <i>Trypanosoma</i> organisms
Presentation Time:	1015 -1030
Authors:	Opara, M. N., Maxwell, J. A⁺, Okoli, I. C. And Fagbemi, B. O⁺⁺. Tropical Animal Health and Production Research Group, Department of Animal Science and Technology, ⁺ Department of Health services, Federal University of Technology, Owerri, Nigeria ⁺⁺ Department of Veterinry Microbiology and Parasitology, University of Ibadan, Nigeria

The grasscutter (*Thryonomys swinderianus*) is a wild hystricomorphic rodent widely distributed in the African sub-region and exploited in most areas as a source of animal protein, thus leading to its recent domestication. Twenty seven (27) captive - reared grasscutters housed in a raised iron cage and fed guinea grass (*Panicum maximum*) and water daily, were used to determine the effects of experimental infection of these rodents with *Trypanosoma congolense* and *T. Vivax* for 21 days. The PCV, MCHC, total WBC and Lymphocytes of grasscutters experimentally infected with *T. congolense* and *T. vivax* significantly decreased ($p < 0.05$), while their MCV significantly increased ($p < 0.05$) 21 days post infection (dpi). Plasma glucose and cholesterol were decreased ($p < 0.05$). Body temperature fluctuated between 37.4°C and 39.2°C with a peak on day 12 (39.2°C) in *T. congolense* infection and 37.5°C to 40.1°C which peaked on day 8 (40.1°C) in *T. vivax*. The livers and kidneys showed vacuolar and tubular epithelial degenerations respectively, with thrombosis in alveolar blood vessels, but no mortalities. The results of this study have shown the ability of the grasscutter to harbour trypanosome organisms without any deleterious effect, a factor which could be investigated to understand the reason for the trypano – tolerance. Following this, the grasscutter could thus serve as a candidate animal for vaccine production against African animal trypanosomosis (AAT).

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Session Details:	8/27/2013 VECTOR BORNE DISEASE - TRYPANOSOMES 1015 - 1130 Meeting Room 1
Oral Presentation Details:	Trypanosome diversity in cattle and tsetse and their implication for zoonotic diseases in Tanzania
Presentation Time:	1030 -1045
Authors:	Malele I, Nyingilili H, Lyaruu E Tsetse & Trypanosomiasis Research Institute

Zoonosis is a disease that naturally infects animals but can also infect humans as exemplified by the Human African Trypanosomiasis (HAT). HAT is one of the zoonotic diseases and is transmitted by tsetse flies from wildlife to livestock and human beings through *Trypanosoma*, the disease causative parasites. The parasites for this zoonotic disease are the trypanozoon, which include the *T. brucei rhodesiense* and *T. b. gambiense*. In Tanzania, only *T. b. rhodesiense* occurs in active foci. Research done from three sites in Tanzania in both livestock and tsetse indicate a rich diversity of trypanosomes which are important for disease transmission to man. The prevalence of *T. brucei* in cattle was 5.4%, 53.4% and 47.8% from North, West and southern zones of Tanzania. In tsetse, the prevalence was 46.73%, 32.7% and 30% from the northern, western and southern Zones. To date two sites (the north and western) are active foci for the zoonotic disease and this was again confirmed by the SRA LAMP test by 5/28 positives in cattle and 7/89 in tsetse from the northern site. From the west, the positive samples were 30/195 in cattle and 13/66 positive samples in tsetse. Presence of human serum resistance associated (SRA) gene confirms the presence of human infective trypanosomes that cause the acute form of HAT. Climate change and changes in land use patterns aggravate the interactions between wildlife-livestock-human and tsetse which are confined in reserved areas. Again, both cattle and tsetse were found to harbor a diverse of parasites that cause Animal trypanosomiasis in various levels. Therefore, HAT being of zoonotic nature, involving livestock, wildlife and human populations call for inter-disciplinary and sustainable control strategies against HAT. Treatment of animals confirmed to have trypanosomiasis is important to curb the spread of both human and animal trypanosomiasis.

Acknowledgements:

URT through ZARDERF for funding the study

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Hutchinson et al (2003). Lancet Infect Dis. 2003 Jan;3(1):42-5.
Gibson W (2001). Trop Med Int Health. 2001 May;6(5):401-6.
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Session Details:	8/27/2013 VECTOR BORNE DISEASE - TRYPANOSOMES 1015 - 1130 <i>Meeting Room 1</i>
Oral Presentation Details:	Identification of the tick (<i>Ixodes australiensis</i>) as the vector for <i>Trypanosoma copemani</i>
Presentation Time:	1045 -1100
Authors:	J.M. Austen ^{1*} , U.M. Ryan ¹ , J.A. Friend ² , W. G. F. Ditcham ¹ and S. A. Reid ¹ ¹ School of Veterinary and Life Sciences, Division of Health Sciences, Murdoch University, South Street, Murdoch, Western Australia, 6150 ² Science Division, Department of Environment and Conservation, 120 Albany Highway, Albany, Western Australia, 6330

Trypanosomes are a diverse group of protozoan parasites that can infect all classes of vertebrate. Little is known of the prevalence, life-cycle and transmission dynamics of trypanosomes in Australia. Recently *Trypanosome copemani* was identified from the critically endangered Gilberts potoroo (*Potorous gilbertii*) and the quokka (*Setonix brachyurus*) from Western Australia and was characterised as belonging to the Stercorarian group of trypanosomes (Austen et al., 2009). The pathogenicity of *T. copemani* in native animals is not known and therefore the identification of the vector for this parasite is important for elucidation of the complete life-cycle of *T. copemani*.

In Australia, ticks are obligate ectoparasites of vertebrates that are capable of transmitting pathogens (viruses, bacteria, rickettsiae, helminths and protozoa) of veterinary and medical importance. Ticks were collected and examined as potential vectors of *T. copemani* from quokkas and the Gilbert's potoroo from Two Peoples Bay and Bald Island, Albany, Western Australia. Faecal examination of tick faeces from ticks isolated from 8 individual quokkas and a Gilbert's potoroo revealed trypanosomes similar to in vitro life-cycle stages of *T. copemani* in one sample. A total of 12 ticks were dissected and trypanosomes found in sections of their midgut and haemolymph, 49 and 117 days after collection. The observations of dividing trypanosomes in stained smears from the gut and gut contents of the tick suggest that the ticks were systemically infected with *T. copemani*. Tick faeces, salivary glands and midguts from *Ixodes australiensis* were screened using an 18S rDNA PCR with amplification seen only from the midguts. Sequencing showed 100% homology to *T. copemani*. We therefore identify a vector for *T. copemani* as *I. australiensis* and given the detection of trypanosomes in the faeces, suggest that transmission is via the faecal-oral route.

References:

Austen JM, Jefferies R, Friend JA, Ryan U, Adams P, Reid SA. 2009. Morphological and molecular characterisation of *Trypanosoma copemani* n. sp. (Trypanosomatidae) isolated from Gilbert's potoroo (*Potorous gilbertii*) and quokka

(*Setonix brachyurus*). Parasitology. 136, 783-792.

Austen JM, Ryan UM, Friend JA, Ditcham WG, Reid SA. 2011. Vector of *Trypanosoma copemani* identified as *Ixodes* sp. Parasitology. 138, 866-872.



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Oral Presentation Details:	Morphological polymorphism of <i>Trypanosoma copemani</i> and description of the genetically diverse <i>T. vegrandis</i> from the critically endangered Australian potoroid, the brush-tailed bettong (<i>Bettongia penicillata</i> (Gray, 1837))
Presentation Time:	1100 -1115
Authors:	Thompson C ¹ , Botero A ¹ , Wayne A ² , Godfrey S ¹ , Lymbery A ¹ , Thompson A ¹ ¹ Murdoch University, ² Department of Environment and Conservation

The trypanosome diversity of the Brush-tailed Bettong (*Bettongia penicillata*), known locally as the woylie, has been part of further investigation. At a species level, woylies are critically endangered and have declined by 90% since 1999. The predation of individuals made more vulnerable by disease is thought to be the primary causes of these declines, but remains to be proven. The trypanosomes in the blood of woylies were grouped into three morphologically distinct trypomastigote forms, encompassing two separate species. The larger of the two species, *Trypanosoma copemani* exhibited polymorphic trypomastigote forms, with morphological phenotypes being distinguishable, primarily by the distance between the kinetoplast and nucleus. The second trypanosome species was only 20 % of the length of *T. copemani* and is believed to be one of the smallest recorded trypanosome species from mammals. No morphological polymorphism was identified for this genetically diverse second species. We described the trypomastigote morphology of this new, smaller species from the peripheral blood of the woylie and proposed the name *T. vegrandis*. Temporal results indicate that during *T. copemani* Phenotype 1 infections, the blood forms remain numerous and are continuously detectable by molecular methodology. In contrast, the trypomastigote forms of *T. copemani* Phenotype 2 appear to decrease in prevalence in the blood to below molecular detectable levels. Here we report for the first time on the morphological diversity of trypanosomes infecting the woylie and provide the first visual evidence of a mixed infection of both the very small *T. vegrandis* and the much larger *T. copemani*. We also provide supporting evidence that overtime, the intracellular *T. copemani* Phenotype 2 may become localised in the tissues of woylies as the infection progresses from the active acute to chronic phase. As evidence grows, further research is necessary to investigate whether the morphologically diverse trypanosomes of woylies have impacted on the health of their hosts during recent population declines.



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Session Details:	8/27/2013 VECTOR BORNE DISEASE - TRYPANOSOMES 1015 - 1130 Meeting Room 1
Oral Presentation Details:	Infection kinetics and drug susceptibility of the Australian <i>Trypanosoma copemani</i> : a comparative in vitro study with the pathogenic <i>Trypanosoma cruzi</i>
Presentation Time:	1115 -1130
Authors:	Adriana Botero ^{1*} , Christopher Peacock ² , Peta Clode ² , Andy Thompson ¹ ¹ Murdoch University, Perth, Australia ² The University of Western Australia, Perth, Australia

Trypanosoma copemani, a parasite found infecting several Australian native marsupials has been shown to have similar biological behaviour in the host to the pathogenic *Trypanosoma cruzi* (Botero et al, 2013). Both species are capable of colonizing different tissues in the host and are able to produce an inflammatory process that may result in damage to vital organs such as heart and liver (Boari et al, 2012; Botero et al, 2013). In the present study three different biological parameters were investigated and compared regarding both, the Australian *T. copemani* and the South American *T. cruzi*. Two genetically different *T. copemani* strains (G1 and G2) were isolated from the blood of woylies, a native marsupial that has suffered a rapid and remarkable decline in the wild (90% reduction over 10 years) and has been found frequently infected with *T. copemani* (Wayne et al, 2013; Botero et al, 2013). *In vitro* growth kinetics of the two new strains and the Tulahuen *T. cruzi* strain, maintained in culture at Murdoch University, were evaluated and compared in three different cell lines. Drug susceptibility against the commercial drugs Benznidazole and Posaconazole, both used against *T. cruzi*, were also assessed and compared. Results revealed significant differences in infection capability and drug susceptibility between the two *T. copemani* strains. However, when both *T. copemani* strains were compared with *T. cruzi*, greater similarity was found between one of the strains and *T. cruzi* than between the two *T. copemani* strains. Similarities in kinetoplast morphology between the two *Trypanosoma* species will be also presented.

Acknowledgements:

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Session Details:	8/27/2013 PARASITES IN THE TROPICS 1 1015 - 1130 <i>Meeting Room 2</i>
Oral Presentation Details:	Prevalence of Gastro-Intestinal helminthes and <i>Coccidia</i> in Indigenous Chicken from different agro-climatic zones in Kenya
Presentation Time:	1015 -1030
Authors:	Kutima L Jomo Kenyatta University Of Agriculture And Technology

In Kenya, rural poultry production represents a significant portion of the economy, as a source of income for smallholder farmers; in addition, both poultry meat and eggs are affordable sources of animal protein. Poultry keeping constitutes a large portion of farming where domestic chicken constitutes over 98% of the total poultry population. Out of an estimated population of 27.7 million domestic chickens, about 70% are categorized as indigenous. Endo-parasites infections in indigenous chicken are common due to the risks of free-ranging. These parasites contribute to low productivity of indigenous chicken. A study on prevalence of Gastro-Intestinal endo-parasites in Indigenous chicken was carried out in three regions in Kenya. The objective of the study was to determine the species and their prevalence rates. A total of 710 adult free-ranging local chickens were sampled from six districts. Kakamega (162), Bondo (81), Narok (81), Bomet (150), Turkana (70) and West pokot (166). Qualitative and quantitative microscopic parasitological examinations were used for faecal examination. The count data for prevalence rates was transformed from non-parametric to a parametric data by the formula $\text{Log}(x+9)$. The test of significance between the districts and prevalence rates was performed using F-test, at 95% confidence interval, in one way ANOVA. Pearson's correlation coefficient measured the linear association between prevalence rates of parasites and their respective egg per gram. The survey showed 192(27.04%) with coccidial oocysts (182(25.63%) with *Ascaris galli*, 10(1.41%) with *Heterakis gallinarum*, 2(0.3%) with *Syngamus trachea*, 37(5.21%) with *Capillaria retunsa*, 8.45% with *Capillaria annulata*, 21(2.96%) with *Raillietina tetragona*, 94(13.24%), while 112(15.8%) were negative, with no helminthes infestation. The findings suggested that endo-parasites are a common health problem in free range Indigenous Chicken in Kenya and agro-climate significantly influenced the distribution of endo-parasites.

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Session Details:	8/27/2013 PARASITES IN THE TROPICS 1 1015 - 1130 <i>Meeting Room 2</i>
Oral Presentation Details:	Ecto and Endo parasites in free range chickens in rainy season in Mbeere District in Kenya
Presentation Time:	1030 -1045
Authors:	Chege, H.W.^{*1} , D. C. Kemboi ¹ , L. C. Bebora ^{1, N} . Maingi ¹ , P. G. Mbuthia ¹ , L.W. Njagi ¹ , P.N. Nyaga ¹ and J. Githinji ² ¹ Department of veterinary Pathology, Microbiology and Parasitology, Faculty of Veterinary Medicine University of Nairobi P.O. Box 29053-0065 Nairobi, Kenya. ² Ministry of Livestock, Central Veterinary Laboratories, Private Bag, 00625, Nairobi, Kenya.

The prevalence of ecto and endo in free range chickens from Mbeere District, Kenya was determined in the rainy month of November 2011. Twenty four birds of all ages (7 chicks, 8 growers and 9 adults) were randomly selected. The birds were obtained from individual farmers using purposive sampling .All birds had mixed infections of ecto parasites and endoparasites. A total of 8 different ectoparasites were identified, and at various prevalence rates in chicks, growers, and adult birds. These were *Menacanthus stramineus* (100, 100, 89), *Menopon gallinae* (71, 100, 100), *Lipeurus caponis* (0, 25, 22) and *Gonoides gigas* (0, 25, 67), *Dermanyssus gallinae* (71, 63, 44) , *Argas persicus* (43, 0,33), *Echidnophaga gallinacea* (71,50,67) and *Cnemidocoptes mutans* (0, 0, 44) in chicks, growers and adult chickens, respectively. The most prevalent nematodes identified in all ages were *Heterakis isolonche* (86, 50, and 89), *Subulura brumpti* (71, 63, and 78), *Tetramere* species (29, 63, and 78) and *Heterakis gallinarum* (14, 0, and 44) in percentage (%). *Raillietina echnobothrida* (71, 75, and 89), *R.tetragona* (57, 38, 68), *Choanotaenia infundibulum* (14, 0, 11) and *Hymenolepis cantaniana* (0, 13, 0) were the cestodes observed in these birds. The coccidial oocysts were only observed in adult birds (21).The prevalence of haemoparasites (chicks growers and adults in %) were *Plasmodium gallinacea* (57, 88, 89), *Leucocytozoon schoutedeni* (14, 38, 22), *Aegyptinella pullorum* (0,13,0) and *Eperythrozoon* species (14, 40, 11).This study showed that endo and ectoparasites are a common health problem in the village chicken in Mbeere District, Kenya during the rainy season.

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Acknowledgments

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Session Details:	8/27/2013 PARASITES IN THE TROPICS 1 1015 - 1130 <i>Meeting Room 2</i>
Oral Presentation Details:	Evaluation of Dry Season Supplementary Feed Ration on Productivity and Parasitic Diseases of Fulani White Cattle in Nigeria
Presentation Time:	1045 -1100
Authors:	Ayodele Majekodunmi ^{1*} , Charles Dongkum ² , Mike Thrusfield ³ , Sue Welburn ¹ ¹ School of Biomedical Sciences, College of Medicine and Veterinary Medicine, University of Edinburgh, EH16 4SB UK. ² Nigerian Institute for Trypanosomiasis Research, P.M.B. 1303, Vom, Plateau State, Nigeria. ³ Veterinary Clinical Sciences, Royal (Dick) School of Veterinary Studies, College of Medicine and Veterinary Medicine, University of Edinburgh, EH25 9RG UK

Increasing human and livestock populations and dwindling natural resources are putting pressure on rural dwellers and current production systems across the world. People have adapted to these changes and there has been a general shift from traditional extensive methods towards more intensive systems of production.

The Jos plateau in North-Central Nigeria is an important cattle producing area, with a cattle density of over 100/km². Lack of tsetse and trypanosomiasis and abundant pasture attracted huge numbers of cattle keeping pastoralists who settled in the area in the early 20th century. By the mid-1970s the Jos Plateau was overgrazed (1). Since then there have been increases in human and livestock populations and expansion and development of arable agriculture. This has led to intense competition and conflict between farmers and herders over natural resources in the area. This is particularly harsh for herders during the dry season when there is very little food and water available and the low plane of nutrition has negative effects on cattle health and productivity (2,3).

To minimise these effects and ease natural resource conflict, more intensive methods of cattle production are required. Dry season supplementary feed is accepted as the best way to achieve these goals but uptake is low amongst herders (4). In this study selected cattle were fed a daily ration of 40% concentrate and 60% fodder from locally available, economically sustainable sources as a supplement to grazing during the dry season. Effects on susceptibility to endemic parasitic diseases and parameters of production such as weight gain, condition score and reproductive performance were assessed. Implications of this modified production system on cattle management in the area are also discussed.

Acknowledgements

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Session Details:	8/27/2013 PARASITES IN THE TROPICS 1 1015 - 1130 Meeting Room 2
Oral Presentation Details:	Prevalence of gastrointestinal parasites in humans, dogs and pigs living in a village in Cambodia
Presentation Time:	1100 -1115
Authors:	Tawin Inpankaew^{1,2*}, Fabian Schär^{3,4}, Virak Khieu^{3,4,5}, K. Darwin Murrell¹, Anders Dalsgaard¹, Stacey A Llewellyn⁶, Wissanuwat Chimnoi², Chhoun Chamnan⁷, Daream Sok⁷, Sorn San⁸, Hanspeter Marti^{3,4}, Muth Sinuon⁵, Peter Odermatt^{3,4}, Rebecca J Traub⁹ ¹ Department of Veterinary Disease Biology, Faculty of Health and Medical Science, University of Copenhagen, Denmark ² Department of Parasitology, Faculty of Veterinary Medicine, Kasetsart University, Bangkok, Thailand ³ Swiss Tropical and Public Health Institute, Basel, Switzerland ⁴ University of Basel, Basel, Switzerland ⁵ National Center for Parasitology, Entomology and Malaria Control, Phnom Penh, Cambodia ⁶ Queensland Institute of Medical Research, 300 Herston Road, Herston, Brisbane 4006, Australia ⁷ Department of Fisheries Post-Harvest Technologies and Quality Control (DFPTQ), Fisheries Administration, Cambodia ⁸ Department of Animal health and Production, National Veterinary Research Institute (NaVRI), Phnom Penh, Cambodia ⁹ School of Veterinary Science, University of Queensland, Gatton, Queensland, Australia

In Cambodia, intestinal parasite infections are prevalent in humans, and particularly in children. Information on zoonotic parasites in animal reservoir hosts is largely lacking. In May 2012, a total of 264 human, 94 dog and 76 pig faecal samples were collected from 41 households in Dong village, Preah Vihear province, Cambodia. Faecal samples were examined microscopically following isolation of parasite eggs by the sodium nitrate and zinc sulphate floatation. The major gastrointestinal parasite infections in humans were hookworms (24.2%), *Entamoeba* spp. (14.0%) and *Giardia duodenalis* (7.6%). In dogs, hookworm (80.8%), *Spirometra* spp. (21.3%) and *Strongyloides* spp. (14.9%) were the most common species, and in pigs *Isospora suis* (75.0%) was the most common parasite followed by *Oesophagostomum* spp. (73.7%) and *Entamoeba* spp. (31.6%). Eleven parasite species were diagnosed in dogs (eight helminths and three protozoa), seven of which have been documented to have zoonotic potential. Four out of twelve parasite species detected in pigs are also recognized as having zoonotic potential. The results from the microscopic examination were compared with those obtained using PCR. Hookworm-positive samples from dogs and humans were further characterised at a species level and those positive for *Ancylostoma ceylanicum* characterised to a haplotype level by analysis of mitochondrial genes. In addition risk factors associated with the prevalence of gastrointestinal parasites infections in both humans and animals will be reported and discussed.



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The authors gratefully acknowledge staffs from The National Center for Parasitology, Entomology and Malaria Control, Cambodia for their help in collecting faecal samples from human, dogs and pigs as well as with the interviews. We also thank Dr. Chhay Somany, deputy director of the provincial health department at Preah Vihear province for his hospitality during sample collection. Financial support of the UBS Optimus Foundation is highly acknowledged. The work is part of a PhD study for Tawin Inpankaew funded by the University of Copenhagen, Denmark. Special thanks got to all participants, and all dog and pig owners at the Dong village for their participation.

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Session Details:	8/27/2013 PARASITES IN THE TROPICS 1 1015 - 1130 Meeting Room 2
Oral Presentation Details:	Zoonotic parasite research in the Caribbean
Presentation Time:	1115 -1130
Authors:	Rosina C Krecek^{1,2*} , Elise Lee ¹ , Helene Lucas ¹ , Michael A Drebot ³ , Heidi Wood ³ , Amanda Loftis ¹ , Lyndon Robertson ⁴ , Kristina Dimitrova ³ , Kai Makowski ³ , Liz Dillon ³ , Eric Dewailly ⁵ , Karen Morrison ⁶ , Martin Forde ⁴ , Patrick Kelly ^{1,7} (presenting author asterisked) ¹ Ross University School of Veterinary Medicine, Basseterre, SAINT KITTS ² University of Johannesburg, Auckland Park, SOUTH AFRICA ³ National Microbiology Laboratory, Winnipeg, CANADA ⁴ Windward Islands Research and Education Foundation, St. George's, GRENADA ⁵ Centre de Recherche du Le Centre Hospitalier Universitaire de Québec, Québec, CANADA ⁶ Ontario Veterinary College, Guelph, CANADA ⁷ Biomedical Research and Training Institute, Harare, ZIMBABWE

One health zoonotic parasitic research was initiated at Ross University School of Veterinary Medicine (RUSVM), St. Kitts, in 2005 in collaboration with Caribbean Ministries of Health and Agriculture. Already, research has provided significant data on existing and emerging zoonotic tick-borne, parasitic diseases and dengue in the Caribbean. Blood samples and external and internal parasites have been collected from ruminants, cats and dogs and humans from 10 Caribbean Community (CARICOM) states. Serological, molecular and routine parasitological techniques were used to identify vector-borne zoonotic diseases and establish prevalences. Zoonotic parasites were found in a high percentage of stray cats on St. Kitts, including hookworms (88%), *Mammomonogamus* spp. (45%), *Toxocara* spp. (4%), taeniids (30%) and *Toxoplasma gondii* reactive antibodies (85%)^{1,2}. The cat flea, *Ctenocephalides felis*, was common on cats and infected with *Rickettsia felis*, the recently described agent of human flea-borne spotted fever. Most cats were infected with *Bartonella henselae*, agent of cat scratch disease, endocarditis and bacillary angiomatosis in people^{3,4}. The spotted fever group rickettsia *Rickettsia africae*, the agent of African tick bite fever was found in 40% of tropical bont ticks, *Amblyomma variegatum*, from eight Caribbean islands while *Rickettsia rickettsia* and *Rickettsia conorii* subsp. *israelensis* (agents of Rocky Mountain spotted fever and Israeli tick typhus in people, respectively) were identified in dog ticks from St. Kitts^{5,6}. Forty percent of maternal blood on 10 CARICOM states was positive with Spotted fever group rickettsiae^{7,8}. The research at RUSVM has significantly expanded the available knowledge on the distribution of a number of important zoonotic pathogens in the Caribbean. A next step is to alert health workers in the Caribbean and those dealing with vacationers from the area of the possibility of these diseases in their patients.

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Oral Presentation Details:	Direct anthelmintic effects of purified chicory extract against cattle nematodes: preliminary results with <i>Cooperia oncophora</i>
Presentation Time:	1015 -1030
Authors:	Peña M ¹ , Williams A ² , Enemark H ¹ , Thamsborg S ²
	¹ Technical University of Denmark, ² University Of Copenhagen

Direct anthelmintic effects of a purified extract from chicory (*Cichorium intybus* L.) were examined *in vitro* on eggs and adults of *C. oncophora*. Chicory leaves (cv. Spadona) were collected from an organic dairy farm in Denmark. Dried leaf tissue was extracted in a Soxhlet apparatus using methanol. The resulting extract was fractionated using solid-phase extraction cartridges to enhance isolation of secondary metabolites, such as sesquiterpene lactones¹. The obtained elutate was dried, dissolved in 100 % DMSO and serially diluted to obtain concentrations ranging from 5 to 0.03 mg dry matter (DM)/mL. Two Jersey calves (4 months old) mono-infected with *C. oncophora* were used for collection of nematode eggs from faeces, and after necropsy, for isolation of adult worms. Isolated eggs and adults were used in an egg hatch assay (EHA) or an adult motility inhibition assay (AMIA), respectively. Eggs or adult worms were incubated in the chicory extract (final DMSO concentration of 2%) or 2 % DMSO in water. In the EHA, hatching percentages were dramatically decreased in the presence of the chicory extract, with more than 95% inhibition at concentrations ≥ 2.5 mg DM/mL and an EC₅₀ value of 0.64 mg DM/mL (95 % CI = 0.49 – 0.83 mg DM/mL). In the AMIA, after 12 hrs of incubation in the chicory extract a total inhibition in worm motility was detected at concentrations > 0.5 mg/mL (EC₅₀ 0.19 mg/mL; 95 % CI = 0.17 – 0.2 mg/mL), and after 48 hrs of incubation a complete inhibition of worm motility was observed at concentrations > 0.25 mg/mL (EC₅₀ 0.07 mg/mL; 95 % CI = 0.06 – 0.09 mg/mL). These results show that chicory leaves can have a significant anthelmintic effect against cattle nematodes. Further studies are ongoing to characterize the active compounds in the extract and determine the mechanism of nematocidal action.

Acknowledgements:

We are grateful to Henrik Toft Simonsen, University of Copenhagen, for advice on the extraction and fractionation methods.

References:

¹Foster, J., Cassida, K., Turner, K. 2011. *Vet Parasitol* 180, 298 - 306



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Session Details:	8/27/2013 DRUG DISCOVERY NATURAL PRODUCTS 1015 - 1130 Meeting Room 3
Oral Presentation Details:	Acaricidal activity of extracts from <i>Caesalpinia gaumeri</i> (Fabaceae) and <i>Havardia albicans</i> (Leguminosae) against the cattle tick, <i>Rhipicephalus microplus</i> resistant to acaricides
Presentation Time:	1030 -1045
Authors:	1*José Alberto Rosado-Aguilar , ¹ Roger Iván Rodríguez-Vivas, ¹ José Rodrigo Carrillo-Peraza ¹ , ² Martha Méndez-González, ² Rocío Borges-Argáez, ¹ Jorge C. Rodríguez-Buenfil, ¹ Iris Trinidad-Martínez, ¹ Manuel Bolio González ¹ Facultad de Medicina Veterinaria y Zootecnia. Universidad Autónoma de Yucatán. Km. 15.5 carretera Mérida-Xmatkuil. CP. 97000. Mérida, Yucatán, México; alberto.rosadoaguilar@gmail.com ² Centro de Investigación Científica de Yucatán. Calle 43 No 130 Colonia Chuburná de Hidalgo. CP 97200. Mérida, Yucatán, México.

Ticks and the diseases they transmit are a major cause of economic losses to cattle. The way to control this pest has been acaricides based. However, as a consequence of extensive use of acaricides this tick specie has developed resistance to the major classes of these. This has led to the search for alternatives to control ticks, as the use of plant extracts. In previous studies by our working group, the methanolic extracts of leaves of *Caesalpinia gaumeri* (Fabaceae) and *Havardia albicans* (Leguminosae) showed acaricidal activity (> 85%) against *Rhipicephalus microplus* larvae multi-resistant to acaricides. Based on these results we evaluated the acaricidal activity of methanolic extracts of leaves from *H. albicans* and *C. gaumeri* against *R. microplus* adults multi-acaricide–resistance, using the adult immersion test. The methanolic extracts were evaluated at 10% (100 mg/ml) and 20% (200 mg/ml) concentrations. To evaluate the acaricidal activity of methanolic extracts percentage of tick mortality, egg laying inhibition and larval hatching inhibition were recorded. Leaf extracts of *H. albicans* at 10% and 20% concentrations showed mortality of 16.7±2.3% and 23.3±5.4% respectively. In addition the extracts at 10% and 20% reduced the ability of engorged females to lay eggs by 24.2±3.4% % and 54.4±12.4%, respectively, and substantially affected the larval hatchability of *R. microplus* by 33.3±5.2% and 48.7±6.8%, respectively. Moreover, extracts of *C. gaumeri* at 10% and 20% concentrations showed mortality of 6.7±2.3% and 30.0±5.4% respectively, egg laying inhibition of 13.9±3.1% and 51.0±11.2% respectively and larval hatching inhibition of 15.0±4.1% and 20.0±3.9%, respectively. The excellent acaricidal activity of both methanolic extracts on *R. microplus* larvae reported previously and the moderate activity to cause mortality on the adult stage and egg laying inhibition found in this study, makes them promising species to be considered as an alternative for the control of *R. microplus* multi-acaricide resistance.

Acknowledgements:

We are very grateful to CONACYT for supporting this project (CB-2012-01-1178216 and SISTPROY: FMVZ-2012-0014). Special thanks to technician Alfredo Dorantes, Mirbella Caceres for their support during sample collection and vegetal material processing.



Session Details:	8/27/2013 DRUG DISCOVERY NATURAL PRODUCTS 1015 - 1130 <i>Meeting Room 3</i>
Oral Presentation Details:	Effect of condensed tannins in gastrointestinal nematodes of sheep under grazing conditions in Uruguay
Presentation Time:	1045 -1100
Authors:	Mederos A ¹, Piaggio J ², Montossi F ¹, Banchero G ¹ ¹ National Research Institute For Agriculture (INIA), ² Veterinary Faculty, Montevideo, Uruguay

Condensed tannins (CT) have been widely evaluated for their potential direct effect on controlling gastrointestinal nematodes (GINs) in ruminants. This study evaluated the effect of a Quebracho tannin extract (QT) on GINs in sheep under a continuous grazing system of Lucerne or *Lotus uliginosus*.

A completely randomized trial was carried out at the Experimental Unit "INIA La Estanzuela", Colonia, Uruguay. The experimental design was based around two forages: *Lotus uliginosus* 'Grassland Maku' (LM) reported as having a high content of CT and *Medicago sativa* L. 'Chana' (Lucerne), with low CT content. Naturally parasitized crossbred female lambs (n=150), were randomly assigned to one of the following treatment groups: G1=Lucerne; G2= LM; G3=Lucerne plus concentrate with 3% QT; G4=LM plus concentrate with 3%QT; G5=Lucerne plus concentrate without QT and G6=LM plus concentrate without QT. Groups 3 to 6 received the corresponding concentrate at 0.7% of the lambs body weight daily in the morning during a period of 49 days. Production traits were recorded and faecal egg counts (FECs) were performed weekly on each individual animal . Presence of infective larvae was recorded both in individual animals and the surrounding pasture. Summary statistics and mixed linear regression model using the logFECs were created using SAS 9.2.

The main GIN genera identified from coprocultures were *Haemonchus* sp. and *Trichostrongylus* spp. FECs were demonstrated to vary significantly between groups on day 0 ($p < 0.0001$), and this was used as a co-variable in the model. We also observed pronounced interaction between treatments x dry matter x protein ($p < 0.0001$). There was significant variation ($p < 0.001$) in the mean logFECs between groups G4 vs G5 (-1.19) and G6 (-1.97) and between groups G3 vs G6 (-1.29).

In summary, the results suggest a positive effect on the reduction of mean logFECs for all groups with the most significant effect shown for the groups of lambs grazing LM or Lucerne and receiving QT. This said, the magnitude of the differences in count ratios was not extremely large (results not shown).

Acknowledgements:

We acknowledge Dr. Andres Salvo for providing Bioquina®; Florencia Isasa for field work; Beatriz Carracelas and Mariana Crudelli for laboratory work.

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Session Details:	8/27/2013 DRUG DISCOVERY NATURAL PRODUCTS 1015 - 1130 <i>Meeting Room 3</i>
Oral Presentation Details:	BioWorma® for control of nematode parasites of livestock.
Presentation Time:	1100 -1115
Authors:	Knox M¹, Healey K², Lawlor C², Lamb J³, Chambers M³, Groves P⁴ ¹ CSIRO Animal, Food And Health Sciences, ² International Animal Health Products Pty Ltd, ³ Veterinary Health Research Pty Ltd, ⁴ Zootechny Pty Ltd

Duddingtonia flagrans, has been shown to have great potential for application to the biological control of the infective stages of nematode parasites of livestock. Previous work has established that a native Australian isolate of *D. flagrans* provided effective control of nematode larvae when delivered within a feed supplement (BioWorma®) to horses, goats and sheep. Here we provide further evidence for the effectiveness of BioWorma for the control of nematode larvae.

For cattle, goats and horses, a series of pasture trials were conducted where faeces was collected from individual animals being offered BioWorma or a placebo supplement and the faeces placed on separate pasture plots. At 2 week intervals for 8 weeks, presence of larvae in any remaining faeces and surrounding pasture was estimated. For sheep, field trials at both Nimmitabel and Armidale, 2 equal groups of 30 infected sheep were allocated to separate paddocks. One group (TRT) was then offered BioWorma for 120 days while the other (CON) was offered a placebo supplement for the same period. At approximately Days 56 and 98 of the trial, 10 worm-free tracer sheep were introduced to each paddock. After 21 days the tracers were moved to pasture free pens and fed hay for 10 days before slaughter for worm burden estimation.

For the combined trials, administration of BioWorma to horses, cattle and goats significantly ($P=0.003$, $P=0.006$, $P=0.01$, respectively) reduced the detection of nematode parasite larvae on pasture surrounding faeces over an 8 week post treatment period. Administration of BioWorma reduced the worm burdens of tracer sheep at Armidale by 18% and 82% and Nimmitabel by 36% and 59% for 56 and 98 Day groups, respectively, when compared to Control group sheep. No adverse reactions to the *D. flagrans* supplement were observed in any BioWorma supplemented animals throughout the trials.

Acknowledgements:

® BioWorma is a registered trademark of International Animal Health Products Pty Ltd

Session Details:	8/27/2013 DRUG DISCOVERY NATURAL PRODUCTS 1015 - 1130 <i>Meeting Room 3</i>
Oral Presentation Details:	Nematocidal Activity Of Medicinal Plants Of Northern Areas Against <i>Haemonchus Contortus</i> In Sheep
Presentation Time:	1115 -1130
Authors:	Farhana Riaz Chaudhary^{1*}, Zainab Wahab¹, Amna Azad¹ ¹ Department of Zoology, Pir Mehr Ali Shah-Arid Agriculture University, Rawalpindi.

Haemonchus contortus is regarded as one of the most prevalent and highly pathogenic parasite, possesses the highest biotic potential, and has a prominent ability to develop anthelmintic resistance against the synthetic drugs all over the world. Instead of resistance development, synthetic drugs have also some other disadvantages, such as cost, environmental pollution and food residues which has provided a spur to seek out alternative control measures. Therefore, screening of plants with anthelmintic properties seems to be an effective alternative strategy, both in terms of parasite control and their low environmental impact in relation to the commercial anthelmintics. By study also different types of female vulvar form were examined and their responses against plant extracts. For said study, eight plants naming *Punica granatum*, *Juglans regia*, *Berberis lycium*, *Zanthoxylum armatum*, peels of *Citrus sinensis*, *Convolvulus arvensis*, seeds and aerial parts of *Eruca sativa* were selected from northern areas, Pakistan to validate the nematocidal activity against *H. contortus* of sheep *in vitro*. By using crude methanolic extracts of eight plants, live tested worms were incubated in different concentrations viz; 1.5mg, 3mg, 6mg, 12.5mg, 25mg and 50mg. Data revealed that CME of *Z. armatum* possess effective nematocidal activity with lowest lethal concentration $LC_{50} = 2.61$ mg/ml and highest percentage efficacy =76.6%. Findings described that knobbed type isoforms (61%), were prominent to be more resistant and still survived in greater medicinal doses for longer time period followed by Linguiform (27.2%) and Smooth (6.6%), respectively. On the basis of current study it is recommended that anthelmintic potential of *Z. armatum* will be investigated *in vivo* which may be used as ethno-veterinary remedy to control the economic losses due to tested worm in small ruminants. Also need to be studied the antigenic structure of isoforms of *Haemonchus* worm to avoid financial losses to farmers and for adequate control programme.

Acknowledgements:

We would like to thank the Department of Zoology, Pir Mehr Ali Shah Arid Agriculture University Rawalpindi for funding this research.



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Session Details:	8/27/2013 PARASITES OF AQUATIC WILDLIFE 1 1015 - 1130 <i>Meeting Room 5</i>
Oral Presentation Details:	Dicyemid parasites as biological tags to assess the population structure of <i>Sepia apama</i> (giant Australian cuttlefish) in southern Australian waters
Presentation Time:	1015 -1030
Authors:	Catalano S^{1, 2}, Whittington I^{1, 2}, Bertozzi T², Donnellan S^{1, 2}, Gillanders B¹ ¹ The University Of Adelaide, ² South Australian Museum

Sepia apama, the largest species of cuttlefish in the world, is endemic to southern Australian waters, distributed from Ningaloo in Western Australian through to Moreton Bay in southern Queensland (Kassahn et al. 2003). A mass breeding aggregation of *S. apama* occurs in Upper Spencer Gulf (USG), South Australia (SA), Australia, during the winter months each year. However, the abundance and biomass of this mass breeding aggregation is in decline (Hall 2008). Differences in host molecular data, morphology and behaviour suggests that the USG breeding aggregation may be distinct (see Rowling 1994, Hall and Hanlon 2002, Gillanders et al. unpublished), and as such, recruitment from neighbouring populations may have no impact on sustaining this aggregation. Therefore, the population structure of this species needs to be investigated further and verified using an innovative approach, as it is important to identify what species are actually present in the system before they can be appropriately managed. In this study, we used dicyemid parasites, microscopic organisms found in the renal appendages of benthic cephalopods, as biological tags to assess the population structure of *S. apama* in southern Australian waters. Four dicyemid species were documented from *S. apama* collected throughout southern Australian waters, although all four species were never found together in the same host individual. Rather patterns of dicyemid fauna composition, inferred via morphological and molecular analyses, varied with capture locality of the host. In particular, the dicyemid parasite fauna of Spencer Gulf (SG) cuttlefish was different to the fauna found from cuttlefish collected in other localities. Due to the highly host-specific nature of these parasites, this result gives strong support to the SG cuttlefish representing a distinct sub-set and potentially a distinct species compared to the other populations in southern Australian waters.

Acknowledgements:

We thank the following people who assisted with sample collections: Dave Barker, Tim Bensen, Kieran Brazell, Dr Cameron Dixon, Kathleen Hill, Graham Hooper, Dr Kate Hutson, Brian Saunders, Dr Richard Saunders, Alex Schnell and Errol Sporer. Thanks are also due to Prof Hidetaka Furuya (Osaka University, Japan) and Dr Eric Hochberg (Santa Barbara Museum Natural History, USA) for tutorials and information on dicyemid morphology and taxonomy. Funding for this project has been provided by the Australian Society for



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Parasitology, Norman Wettenhall Foundation, Holsworth Wildlife Research Endowment, Sir Mark Mitchell Research Foundation, Lirabenda Endowment Fund, Nature Foundation South Australia, Nature Conservation Society of South Australia and Australian Federation of University Women South Australia. SC is funded by an Australian Postgraduate Award

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Session Details:	8/27/2013 PARASITES OF AQUATIC WILDLIFE 1 1015 - 1130 Meeting Room 5
Oral Presentation Details:	Gastrointestinal infections of free-living Indo-Pacific bottlenose dolphins (<i>Turiops aduncus</i>) from the Northern Red Sea, Egypt
Presentation Time:	1030 -1045
Authors:	Kleinertz S ¹, Hermosilla C ¹, Hirzmann J ¹, Abel-Ghaffar F ², Taubert A ¹ ¹ 1Institute of Parasitology, Justus Liebig University Giessen, D-35392 Giessen, Germany, ² 2Zoology Department, Faculty of Science, Cairo University, Cairo, Egypt

The present study represents to our knowledge the first survey on the gastrointestinal parasite fauna of free-living Indo-Pacific bottlenose dolphins (*Turiops aduncus*) within waters of the Red Sea, Egypt. In total 94 individual faecal samples of bottlenose dolphins (*T. aduncus*) were collected throughout several diving expeditions for individual cataloguing by using photo identification techniques as well as for behavioral studies during the year 2012. Additionally, two individual vomitus samples were collected, which contained nematode species, identified as *Anisakis typica*, by using molecular analysis and one isopod (Cymothoidae) species, based on morphological features. The study revealed 21 different parasite species belonging to protozoans (10 species) and metazoans: trematoda (7 species), cestoda (1 species), nematoda (2 species) and crustacea (1 species), using different standardized diagnostic techniques such as SAF-method, carbol-fuchsin stained faecal smears, copro-ELISA, PCR and microscopy analyses. Parasitological findings represent, in several cases, new host and locality records for Red Sea waters. The present study aims to identify the parasites which occur in free-living Indo-Pacific bottlenose dolphins (*Turiops aduncus*) from the Red Sea in order to gain some insights on gastrointestinal parasites for conservation purposes as some of these parasites can induce severe diseases. Continued parasite monitoring of wild bottlenose dolphins (*T. aduncus*) as well as stranding patterns is warranted for early detection of changes, such as the detection of zoonotic parasitosis, and the possibility of taking timely management actions.

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Session Details:	8/27/2013 PARASITES OF AQUATIC WILDLIFE 1 1015 - 1130 <i>Meeting Room 5</i>
Oral Presentation Details:	Morphological and molecular characterisation of cardiovascular flukes (Digenea: Spirorchiiidae) from marine turtles in Moreton Bay, Queensland.
Presentation Time:	1045 -1100
Authors:	Phoebe Chapman^{1*}, Rebecca Traub¹, Thomas Cribb², Myat Kyaw-Tanner¹, Mark Flint¹, David Blair³, Paul Mills¹, Paul Eden¹ ¹ School of Veterinary Science, The University of Queensland, Gatton, AUSTRALIA ² School of Biological Science, The University of Queensland, St Lucia, AUSTRALIA ³ School of Marine and Tropical Biology, James Cook University, Townsville, AUSTRALIA

Spirorchiid flukes inhabit the cardiovascular systems of endangered marine turtles and contribute to strandings and mortalities worldwide. Few studies have explored spirorchiid species assemblages, host-parasite relationships and species-specific pathogenicity. Spirorchiid eggs, rather than adults, are the cause of most significant pathology. Morphological identification of eggs beyond genus level is generally not possible due to inherent similarities, therefore it is difficult to attribute pathogenic effects of eggs to a particular species. This study aims to expand the currently very limited genetic database for spirorchiids to provide a means for identifying spirorchiid eggs to species level. This in turn allows the proper investigation of relative pathogenicity of individual species, leading to development of targeted diagnostics for surveillance and control purposes, as well as improving understanding of spirorchiid diversity and host-parasite relationships in Queensland. Stranded or recently deceased turtles were obtained from government or rehabilitation organisations and adult flukes and eggs collected during detailed necropsies. Adult flukes were stained and mounted for morphological identification after initial examination and categorisation. Portions of adult worms were removed to provide genetic material prior to staining, or additional corresponding whole adults were used. The 28S (partial) and ITS2 nuclear ribosomal genes were amplified by PCR using custom primers and sequenced. The resulting sequences, once matched to morphological identifications and sequences stored in Genbank (where available), were then matched with sequences obtained from eggs to determine species and subsequently identify relationships between species and significant pathology. It is envisioned that the results of this study will lead to the development of a diagnostic test for the surveillance of pathogenic spirorchiids in endangered marine turtles in the Moreton Bay region.

Acknowledgements:

Funding for this project was provided by an ARC Linkage Grant. Turtles were obtained through the services and staff of Australia Zoo and the Queensland Parks and Wildlife Service.

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Session Details:	8/27/2013 PARASITES OF AQUATIC WILDLIFE 1 1015 - 1130 <i>Meeting Room 5</i>
Oral Presentation Details:	Parasites of introduced freshwater fish species in Murrumbidgee Basin
Presentation Time:	1100 -1115
Authors:	Margriet van Keulen^{1,2*} Anna Turner ¹ , Gerrieke Eulink ^{1,2} , Skye Wassens ³ , Shokoofeh Shamsi ¹ ¹ School of Animal and Veterinary Sciences and Graham Centre for Agricultural Innovation, Charles Sturt University, Wagga Wagga, Australia; ² Faculty of Veterinary Medicine, University of Utrecht, the Netherlands; ³ School of Environmental Sciences, Charles Sturt University, Albury, Australia

There has been significantly less research on parasites from Australia's freshwater fish fauna compared with work on these parasites from marine fishes. Exotic freshwater fishes have been known to cause many changes in Australian rivers and lakes from depletion of native fish stocks to increased turbidity. However, one area that did not attract many attentions is parasite fauna of the introduced fishes. In the current preliminary study, we examined carps (*Cyprinus carpio*), perch (*Perca fluviatilis*) and gambusia (*Gambusia holbrooki*) caught from Murray-Darling Basin in New South Wales (NSW) for infection with parasites. Various parasitic groups, including apicomplexa, monogeneans, cestodes and crustaceans were found. Although some of these parasites, such as monogeneans are known as having the potential to cause serious disease and massive mortalities both in farmed and wild fish, all infected fish in the present study had a healthy appearance. These introduced fish are known to be resilient against many parasitic diseases therefore they can act as reservoirs for dangerous parasites and can be a major threat to the aquatic biodiversity as well as aquaculture development in regional areas. Flooding events in recent years increased fish movement through inland river systems and , could have facilitated parasite transfer between introduced species and native fish and further distribution of parasites in the region.

Acknowledgements:

We would like to acknowledge the staff at Narrandera Fisheries Research Centre for assistance in fish sampling, the Graham Centre for Agricultural Innovation and CSU School of Animal and Veterinary Sciences for financial support toward conducting this project and financial assistance for attending WAAVP 2013.



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Oral Presentation Details:	Host specificity of digenean parasites of nassariid gastropods
Presentation Time:	1115 -1130
Authors:	Barnett L Central Queensland University

The Nassariidae is a large family of marine gastropods containing approximately 500 species in the Superfamily Buccinoidea. The parasite fauna of only a few nassariid gastropods has been thoroughly studied; these include *Ilyanassa obsoleta*, an intertidal snail found along the east and west coasts of North America, and *Nassarius reticulatus*, a snail common to the north-eastern Atlantic and the Mediterranean, Black and Azov Seas. Nassariid gastropods are well represented in Australia, and *Nassarius dorsatus*, *Nassarius olivaceus* and *Nassarius pullus* are common in the intertidal mangroves of the Capricornia region in Central Queensland. Twelve species of cercariae in six families of digenean trematodes were associated with these gastropods. No infections were found by families that had not been previously reported from other nassariids. Six species of acanthocolpids were found, including three putative species of the genus *Stephanostomum* and one of the genus *Stephanostomoides*. There were two species of echinostomatid cercariae and one species each of microphallid, opecoelid, zoogonid and lepocreadiid cercariae. The majority of the cercariae were host specific; only four infected two species. Sixteen new host-parasite records were added to the Nassariidae, and examination of the host-parasite associations shows that common families using nassariids as first intermediate host are the Acanthocolpidae, Echinostomatidae, Lepocreadiidae and Zoogonidae. Nassariid gastropods are also the dominant marine first intermediate hosts for the Acanthocolpidae, Lepocreadiidae and Zoogonidae and one of the three most common first intermediate host families for marine species of *Himasthla* (Echinostomatidae).

Session Details:	8/27/2013 COMPANION ANIMAL ZOONOSES 1015 - 1130 Meeting Room 6
Oral Presentation Details:	<i>Onchocerca lupi</i>: a neglected canine vector-borne helminth of zoonotic concern
Presentation Time:	1015 -1030
Authors:	Domenico Otranto^{1*} , Filipe Dantas-Torres ^{1,2} ¹ Università degli Studi di Bari, Valenzano, ITALY ² Centro de Pesquisas Aggeu Magalhães, Recife, BRAZIL

The zoonotic potential of *Onchocerca lupi*, a neglected parasite of dogs, has only recently been demonstrated in a patient from Turkey. Since this first case report, human ocular cases have been increasingly reported worldwide, including in Iran, Turkey, Tunisia, and the United States, where *O. lupi* was recently diagnosed about the rachidian channel of a 22 years-old patient. In dogs the parasite causes nodular lesions associated with acute or chronic ocular disease (i.e., conjunctivitis, ocular swelling, photophobia, lacrimation, discharge, exophthalmia), but asymptomatic infestations also occur making an estimation of the actual distribution of the parasite a challenging task. Indeed, the difficulties in achieving a reliable diagnosis through the skin snip technique, might explain the scant data available on *O. lupi*. Since its first description in a Caucasian wolf (*Canis lupus*) from Georgia, *O. lupi* remained almost unknown for decades until reports in clinically suffering dogs from southern (Greece, Portugal) and central (Germany, Hungary) Europe, and in cats and dogs from United States. Recently, an epidemiological survey was conducted to estimate the occurrence of *O. lupi* in dog populations from areas of Greece and Portugal where a single or multiple cases, respectively, were previously reported. Of 107 animals sampled, 9 (8.4%) scored positive by cytology. Recent data showed that *O. lupi* infestation is featured by different clinical presentations, from no apparent clinical sign to blindness. The genetic make-up of specimens collected from distinct animal populations displayed differences according their provenience (e.g., Portugal). Nevertheless, many aspects of the biology and ecology of *O. lupi* remain unknown to science and knowledge of its actual distribution, limited to a few case reports. Therefore, further studies are needed to improve current understanding of the biology of this parasite in its hosts and vectors, gain information about the efficacy of antihelminthic treatments against microfilariae and adults and setting an easy and non invasive diagnosis. Medical physicians and ophthalmologists should be aware about the risk for humans and their pets (cats and dogs) to become infested by this important, yet neglected helminth.

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Otranto D, Dantas-Torres F, Papadopoulos E, Petrić D, Čupina AI, Bain O. 2012. Tracking the vector of *Onchocerca lupi* in a rural area of Greece. Emerg Infect Dis. 18:1196-200.

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Session Details:	8/27/2013 COMPANION ANIMAL ZOONOSES 1015 - 1130 Meeting Room 6
Oral Presentation Details:	The Prevalence, clinical impact and zoonotic significance of <i>Giardia</i> species in dogs and cats in Germany.
Presentation Time:	1030 -1045
Authors:	Pallant L ¹ , Barutzki D ² , Schaper R ³ , Thompson R ¹ ¹ Murdoch University, Western Aualtia, ² Tierärztliches Labor Freiburg, Germany, ³ Bayer Animal Health, Leverkusen, Germany

Giardia is now the most common enteric parasite in well cared for dogs and cats in developed countries. This raises questions of the need for treatment in terms of the clinical effects of infection and potential impact on public health. With the former, it is still uncertain whether *Giardia* is always a clinical problem and if this varies between different breeds. It is also not known if the different species of *Giardia* to which dogs and cats are susceptible vary in virulence. Further, it is possible that concurrent infections with co-habiting protozoa such as *Cystoisospora* may exacerbate the consequences of *Giardia* infections.

Since dogs and cats are susceptible to different species of *Giardia* which vary in zoonotic potential, and possibly their clinical impact, it is important to obtain data on the frequency of infection in urban areas. The few randomised surveys so far undertaken have reported contrasting results in the prevalence of the different species of *Giardia* in dogs and cats. The present study was undertaken to provide additional data on the prevalence of *Giardia* in cats and dogs in central Europe where previous studies with limited numbers of dogs have demonstrated differences in the frequency of zoonotic species in dogs.



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Session Details:	8/27/2013 COMPANION ANIMAL ZOONOSES 1015 - 1130 <i>Meeting Room 6</i>
Oral Presentation Details:	Prevalence of <i>Cheyletiella parasitovorax</i> and <i>Trichophyton mentagrophytes</i> in rabbits and guinea pigs in Dutch pet
Presentation Time:	1045 -1100
Authors:	Paul A.M. Overgaauw^{1*} , Nico J. Schoemaker ² , Rob A. Samson ³ , Kim H.A. van Avermaete ⁴ , Carlijn A.R.M. Mertens ⁴ ¹ Division Veterinary Public Health, Institute for Risk Assessment Sciences, Faculty of Veterinary Medicine, Utrecht University, Yalelaan 102, 3584 CM Utrecht, the Netherlands ² Division of Zoological Medicine, Department of Clinical Sciences of Companion Animals, Faculty of Veterinary Medicine, Utrecht University, Yalelaan 108, 3584 CM Utrecht, the Netherlands ³ CBS-KNAW Fungal Biodiversity Centre, Uppsalalaan 8, 3584 CT Utrecht, The Netherlands ⁴ MSc students, Faculty of Veterinary Medicine, Utrecht University

Fur mites and dermatophytosis cause skin diseases and may be zoonotic infections. In rabbits and guinea pigs, dermatophytosis is primarily caused by *Trichophyton mentagrophytes*. The nonburrowing fur mite *Cheyletiella parasitovorax* is a common ectoparasite on rabbits (very rare on guinea pigs) and a possible risk factor for acquiring dermatophytosis due to skin lesions. To estimate the risk of acquiring cheyletiellosis and dermatophytosis for new owners, often children, the prevalence on rabbits and guinea pigs in Dutch pet shops was investigated.

Ninety-one pet shops (7.4% of all Dutch pet shops), randomly spread throughout the Netherlands, were visited. The presence of *Cheyletiella* mites was investigated using a flea comb and a magnifying glass and the MacKenzie toothbrush method was used to sample the fur for dermatophytes. The samples were cultured on Sabouraud's dextrose agar plates in the dark at 25 °C for three weeks. Suspected colonies were subcultured on malt extract agar plates at 25 °C for another three weeks. Growth of *T. mentagrophytes* was confirmed by PCR.

In total 213 rabbits and 179 guinea pigs were investigated. None of the animals was infected with *C. parasitovorax*. *T. mentagrophytes* was found on 17% of the sampled guinea pigs (31/179) and on 4% of the sampled rabbits (8/213). None of the positive tested animals showed lesions on visual control. In 27% of the participating pet shops (24/88) infected guinea pigs were present, while in 6% participating shops (5/90) infected rabbits were present.

The results demonstrate that Dutch pet shops play an important role in the distribution of *T. mentagrophytes* and that fur mites are not required in the epidemiology. Educating pet shop owners and routine testing of new introduced rabbits and guinea pigs is recommended to reduce the prevalence of zoonotic dermatophytes in pet shops.

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Session Details:	8/27/2013 COMPANION ANIMAL ZOONOSES 1015 - 1130 <i>Meeting Room 6</i>
Oral Presentation Details:	Emphasising the Importance of Travel History and Clinical Awareness: Cases of Canine Leishmaniasis in Australia
Presentation Time:	1100 -1115
Authors:	Emily Cleare ^{1*} , Ken Mason ² , Jenny Mills ¹ , Peter Irwin¹ ¹ College of Veterinary Medicine, School of Veterinary and Life Sciences, Murdoch University, Perth, Western Australia ² Springwood, Brisbane, Queensland 4127, Australia

Canine leishmaniasis caused by *Leishmania infantum* is a life-threatening zoonotic disease with a wide geographical distribution. Australia is currently considered to be free of endemic canine leishmaniasis; mandatory pre-import serological testing of dogs has been enforced by Australian Biosecurity authorities for approximately six years. This report describes five dogs living in Australia and diagnosed with canine leishmaniasis, all of which were imported from southern Europe before 2007. Four dogs were male, one was female, and they ranged in age from five to eight years old. Breeds included a miniature Poodle, Jack Russell Terrier crosses (n=2) and Boxers (n=2). Most dogs showed clinical abnormalities within a short time after leaving quarantine but one dog took approximately six years to develop systemic illness, by which time the clinical suspicion of leishmaniasis was very low. The severity and nature of the clinical signs varied greatly between dogs in this small study cohort, from sub-clinical infection in one Boxer to widespread organ involvement and renal failure, typical of fulminant visceral leishmaniasis in three dogs. Skin disease, characterised by varying degrees of alopecia and scale, were evident in four dogs. Nodular ulcerative lesions and nail bed pathology that prompted the initial veterinary consultations were present in two dogs. Clinicopathological abnormalities included hypoalbuminaemia, hyperglobulinaemia, non-regenerative anaemia, leukocytosis, thrombocytopenia and proteinuria. One dog exhibited a monoclonal gammopathy. A range of treatments were given to these dogs, including allopurinol, levamisole and meglumine antimoniate, together with supportive treatment as indicated. Two dogs were euthanized, one remains subclinical, and there are two that were lost to follow up, which is of particular concern since the vectorial capacity of various insect species in Australia remains unanswered. Veterinarians need to be vigilant and enquire about travel history when presented with dogs exhibiting dermatological signs and systemic clinical illness.

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Session Details:	8/27/2013 COMPANION ANIMAL ZOONOSES 1015 - 1130 Meeting Room 6
Oral Presentation Details:	Fasciolosis of donkeys and their epidemiological and zoonotic role in Ethiopia.
Presentation Time:	1115 -1130
Authors:	Getachew M, Innocent G, Burden F, Trawford A, Reid S, Love S Donkey Sanctuary

Background: Fasciolosis is an important livestock disease worldwide because of the substantial production and economic losses it causes. The public health importance of human fasciolosis has also increased in recent years and is recognized as an important re-emerging zoonotic disease. Although fasciolosis is widespread in Ethiopia, and it is one of the most significant constraints on livestock production, its epidemiology and pathogenicity in donkeys, and the epidemiological role they may play have not been determined.

Methods: A cross-sectional coprological survey and a retrospective post-mortem investigation were conducted to study the epidemiology of fasciolosis in working donkeys in the central regions of Ethiopia. Faecal samples collected from 803 donkeys, and the number of liver flukes recovered from 112 donkeys that died either of various clinical ailments or were euthanized on welfare grounds were analysed.

Results: The overall infection prevalence of fasciolosis was 44.4% in coprologically examined donkeys. The prevalence was significantly higher in the highland region (72.6%) than in the mid-lowland regions (21.5 - 52.6%) (P<0.001). Among donkeys positive for *Fasciola* species eggs, the egg output ranged from 10 to 960 epg.

The infection prevalence in donkeys examined post-mortem was 41.9%. Both *Fasciola hepatica* and *Fasciola gigantica* were identified with the mean infection intensities of 19 and 11, respectively. The overall mean infection intensity was 30 flukes ranging from 3 to 79. Gross pathological lesions of hyperplasia of the bile ducts were observed in most donkeys. Histopathology also revealed fibrosis of large portal areas, marked and irregular bile duct proliferation and hypertrophy in some of the donkeys.

Conclusions: The high infection prevalence of fasciolosis in working donkeys shows the endemic nature of the disease in all regions and the total absence of treatment against trematode infection in equids in Ethiopia. Such high infection prevalence also indicates the important role that donkeys can play in the epidemiology of both livestock and human fasciolosis, and the need for these animals to be considered in the overall epidemiological studies and for sound control strategies and prevention of fasciolosis. The gross and microscopic lesions observed indicate the need to further investigate the pathogenicity and immunity of working donkeys against liver flukes.





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Session Details:	8/27/2013 DRUG RESISTANCE - ECTOPARASITES 1015 - 1130 <i>Meeting Room 7</i>
Poster Display Details:	Cross-Resistance Between Fipronil And Lindane In <i>Rhipicephalus (Boophilus) Microplus</i>
Presentation Time:	1015 -1030
Authors:	Castro Janer, E^{*1} ; Klafke, G.M. ² ; Capurro, M. ³ ; Schumaker, T.T.S. ³ ¹ Department of Parasitology, School of Veterinary-UDELAR, Montevideo, Uruguay ² Laboratory of Parasitology, FEPAGRO Animal Health, Eldorado do Sul, RS. Brazil. ³ Department of Parasitology, Instituto de Ciências Biomédicas-USP, São Paulo, SP, Brazil.
Poster Number:	96

The southern cattle tick, *Rhipicephalus (Boophilus) microplus* (Canestrini), is one of the most damaging pests that parasites cattle in tropical and subtropical regions of the world. For its control, several chemical groups have been used, including fipronil and lindane. In Uruguay and Brazil, cyclodienes (lindane, dieldrin) were used to control ticks at the beginning of 60's and later, organophosphates and other chemical groups substituted those molecules. Fipronil and lindane exert action in the same target site. In some cases, in both countries, cattle tick resistance to fipronil has developed quickly, after only a few acaricide treatments (three to seven). The objective of the present study was to determine the cross-resistance between fipronil and lindane in the cattle tick from Uruguay and Brazil. Initially, the FAO's larval packet test with lindane was applied to a fipronil-resistant strain and five susceptible field populations. Mozo and POA strains were used as susceptible controls. Larval immersion test was used to assess fipronil toxicity. Seventeen fipronil-resistant field populations were tested with lindane. Fourteen were lindane-resistant and three were susceptible. The last three populations had incipient resistance to fipronil. Recently, the persistence of dieldrin-resistant phenotypes was demonstrated in Australia. However, in Brazil and Uruguay, cyclodienes were used for a short period in cattle tick control. Probably, the high occurrence of cross-resistance could be explained by the indirect selection by endosulfan, used for crop pest control. Finally, cross-resistance between fipronil and lindane is reported for the first time.

Session Details:	8/27/2013 DRUG RESISTANCE - ECTOPARASITES 1015 - 1130 <i>Meeting Room 7</i>
Oral Presentation Details:	Investigation into the variability of response to the insect growth regulator compounds, dicyclanil and triflumuron in field strains of <i>Lucilia</i> spp blowflies in New Zealand.
Presentation Time:	1030 -1045
Authors:	Brown B¹, McKay C², Waghorn T³ ¹ Novartis Animal Health Australia, North Ryde, AUSTRALIA, ² Novartis Animal Health New Zealand, Mairangi Bay, Auckland, NEW ZEALAND, ³ AgResearch Grasslands, Palmerston North, NEW ZEALAND

The Australian green blowfly (*Lucilia cuprina*) and the common green blowfly (*Lucilia sericata*) are major ectoparasites of sheep in New Zealand.

Prevention of flystrike caused by the larvae of these species is by application of a range of insecticides to the fleece of at risk animals. The most commonly used compounds in New Zealand fall into the insect growth regulator (IGR) group.

Within the IGRs there are two distinct chemical classes, with unrelated modes of action.

- 1) The triazine/pyrimidine derivatives e.g. cyromazine and dicyclanil and
- 2) The benzoyl phenyl urea (BPU) compounds e.g. diflubenzuron and triflumuron

Resistance by *Lucilia cuprina* to diflubenzuron was confirmed in Australia in 2002, the registration of diflubenzuron for the prevention of flystrike in sheep in Australia was subsequently removed in 2008.

Previous studies presented in conference proceedings and anecdotal reports from field veterinarians in New Zealand have suggested that similar BPU resistant strains of fly are also present in New Zealand.

A pilot study conducted in 2010, investigating variability of response to two insect growth regulator chemicals, dicyclanil and triflumuron, suggested that triflumuron resistant strains of the European Green blowfly, *L. sericata* were present in the South Auckland and Waikato regions.

A larger survey testing the response of 34 field strains of *Lucilia* spp blowflies was conducted over the summer/autumn of 2010 /2011.

Fifteen strains of *L. sericata* were tested with five appearing to have a high level of tolerance to triflumuron. Responses by *L. sericata* to dicyclanil were relatively uniform indicating little likelihood of any decrease in susceptibility to this chemical.

Conversely nineteen strains of *L. cuprina* were tested, with little variation in response to either active ingredient.



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The wide variability of response to triflumuron suggests a loss of reliability for flystrike preventative treatments based on this active ingredient.

Acknowledgements:

The sheep graziers of the Waikato and South Auckland regions that allowed access to their properties to collect flies for testing.

References:

Levot GW & Sales N. 2002. New high level resistance to diflubenzuron detected in the Australian sheep blowfly, *Lucilia cuprina* (Wiedemann) (Diptera: Calliphoridae). *General and Applied Entomology* 31, 43–45.

Session Details:	8/27/2013 DRUG RESISTANCE - ECTOPARASITES 1015 - 1130 <i>Meeting Room 7</i>
Oral Presentation Details:	Investigations of a suspected cyromazine resistant strain of <i>Lucilia cuprina</i>, the Australian sheep blowfly, and the implications for fly strike control.
Presentation Time:	1045 -1100
Authors:	Brown B¹, Bailey J¹, Kluver P¹, Rolfe P², George A², Vanhoff K², Baker K² ¹ Novartis Animal Health Australia, North Ryde, AUSTRALIA, ² Novartis Animal Health Australia, Yarrandoo R&D Centre, Kemps Creek, Sydney, AUSTRALIA

The protective period of *Vetrazin*[®] spray-on and *CLiK*[®] was investigated on sheep against an Australian field isolate of *Lucilia cuprina* (Nimmitabel strain) that demonstrated increased in-vitro tolerance to cyromazine.

Two studies were conducted; a larval implant, laboratory-based study and a field study on the original farm of isolation.

Larval implant studies were carried out using both *Vetrazin* spray-on (60mg/mL cyromazine) and *CLiK* (50mg/mL dicyclanil) to estimate the protective period of these products against 2 strains of fly: the Nimmitabel strain and a triazine-susceptible reference strain. The implant study was conducted in Merino sheep treated at the minimum recommended dose for the specified weight range. First stage instars were placed in the top third of the staple above a small incision adjacent to the treatment zone of 6 sheep per treatment group, and assessed for larval viability for the next three days.

In the field study three hundred and eighty-five merino lambs were treated with *Vetrazin* and 198 merino lambs were treated with *CLiK*. The presence of *L. cuprina* was monitored using fly traps. All sheep were monitored several times a week for fly strikes up to 18 weeks after treatment.

In the implant study *Vetrazin* prevented the establishment of viable strikes for 13 weeks. No strikes were established in the *CLiK* treated groups up to week 18, (study end). In the field study, the numbers of *L. cuprina* were moderate to high through the study period. Five lambs were struck in the *Vetrazin* group at week 18, outside the Australian registered label claim of protection for 11 weeks. No sheep were struck in the *CLiK* treated group.

These studies demonstrated that, against this field isolate and under both field and controlled laboratory conditions, *Vetrazin* spray-on and *CLIK* each maintained the registered protective period after treatment.

Acknowledgements:

The owners of the Nimmitabel property for allowing access and providing sheep for the field study.
Dr Garry Levot for supply of the Nimmitabel strain of *Lucilia cuprina*.

References:

Levot GW. Cyromazine resistance detected in Australian sheep blowfly. *Aust Vet J* 2012;90:433–437.



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Session Details:	8/27/2013 DRUG RESISTANCE - ECTOPARASITES 1015 - 1130 <i>Meeting Room 7</i>
Oral Presentation Details:	Determination of Acaricide Resistance in <i>Rhipicephalus (Boophilus) microplus</i> (Acari: Ixodidae) Field Populations of Argentina, South Africa and Australia with the novel Larval Tarsal Test
Presentation Time:	1100 -1115
Authors:	Lovis L ^{1,2} , Reggi J ³ , Berggoetz M ¹ , Betschart B ¹ , Sager H ² ¹ University of Neuchâtel, Inst. of Biology, Neuchâtel, Switzerland, ² Novartis Animal Health Research Center, St-Aubin, Switzerland, ³ Novartis Animal Health, Ciudad Autónoma de Buenos Aires, Argentina

Infestations with ticks have an important economic impact on the cattle industry worldwide and resistance to acaricides has become a widespread phenomenon. In order to optimize their treatment strategy, farmers need to know if and against which acaricide-classes potential resistance does occur. Bioassays are used to assess the resistance level and pattern of *Rhipicephalus (Boophilus) microplus* populations. In the past years we have been able to validate the Larval Tarsal Test (LTT) as an alternative test method to the Larval Packet Test and to collect first experience with field samples from Brazil (Lovis et al., 2011 and 2013). In the present study the LTT was used to assess the susceptibility of field populations originating from Argentina (8), South Africa (3) and Australia (2) to nine acaricidal compounds from five major classes: organosphosphates (OP), synthetic pyrethroids (SP), macrocyclic lactones (ML), phenylpyrazols (PYZ) and amidines. The resistance ratios at concentrations inducing 50% and 90% mortality were used to detect established and emerging resistance. This study confirmed the newly reported presence of amitraz resistance in populations from Argentina. In addition, resistance to SP appeared to be widespread (7/8, 88%) in the Argentinean farms, which had been selected based on the observation of lack of treatment efficacy by farmers. In South Africa one of the three populations was found to be resistant to SP and to a PYZ compound (pyriprol). Furthermore, resistance to OP and SP was observed in Australia. Finally, the LTT proved to be a suitable test to evaluate the susceptibility of *R. microplus* field populations to the most relevant acaricidal classes.

References:

Lovis L, Perret JL, Bouvier J, Fellay JM, Kaminsky R, Betschart B, Sager H. 2011. A new in vitro test to evaluate the resistance level against acaricides of the cattle tick, *Rhipicephalus (Boophilus) microplus*. *Vet Parasitol* 182:269-280.

Lovis L, Mendes MC, Perret JL, Martins JR, Bouvier J, Betschart B, Sager H. 2013. Use of the Larval Tarsal Test to determine acaricide resistance in *Rhipicephalus (Boophilus) microplus* Brazilian field populations. *Vet Parasitol* 191:323-331.



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Session Details:	8/27/2013 VACCINES - NEMATODES 1015 - 1130 <i>Meeting Room 8</i>
Oral Presentation Details:	RNA interference (RNAi) in the parasitic nematode <i>Teladorsagia circumcincta</i> and the search for potential marker genes that indicate the activation or not of the RNAi pathway in <i>Caenorhabditis elegans</i>
Presentation Time:	1015 -1030
Authors:	Tzelos T¹, Knox D¹, Matthews J¹, Whitelaw B² ¹ Moredun Research Institute, Edinburgh, ² Roslin Institute, Edinburgh

Teladorsagia circumcincta is a major cause of ovine parasitic gastroenteritis in temperate climatic regions. The developed resistance to the major anthelmintic drug classes challenges its future control. Vaccination is a potential alternative control method and potential vaccine candidates have been revealed. However, increasing gene datasets suggest that target selection may be aided by screening methods such as RNAi, a reverse genetic mechanism that causes highly specific gene silencing. It was initially described and used in *Caenorhabditis elegans* for the functional analysis of its genome. Nevertheless, its application was more difficult than anticipated in parasitic nematodes because of the inconsistency of the silencing effect. In the unsuccessful cases, did the dsRNA penetrate the parasite and activate the RNAi pathway? Thus far, there are no internal controls that indicate the activation of the pathway. The aims of the study were: to determine potential marker genes in the RNAi pathway that could indicate the activation of the pathway in *C. elegans*; and to apply these markers to test the efficacy of RNAi in *T. circumcincta*. Two targets were selected for the former aim (*Ce-cpr-4*, *Ce-sod-4*) which had been proven to be consistently susceptible and refractory to RNAi, respectively. After the exposure to the dsRNA the transcript levels of candidate marker genes (*Ce-dcr-1*, *Ce-ego-1* and *Ce-rsd-3*) were examined and showed that exposure to dsRNA has no effect on the levels of those genes making them inappropriate markers for the activation of the RNAi pathway. In *T. circumcincta*, the selected RNAi targets were members of a secreted protein group (ASPs) common to gastrointestinal nematodes and known to provide some protection against other nematode species. The results have shown a successful silencing of two members of the group and an *in vivo* RNAi experiment is planned to define the effect of ASP knockdown on infection outcome.

Acknowledgements:

I would like to thank my supervisors for their support and guidance throughout this project. Moreover I would like to thank my sponsors EBRC and Pfizer.



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Session Details:	8/27/2013 VACCINES - NEMATODES 1015 - 1130 <i>Meeting Room 8</i>
Oral Presentation Details:	Generation of a recombinant <i>Teladorsagia circumcincta</i> antigen using <i>Caenorhabditis elegans</i>
Presentation Time:	1030 -1045
Authors:	Cassandra Longhi ^{1*} , Alasdair Nisbet ¹ , Alexa Brett Roberts ² , Collette Britton ² , Tom N. McNeilly ¹ ¹ Moredun Research Institute, Edinburgh, SCOTLAND ² Institute of Infection, Immunity and Inflammation, University of Glasgow, Glasgow, SCOTLAND

Teladorsagia circumcincta is a parasite of sheep in temperate areas, and main cause of parasitic gastroenteritis (PGE) in lambs [1]. Strains resistant to commonly used drugs have been described [2-3]. Repeated exposure to infection elicits immunity [4-5], suggesting vaccination is a promising alternative to the current unsustainable use of anthelmintics. Immuno-screening and proteomics studies have identified potential vaccine candidates in *T. circumcincta* Excretory/Secretory (ES) products. One candidate is Cathepsin F (Tci-CF-1), a cysteine protease [6]. A recombinant version was expressed in the yeast, *Pichia pastoris*; however, this protein lacked enzymatic activity and, compared to native Tci-CF-1, was poorly recognised by the host immune response in ELISA experiments. This may be due to incorrect folding or altered post-translational modifications (PTMs) of the recombinant yeast version, which may affect ability to induce protective immune responses.

To express Tci-CF-1 in a more similar form to the native protein, we have used the free-living nematode *Caenorhabditis elegans* as a novel expression system. A gene construct coding for Tci-CF-1 was micro-injected into *C. elegans* and the recombinant protein was purified from stable expressing lines. Using immune gastric lymph, no immune reactivity to either recombinant Tci-CF-1 was observed in ELISA experiments, however a small degree of antibody binding was observed in western blots, suggesting conserved linear epitopes became available once either protein was denatured. Glycosylation was confirmed in each Tci-CF-1 version, with *P. pastoris*-expressed Tci-CF-1 showing hyperglycosylation compared to native and *C. elegans*-expressed version. As a measure of correct protein folding, we investigated the enzymatic activity of both recombinant Tci-CF-1 versions. Neither proenzyme showed the ability to *self*-activate, however once *trans*-activated by an exogenous protease, both recombinant Tci-CF-1 versions were able to digest the cysteine protease-specific substrate Z-FR-AMC. This is the first successful attempt to generate *T. circumcincta* antigens using *C. elegans* as expression system.

Acknowledgements:

Moredun Research Institute, University of Glasgow, Dave Bartley, Louise McLean, Alison Morrison

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Session Details:	8/27/2013 VACCINES - NEMATODES 1015 - 1130 <i>Meeting Room 8</i>
Oral Presentation Details:	Mitigating the impact of infection by desensitising sheep to nematode antigens
Presentation Time:	1045 -1100
Authors:	AW Greer¹ , A Hogan ¹ , CM Logan ¹ , RW McAnulty ¹ , JF Huntley ² , TN McNeilly ² ¹ Lincoln University, Christchurch, NEW ZEALAND ² Moredun Research Institute, Penicuik, UNITED KINGDOM

Gastro-intestinal nematodes cause considerable production loss in grazing livestock. Recent advances in our understanding of the host x nematode relationship have identified a majority of lost animal productivity during infection with some species of sheep parasites are a consequence of the host immune response. As such, manipulating the immune response by desensitising to nematode antigens may provide novel methods of mitigating the impact of infection and improve animal productivity. Twenty-one helminth-free 4 month old lambs sheep were allocated hierarchically by live weight into one of three treatment groups (n=7). One group (group DES) was subjected to a desensitising regime that consisted of repeated exposure to a *Trichostrongylus colubriformis* antigen preparation while the remaining two groups (CON and INF) were sham treated with PBS. Following the desensitising regime, DES and INF groups were infected with 2500 *T. colubriformis* L3 larvae per day, leaving CON animals as an uninfected control. As expected during infection with this nematode, liveweight gain of all groups was similar for the first three weeks of infection, being 258 ± 46.2 , 263 ± 44.1 and 264 ± 31.6 g per d for CON, INF and DES groups, respectively ($P>0.05$). In comparison, during weeks three to seven of infection, mean liveweight gains were 265 ± 25.4 , 61 ± 30.5 and 184 ± 26.7 g per d for CON, INF, and DES, respectively ($P<0.001$). No difference in faecal egg output between INF and CON animals were observed ($P>0.05$). Overall, despite nematode infection reducing lamb growth rates by 77% compared with the uninfected controls, the desensitising regime was able to recover 60% of the loss in performance associated with infection. Although further investigation and refinement is required, manipulating the immune response through desensitising animals to nematode antigens provides a novel avenue for mitigating the impacts of parasitism in grazing livestock.

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Session Details:	8/27/2013 VACCINES - NEMATODES 1015 - 1130 Meeting Room 8
Oral Presentation Details:	Vaccination with double-domain ASP confers significant protection against <i>Cooperia oncophora</i> challenge infection
Presentation Time:	1100 -1115
Authors:	Claerebout E, Borloo J, Peelaers I, De Wilde N, Casaert S, Van Coppernelle S, Sarre C, Vercruysse J, Geldhof P Ghent University

Infections with gastro-intestinal nematodes are a major constraint on ruminant welfare and production worldwide. *Cooperia oncophora* is one of the most prevalent gastrointestinal parasites in grazing cattle. Current control of GI nematode infections mainly relies on anthelmintic treatments. Vaccination may be a future alternative or complementary strategy to control *Cooperia* infections. In an attempt to identify protective antigens, excretory-secretory (ES) proteins were produced from adult *C. oncophora*. Fractionation of adult worm ES proteins using size-exclusion chromatography resulted in three distinct groups of proteins, in the high, medium and low molecular weight regions, respectively. Mass spectrometry analysis showed that the high molecular weight (HMW) fraction mainly consists of a double-domain activation-associated secreted protein-like protein (ASP).

Immunisation of calves with the HMW fraction and Quil A adjuvant resulted in a 91% reduction of cumulative faecal egg counts and 50% reduction in worm counts after a trickle challenge infection with 25,000 infective larvae. A higher percentage of inhibited L4 larvae and smaller adult worms were also observed in the vaccinated calves. This is the highest level of protection that has been obtained with a vaccine against *C. oncophora* up to date.

ASP-specific IgG1 levels were significantly higher in the vaccinated calves and a significantly higher proliferation of natural killer cells was measured after *in vitro* stimulation of mesenteric lymph node cells in calves vaccinated with the ASP antigens, compared to the control group. Further characterisation of the immune responses induced by vaccination and of the protein structure of double-domain ASP may be helpful to design a protective recombinant vaccine and to optimise antigen delivery.

Acknowledgements:

This study received funding from FP7 (Paravac project) and Zoetis



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Session Details:	8/27/2013 VACCINES - NEMATODES 1015 - 1130 Meeting Room 8
Oral Presentation Details:	Structural and functional studies with H-gal-GP, a major antigenic component of “Barbervax”.
Presentation Time:	1115 -1130
Authors:	G.F. Newlands ^{1*} , S Meunsch ² , J. Trinick ² , W.D. Smith ¹ ¹ Moredun Research Institute, Bush Loan, Penicuik, Midlothian, EH26 0PZ, UK ² University of Leeds

Haemonchus galactose containing glycoprotein (H-gal-GP) complex has been known for almost 20 years to possess protease activity and to have a protective function if used to immunise sheep against a challenge infection of Haemonchus. Localised on the intestinal micro-villar membrane of the parasite, H-gal-GP has a molecular weight of about 1 million Daltons and consists mainly of families of four metallo and two aspartyl proteases. More recent electron microscopy studies have revealed that the complex has a fascinating symmetrical structure, apparently containing an internal chamber which has two larger and three smaller apertures. Molecular modelling suggests that the active sites of the proteases face into the chamber and that the most abundant blood proteins, haemoglobin and albumin could fit through the larger apertures. Thus it is speculated that these proteins are digested in the chamber and that the whole complex behaves like a protease machine. Further modelling suggests that if immunoglobulin molecules were to bind to the complex near its larger apertures, entry of host blood proteins into the chamber would be blocked. Thus it is possible that the vaccine induced antibodies could reduce efficient blood meal digestion in this way, leading to starvation, reduced egg output and eventual loss of worms.



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Session Details:	8/27/2013 DRUG RESISTANCE SMALL - RUMINANTS 1 1330 - 1445 Riverside Theatre
Oral Presentation Details:	Can combination anthelmintics be used once resistance to multiple actives has developed?
Presentation Time:	1330 -1345
Authors:	Waghorn T¹, Leathwick D¹, Rhodes T², Pomroy B³ ¹ AgResearch, ² PGG Wrightsons, ³ Massey University

In 2010 a programme to evaluate Best Practice Parasite Management practices on commercial farms in New Zealand was initiated. Sheep farms were selected on the basis of having significant problems involving resistance to 2 or more anthelmintic classes. The aims were to manage parasitism, maintain or improve on existing production figures, and ensure that the efficacy of anthelmintics did not decline further.

A management programme was designed specifically for each farm by a parasitologist, a farm consultant, a local veterinarian and the farmer. Strategies implemented included minimising unnecessary treatments whilst maintaining a strategic preventive drenching programme, maintaining refugia of susceptibility and the use of combinations of different anthelmintic classes. Regular monitoring included multiple faecal egg counts combined with an annual faecal egg count reduction test.

Resistance levels varied between farms with some (n=3) having significant resistance to all of the older anthelmintic classes, whilst all except 1 of the remainder had resistance to 2 classes. In most cases the resistant parasite was *Teladorsagia (Ostertagia) circumcincta*. On all farms combination anthelmintics were used almost exclusively, the exceptions being strategic use of new actives or moxidectin.

Uptake of resistance management practices by farmers was high as long as strategies were simple, practical and the rational for use understood. Monitoring indicated that in most cases parasite load was acceptable and farmers were happy with animal performance. The effectiveness of anthelmintics against *T. circumcincta* over time showed a significant positive slope indicating that overall, efficacy increased over the duration of the study. The use of combination anthelmintics in conjunction with other resistance management strategies appears to have resulted in meaningful improvements in treatment efficacy despite significant multiple-resistance being present initially. The hypothesis that combinations cannot be usefully employed once resistance has developed is not supported by the results of this study.

Acknowledgements:

This project was funded by MAF-SFF, Beef+LambNZ, AgMardt and MSD.



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Session Details:	8/27/2013 DRUG RESISTANCE SMALL - RUMINANTS 1 1330 - 1445 Riverside Theatre
Oral Presentation Details:	Lack of efficacy of monepantel against <i>Teladorsagia circumcincta</i> and <i>Trichostrongylus colubriformis</i>
Presentation Time:	1345 -1400
Authors:	Ian S ¹ , Bill P ¹ , Paul K ¹ , Greg S ² , Barbara A ¹ , Moss A ¹ ¹ Massey University, ² Totally Vets, Fielding, New Zealand

Cases of parasitic gastroenteritis were observed in goats on a small, 3ha property grazing small numbers of goats and sheep. These cases arose despite recent treatment with monepantel. The property had a history of resistance occurring to all three of the traditional drench families (benzimidazole, imidathiazole and macrocyclic lactone) and had thus switched to using monepantel approximately 2 years beforehand. To investigate the problem further, 2 faecal egg count reduction tests (FECRT) were conducted using goats and sheep resident on the property. In the first, 12, mixed age goats were treated with approximately 1.5x (n=8) and 3x (n=4) the sheep dose of monepantel (3.9 and 7.7 mg/kg respectively) and resampled 8 days later. In the FECRT in sheep, 15, 2 to 3 month old lambs were treated with 3.0mg/kg monepantel, followed 7 days later by treatment with a triple combination (5mg/kg oxfendazole, 8.8mg/kg levamisole HCl and 0.22mg/kg ivermectin). In the slaughter study, 12, 9 month old lambs were grazed on the goat property for 5 weeks, before being brought indoors for 2 weeks after which time half were treated with monepantel (2.9mg/kg). All 12 lambs were killed for worm counts 9 days after treatment. In the FECRT in goats, neither the 1.5x nor the 3x dose of monepantel were associated with any reduction in egg output. Likewise, in the FECRT in lambs, egg counts were unaffected by treatment with monepantel and were only reduced by 91.5% by the triple combination. In the slaughtered animals, the worm counts indicated that monepantel had negligible efficacy against both *Teladorsagia circumcincta* and *Trichostrongylus colubriformis*.

Acknowledgements:

The monepantel for the slaughter study was kindly provided by Novartis New Zealand Ltd. The assistance of the farm owners is gratefully acknowledged.



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Session Details:	8/27/2013 DRUG RESISTANCE SMALL - RUMINANTS 1 1330 - 1445 <i>Riverside Theatre</i>
Oral Presentation Details:	First evidence for on-farm multi-drug resistance in sheep parasites in Northern Ireland
Presentation Time:	1400 -1415
Authors:	Blair S , Maule A, Marks N Queens University Belfast

The over-reliance on a small portfolio of anthelmintics, coupled with their misuse means that their utility as long-term parasite control options has been undermined. Although supporting evidence includes ever-increasing reports of anthelmintic resistance in sheep flocks^{1,2,3}, there has been a significant lack of data on anthelmintic resistance levels in Northern Ireland (NI). A recent faecal egg count reduction test (FECRT) study via postal survey conducted by McMahon et al. (2013) reported resistance levels of 77% to Benzimidazoles (BZ), 47% to Avermectins (AVM) and 12.5% to Levamisole (LV) in flocks from across NI. Here we used FECRT to detect evidence of resistance on 42 sheep farms across NI. To ensure experimental consistency and data integrity, all sample collections, drug administrations and FERCTs were performed by the lead author. Egg count reductions post treatment of less than 95% (where pre treatment counts were over 150 eggs per gram of faeces [EPG]) were seen 8-10 days post BZ treatment on 65.7% of farms, 14-17 days post AVM treatment on 56% of farms, 3-7 days post LV treatment on 23% of farms and 7 days post AAD treatments on 0% farms. ML and BZ were tested together on 19 of the farms, with FECR below 95% on 31.6%. BZ and LV were tested together on 11 farms with FECR below 95% on 20%. This is the first evidence of multi-drug resistant sheep parasites on farms in NI and demands an alteration to the prevailing parasite control strategies in use in the province.

Acknowledgements:

Department of Agriculture and Rural Development for Northern Ireland
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References:

^{1,2,3} Besier 2007; Jones et al. 2012; Mitchel et al. 2010



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Session Details:	8/27/2013 DRUG RESISTANCE SMALL - RUMINANTS 1 1330 - 1445 <i>Riverside Theatre</i>
Oral Presentation Details:	Resistance to monepantel in two nematode species in goats
Presentation Time:	1415 -1430
Authors:	Leathwick D , Miller C, McMurtry L AgResearch

A small commercial goat farm running approximately 70 mixed breed meat goats began using monepantel (Zolvix™, Novartis Animal Health) on a limited basis in 2009. In a 2012 post-treatment faecal egg count (FEC) 7 of 8 samples were positive with a mean egg count of 125. As a result of this finding a faecal egg count reduction test was conducted. Twenty six does were weighed, sampled for FEC and treated to individual liveweight with 3.75 mg/kg monepantel. The resulting percentage reduction in mean FEC, 10 days later, was 21.8% (means of 192 epg and 150 epg pre- and post-treatment, respectively). The same animals were then divided into groups of 8-9 and treated with either, abamectin at 0.3 mg/kg, levamisole at 12.0 mg/kg or albendazole at 7.5 mg/kg. A further 7 days later the reductions in FEC for abamectin, levamisole and albendazole were 68.1%, 63.6% and 38.1% respectively. Subsequent treatment with a derquantel + abamectin combination product was 100% effective at eliminating FEC.

Twenty eight, previously worm free lambs grazed pastures on the farm for 14 days before being housed indoors. Three weeks after housing they were randomly divided on FEC into 5 groups and treated with either monepantel at 2.5 mg/kg, abamectin at 0.2 mg/kg, levamisole at 8 mg/kg or albendazole at 5.0 mg/kg. Fifteen days after treatment all lambs were euthanased for worm count. Efficacy of all treatments against *Haemonchus contortus* and *Trichostrongylus axei* were >99%. Efficacy of monepantel against adult worms of *Teladorsagia (Ostertagia) circumcincta* and *Trichostrongylus colubriformis* was zero and 7%, respectively. Resistance to the other anthelmintics tested in both these worm species was confirmed.

This study confirms the development to high levels of resistance to monepantel in two common nematode species in goats.





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Session Details:	8/27/2013 DRUG RESISTANCE SMALL - RUMINANTS 1 1330 - 1445 <i>Riverside Theatre</i>
Oral Presentation Details:	A survey investigating gastro-intestinal nematode egg output of sheep following treatment with long acting anthelmintics on farms in New Zealand and Australia
Presentation Time:	1430 -1445
Authors:	Bailey J ¹ , Brown B ¹ , McKay C ¹ ¹ Novartis Animal Health Australasia Pty Ltd, North Ryde NSW 2113, Australia, ² Novartis Animal Health Australasia Pty Ltd, North Ryde NSW 2113, Australia, ³ Novartis Animal Health Australasia Pty Ltd, North Ryde NSW 2113, Australia

The development of bolus anthelmintic delivery technology and novel chemistry has given sheep farmers the option of treating animals with long acting (LA) anthelmintic products prior to or during periods of high larval challenge or low immunity. The aim of these treatments is to control parasitic nematode infections present at time of treatment, prevent the establishment of new infections by killing incoming larvae and to significantly reduce the subsequent exposure of other sheep to incoming third stage infective larvae. This technology has been embraced by farmers in Australia and New Zealand such that LA products currently account for approximately 25% of the sheep drench market by value, largely associated with pre-lambing treatment of ewes. However, the major downside of treatment with LA products is that they are widely considered to be a high risk activity in terms of selection for anthelmintic resistance.

A reduction in the claimed period of protection is usually the first indication of development of resistance to long acting anthelmintics. To get a current indication of the possible level of resistance to these anthelmintics and their ability to achieve their desired aims, surveys were conducted on sheep farms in Australia and New Zealand. These surveys assessed the presence and level of gastro-intestinal nematode egg output from sheep following treatment with LA products and prior to expiry of the claimed payout period. In ewes and ewe hoggets in New Zealand, positive faecal egg counts were found during the payout period in 19 of the 30 flocks tested. The results of this study support the incorporation of “exit” treatments using an active (or actives) from a different anthelmintic family to the active present in the LA product, along with adoption of other risk mitigation strategies to facilitate more sustainable use of LA anthelmintic products.

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Session Details:	8/27/2013 DIAGNOSTICS - APICOMPLEXA 1330 - 1445 <i>Meeting Room 1</i>
Oral Presentation Details:	Results of a nationwide coccidiosis survey using a simple, one-tube assay for the simultaneous detection and diagnosis of the ten Australian <i>Eimeria</i> of chicken.
Presentation Time:	1330 -1345
Authors:	RM Godwin and JAT Morgan (1) Animal Science, Queensland Department of Agriculture, Fisheries and Forestry, The University of Queensland, St Lucia, Queensland, Australia and (1) Queensland Alliance for Agriculture and Food Innovation (QAAFI), The University of Queensland, St Lucia, Queensland, Australia

Coccidiosis is a costly worldwide enteric disease of chickens caused by parasites of the genus *Eimeria*. The aim of this project was to examine the genetic diversity of *Eimeria* species within Australia. Broad-scale screening of faeces from unvaccinated backyard and commercial flocks were conducted bi-annually over 3 years. Samples were screened using a newly developed PCR based assay which is capable of detecting all 10 species of *Eimeria*, including OTUs X, Y and Z. This one tube assay is simple, low cost and has the capacity for high-throughput screening. The nationwide survey of 125 commercial flocks and 136 back yard flocks detected all seven species and three OTU's. Overall 80% of the samples were infected with *Eimeria* and most were mixed-species infections (90%). The most common species found in commercial flocks are *E. acervulina* and *E. maxima*. In contrast, coccidiosis in backyard flocks was largely due to *E. mitis* and OTU-Y.





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Session Details:	8/27/2013 DIAGNOSTICS - APICOMPLEXA 1330 - 1445 <i>Meeting Room 1</i>
Oral Presentation Details:	Advanced studies on coccidian parasites of cattle
Presentation Time:	1345 -1400
Authors:	El-Seify M ¹ , Desouky A ¹ , Khalfalla R ¹ , Ahmed A ² , Sorour S ¹ ¹ ¹ Deaprtment Of Parasitology, Faculty Of Veterinary Medicine, Kafrelsheikh University, ² ² Central diagnostic lab, Faculty of Veterinary Medicine, Kafrelsheikh University, 33516 Kafr El-Sheikh, Egypt

In the present study, examination of faecal samples of 698 animals (592 cattle and 106 buffaloes). The results showed that:

1. Prevalence of *Eimeria* and *Cryptosporidium* species were 28.9% and 34.1%, respectively.
2. Eleven *Eimeria* species were identified and *E. bovis* and *E. zuernii* were the most pathogenic in both cattle and buffaloes.
3. Two species of *Cryptosporidium* were identified *C.andersoni* and *C.parvum*.
4. Genomic DNA samples obtained from 30 faecal samples, which were divided into 3 groups according to mean number of *Cryptosporidium* oocysts/ per field (group A 1-10 oocysts/ field), group B (11-20 oocysts/ field), group C (more than 20 oocyst/ field). All samples were screened by nested PCR (primary and secondary PCR) using Cowp gene specific primers. Only 18(60%) of samples showed primary PCR amplification of ~ 422bp products with Cowp₁ and Cowp₂ primers. While secondary PCR showed positive amplification of ~ 312bp products by using Cowp₃ and Cowp₄ primers. The entire samples which were positive in primary PCR were also positive in secondary PCR.

The *Cryptosporidium* spp. samples, group A (Less than 10 oocysts/ field) were difficult to be detected by PCR than those group B (10- 20 oocysts/ field) or group C (over 20 oocysts/ field).

This study demonstrates the advantages of molecular diagnosis of coccidian protozoans in the farm animals. Further studies are encouraged to clarify the taxonomic status of coccidian protozoans infects farm animals.

Key words: Cattle, Coccidia, Cryptosporidium, Molecular, Diagnosis

Session Details:	8/27/2013 DIAGNOSTICS - APICOMPLEXA 1330 - 1445 <i>Meeting Room 1</i>
Oral Presentation Details:	Immuno-PCR for detection of <i>Giardia lamblia</i> cysts in water
Presentation Time:	1400 -1415
Authors:	Deng M¹ , Xiao X, Ji X ¹ Shandong Entry-Exit Inspection And Quarantine Bureau, ² Shandong Entry-Exit Inspection And Quarantine Bureau, ³ Xinjiang Entry-Exit Inspection And Quarantine Bureau

The protozoan pathogens *Giardia lamblia* is one of the major causes of waterborne enteric disease throughout the world. For many years, microscopic examination of water and stool samples has been considered to be the “gold standard” for diagnosis of *Giardia lamblia*. Many diagnostic methods, including PCR, real time PCR, and LAMP techniques were often used as a rapid screening tool for the initial diagnosis of *Giardia lamblia* in most laboratories. However, many factors, such as inhibitory substances in the samples and inefficient DNA extraction, may greatly affect the sensitivity of the gene assay. DNA detection of *Giardia lamblia* tends to result in a false negative result. In our study, detecting *Giardia lamblia* cysts at low concentrations for the water was carried out using a highly sensitive immunological-polymerase chain reaction (immuno-PCR, IPCR) method. Magnetic gold particles were pre-coated with a monoclonal anti-Giardia, and *Giardia lamblia* cysts were diluted in 500 µl water ranging from 1-100 cysts. A biotinylated detection antibody bound to the *Giardia lamblia* cysts was then linked via a streptavidin bridge to biotinylated Giardia-reporter DNA. After extensive washing, reporter DNA was released by denaturation, transferred to PCR tubes, amplified, electrophoresed and visualized. An optimized IPCR method was able to detect as little as 5 *Giardia lamblia* cysts. To further evaluate the specificity and the clinical application of this immuno-PCR (IPCR) assay for *Giardia lamblia* cysts, the *Entamoeba histolytica* and *Cryptosporidium parvum* were collected and detected by IPCR. Our data demonstrated that this monoclonal antibody-based immuno-PCR method is especially the case for analysis of environmental water samples in which the densities of *Giardia lamblia* cysts is very low, and provides us a platform capable of rapid screening of water samples from drinking water, wells, rivers, lakes, and recreational swimming pools for trace levels of *Giardia lamblia* cysts.

Acknowledgements:

This study received financial support from public welfare project of china (201110039). We thank colleagues in animal disease laborioried of Shandong entry-exit inspection and quarantine bureau for the dilution and Enumeration of the *Giardia lamblia* cysts and the collection and purification of the *Entamoeba histolytica* eggs.

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Session Details:	8/27/2013 DIAGNOSTICS - APICOMPLEXA 1330 - 1445 <i>Meeting Room 1</i>
Oral Presentation Details:	A comparison of sequencing technologies for the screening of <i>Cryptosporidium</i> infections in biological samples
Presentation Time:	1415 -1430
Authors:	Paparini A¹, Bunce M², Haile J², White N², Ryan U¹ ¹ School of Veterinary and Life Sciences, Murdoch University, Murdoch WA, AUSTRALIA, ² Australian Wildlife Forensic Services and Ancient DNA Laboratory, School of Veterinary and Life Sciences, Murdoch University, Murdoch, AUSTRALIA

The advent of second generation, high-throughput pyrosequencing (HTS) platforms is rapidly revolutionizing several research areas in the Life Sciences. Sequencing of genes, genomes, and metagenomes is now routinely carried out in many laboratories, however, the application of HTS technologies to characterize *Cryptosporidium* infections in biological samples has not been previously attempted. This approach may likely prove to be an ideal technique to genetically audit the species composition of multiple samples in parallel, in a rapid and cost-effective fashion.

In the present study, we conducted a targeted HTS analysis of 18 *Cryptosporidium*-positive faecal samples, and compared the results to Sanger sequencing, and PCR-RFLP, of the 18S rRNA gene.

All species detected by Sanger sequencing were also detected by pyrosequencing, with the exception of one sample, for which pyrosequencing provided too few reads. Pyrosequencing proved to be highly sensitive, rapid, cost-effective and more efficient than the other approaches, in detecting mixed *Cryptosporidium* infections.

In one third of the samples, HTS also detected possibly novel parasite genotypes, which were not detected by Sanger sequencing. As some of these rare DNA variants probably represent experimental artefacts, rather than evidence of actual infections, the need of a rational laboratory setup and a careful interpretation of the results is discussed. Despite this, the superior depth of coverage, offered by HTS, still represents a clear advantage over more traditional approaches, especially when rare genetic variants and/or mixed infections are present in a clinical sample.

Acknowledgements:

The authors wish to thank Ms. Josephine Ng for the PCR-RFLP results

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Session Details:	8/27/2013 DIAGNOSTICS - APICOMPLEXA 1330 - 1445 <i>Meeting Room 1</i>
Oral Presentation Details:	Phylogenetic analysis of <i>Trypanosoma congolense</i> and <i>Trypanosoma vivax</i> detected in naturally infected Nigerian cattle breeds
Presentation Time:	1430 -1445
Authors:	Michael I. Takeet^{1,2,3*} , Benjamin O. Fagbemi ² Marcos De Donato ^{3,4} , Abdulmojeed Yakubu ^{3,5} , Hectorina E. Rodulfo ⁴ , Sunday O. Peters ^{1,3} , Matthew Wheto ¹ , and Ikhide G. Imumorin ³ ¹ Federal University of Agriculture, Abeokuta, NIGERIA ² University of Ibadan, Ibadan, NIGERIA ³ Cornell University, Ithaca, USA ⁴ Universidad de Oriente, Cumana, VENEZUELA ⁵ Nasarawa State University, Lafia, NIGERIA

Genetic diversity of *Trypanosoma congolense* and *Trypanosoma vivax* detected in naturally infected cattle in Northern Guinea Savannah and rain forest of Southwestern Nigeria was assessed using the variable region of internal transcribed spacer 1 (ITS1) of ribosomal DNA sequences for the first time. Of 411 samples analyzed, species specific primers detected 262 positive samples and the ITS1 primers detected 186 positive samples with the sizes of the amplified ITS1 PCR products ranging from 250bp to 700bp. Alignment of the ITS1 rDNA sequences of *T. congolense* and *T. vivax* with the available sequences in the GenBank revealed 91% to 95% and 97% to 100% homology, respectively, with GC content ranging from 49.4 and 61.9% for *T. congolense* and *T. vivax*, respectively. Extensive sequence variations and length polymorphisms were noted in both species but sequence similarity of the ITS1 was higher in *T. vivax*. Phylogenetic analysis of the two species of trypanosomes based on maximum-likelihood (ML) and unweighted pair group with arithmetic mean (UPGMA) methods revealed similar topologies. While *T. congolense* and *T. vivax* sequences from Nigeria cattle clustered together within each clade formed by the two species, the *T. congolense* and *T. vivax* from East Africa were distantly placed from the Nigerian isolates of respective species but *T. vivax* from Venezuela clustered within Nigeria isolates of *T. vivax* clade. This study supports the hypothesis that trypanosomes isolates from Nigeria are clearly separated from the East African species, but more related to Latin American isolates which may have some consequences for treatment and control.

Acknowledgement:

This research was funded by Education Trust Fund for Staff Training and Development of the Federal Republic of Nigeria and supported by College of Agriculture and Life Sciences, Cornell University. Ithaca, New York, USA.



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Session Details:	8/27/2013 DOG AND CAT PARASITES 1 1330 - 1445 Meeting Room 2
Oral Presentation Details:	Recent <i>Dirofilaria</i> Spp. Distribution Information In Northern Europe
Presentation Time:	1330 -1345
Authors:	Oksanen A ¹ , Nygren K ² , Heikkinen P ¹ , Laaksonen S ³ , Petkevièius S ⁴ , Näreaho A ³ ¹ Finnish Food Safety Authority Evira, Production Animal And Wildlife Health Research Unit (FINPAR), ² Finnish Game and Fisheries Research Institute, ³ University of Helsinki (FINPAR), ⁴ Lithuanian University of Health Sciences

The bloodsucking insect vector –borne nematode genus *Dirofilaria* comprises 2 species known to exist in Europe; *D. immitis* and *D. repens*. They are both zoonotic, but principally parasites of dogs. *Dirofilaria immitis*, the causative agent of heartworm disease, is still confined to the Mediterranean countries. The cause of subcutaneous dirofilariosis, *D. repens*, has been increasing its distribution northward from Southern Europe during the last decades. We review the recently observed occurrence of *D. repens* infection in the Baltic States, as well as present data about the distribution of *Dirofilaria ursi* in the brown bear (*Ursus arctos*) in Finland.

In Latvia, *D. repens* microfilariae were found in 3 % of a large number of canine blood samples investigated 1n 2008-2011. The first clinical dog case was found in 2011, and a human infection was described the same year. In Lithuania, two *D. repens* infected dogs were found in 2011. Both were domestic born and raised, infection considered autochthonous. From this cluster of cases, it appears clear that *D. repens* has in the early 2010s already been established in the Baltic States. This fits in the *Dirofilaria*-in-mosquito-development models published recently, with L3 development possible in Latvia in July and August. With climate change, the development threshold is expected to move northward, facilitating *D. repens* life cycle even more northerly in Europe.

Dirofilaria ursi parasites have been seen in hunted brown bears at least for 3 decades with a high prevalence in Finnish Karelia, around 70-80 % of adult bears. The identified range of the parasite includes North America, Japan and Siberia, but there appear to be no properly published records from Europe. Mosquitoes are the vectors of *D. immitis* and *D. repens*, but blackflies are described as the vectors of *D. ursi*. Its in-vector developmental temperature and Growing-Degree-Days requirements are apparently lower than those of *D. immitis* and *D. repens*. What climate change will do to the distribution of *D. ursi* is to be seen, but, however, first its current distribution in Europe should be clarified.





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Session Details:	8/27/2013 DOG AND CAT PARASITES 1 1330 - 1445 <i>Meeting Room 2</i>
Oral Presentation Details:	New insights into diagnosis and epidemiology of <i>Angiostrongylus vasorum</i> in European countries
Presentation Time:	1345 -1400
Authors:	Schnyder M¹, Schaper R², Morgan E³, Deplazes P¹ ¹ Institute of Parasitology, University of Zurich, ² Bayer Animal Health, Leverkusen, Germany, ³ School of Biological Sciences, University of Bristol, Woodland Road, Bristol, BS8 1UG, United Kingdom

Canine angiostrongylosis is a cardiopulmonary disease which can be fatal if left untreated. Adults of *Angiostrongylus vasorum* live in the right heart and the pulmonary arteries of dogs and foxes, while gastropods act as intermediate hosts. Routine diagnosis is currently performed through the isolation of first stage larvae (L1) by larval migration methods (Baermann method) from multiple, fresh faecal samples. However, this method has a restricted sensitivity in case of low worm burdens, and it is unsuitable during prepatency. Novel tools such as serological methods and PCR have been described, and they may overcome these shortcomings. Experimentally infected dogs were available for a comparative analysis of Baermann results, PCR-based detection of *A. vasorum* DNA in tracheal swabs, blood and faecal samples, and ELISAs for detecting circulating antigens of *A. vasorum* or specific antibodies against *A. vasorum*. Thus, a high performance of the serological methods was demonstrated. Both ELISAs were validated in a field study with sera of dogs from Italy from which also Baermann results were available, proving their validity as alternative, rapid and affordable tests. *A. vasorum* originally was known from endemic foci in e.g. south-western France, Ireland and Italy but has increasingly been reported in extended areas in central and western European countries and also in Canada during the last decades. In large scale surveys with canine sera from Germany, Great Britain, Poland and further European countries, the endemic presence of *A. vasorum* in known regions was confirmed, and additional cases were detected outside of the known endemic foci. In these areas, it is crucial to disseminate the information of the occurrence of *A. vasorum* and to increase disease awareness among veterinarians in order to prevent fatal cases. Early diagnosis has a good prognosis for *A. vasorum* affected dogs through adequate anthelmintic treatment before the onset of pathological changes, which can precede evident clinical signs. Monthly use of adequate anthelmintics or routine screening of dogs are recommended in endemic areas.

Acknowledgements:

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Session Details:	8/27/2013 DOG AND CAT PARASITES 1 1330 - 1445 <i>Meeting Room 2</i>
Oral Presentation Details:	The efficacy of a topically applied imidacloprid 10% / moxidectin 2.5% formulation (Advocate®, Advantage Multi® Bayer) against immature and adult <i>Spirocerca lupi</i> worms in experimentally infected dogs.
Presentation Time:	1400 -1415
Authors:	Austin C^{1,2}, Kok D³, Crafford D³, Schaper R⁴ ¹ Bayer (Pty) Ltd, P.O. Box 143, Isando, 1600, South Africa, ² Faculty of Veterinary Science, University of Pretoria, Private Bag X20, Hatfield, 0028, South Africa, ³ Clinvet International (Pty) Ltd, P. O. Box 11186, Universitas, Bloemfontein, 9321, South Africa, ⁴ Bayer Animal Health GmbH, 51368 Leverkusen, Germany

This study investigated the efficacy and safety of an imidacloprid 10% / moxidectin 2.5% spot-on combination (Advocate®, Advantage Multi®, Bayer) against immature and mature stages of *Spirocerca lupi* in experimentally infected dogs. 24 dogs were allocated to 3 groups and infected with approximately 10 L3 larvae of *S. lupi* orally on study day (SD) +2, +14, +28 and +42. Group 1 remained as untreated control group. Group 2 dogs were treated on SD -28, 0, and thereafter monthly until day 280 (12 treatments). Group 3 dogs were treated weekly on 19 occasions starting on SD +170. The dosage for all treatments was the licensed dose of 10 - 25 mg imidacloprid / 2.5 – 6.25 mg moxidectin per kg bodyweight. All dogs were examined on SD +169 or +176 by endoscopy. Group 3 dogs were additionally examined regularly up to day 296. On SD +308 or +310 all dogs were necropsied to recover *S. lupi* worms and to quantify lesions in the thoracic aorta and oesophagus. Dogs in the control group were adequately infected with *S. lupi*, demonstrated by the extensive damage to the thoracic aorta, the nodules in the oesophagus and the large numbers of worms recovered. In total 144 worms were collected (gm of 16.8 worms per dog). Dogs in group 2 had no or very slight damage to the thoracic aorta and no nodules or worms in the oesophagus, indicating 100 % efficacy. Dogs in group 3 were also adequately infected, showing extensive damage in the thoracic aorta and nodules in the oesophagus. After treatment three dogs of 8 still had few nodules and in total three worms (GM of 0.25 per dog) were recovered, demonstrating an efficacy of 98.5 % against adult *S. lupi*. All dogs tolerated the treatment well and no treatment related adverse events occurred.



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Session Details:	8/27/2013 DOG AND CAT PARASITES 1 1330 - 1445 <i>Meeting Room 2</i>
Oral Presentation Details:	Host-parasite proteome from canine faecal samples
Presentation Time:	1415 -1430
Authors:	Jones F¹ , Lipscombe R ² , Thompson A ¹ ¹ Murdoch University, ² Proteomics International

Gastrointestinal tract infections are important in a medical context. The clinical practitioner relies on patient history and clinical diagnostics to eliminate causative factors. Research has clearly indicated the need to include enteric protozoan parasites in the differential diagnosis of gastro-intestinal tract infections. An increasing incidence of human gastroenteritis infections and associated changes in lifestyle patterns are modern day dilemmas, and recent reports allude to increasing demands on health systems.

Equally, human lifestyles are reflected in the nature of relationships with animals, particularly companion animals. Australians are pet lovers, with 36% of Australian households owning a dog, although most pet owners are unaware of recent research indicating that over twenty percent of all dogs are infected with parasites. *Giardia* spp. rely upon a faecal-oral transmission route and infections are not always straightforward to diagnose. Existing tests to diagnose *Giardia duodenalis* examine faecal material for the presence of *Giardia* cysts using light microscopy. Increasingly copro-antigen diagnostic tests, based upon the detection of *Giardia* surface proteins, have become commercially available. These methods are unable to differentiate between host specific and potentially zoonotic *Giardia* infections and the diagnosis of *Giardia* infections is often unreliable.

In a proteomic approach to identify proteins associated with *Giardia* infections and seek biomarkers to differentiate between *Giardia* genotypes, canine faecal samples were collected from dogs naturally infected with *Giardia duodenalis*. Freshly collected samples were homogenised and precipitated to extract total faecal protein content. Tryptic digestion of extracted protein pellets released peptides that were further separated using a strong cation exchange column; fractions were collected and submitted for ion fragmentation using MALDI-TOF/TOF mass spectrometry. Spectra generated were analysed and compared to existing protein databases.

The results confirm detection of proteins from canine faecal matter originating from *Giardia*, together with host proteins, providing a new insight into host-parasite interactions.

Acknowledgements:

State Agricultural Biotechnology Centre (SABC) of Western Australia

West Australian Institute for Medical Research (WAIMR)

References:

Palmer et al. (2008)

Steuart et al. (2008)



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Session Details:	8/27/2013 DRUG DISCOVERY 1330 - 1445 <i>Meeting Room 3</i>
Oral Presentation Details:	Haem Uptake in <i>Schistosoma mansoni</i>
Presentation Time:	1330 -1345
Authors:	Shu Qin Toh^{1,2*} , David Malagon Martinez ¹ , Geoffrey Gobert ¹ , Malcolm Jones ^{1,2} ¹ Queensland Institute of Medical Research, Brisbane, AUSTRALIA ² University of Queensland, Brisbane, AUSTRALIA

Schistosomes are parasitic blood flukes that feed on red blood cells and other blood components to obtain essential nutrients and amino acids for growth, development and reproduction. In the process of ingesting and breaking down erythrocytes, large quantities of haem are released. Despite its potential toxicity when in abundance, haem is a biologically important molecule for schistosomes, as demonstrated by the numerous haemoproteins expressed by the parasites. However, knowledge on haem biosynthesis and the associated uptake in schistosomes is limited and contradictory. The aim of this study is to provide a better understanding of the uptake of haem and the underlying molecular mechanisms involved. To demonstrate the presence of a haem uptake system in adult schistosome, pulse-chase experiment using fluorescent haem analogue, palladium mesoporphyrin IX, have been performed. As the presence of transporter proteins have been demonstrated to be involved in the transmembrane transport of haem in other organisms, bioinformatics tools are being utilized to identify possible haem transporter protein from *S. mansoni* genome database. The results in this study showed that schistosomes take up exogenous haem, which accumulates in the ovary of the female parasite. This suggests that host haem could be involved in supporting embryogenesis in *S. mansoni*. Understanding the underlying molecular mechanism in this transmembrane transport of haem in schistosomes could reveal potential molecular targets for control of this important group of human parasites.

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Session Details:	8/27/2013 DRUG DISCOVERY 1330 - 1445 <i>Meeting Room 3</i>
Oral Presentation Details:	In vitro and in vivo activities of dicationic diguanidino-compounds against Echinococcus multilocularis metacestodes
Presentation Time:	1345 -1400
Authors:	Hemphill A ¹ , Küster T ¹ , Kriegel N ¹ , Boykin D ² , Stephens C ¹ Institute Of Parasitology, University Of Bern, ² Georgia State University, Atlanta, ³ Georgia Regents University, Augusta

Alveolar echinococcosis (AE) is a disease affecting predominantly the liver, with metacestodes (larvae) of the tapeworm *Echinococcus multilocularis* proliferating, and exhibiting tumor-like infiltrative growth in Man, but also in many animal species. Since many years, the chemotherapeutical treatment against alveolar echinococcosis relies on the benzimidazoles albendazole and mebendazole, and encompasses long treatment durations and parasitostatic rather than parasitocidal efficacy. Recurrence rates after termination of benzimidazole treatment are high. Although benzimidazoles have been and still are beneficial for the patients and have improved the life quality and life expectancy of affected patients, there is clearly a demand for alternative and more efficient treatment options with respect to efficacy, timing and costs. Aromatic dications, more precisely a small panel of di-*N*-aryl-diguanidino compounds, essentially pentamidine derivatives, were screened for efficacy against *E. multilocularis* metacestodes *in vitro*. Only those with a thiophene core group were active against metacestodes, while furans were not. The most active compound, DB1127, was further investigated in terms of *in vivo* efficacy in mice experimentally infected with *E. multilocularis* metacestodes. This di-guanidino compound was effective against AE when administered intraperitoneally, but not when applied orally. Thus thiophene-di-guanidino derivatives with improved bioavailability when administred orally could hold an immense potential as treatment options against AE.

Acknowledgements:

The study was financed by the Swiss National Science Foundation (grant No. 31003A-125990), the Swiss Life Foundation, and the Bangerter Rhyner Foundation.



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Session Details:	8/27/2013 DRUG DISCOVERY 1330 - 1445 <i>Meeting Room 3</i>
Oral Presentation Details:	Investigation and validation of a potential new drug target for parasitic nematodes
Presentation Time:	1400 -1415
Authors:	Behm C¹, Fritz J¹, Zawadzki J², Knight A¹, Johnson N¹, Hetherington S¹, Hemsworth J² ¹ Australian National University, ² Department of Primary Industries, Victoria, Australia

In a screen for conserved nematode proteins that exhibit highly compromised RNA interference (RNAi) phenotypes in *Caenorhabditis elegans* we identified UDP-galactopyranose mutase (GLF-1; E.C.4.4.99.9) as a potential anti-nematode drug target. RNAi of *glf-1* in *C. elegans* confirmed the published phenotypes (Kamath *et al.* 2003 *Nature* **421**, 231; Novelli *et al.* 2009 *Devel. Biol.* **335**, 340), including locomotory defects progressing to paralysis, abnormal larval development, and cuticular permeability to the fluorescent DNA-binding dye, Hoechst 33258. RNAi of *glf-1* in wild-type *C. elegans* also led to potentiation of the effects of levamisole, ivermectin and mebendazole.

We cloned the putative orthologue of *glf-1* from *Haemonchus contortus* and used RNAi of the free-living larval stages of *H. contortus* (Zawadzki *et al.* 2012 *Parasitol.* **139**, 613) to show that knockdown of *Hc-glf-1* caused abnormal development from L1 to L3, reduced locomotory activity and permeability to Hoechst 33258.

To assess the physiological functions of *Hc*-GLF-1 we tested whether expression of *Hc-glf-1* could rescue the functions of *glf-1* in *C. elegans* using 'differential RNAi' technology (Britton and Murray 2002 *Parasitol.* **122**, 21; Zawadzki *et al.* 2012 *Parasitol.* **139**, 613). We constructed transgenic strains of *C. elegans* that expressed both *Hc-glf-1* and *C. elegans glf-1*. When *C. elegans glf-1* was selectively knocked down by RNAi, the strains expressing *Hc-glf-1* did not exhibit the *glf-1* RNAi phenotype, indicating that expression of *Hc*-GLF-1 effectively replaced the critical functions of GLF-1.

This work validates GLF-1 as a potential new drug target for parasitic nematodes and shows that a drug targeting nematode GLF-1 could act potentially both as a nematotoxin and a potentiating agent for other anti-nematode drugs.

Acknowledgements:

This research was funded by Meat and Livestock Australia and Australian Wool Innovation.





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Session Details:	8/27/2013 DRUG DISCOVERY 1330 - 1445 <i>Meeting Room 3</i>
Oral Presentation Details:	In vitro efficacy of Toltrazuril against <i>Besnoitia besnoiti</i> infection in Vero and HFF cells
Presentation Time:	1415 -1430
Authors:	Gottstein B¹, Mueller J², Greif G³, Cortes H⁴ ¹ Institute of Parasitology, ² Institute of Parasitology, ³ Bayer Animal Health GmbH, Leverkusen, Germany, ⁴ 3Laboratório de Parasitologia Victor Caeiro, Universidade de Évora, Portugal

Besnoitia besnoiti is the causative agent of bovine besnoitiosis, a parasitic disease of cattle widely distributed in subsaharian areas, which has recently received increased attention in Mediterranean countries. *B. besnoiti* tachyzoites were maintained in Vero cell cultures. For in vitro drug treatment assays, human foreskin fibroblasts (HFF) were maintained in T-75 flasks, DMEM containing 10% FCS and supplements. Toltrazuril was obtained from Bayer and used at a concentration of 30 µg per ml. Infected HFF cells were maintained in culture medium containing the drug dilutions. In order to assess selective toxicity, uninfected HFF cells were treated identically. Samples for monitoring parasite proliferation were taken at different times post-initiation of drug treatment. Each assay in a given experiment was carried out in triplicate. DNA purification was performed using the DNAeasy kit (QIAGEN, Basel, Switzerland). For quantitative PCR, primers directed to ITS1 region of *B. besnoiti* were used. The quantification was referenced with a parallel investigation using defined titrated amounts of *Besnoitia* tachyzoites. For the time-course experiments, the significance of the differences between end-point values of the control and experimental assays was determined by Student's t-test, using the Microsoft Excel program. P values <0.05 were considered statistically significant.

Results indicated that Toltrazuril significantly inhibited parasite proliferation in vitro after approximately 2-4 days of treatment of preinfected Vero cells (for this, host cells were washed after 3 or 24 hours after infection / inoculation had been initiated, such as to remove non-infection parasites). Our results suggest that Toltrazuril acts against *B. besnoiti* tachyzoites, suggesting that it could be potentially applied to control parasite dissemination and transmission at the tachzoite stage level.

References:

Cortes HC et al. (2006). Isolation of *Besnoitia besnoiti* from infected cattle in Portugal. Veterinary Parasitology 141, 226-233.

Cortes et al. (2011). In vitro effects of arylimidamides against *Besnoitia besnoiti* infection in Vero cells. *Parasitology* 138, 583-592.

Cortes et al. (2007). Application of conventional and real-time fluorescent ITS1 rDNA PCR for detection of *Besnoitia besnoiti* infections in bovine skin biopsies. *Veterinary Parasitology* 146, 352-356.



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Session Details:	8/27/2013 DRUG DISCOVERY 1330 - 1445 <i>Meeting Room 3</i>
Oral Presentation Details:	Metaphylactic toltrazuril treatment of dairy calves at risk of coccidiosis – short and long term effects on weight gain
Presentation Time:	1430 -1445
Authors:	Enemark H¹, Dahl J², Enemark J³ ¹ Technical University Of Denmark, ² Jan Dahl Consult, ³ Bayer HealthCare Nordic

Coccidiosis caused by *Eimeria* spp. remains an important health problem in modern calf rearing. Although the effect of metaphylactic treatment with toltrazuril has been proven in previous studies in calves at risk of coccidiosis, the long-term effect on weight gain is poorly investigated. In the present randomized, blinded and placebo-controlled field study, the effect of metaphylactic treatment with toltrazuril (Baycox Bovis®, Bayer Animal Health, Germany) on daily weight gain of dairy in-housed calves was studied in a Danish dairy cattle farm with confirmed history of coccidiosis caused by *E. zuernii* and *E. bovis*. Five groups of 10 calves aged 4-6 weeks were randomly allocated to the treatment group ($n=25$) which received one dose toltrazuril (15 mg/kg) and the control group ($n=25$) receiving placebo. Treatment was initiated one week before expected outbreak of coccidiosis after regrouping of calves within the farm. Body weight was quantified at treatment day 0, after 8 weeks (56 days), and after 22 weeks (155±7 days). Mean daily weight gains throughout the study periods were calculated statistically (Wilcoxon-Man-Whitney-U Test, two sided 95% CI): 0.6765±0.0174 kg and 0.6290±0.0254 kg (treated and controls; 8 weeks); 0.6180±0.0163 kg and 0.5670±0.0173 kg (treated and controls; 22 weeks) ($p<0.005$). Differences in mean total weight gain between treated and controls were 2.7 kg and 6.1 kg 8 and 22 weeks post treatment respectively. Weekly faecal samples demonstrated that prevalence and OPG of *E. zuernii* and *E. bovis* were reduced significantly in the treatment group during 5 weeks post treatment. The study showed that metaphylactic treatment with toltrazuril in dairy calves at risk of coccidiosis controlled oocyst shedding of pathogenic *Eimeria* sp., improved daily weight gain and resulted in significantly increased body weight 5 months post treatment. Follow-up studies will investigate the long-term effects on other production parameters e.g. milk yield.

Acknowledgements:

The study was funded by Bayer HealthCare Nordic.

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Session Details:	8/27/2013 TEACHING WORKSHOP 1330 - 1445 <i>Meeting Room 5</i>
Oral Presentation Details:	The ParSCo (Parasitology Summer Course): an EVPC Residential-Practical Course in the Heart of the Mediterranean Sea
Presentation Time:	1330 -1345
Authors:	Andreas L. Chryssafidis¹ , Filipe Dantas-Torres ^{2,3} , Domenico Otranto ³ ¹ School of Veterinary Medicine, University College Dublin – Belfield, IRELAND ² Laboratory of Immunoparasitology, Aggeu Magalhães Research Center, Recife, BRAZIL ³ Department of Veterinary Medicine, University of Bari, Valenzano, ITALY

The Parasitology Summer Course (ParSCo) is an intensive one-week long practical course on advanced level Veterinary Parasitology, organized in southern Italy by the Parasitology Unit of the Department of Veterinary Medicine, University of Bari (Italy), together with the European Veterinary Parasitology College (EVPC). Following the success of its first edition in 2012, the ParSCo II, took place at the Parco Regionale di Gallipoli Cognato Matera, Basilicata, Italy, on July 6th- 13th, 2013. This location is a perfect example of Mediterranean climate, fauna, and flora. For its natural characteristics, the Mediterranean region offers an optimal environment for the development of arthropods, therefore for the spread of many arthropod vectors of vector-borne disease (VBD) causing pathogens. Ten researchers with interest in the field of parasitology, from different nationalities and with distinct backgrounds, were trained mainly on practical aspects of the discipline, such as arthropod (ticks, sand flies, and *Phortica variegata*) collection from field and hosts, their identification and dissection, as well as on the diagnosis of VBDs pathogens (*Leishmania infantum*, *Babesia* spp., *Thelazia callipaeda*, cat lungworms, and filarioids) in vectors and hosts. Attendants were also involved in bird trapping sessions and tick collections from birds. All attendants were tested at the end of the course in order to assess their knowledge acquired during the course and as a pre-requisite to receive the final certificate. An overview of all activities carried out during ParSCo II will be presented.

Acknowledgements:

This course was sponsored by Bayer Health Care, Merial Animal Health and Società Italiana di Parassitologia.



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Session Details:	8/27/2013 TEACHING WORKSHOP 1330 - 1445 <i>Meeting Room 5</i>
Oral Presentation Details:	Progress in developing a “downunder” parasitology e-text
Presentation Time:	1345 -1400
Authors:	I. Beveridge ¹ and D.Emery² ¹ University of Melbourne; ² University of Sydney

To generate a parasitology textbook to facilitate future training of veterinary and animal bioscience undergraduate and postgraduate students, veterinary parasitologists from each of the Australasian Vet Schools concurred on a function, template and content of a hardcopy textbook. With recent developments in software and hardware for electronic provision, a survey monkey of undergraduates identified a suitable e-format. With funding from the Australian society for Parasitology, sections were written by various single authors and group contributions and formatted into “i-design”. A final downloadable version is projected to be ready for launch in 2014. Lessons from the exercise will be provided and discussed.

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Session Details:	8/27/2013 TEACHING WORKSHOP 1330 - 1445 <i>Meeting Room 5</i>
Oral Presentation Details:	So, if the only teaching aid in the budget is an old shoebox...
Presentation Time:	1400 -1415
Authors:	Dwight D. Bowman Department of Microbiology and Immunology, College of Veterinary Medicine, Cornell University, Ithaca, NY, 14853, USA.

As is the case with most parasitologists working as educators, didactic training in education per se was not required as part of the skill set passed along in the different courses taken and positions held over the years. Thus, like others in the profession, I have tried to assimilate the best from various mentors and colleagues with whom I have worked. From this assimilation, much of what determines what I do in my daily work is the application of what has developed into a simple set of platitudes that have grown out of interactions had with those I have worked with over the last forty or so years. Usually, it has been as simple as hearing or being told a phrase or story that rings true and which has been verified as to its value through its application and observed results. Sometimes, as would also be expected, my personal bias has led me to take a slightly different course than the mentor intended. And, some of these basic educational planks are more personal in that they have been developed from my own quirks and idiosyncrasies. A few of these simple educational platitudes and their sources will be presented along with how they are regularly applied in my own teaching.



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Session Details:	8/27/2013 TEACHING WORKSHOP 1330 - 1445 <i>Meeting Room 5</i>
Oral Presentation Details:	Core competencies in veterinary parasitology practicals – A LOGical appropach
Presentation Time:	1415 -1430
Authors:	Ryan O’Handley* ¹ School of Animal and Veterinary Sciences, University of Adelaide, Roseworthy, South Australia University,

Teaching practical skills in veterinary parasitology can be challenging. Traditional methods of evaluating students using a practical exam requires a great deal of time and resources, both of which are becoming scarce. In this presentation, a method of teaching pracicals based on core competencies combined with the use of a log book to evaluate students will be discussed. This method does not require a final practical examination as numerous formative evaluations are used throughout the year. The positive and negatives of this approach to teaching practicals will be presented.



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Session Details:	8/27/2013 FUNCTIONAL GENOMICS 2 1330 - 1445 Meeting Room 6
Oral Presentation Details:	The genome and transcriptome of <i>Haemonchus contortus</i> : a key model parasite for drug and vaccine discovery
Presentation Time:	1330 -1345
Authors:	Roz Laing¹, Taisei Kikuchi^{2,3}, Axel Martinelli², Isheng J. Tsai^{2,3}, Robin N. Beech⁴, Elizabeth Redman⁵, Nancy Holroyd², David J. Bartley⁶, Helen Beasley², Collette Britton¹, David Curran⁵, Eileen Devaney¹, Aude Gilabert⁵, Martin Hunt², Frank Jackson⁶, Stephanie Johnston¹, Ivan Kryukov⁵, Keyu Li⁵, Alison A. Morrison⁶, Adam J. Reid², Neil Sargison⁷, Gary Saunders^{1,2}, James D. Wasmuth⁵, Adrian Wolstenholme⁸, Matthew Berriman², John S. Gilleard⁵, James A. Cotton² ¹ University of Glasgow, Glasgow, UNITED KINGDOM ² Wellcome Trust Sanger Institute, Cambridge, UNITED KINGDOM ³ University of Miyazaki, Miyazaki, 889-1692 JAPAN ⁴ McGill University, Quebec, CANADA ⁵ University of Calgary, Calgary, CANADA ⁶ Moredun Research Institute, Edinburgh, UNITED KINGDOM ⁷ University of Edinburgh, Edinburgh, UNITED KINGDOM ⁸ University of Georgia, Athens, USA

Anthelmintic resistance in strongylid worms threatens the viability of the sheep industry worldwide and provides a cautionary model of mass drug administration to control parasitic disease. *Haemonchus contortus*, a gastrointestinal parasite of small ruminants, is one of the most intensively studied parasitic nematodes and is the most established parasite species in drug discovery, drug mode-of-action and drug resistance research. Its close phylogenetic relationship to the free-living nematode *Caenorhabditis elegans* enables powerful comparative and functional genetics, and its close relationship to other parasitic nematodes of devastating medical and veterinary importance, underpin its proven value as a parasitic model for the strongylid group.

The 370 Mb genome consists of 26 044 scaffolds with a N50 of 83,287 bp. Around 93% of conserved eukaryotic genes (CEGs) can be identified, suggesting our draft assembly represents at least that fraction of the *H. contortus* genome. We find a general pattern of conservation of genome structure and gene content between *H. contortus* and *C. elegans* but also a dramatic expansion of important parasite gene families. We identify genes involved in blood feeding, drug metabolism and neurological function, and describe complete gene repertoires for known drug target families, providing the most comprehensive understanding yet of the action of several important anthelmintics. Transcriptome (RNA-seq) libraries of eggs, L1, L3, L4, male adults and female adults show differential expression of genes throughout the parasite lifecycle and identify key differences between free-living and parasitic life-stages. Transcriptome libraries of the parasite gut are of particular interest as a rich source of potential vaccine and drug targets.

The draft genome and transcriptome are expected to provide a wealth of new information for the extensive research effort already focused on *H. contortus* and for other important parasites in the strongylid group.



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Session Details:	8/27/2013 FUNCTIONAL GENOMICS 2 1330 - 1445 <i>Meeting Room 6</i>
Poster with a 2 minute oral Details:	<i>Haemonchus contortus</i> genome and developmental transcriptome
Presentation Time:	1345 -1400
Authors:	Pasi K. Korhonen1* , Erich M. Schwarz1,2, Bronwyn E. Campbell1, Neil D. Young1, Aaron R. Jex1, Abdul Jabbar1, Ross S. Hall1, Alinda Mondal1, Adina Howe3, Jason Pell4, Andreas Hofmann5, Xing-Quan Zhu6, Alex Loukas7, Brian A. Williams2, Igor Antoshechkin2, C. Titus Brown3,4, Paul W. Sternberg2, Robin B. Gasser1 1 Faculty of Veterinary Science, University of Melbourne, Parkville 3010, Victoria, AUSTRALIA 2 HHMI, California Institute of Technology, Pasadena, California, USA; present address: Cornell University 3 Microbiology and Molecular Genetics & 4Computer Science and Engineering, Michigan State University, MI, USA 5 Eskitis Institute for Cell & Molecular Therapies, Griffith University, Brisbane, AUSTRALIA 6 State Key Laboratory of Veterinary Etiological Biology, Lanzhou Veterinary Research Institute, Chinese Academy of Agricultural Sciences, Lanzhou, Gansu, CHINA

We produced a draft genome and transcriptomes of key developmental stages of *Haemonchus contortus* (Australia) using advanced sequencing and bioinformatic techniques. The genome is estimated at 453 Mb in size, has a repeat content of 13.1% and 23,610 protein-coding genes. A deep exploration of the genome and transcriptomes provides new insights into the molecular biology of *Haemonchus contortus*. We studied, in detail, transcriptional alterations taking place during the life cycle, particularly, in the transition from the free-living to the parasitic stages, and molecules involved in host interactions and immune responses. We also characterised the full complement of gene silencing machinery to support functional genomic work in selected stages/tissues of the parasite. The present genomic and transcriptomic datasets for *H. contortus* will be made available publicly in due course and should assist a wide range of fundamental discovery and applied research projects, particularly post-genomic investigations of genes and gene products involved in nematode development and reproduction, proteomic and metabolomic studies, parasite-host interactions, pathogenesis of disease, and the genetics and mechanisms of drug resistance. We hope that this resource, together with other data sets, will pave the way for a rapid acceleration in our understanding of the systems biology of *H. contortus* and related nematodes.





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Session Details:	8/27/2013 FUNCTIONAL GENOMICS 2 1330 - 1445 <i>Meeting Room 6</i>
Oral Presentation Details:	Development of RNA interference in the human hookworm <i>Necator americanus</i>
Presentation Time:	1400 -1415
Authors:	Dougall A , Susianto A, Pickering D, Loukas A Queensland Tropical Health Alliance, James Cook University, Cairns, QLD, Australia

RNA interference (RNAi) has been successfully demonstrated in the sheep parasitic nematode, *Haemonchus contortus*, by targeting accessible genes such as those expressed in the gut, excretory cell and amphids. To date successful application of RNAi to hookworms has not been described. Given the similarities of *H. contortus* to hookworm, we have applied RNAi approaches that proved successful for silencing expression of some *H. contortus* larval genes in an attempt to develop RNAi as a tool for exploring gene function in hookworms. Presented are the first trials using dsRNA delivery by soaking L3 in DMEM media containing 20% human serum with dsRNAs (10 µg/mL). Two genes targeting a digestive aspartic protease (*Na-apr-1*) and β -tubulin (β -tub) appeared to be susceptible to knockdown. After 24-48 hours significant mRNA knockdown was observed in biological replicates of *Necator americanus* infective larvae (L3) treated with β -tub compared to negative control L3 that were incubated with *luciferase* dsRNA. Knockdown of *Na-apr-1* was evident but less dramatic than that observed for β -tub. Further experiments are underway to optimise experimental conditions and assess any phenotypes associated with silencing of these and other genes. Alternative delivery strategies such as electroporation with small interfering (si)RNAs are also underway. RNAi is a notoriously difficult technique to apply in a robust fashion to parasitic nematodes. Successful application of this technique to hookworm biology will allow researchers to assess gene function and lethality in the search for new drug and vaccine candidates for hookworm disease.

Session Details:	8/27/2013 FUNCTIONAL GENOMICS 2 1330 - 1445 <i>Meeting Room 6</i>
Oral Presentation Details:	Functional analysis of the bovine immunological response against <i>in silico</i> predicted B and T cell epitopes in <i>Rhipicephalus microplus</i> lipocalins (LRMs).
Presentation Time:	1415 -1430
Authors:	Manuel Rodriguez-Valle ^{1*} , Paula Moolhuijzen ² , Emily K. Piper ³ , Olivia Weiss ³ , Matthew Bellgard ² and Ala Lew-Tabor ^{1,2} ¹ The University of Queensland, Queensland Alliance of Agriculture & Food Innovation, St. Lucia, Brisbane, Qld, Australia ² Murdoch University, Centre for Comparative Genomics, Perth, Western Australia, Australia ³ The University of Queensland, School of Veterinary Science, Gatton, Qld, Australia

The host-parasite interaction can induce a rejection larvae, as is frequently observed in *Bos t. indicus* cattle, and under certain conditions in *Bos t. taurus* cattle. Ticks deactivate the host rejection response by secreting specific proteins that play an essential role in the manipulation of the host immune response. The available genomic information for *R. microplus* ticks was mined using bioinformatics approaches to identify *R. microplus* lipocalins (LRMs). This *in silico* examination revealed a total of 269 lipocalin-related sequences. Twelve different putative *R. microplus* lipocalins groups (LRM1 through LRM12) were identified. The identity of the LRM family showed high sequence variability: from 6% between LRM7 and LRM8 to 55.9% between LRM2 and LRM6. The B and T cell epitopes in these lipocalins were then predicted, and 6 of the LRMs (5, 6, 9, 10, 11 and 12) were used to examine the host immune interactions with sera and peripheral blood mononuclear cells (PBMCs) collected from tick-susceptible and tick-resistant cattle previously challenged with *R. microplus*. On days 28 through 60 after tick infestation, the anti-LRM titres were higher in the resistant group compared with the susceptible cattle. After 60 days, the anti-LRM titres (except LRM9 and LRM11) decreased to zero in the sera of both the tick-resistant and tick-susceptible cattle. Using cell proliferation assays, the PBMCs challenged with some of the predicted T cell epitopes (LRM1_T1, T2; LRM_T1, T2 and LRM12_T) exhibited a significantly higher abundance of IFN- α ?-secreting cells in tick-susceptible Holstein compared with tick-resistant Brahman cattle. In contrast, the expression of IL-4 was lower in Holstein cattle compared with Brahman cattle. Moreover, this study found that LRM6, LRM9 and LRM11 play important roles in the mechanism by which *R. microplus* interferes with the host's haemostasis mechanisms.

Acknowledgments

This work was supported by the CRC for Beef Genetic Technologies and Queensland Smart State Innovation Fund (National and International Research Alliances Program). The authors want to give special thanks to Sandy Jarrett, Catherine Minchin and Anthea Bruyeres (Qld Department of Agriculture, Fisheries & Forestry) for their technical support. Thanks to Dr. Louise Jackson (DAFF) for providing access to the Santa Gertrudis sera and ticks.

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Session Details:	8/27/2013 FUNCTIONAL GENOMICS 2 1330 - 1445 Meeting Room 6
Oral Presentation Details:	Functional study of a genetic marker allele associated with resistance to <i>Ascaris suum</i> in pigs
Presentation Time:	1430 -1445
Authors:	Skallerup P ^{1,2}, Thamsborg S ¹, Jørgensen C ², Enemark H ³, Yoshida A ⁴, Göring H ⁵, Fredholm M ², Nejsum P ^{1,2} ¹ Department For Veterinary Disease Biology, University of Copenhagen, Frederiksberg, DENMARK, ² Department of Veterinary Clinical and Animal Sciences, University of Copenhagen, Frederiksberg, DENMARK, ³ National Veterinary Institute, Frederiksberg, DENMARK, ⁴ Department of Infectious Diseases, University of Miyazaki, JAPAN, ⁵ Texas Biomedical Research Institute, San Antonio, TX, USA

Mapping of quantitative trait loci (QTLs) has helped dissecting the genetics underlying the variation in resistance to helminth infections. In pigs, two single nucleotide polymorphisms (SNP TXNIP and SNP ARNT), both on chromosome 4, have been reported to be associated with roundworm (*Ascaris suum*) burden. In the present study, we selected pigs with two SNP TXNIP genotypes (AA; n=24 and AB; n=24) which, from eight weeks of age were trickle-infected with *A. suum* until necropsy at week 8 post first infection (PI), to test the hypothesis that pigs with the AA genotype would have higher levels of resistance (lower worm burdens) than pigs of the AB genotype. We used different indicators of resistance (worm burden, faecal egg counts, number of liver white spots and *A. suum*-specific serum IgG antibody levels). Pigs of the AA genotype had lower mean macroscopic worm burden (2.4 vs. 19.3; P=0.06), lower mean total worm burden (26.5 vs. 70.1; P=0.06) and excreted fewer *A. suum* eggs at week 8 PI (mean number of eggs/g faeces: 238 vs. 1259; P=0.14) than pigs of the AB genotype. In addition, pigs of the AA genotype had lower (though not significant) serum IgG antibody titres against three different *A. suum* antigens. There was no significant difference between genotypes in the number of liver white spots. The pigs were also genotyped at another locus (SNP ARNT) which showed a similar trend. The data presented here provide suggestive evidence that resistant pigs can be selected using a genetic marker, TXNIP, and that the B allele is associated with susceptibility to *A. suum* infection. Our work confirmed that SNP ARNT is another diagnostic marker candidate for *A. suum* resistance and provides further support to the QTL on porcine chromosome 4 detected previously.



Session Details:	8/27/2013 IMMUNOLOGY GENERAL 1330 - 1445 <i>Meeting Room 7</i>
Oral Presentation Details:	Gene expression in abomasal lymph node of Scottish Blackface lambs challenged with <i>Teladorsagia circumcincta</i>.
Presentation Time:	1330 -1345
Authors:	McRae K ^{1,2} , Good B ³ , Hanrahan J ³ , Sweeney T ⁴ , O'Connell M ² , Keane O ¹ ¹ Teagasc, Grange, Dunsany, Co. Meath, IRELAND, ² Dublin City University, Dublin, IRELAND, ³ Teagasc, Athenry, Co. Galway, IRELAND, ⁴ University College Dublin, Dublin, IRELAND

Infection with gastrointestinal nematodes (GIN) is one of the major constraints of sheep production worldwide. An increase in the incidence of anthelmintic resistance has led to a search for alternative options for GIN control, such as selective breeding for resistance. The objective of this study was to identify lambs that differed in their response to natural GIN infection and characterise their response to a controlled challenge.

Scottish Blackface lambs, grazed together from birth, were monitored for faecal egg count (FEC; 2 samples following each of 2 independent natural infections). These observations were used to identify the most resistant (n=10, Low FEC) and susceptible (n=10, High FEC) individuals. Lambs were challenged with 30,000 *Teladorsagia circumcincta* larvae (L3), and slaughtered at 7 or 14 days post infection (dpi). Samples were collected at slaughter for worm burden enumeration, haematology and gene expression analysis. Total RNA was extracted from abomasal lymph nodes and cDNA libraries generated and sequenced (50 bp paired-end). Reads (790 million) were aligned to the *Ovis aries* reference genome (Oarv3.1) using TopHat. *De novo* transcript assembly was carried out using Cufflinks. Transcript abundances were normalised, and used to detect differentially expressed genes.

Worm burden was not significantly different between High and Low FEC animals, consistent with previous studies, which showed the time taken for animals to activate a protective immune response and expel worms is greater than 14 days (Hassan *et al.* 2011). Low FEC animals had a higher number of circulating basophils ($P < 0.05$); however all other haematology variables were not significantly different. A total of 82 (7 dpi) and 63 (14 dpi) genes were differentially expressed ($FDR < 0.05$) between High and Low FEC animals. Genes will be annotated by searching for orthologs in *Homo sapiens* and *Bos taurus*, and over-represented pathways discovered using GO and KEGG.

Acknowledgements:

We acknowledge the Teagasc Walsh Fellowship Scheme for financial support.

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Hassan, M., Good, B., Hanrahan, J. P., Campion, D., Sayers, G., Mulcahy, G. & Sweeney, T. (2011). *Vet. Res.*, 42(1): 46.



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Session Details:	8/27/2013 IMMUNOLOGY GENERAL 1330 - 1445 <i>Meeting Room 7</i>
Oral Presentation Details:	Immune responses of sheep against <i>Oestrus ovis</i> (Diptera: Oestridae) associated to gastrointestinal nematode infection
Presentation Time:	1345 -1400
Authors:	Silva B ^{1 and 2} , Bassetto C ² , Amarante A ² ¹ Universidade do Planalto Catarinense, ² Universidade Estadual Paulista

Sheep are frequently parasitized simultaneously by gastrointestinal nematodes (GIN) and by *Oestrus ovis* larvae. Thus, this study was carried out to evaluate the immune response in young Ile de France (IF) and Santa Ines (SI) sheep naturally infected by *O. ovis* and gastrointestinal nematodes (GIN). Mast cells, eosinophils and globule leucocytes were enumerated in the upper respiratory tract (septum, middle meatus and ventral nasal conchae) and in the mucosa of abomasum and small intestine. Immunoglobulin G (IgG) levels in serum samples and immunoglobulin A (IgA) levels in mucus from the nasal, abomasum and small intestinal mucosae were determined against *O. ovis*, *Haemonchus contortus* and *Trichostrongylus colubriformis* antigens. In both breeds, animals with the highest levels of IgG and IgA against *O. ovis* had the highest numbers of *O. ovis* larvae, while inflammatory cell numbers did not present any consistent association with *O. ovis* larval burden. Apparently, the presence of antibodies in the serum or nasal mucus, as well as inflammatory cells, was not able to efficiently protect against *O. ovis* infestation. With regard to GIN, the levels of immunoglobulins and the inflammatory cell numbers in the gastrointestinal mucosa presented a significant inverse relationship only with *H. contortus* worm burden in SI animals and this may have contributed to the fact that these animals presented the lowest FEC and worm burden compared to IF. In conclusion, the immune responses against *O. ovis* and GIN were very similar and involved the recruitment of inflammatory cells and production of immunoglobulins against the parasites. However, the host-parasite interaction may be more well balanced for *O. ovis*, allowing parasites infestation without acute disease; while is less balanced for *H. contortus*, that frequently cause acute disease and death in sheep.

Acknowledgements:

This study was funded by Fundação de Amparo à Pesquisa do Estado de São Paulo (FAPESP, Grant number 2008/53494-2). Bruna F. Silva (Grant number 2007/58244-1) and César C. Bassetto (Grant number 2009/03504-4) received financial support from FAPESP and Alessandro F. T. Amarante from CNPq (Conselho Nacional de Desenvolvimento Científico e Tecnológico, Brazil).

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Session Details:	8/27/2013 IMMUNOLOGY GENERAL 1330 - 1445 Meeting Room 7
Oral Presentation Details:	Predominant natural killer cell proliferation in Belgian Blue cattle with aggravating Psoroptes ovis mange.
Presentation Time:	1400 -1415
Authors:	Sarre C, Van Coppernolle S, Vercruysse J, Claerebout E Ghent University

Psoroptes ovis is one of the most common ectoparasites in cattle and causes important economic losses, especially in the highly sensitive Belgian Blue (BB) breed. Within this breed, resistant and susceptible phenotypes to *P. ovis* infection can be distinguished. In humans with *Sarcoptes scabiei* infections, different scabies phenotypes have been associated with different T-cell responses to mite antigen (Walton et al., 2010). Therefore we investigated whether this would also be the case for cattle with mild versus severe *P. ovis* infection. Peripheral blood mononuclear cells (PBMCs) were isolated from uninfected BB heifers and from BB heifers with a natural *P. ovis* infection, which either had mild or severe mange. After *in vitro* stimulation of PBMCs with crude *P. ovis* extract, a significantly higher antigen-specific PBMC proliferation was observed in infected animals than in uninfected heifers. Moreover, proliferation was significantly higher in animals with severe mange, compared to animals with mild mange. PKH labelled PBMCs were used to identify the proliferating cell populations using flow cytometry. No significant proliferation was observed in any cell type in the uninfected animals. In both infected groups, there was a significant proliferation of CD3⁺ CD335⁺ natural killer cells (NK). Animals with mild mange also showed a T-cell response with proliferation of mainly CD3⁺ TCRγδ⁺ cells. This CD3⁺ TCRγδ⁺ response was virtually absent in animals with severe mange.

In conclusion, *P. ovis* infection induced strong *P. ovis* specific *in vitro* proliferation of PBMCs. The magnitude of this response was highest in the animals with severe mange. Surprisingly, in contrast to *S. scabiei* infection in humans, the main proliferating population seemed to be NK cells. Experiments to identify the cytokine profiles of the proliferating PBMCs are ongoing to further differentiate the cellular responses to mite antigen in cattle with severe versus mild psoroptic mange.

Acknowledgements:
The authors thank Grietje Grit for her assistance during the flow cytometry.

References:
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Session Details:	8/27/2013 IMMUNOLOGY GENERAL 1330 - 1445 Meeting Room 7
Oral Presentation Details:	Semi maturation of bovine monocyte-derived dendritic cells after incubation with <i>Giardia duodenalis</i>
Presentation Time:	1415 -1430
Authors:	Grietje Grit ¹ , Stefanie Van Coppernolle ¹ , Bert Devriendt ¹ , Thomas Geurden ¹ , Jayne Hope ² , Jozef Vercruysse ¹ , Peter Geldhof ¹ , Eric Cox ¹ , Edwin Claerebout^{1*} ¹ Dept. of Virology, Parasitology & Immunology, Ghent University, Merelbeke, Belgium ² The Roslin Institute, University of Edinburgh, UNITED KINGDOM

Giardia duodenalis is an important intestinal parasite in animals and humans. The role of dendritic cells in the immune response against *G. duodenalis* is poorly documented and has only been studied in the mouse, which is not a natural host for this parasite. In this study we addressed the effect of *G. duodenalis* trophozoites and excretion/secretion (ES) products on the expression of maturation markers and cytokine production by bovine monocyte-derived dendritic cells (MoDCs) *in vitro*. Moreover, the ability of stimulated MoDC to take up antigen and to induce mononuclear cell proliferation was assessed.

Although none of the maturation markers CD40, CD80 and MHCII were up-regulated in MoDC cultures after stimulation with *Giardia* trophozoites or ES, a dose-dependent decrease in ovalbumin uptake was observed. IL-15 transcription was significantly increased after 24h of stimulation with *Giardia* trophozoites. Other cytokines were not significantly up- or down-regulated. MoDC stimulated with *Giardia* trophozoites or ES induced dose-dependent proliferation of allogeneic $\gamma\delta$ -T-cells and TRC $\alpha\beta^+$ CD4 $^+$ and -CD8 $^+$ T-cells *in vitro*, which was not observed in cultures with unstimulated MoDC. Induction of TCR $\alpha\beta^+$ CD4 $^+$ proliferation by *Giardia*-stimulated MoDC was confirmed in an autologous lymphocyte proliferation assay, using MoDC and PBMC from calves artificially infected with *G. duodenalis* cysts.

Our data show that, despite the absence of co-stimulatory molecules, *G. duodenalis* trophozoites induce functional maturation of bovine MoDC. This is illustrated by their ability to induce both allogeneic and autologous T cell proliferation, which is probably induced by the *G. duodenalis* induced expression of IL-15. Functionally active MoDC, lacking the expression of co-stimulatory molecules are described in literature as semi-mature DC and are known for their ability to induce T cell tolerance. Proliferating TCR $\alpha\beta^+$ CD4 $^+$ T-cells from our MoDC cultures will be further characterised to determine the functional phenotype of the *G. duodenalis* induced T cell response.

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Session Details:	8/27/2013 IMMUNOLOGY GENERAL 1330 - 1445 Meeting Room 7
Oral Presentation Details:	Leishmania australiensis infection in BALB/c nude mice
Presentation Time:	1430 -1445
Authors:	Calila Sena Santos^{1, 2*}, Ace Yu Leng Choo^{1, 2}, Joyce Oommen² and Christopher Peacock^{1, 2} ¹School of Pathology & Laboratory Medicine, Faculty of Medicine, Dentistry and Health Sciences, The University of Western Australia, Australia ²Telethon Institute for Child Health Research, Western Australia, Australia

The recent discovery of a novel species of *Leishmania* infecting marsupials in the Australian Northern Territory, namely, *Leishmania australiensis*, has raised many questions and concerns, including the risk of human leishmaniasis becoming endemic in Australia. Although *L. australiensis* is considered to be non-pathogenic to humans, it has high degree of similarity to human pathogenic species, which makes it an ideal candidate for identifying mechanisms of pathogenicity and virulence in human leishmaniasis. Previous work done in our laboratory has showed that *L. australiensis* is able to infect and survive as amastigotes in a variety of human and murine *in vitro* cells, including macrophages, neutrophils and dendritic cells. In addition, this parasite appears to modulate such cells and is resistant to complement mediated killing. In this study we show the effects of *in vivo* infection using BALB/c *nu/nu* mice as models. The subjects were infected with 10⁵ stationary phase *L. australiensis* promastigotes in the ear pinna and examined weekly for skin lesions. The serum monitored for the presence of antibodies and cytokines and post mortem analysis of infected tissues as well as draining lymph nodes. The increased susceptibility of nude mouse to *Leishmania* infections in general will provide an ideal initial mouse model to study *L. australiensis*, analyse the infection in the absence of T cell lymphocytes and more importantly, compare to human pathogenic *Leishmania* species. The relevance of such a study is not limited to clarifying the pathogenicity of human pathogenic species but, as shown recently with *L. tarentolae*, non-human pathogenic *Leishmania* species may represent a safe alternative to either attenuated or subunit vaccines.



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Session Details:	8/27/2013 ONE HEALTH 3 1330 - 1445 <i>Meeting Room 8</i>
Oral Presentation Details:	Update of current knowledge of <i>toxoplasmosis</i> in Australia
Presentation Time:	1330 -1345
Authors:	James Conlan¹ , Duncan Craig ¹ and Marion Healy ¹ ¹ Risk Assessment Branch, Food Standards Australia New Zealand, Canberra, AUSTRALIA

There is growing international interest in the potential role of food in the transmission of toxoplasmosis to vulnerable populations. In 2011, Food Standards Australia New Zealand (FSANZ) collated existing Australian data on toxoplasmosis and other foodborne parasites for the Joint FAO/WHO expert meetings on microbiological risk assessment (JEMRA) but were unable to definitively identify a food vehicle or the risk associated with a food. Data on foodborne cases in Australia is scarce, toxoplasmosis is not a notifiable disease and prenatal screening is not routine. *Toxoplasma gondii* is endemic in the domestic and feral cat populations of Australia, and known intermediate hosts include sheep, goats, free-range poultry, feral and free-range domestic pigs and a variety of native marsupials and birds. There is, at present, only limited data on meat contamination in Australia. Further studies to determine the prevalence and concentration of toxoplasma contamination in meat and other foods in Australia would advance our understanding of the potential role of food in toxoplasma transmission. Further still, the contribution of environmental contamination to human toxoplasmosis in Australia is not well defined and requires further study. This presentation provides an update of current and historical research on toxoplasmosis in Australia and identifies key knowledge gaps that should be addressed to better understand the potential role of food in toxoplasma transmission and the risk posed to vulnerable populations.

Session Details:	8/27/2013 ONE HEALTH 3 1330 - 1445 <i>Meeting Room 8</i>
Oral Presentation Details:	Four cases of fatal toxoplasmosis in three species of endemic New Zealand birds.
Presentation Time:	1345 -1400
Authors:	Howe L ¹ , Hunter S ¹ , Burrows E ¹ , Hardcastle M ² , Roe W ¹ ¹ Wildbase, Massey University, ² Gribbles Veterinary Pathology

Mammals were introduced to New Zealand with the arrival of Maori and Europeans. Prior to this time, New Zealand's only native land mammals were three species of bat and the wide range of unique avifauna occupied the ecological niches normally filled by mammals. With no native felines, the introduction of the domestic cat (*Felis catus*) in the mid-19th century allowed *Toxoplasma gondii* to cycle which then exposed the native avifauna to this new pathogen.

To our knowledge, this is the first report of fatal toxoplasmosis in endemic New Zealand birds. Between 2010 and 2012, two kereru, one North Island brown kiwi, and one kaka were submitted for necropsy examination. On gross post mortem the kiwi had marked hepatosplenomegaly while the kaka and two kereru had swollen, slightly firm deep red lungs. Histologically, there was extensive hepatocellular necrosis in the liver of the kiwi while the kaka and kereru showed fibrinous bronchointerstitial pneumonia. In the kiwi, protozoal organisms were present within the Kupffer cells of the liver and within the macrophages of the pulmonary interstitium of the lung in the kiwi kaka and two kereru. The diagnosis of toxoplasmosis was confirmed with immunohistochemistry and PCR. Genotyping revealed an atypical Type II isolate of *T. gondii* was present in all four cases. This study provides the first evidence that *T. gondii* is causing mortality in these endemic species and suggests further research is needed to determine that full extent of morbidity and mortality caused by this parasite in New Zealand's unique avifauna.

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Session Details:	8/27/2013 ONE HEALTH 3 1330 - 1445 <i>Meeting Room 8</i>
Oral Presentation Details:	An Atypical Genotype Of Toxoplasma Gondii As A Cause Of Mortality In Hector's Dolphins (<i>Cephalorhynchus Hectori</i>)
Presentation Time:	1400 -1415
Authors:	Howe L¹, Roe W¹, Baker E², Burrows L¹, Hunter S¹ ¹ Wildbase, Massey University, ² University of Edinburgh

Hector's dolphins (*Cephalorhynchus hectori*) are a small endangered coastal species that are endemic to New Zealand. Anthropogenic factors, particularly accidental capture in fishing nets, are believed to be the biggest threat to survival of this species. The role of infectious disease as a cause of mortality has not previously been well investigated.

This study investigates *Toxoplasma gondii* infection in Hector's dolphins, finding that 7 of 28 (25%) dolphins examined died due to disseminated toxoplasmosis, including 2 of 3 Maui's dolphins, a critically endangered sub-species. A further 10 dolphins had one or more tissues that were positive for the presence of *T. gondii* DNA using PCR. Genotyping revealed that 7 of 8 successfully amplified isolates were an atypical Type II genotype. Fatal cases had necrotising and haemorrhagic lesions in the lung (n = 7), lymph nodes (n = 6), liver (n = 4) and adrenals (n = 3). Tachyzoites and tissue cysts were present in other organs including the brain (n=5), heart (n = 1), stomach (n = 1) and uterus (n = 1) with minimal associated inflammatory response. One dolphin had a marked suppurative metritis in the presence of numerous intra-epithelial tachyzoites. No dolphins had underlying morbillivirus infection.

This study provides the first evidence that infectious agents could be important in the population decline of this species, and highlights the need for further research into the route of entry of *T. gondii* organisms into the marine environment worldwide.

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Session Details:	8/27/2013 ONE HEALTH 3 1330 - 1445 <i>Meeting Room 8</i>
Oral Presentation Details:	Predilection sites of <i>Toxoplasma gondii</i> in goats, sheep and pigs determined by magnetic capture and real-time PCR
Presentation Time:	1415 -1430
Authors:	Jurankova J¹, Opsteegh M², Basso W³, Neumayerova H¹, Balaz V¹, Frencova A¹, Volf J⁴, Sidler X³, Deplazes P³, Koudela B¹ ¹ University of Veterinary and Pharmaceutical Sciences, ² National Institute for Public Health and the Environment, Bilthoven, THE NETHERLANDS, ³ Institute of Parasitology, University of Zurich, SWITZERLAND, ⁴ Veterinary Research Institute, THE CZECH REPUBLIC

Toxoplasma gondii is an obligate intracellular coccidian, parasitizing many warm-blooded animals including humans all over the world. One of the most common ways of *T. gondii* infection in humans is the consumption of undercooked meat containing tissue cysts.

In order to determine the predilection sites and estimate the parasite burden of *T. gondii* in three food animal species, we performed a sequence-specific magnetic capture method for isolation of *T. gondii* DNA from the tissues (brain, lung, heart, spleen, kidney, liver, muscles from both fore limbs, both hind limbs and dorsal muscle) of goats (n=16), sheep (n=6) and pigs (n=6), experimentally inoculated with 5,000 to 20,000 *T. gondii* oocysts, followed by a quantitative real-time PCR targeting the 529 bp repeat of *T. gondii*.

After euthanasia at 11-12 weeks after inoculation, *T. gondii* DNA was detected (at least once) in all types of tissues in goats, in brain, lungs, skeletal and cardiac muscle in sheep and in all tested tissues except spleen in pigs. According to our results, the most frequently affected tissues, with the highest parasite counts, appeared to be brain, lung and dorsal muscle in goats, and brain in sheep and pigs, representing appropriate tissues for detection of *T. gondii* when performing non-serological surveys in each selected animal species. Moreover, the importance of all tested tissues as a possible source of toxoplasmosis in humans was considered and thorough cooking of meat and offal before human consumption is highly recommended.

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Oral Presentation Details:	Evidence of the three main clonal <i>Toxoplasma gondii</i> lineages in British wild carnivores.
Presentation Time:	1430 -1445
Authors:	Alison Burrells^{1*}, Paul Bartley¹, Irene Zimmer², Sugoto Roy², Andrew Kitchener^{3,4}, Anna Meredith⁵, Steve Wright¹, Elisabeth A. Innes¹, Frank Katzer¹ ¹Moredun Research Institute, Edinburgh, UNITED KINGDOM ²The Food and Environment Research Agency, York, UNITED KINGDOM ³Department of Natural Sciences, National Museums Scotland, Edinburgh, UNITED KINGDOM ⁴Institute of Geography, School of GeoSciences, University of Edinburgh, UNITED KINGDOM ⁵Royal (Dick) School of Veterinary Studies, University of Edinburgh, UNITED KINGDOM

Toxoplasma gondii is a zoonotic pathogen that has the ability to infect all warm blooded animals including humans (Tenter *et al* 2000). Wildlife can act as reservoirs for *T. gondii* infection. Studying the genotype of *T. gondii* in wildlife provides an indication of strains which can potentially be transmitted from the environment to livestock and humans. Three main clonal lineages exist (type I, II and III) and within Europe type II is the most commonly identified type found in humans and animals. Currently very little information exists relating to strains in Britain.

DNA was extracted from tissue samples from ferrets, polecats, badgers, foxes, mink and stoats, which had originated from various locations throughout the UK. A nested PCR, specific for *T. gondii*, was used to detect the presence of the parasite DNA, this was followed by strain genotyping (PCR-RFLP) and sequence analysis.

The prevalence of *T. gondii* within these animals varied from 6% to 44% depending on host species. Type II was the predominant lineage found, however type III and two alleles for type I were also identified, though no atypical genotypes were observed.

The influence of genotype on human infection is still not fully understood, however certain genetic types may be associated with human clinical toxoplasmosis. This study highlights the presence of alleles for all three lineages with potential for their transmission to humans via infected livestock, or directly by cats.

Acknowledgements:

The Scottish Government, Rural and Environmental Sciences and Analytical Services (RESAS) and the Moredun Foundation.

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Session Details:	8/27/2013 ELANCO (GOLD SPONSOR) 1515 - 1630 Riverside Theatre
Oral Presentation Details:	The Spinosyns: Discovery and Development of a Novel Parasiticide
Presentation Time:	1515-1530
Authors:	Daniel E. Snyder* Elanco Animal Health, Greenfield, IN USA

Despite progress in parasiticide development, there remains an ongoing need for new chemistries to enhance effectiveness through novel modes of action or innovative formulations. A source to identify new chemistries consists of soil sampling programs. During the last third of the 20th century, such programs led to discovery of actinomycetes that produced highly active compounds that would revolutionize parasite control in domestic animals. The first of these to have widespread commercial success was ivermectin. The most recent is spinosad, a mixture of two spinosyns—A and D—identified in a soil sample collected from an abandoned Caribbean rum still.¹ Spinosyns paralyse insect and acarine parasites primarily by unique binding to sites on nicotinic acetyl choline receptors, and secondarily to sites on γ-amino butyric acid gated receptors.² Initially developed for agricultural use, spinosad was accepted for organic farming because of its relatively low impact on non-target organisms.² Spinosad containing formulations have been approved for use in livestock (sheep blow-fly strike, lice infestations of cattle and sheep) and for use in companion animals. Although initial work on a topical formulation for dogs showed promise, the crowded field of spot-on flea control products and absence of oral alternatives stimulated development of a tablet formulation. First registered for dogs in 2007 and cats in 2012, both in the USA, spinosad tablets were shown to provide very rapid knockdown and one month activity against *Ctenocephalides felis*. Subsequent registrations have been achieved in numerous countries. Recent data indicate that spinosad continues to maintain a high level of flea control, regardless of the level of initial challenge.³ Further refinement of the spinosyns has led to the development of a combination of 2 additional family members—spinosyns J and L—which has now achieved initial registrations as a topical treatment of flea infestations on cats.

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1. Mertz FP, Yao RC. *Saccharopolyspora spinosa* sp. nov. Isolated from Soil Collected in a Sugar Mill Rum Still. Int J Syst Bacteriol. 1990;40:34-9
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3. Dryden MW, Ryan WG, Bell M, Rumschlag AJ, Young LM, Snyder DE. Assessment of owner-administered monthly treatments with oral spinosad or topical spot-on fipronil/(S)-methoprene in controlling fleas and associated pruritus in dogs. Vet Parasitol. 2013, 191:340-6.

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Session Details:	8/27/2013 ELANCO (GOLD SPONSOR) 1515 - 1630 <i>Riverside Theatre</i>
Oral Presentation Details:	The Efficacy of Spinosad for the Control of Pests Infesting Poultry
Presentation Time:	1515 -1530
Authors:	* Richard Hack ¹ , Ignacio Dominguez ² , Donato Pennelli ³ , Gosse Smid ⁴ , Fabio Mello ⁵ Elanco Animal Health, ¹ United States, ² Spain, ³ Italy, ⁴ Netherlands, ⁵ Brazil

Spinosad is in the chemical class spinosyns with no known cross resistance to other classes of pesticides. Spinosad's unique mode of activity provides efficacy against the Lesser mealworm (Darkling Beetle): *Alphitobius diaperinus* (Panzer, 1797), the Poultry Red Mite: *Dermanyssus gallinae* (De Geer, 1778), the Northern Fowl Mite: *Ornithonyssus sylviarum* (Canestrini et Fanzago, 1877), the Poultry Louse: *Menopon gallinae* (Linnaeus, 1758) and the House fly: *Musca domestica* (Linnaeus, 1758). The formulation is 44.2% spinosad. Depending upon the pest, spinosad is applied to the facilities or a topical application directly to the birds. When used as a topical application to control Northern Fowl Mites or Poultry lice, a single application will control the infestation with a thorough application. When used as a facility treatment, the duration of effect is dose dependent, with the higher dose providing a longer duration. The duration of effect for house flies is approximately two weeks and red mites 5 to 8 weeks with a thorough application. The duration of effect in litter to control Darkling Beetles is 4 to 6 weeks when applied as a banded treatment. Spinosad has an excellent safety profile and is non toxic to the birds and the applicators. In all countries except Australia (21 day) there is a 0 day withdraw on meat and eggs. Since there is no known cross resistance to other chemistries, spinosad is recommended to be used in a rotational pesticide program to reduce the potential of resistance.

References:

Elanco Reports:

- T9CDE090011
- T9CGB090002
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- T9C370608
- Red Mite Technical Manual

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Session Details:	8/27/2013 ELANCO (GOLD SPONSOR) 1515 - 1630 <i>Riverside Theatre</i>
Oral Presentation Details:	The Spinosyns: Discovery and Development of a Novel Parasiticide
Presentation Time:	1515-1530
Authors:	Daniel E. Snyder* Elanco Animal Health, Greenfield, IN USA

Despite progress in parasiticide development, there remains an ongoing need for new chemistries to enhance effectiveness through novel modes of action or innovative formulations. A source to identify new chemistries consists of soil sampling programs. During the last third of the 20th century, such programs led to discovery of actinomycetes that produced highly active compounds that would revolutionize parasite control in domestic animals. The first of these to have widespread commercial success was ivermectin. The most recent is spinosad, a mixture of two spinosyns—A and D—identified in a soil sample collected from an abandoned Caribbean rum still.¹ Spinosyns paralyse insect and acarine parasites primarily by unique binding to sites on nicotinic acetyl choline receptors, and secondarily to sites on γ-amino butyric acid gated receptors.² Initially developed for agricultural use, spinosad was accepted for organic farming because of its relatively low impact on non-target organisms.² Spinosad containing formulations have been approved for use in livestock (sheep blow-fly strike, lice infestations of cattle and sheep) and for use in companion animals. Although initial work on a topical formulation for dogs showed promise, the crowded field of spot-on flea control products and absence of oral alternatives stimulated development of a tablet formulation. First registered for dogs in 2007 and cats in 2012, both in the USA, spinosad tablets were shown to provide very rapid knockdown and one month activity against *Ctenocephalides felis*. Subsequent registrations have been achieved in numerous countries. Recent data indicate that spinosad continues to maintain a high level of flea control, regardless of the level of initial challenge.³ Further refinement of the spinosyns has led to the development of a combination of 2 additional family members—spinosyns J and L—which has now achieved initial registrations as a topical treatment of flea infestations on cats.

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3. Dryden MW, Ryan WG, Bell M, Rumschlag AJ, Young LM, Snyder DE. Assessment of owner-administered monthly treatments with oral spinosad or topical spot-on fipronil/(S)-methoprene in controlling fleas and associated pruritus in dogs. *Vet Parasitol.* 2013, 191:340-6.





Session Details:	8/27/2013 ELANCO (GOLD SPONSOR) 1515 - 1630 Riverside Theatre
Oral Presentation Details:	Broadening the spectrum - the combination of spinosad with milbemycin oxime
Presentation Time:	1600 -1615
Authors:	Beate Schnitzler* Elanco Animal Health, Priestley Road, Basingstoke, Hants RG24 9NL, UK

Breadth of spectrum is a desirable characteristic of products used to control parasites of domestic animals. Milbemycin oxime (MBO) is a well established broad spectrum anthelmintic with known safety and efficacy against heartworm, ascarid, hookworm and whipworm infections. Initial safety studies demonstrated that concurrent doses of MBO and spinosad, both at elevated levels, would allow a very wide therapeutic index in avermectin sensitive dogs.¹ Studies subsequently demonstrated the non-interference of spinosad with MBO, and dose titration and dose confirmation studies were completed against flea infestations and infections with adult and/or larval stages of gastrointestinal nematodes, including *Ancylostoma caninum*, *Toxocara canis*, *Toxascaris leonina*, and *Trichuris vulpis*.^{2,3} Effectiveness was then further confirmed against these parasites in natural infections. The results consistently demonstrated that the spinosad/MBO combination would at least maintain the established efficacy profile of either product administered as a single entity. Against *Dirofilaria immitis* infections, studies demonstrated equivalent efficacy of the combination product to the well-established heartworm preventives, while elevated dose assessment of the spinosad/MBO combination verified its broad therapeutic index.⁴ A recent European laboratory study demonstrated 99% efficacy of this spinosad/MBO combination in the prevention of infections with *Angiostrongylus vasorum*, a parasite which, although having apparently limited distribution, is a cause of increasing concern in potentially endemic areas, particularly in Europe⁵ and Canada.^{6,7}

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Session Details:	8/27/2013 CONSERVATION AND WILDLIFE GENERAL 1515 - 1630 Meeting Room 1
Oral Presentation Details:	Christmas Island's parasitic plight
Presentation Time:	1515 -1530
Authors:	Narelle Dybing ^{1*} , Caroline Jacobson ¹ , Peter Irwin ¹ , Dave Algar ² and Peter Adams ¹ ¹ Murdoch University, School of Veterinary and Biomedical Science, South street campus, Western Australia, 6150 ² Department of Environment and Conservation, Wildlife place, Woodvale, Western Australia 6026

Christmas Island is a strategic surveillance site for Australian biosecurity given its proximity to South East Asia and Northern Australia. Additionally the tropical climate and rainforest environment of Christmas Island are conducive to the establishment of a wide range of parasites of zoonotic and conservation importance which may involve both feral and/or native wildlife and their respective ectoparasite communities. Feral cats and black rats, two species commonly introduced to island ecosystems, have been introduced on Christmas Island along with their parasites. Pathogens previously reported from cats and rats on Christmas Island include *Bartonella* and *Trypanosoma*, both presumably introduced by black rats, with the latter being attributed with the subsequent demise of two endemic rodent species (*R. macleari* and *R. nativitatis*). However little is known regarding the true prevalence of these pathogens or those species it colonises. The current use of the island as a processing site for refugees from Middle Eastern origins also increases the potential for the introduction of *Leishmania* spp. In conjunction with these blood pathogens, black rats and feral cats harbour a range of helminth parasites. Black rats (n=101) and feral cats (n=67) from Christmas Island were examined for parasites in conjunction with a management and eradication program run by the Department of Environment and Conservation (DEC). Eighty-five percent of cats harboured helminths with the three most common being *Ancylostoma* spp (69%), *Toxocara cati* (49%), *Dipylidium caninum* (40%) and 79% of black rats harboured helminths with the 3 most common being *Rictularia* spp. (42%), *Protospirura muris* (40%), *Syphacia muris* (29%). This study investigates the parasite status of two competent host populations (feral cats and black rats) present on Christmas Island with particular emphasis on pathogens of zoonotic and conservation significance.

Acknowledgements:

Department of Environment and Conservation; Christmas Island Phosphates; Christmas Island National Parks; Murdoch University Veterinary Trust.





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Session Details:	8/27/2013 CONSERVATION AND WILDLIFE GENERAL 1515 - 1630 <i>Meeting Room 1</i>
Oral Presentation Details:	The susceptibility of native and introduced freshwater fish species to the exotic parasite <i>Lernaea cyprinacea</i>
Presentation Time:	1530 -1545
Authors:	Alan L , Basile S, Morine M, Morgan D, Beatty S Murdoch University

The south west of Western Australia has a unique and threatened freshwater fish fauna. One of the major threatening processes is the introduction of exotic fish species, which affect native species by habitat alteration, competition, predation and the introduction of new parasites and pathogens. The copepod parasite *Lernaea cyprinacea* L., most likely introduced with goldfish, has recently been found in a number of river systems in the south west of Western Australia. Field data indicate that this parasite is more prevalent, and has greater pathogenic consequences on native fish species than on goldfish. Laboratory studies suggest that native fish species are more readily infected than goldfish, due to differences in innate and acquired immune response, and in behavioural reactions to infection. Goldfish are therefore less competent hosts for *L. cyprinacea* than native fish species and their continued presence in south west rivers may be beneficial in reducing infection pressure on native fishes.

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Session Details:	8/27/2013 CONSERVATION AND WILDLIFE GENERAL 1515 - 1630 Meeting Room 1
Oral Presentation Details:	Centrocestus armatus metacercariae (Digenea: Heterophyidae) induced changes in fish host behavior and susceptibility to predation
Presentation Time:	1545 -1600
Authors:	Paller V ¹ , Uga S ² , Ishiyama S ² ¹ Animal Biology Division, Institute Of Biological Sciences, ² Department Of Parasitology, Graduate School Of Health Sciences, Kobe University, Japan

Centrocestus armatus is a digenean trematode transmitted by second intermediate fish hosts, such as *Zacco temminki*, to its definitive avian host. Parasites that are transmitted from prey to predator are often associated with altered prey behavior. Hence, we hypothesized that *C. armatus* can modify the behavior of its fish host for easy transmission to the avian definitive host. In this study, we conducted a 2-fold experiment on field collected and artificially infected fish to demonstrate the possible effects of a parasite on the behavior of the hosts. We tested whether *C. armatus* induce changes in the behavior of the fish that would increase their susceptibility to predation. Factors such as escape response, shelter use, and predation experiments were performed to determine its vulnerability to predation. Results revealed that parasitized fish were substantially more susceptible to predation. The results of escape response from the strike of simulated avian predator and shelter use were less than those of uninfected fish. For the predation experiments, the infected fish were more likely to be caught than uninfected fish. All infected fish were parasitized and the average *C. armatus* burden $\pm$ SD in the brain and eyes of naturally infected fish were 252 ± 107.55 and 28 ± 19.87 , respectively, while that of artificially-infected fish were 62 ± 16.68 and 18 ± 10.23 . These results support the behavior-modification hypothesis and emphasize the importance of parasites in predator-prey interactions.





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Session Details:	8/27/2013 CONSERVATION AND WILDLIFE GENERAL 1515 - 1630 <i>Meeting Room 1</i>
Oral Presentation Details:	Reappearance of <i>Taenia ovis krabbei</i> muscle cysts in a roe deer (<i>Capreolus capreolus</i>) in Denmark after 60+ years, with a possible role of a grey wolf (<i>Canis lupus</i>) as definitive host
Presentation Time:	1600 -1615
Authors:	Al-Sabi M, Chriel M, Holm E, Jensen T, Ståhl M, Enemark H National Veterinary Institute, Technical University of Denmark

Taenia ovis krabbei has a semi-sylvatic life cycle with carnivore definitive hosts and cervid intermediate hosts. Cervids become infected by foraging on pasture contaminated with the eggs. Larval stages usually develop in heart and skeletal muscles causing pathological changes and severe illness^{1,2}. Meat infected with *T. o. krabbei* entails no zoonotic risk, but for aesthetic reasons the infected meat is usually discarded³. Here, we report the reappearance of *T. o. krabbei* in a roe deer in Denmark after more than 60 years. The cysticerci were diagnosed after histology, morphology⁴ and sequencing of the *cox1* gene⁵. Shortly after this discovery, a wolf died in a nearby locality, and worms of *T. o. krabbei* were recovered from its intestine. By phylogenetic analysis, the Danish roe deer and wolf isolates were clearly grouped together with other isolates of *T. o. krabbei* from wolves in Fennoscandinavia. In mainland Europe, *T. o. krabbei* is primarily a parasite of wolves^{6,7}. The unexpected reappearance of a wolf in Denmark in 2012 after almost two decades of absence could be a mere coincidence, but may also explain the introduction of this parasite along with the wolf. Domestic dogs, on the other hand, could play a role in transmission of *T. o. krabbei* in the area, but this has yet to be tested. Deer infections with *T. o. krabbei* were previously reported in the German county that borders Denmark³, and may have spread from there. But it is also possible that deer infections were already present, but unnoticed, in other areas of Denmark. The helminth burden of invading animals is normally expected to decrease⁸. However, invading wolves can support their establishment in new areas by carrying worms of *T. o. krabbei* that cause severe illness in native deer that subsequently become prey to the wolves.

Acknowledgements:

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Session Details:	8/27/2013 CONSERVATION AND WILDLIFE GENERAL 1515 - 1630 Meeting Room 1
Oral Presentation Details:	Why history matters? A tale of lungworms and their hosts
Presentation Time:	1615 -1630
Authors:	Guilherme G. Verocai ^{1*} , Eric P. Hoberg ² , Susan J. Kutz ^{1,3} ¹ University of Calgary, Calgary, CANADA ² United States Department of Agriculture, US National Parasite Collection, Beltsville, USA ³ Canadian Cooperative Wildlife Health Centre, Calgary, CANADA

Parasitism does not occur in a vacuum of space and time and the current patterns of parasite community structure and host associations are a product of historical and ongoing processes. Knowledge of historical biogeography and phylogenetic relationships for hosts and parasites can provide critical insights into contemporary parasite biodiversity and host-parasite associations¹. Conversely, information on current host-parasite systems also help us to decipher past events that shaped these faunas.

Herein, we explore the diversity of nematodes within the Protostrongylidae, pathogenic parasites of ungulates globally. Apart from introductions with domestic or wild hosts, Eurasian and North American protostrongylid faunas are distinct, reflecting historical events of expansion and isolation.

Recent discovery of a new lungworm species from North America (*Varestrongylus* sp.)^{2,3} and the resurrection of a *Varestrongylus* species from Eurasia (*V. alces*)⁴ have changed our understanding of biodiversity within this genus and the historical processes that shaped this diversity. Although there are two North American species of *Varestrongylus*, *V. alpenae* in *Odocoileus virginianus* and the putative new species primarily in *Rangifer tarandus*, phylogenetically these didn't appear to be sibling species. Subsequent morphological and molecular analyses of all three species demonstrated a closer phylogenetic relationship of the new species with the Eurasian *V. alces*, as opposed to *V. alpenae*. These results indicate at least two independent events of geographic expansion for *Varestrongylus* from Eurasia into North America with cervids during the late Pliocene and Quaternary.

Our findings further predict a yet undetected *Varestrongylus* may occur in *Rangifer* from Eurasia. It is apparent that evaluation of parasite diversity and distributions in light of historical processes constitutes a powerful tool for exploring biodiversity and anticipating host-parasite associations. Moreover, such integrated approaches may be particularly valuable for the investigation of data poor systems.

Acknowledgements:

This research was partially funded by Alberta Innovates Health Solutions, Faculty of Veterinary Medicine of the University of Calgary, Alberta Conservation Association – Grants in Biodiversity, Wildlife Conservation Society, Natural Sciences and Engineering Research Council (NSERC), and the Government of Canada International Polar Year program. We also thank the various collaborators in different aspects of the overall project that allowed us to build this conceptual framework.



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Hosted by The Australian Society for Parasitology Inc.

Session Details:	8/27/2013 PARASITES OF AQUATIC WILDLIFE 2 1515 - 1630 <i>Meeting Room 2</i>
Oral Presentation Details:	Global diversity of parasitic isopods of the Family Cymothoidae
Presentation Time:	1515 -1530
Authors:	Nico J. Smit^{1*} , Kerry-Ann Hadfield ¹ , Niel L. Bruce ² ¹ Water Research Group (Ecology), Unit for Environmental Sciences and Management, North West University, Potchefstroom, SOUTH AFRICA, ² Museum of Tropical Queensland, and School of Marine and Tropical Biology, James Cook University, Townsville, Qld 4810, AUSTRALIA.

Of the 95 known families of Isopoda only a few are parasitic namely, Bopyridae, Cryptoniscidae, Cymothoidae, Dajidae, Entoniscidae, Gnathiidae and Tridentellidae. Representatives from the family Cymothoidae are obligate parasites of both marine and freshwater fishes and there are currently 43 recognised cymothoid genera worldwide. These isopods are large (> 6 mm) parasites, thus easy to observe and collect, yet many aspects of their biodiversity and biology are still unknown. They are widely distributed around the world and occur in many different habitats, but mostly in shallow waters in tropical or subtropical areas. A number of adaptations to an obligatory parasitic existence have been observed, such as the body shape, which is influenced by the attachment site on the host. Cymothoids generally have a long, slender body tapering towards the ends and the efficient contour of the body offers minimum resistance to the water flow and can withstand the forces of this particular habitat. Other adaptations to this lifestyle include small sensory antennae and eyes; a very heavily thickened and calcified cuticle for protection; and sharply curved hooks on the ends of the pereopods which allows these parasites to attach to the host. Most cymothoids are highly site and host specific. Some of these parasitic cymothoids have been reported to parasitise the same host fish species for over 100 years, showing this species specificity. The site of attachment on the host (gills, mouth, external surfaces or inside the host flesh) can also be genus or species specific. This paper aims to provide a summary of our current knowledge of cymothoid biodiversity and will highlight their history of discovery, morphology, relationships and classification, taxonomic diversity and ecology.



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Session Details:	8/27/2013 PARASITES OF AQUATIC WILDLIFE 2 1515 - 1630 <i>Meeting Room 2</i>
Oral Presentation Details:	Review of the fish tongue biter <i>Cymothoa</i> Fabricius, 1793 (Crustacea: Isopoda: Cymothoidae) in Australian waters
Presentation Time:	1530 -1545
Authors:	Martin M^{1, 2}, Bruce N^{3, 4, 5}, Nowak B¹ ¹ National Centre for Marine Conservation and Resource Sustainability, University Of Tasmania, ² Faculty of Maritime and Marine Sciences, University Malaysia Terengganu, ³ Museum of Tropical Queensland, Queensland Museum, ⁴ School of Marine and Tropical Biology, James Cook University, ⁵ Department of Zoology, University of Johannesburg

Cymothoids are parasitic crustaceans of fish, known to burrow in the flesh or attach externally on the fins, gill chambers or mouth region of its host. The Cymothoidae is the second largest family of marine isopods in the suborder Cymothoidea, with 280 species of 34 genera known worldwide. Species of the mouth-attaching genus *Cymothoa* are economically important parasites as they have been shown to have a detrimental effect on fish such as buccal malformation, growth inhibition and anaemia. The World Register of Marine Species lists 47 species of *Cymothoa* worldwide, 13 of which occur in Australia. Knowledge on *Cymothoa* from Australia rests with the early works of Schioedte and Meinert (1884), Hale (1926), Trilles (1975) and Avdeev (1978,1979). *Cymothoa* is one of the most difficult of the cymothoid genera to identify correctly to species level due to poor description in the historical literature, lack of type material, lack of identified hosts and localities and morphological variability.

Research to date has revealed three new species in Australian waters, including one species previously known only from South Africa, which indicates that at least some species from the genus *Cymothoa* have a wide geographical distribution. We also have three new host records, providing a better understanding of host preference for *Cymothoa*. We demonstrate how our results will be developed into a user-friendly DELTA key, which will include digital images, illustrations and descriptions suitable for aquaculturists, biologists and parasitologists.

Acknowledgements:

The senior author would like to acknowledge the Australian Museum for the Geddes Postgraduate Award, enabling her to have access to their cymothoid and fish collections. This project was made possible by the provision of facilities and collections of The Museum of Tropical Queensland–Queensland Museum, South Australian Museum and The Tasmanian Museum and Art Gallery. Gratitude is also extended to the National Centre for Marine Conservation and Resource Sustainability and the Public Service Department of the Malaysian Government for their generosity in awarding the senior author a postgraduate scholarship.

References:

Avdeev, V.V. (1979a) New species of the genus *Cymothoa* (Isopoda, Cymothoidae) from the coastal regions of north-western Australia. *Parazitologiya*, 13, 50–55.



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Session Details:	8/27/2013 PARASITES OF AQUATIC WILDLIFE 2 1515 - 1630 <i>Meeting Room 2</i>
Oral Presentation Details:	Revision of taxonomy and biology of anisakid nematodes in Australia
Presentation Time:	1545 -1600
Authors:	Shamsi S Charles Sturt University

Anisakid nematodes have a cosmopolitan distribution and infect a wide range of invertebrates and vertebrates during their life cycles. Since first report of these parasites from humans (1961), anisakid nematodes have attracted considerable attention as emerging zoonotic parasites. This, along with rapid development of various molecular techniques during last decades, caused a significant change in the taxonomy and systematics of these parasites. Australian anisakids are mainly known by works of Johnson and Mawson in mid 20th century. Although employing advanced morphological and molecular techniques to study anisakids had a late start in Australia, great biodiversity was found and unique species were discovered. This presentation will review the current state of knowledge on Australian anisakids. An updated list of members within the family will be presented and some common confusion on nomenclature and assigning genera to this family will be discussed. Different patterns of the life cycle within this family and the potential impact of these parasites on wildlife as well as humans health will be reviewed. Given that employing advanced techniques to study these important emerging zoonotic parasites in Australia is recent, more research is needed to understand ecology and biology of these socio economically important parasites. After several human cases of anisakidosis in Australia in recent years, such understanding is crucial if control and preventive strategies are to be established in the country.

Acknowledgement:

I am very grateful of my former PhD supervisor, Professor Ian Beveridge for all his support during and after my candidature. Also many thanks to all researchers across the world who contributed to our today’s knowledge on these important parasites.



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Session Details:	8/27/2013 PARASITES OF AQUATIC WILDLIFE 2 1515 - 1630 <i>Meeting Room 2</i>
Oral Presentation Details:	Larval anisakid nematodes from teleost fishes from Lizard Island, Queensland, Australia
Presentation Time:	1600 -1615
Authors:	Jabbar A¹ , Norbury L ² , Eisenbarth A ² , Shamsi S ³ , Gasser R ¹ , Lopata A ^{2,4} , Beveridge I ¹ ¹ The Unievrsity Of Melbourne, ² School of Applied Science, RMIT University, Bundoora, ³ School of Animal & Veterinary Sciences Charles Sturt University, ⁴ James Cook University, Townsville

This study characterised larval anisakid nematodes in teleost fishes from Lizard Island on the northern Great Barrier Reef. A total of 464 fish was examined, encompassing 32 families, 62 genera and 107 species. Anisakid nematodes were found in 46 (9.9%) of the fish examined. Infections in Atherinidae, Lethrinidae, Lutjanidae and Serranidae were more prevalent with intensities of infection ranging from 1 to 80; whereas in the Sphyraenidae and Scombridae, the prevalence of infection was very high with intensities raging from 1 to >375. A combined morphological and molecular-phylogenetic approach was employed to identify larval anisakid nematodes to species and/or genotypes. For the molecular characterisation of nematodes (n = 424), we used an integrated PCR-coupled mutation scanning-sequencing-phylogenetic analysis of sequence variation in the internal transcribed spacers of nuclear ribosomal DNA. This analysis revealed eight morphotypes representing, *Anisakis typica*, *Terranova* larval types I and II, *Hysterothylacium* larval types IV, Vb, Vc, VI and X. Mutation scanning analysis of all the PCR-amplicons revealed 20 profiles which were confirmed by sequencing the representative amplicons. The findings of the present study provide some insights into the distribution of larval anisakid nematode in coral reef fishes and basis for future investigations of the genetic composition of anisakid populations in a wide range of fish hosts in Australia.



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Session Details:	8/27/2013 PARASITES OF AQUATIC WILDLIFE 2 1515 - 1630 <i>Meeting Room 2</i>
Oral Presentation Details:	Trematodes of New Zealand rocky shore littorinid snails and desiccation stress
Presentation Time:	1615 -1630
Authors:	O'Dwyer K, Poulin R University Of Otago

Trematode parasites are well known for their fascinating and complex life cycles, in some cases involving up to four host species. Many species have secondarily adopted simpler life cycles by omitting a host, thereby abbreviating their life cycle. Rocky shore littorinid gastropods serve as first intermediate hosts to a suite of trematode species. However, in the Southern Hemisphere littorinid species have thus far not been seriously investigated as hosts to trematodes. In the present study, the transmission modes of trematode species utilising two closely related species of littorinid as first intermediate host were investigated. One of these trematodes (family Philophthalmidae) was found to facultatively develop into the next stage of its life cycle (metacercarial cyst) while still inside the tissue of the preceding stage (redia). To investigate this further, an experiment was carried out to test the effect of long-term desiccation stress on the development route taken by this trematode. Precocious encystment as a metacercaria increased in frequency with the size of the snail host, with some differences in encystment frequency also observed between desiccation treatments for the two littorinid species. One littorinid species was found to have more individuals containing metacercarial cysts when kept in wet conditions, while for the other host species there was an increase in the occurrence of cysts under dry conditions. Mortality of both littorinid species was similarly affected, being greater in dry conditions than when water was available, and was higher for infected snails. The large temporal variation in factors affecting the biota found on rocky shores has been well documented. The same abiotic stresses affect parasites, which have had to adapt in varying ways to persist in these harsh habitats. The success of this parasite and the likely adaptive significance of precocious encystment will be discussed.



Session Details:	8/27/2013 DOG AND CAT PARASITES 2 1515 - 1630 <i>Meeting Room 3</i>
Oral Presentation Details:	Molecular characterization and PCR detection of <i>Gurltia paralysans</i>.
Presentation Time:	1515 -1530
Authors:	Gomez M ¹ , Hirzmann J ² , Hermosilla C ² , Taubert A ² , Muñoz P ¹ , Moroni M ¹ , Mieres M ¹ , Acosta-Jamett G ¹ , López F ¹ , Morera F ¹ ¹ Universidad Austral de Chile, Valdivia, CHILE, ² Justus-Liebig University of Giessen, Giessen, GERMANY

Gurltia paralyans (Metastrongyloidea, *Angiostrongylidae*) is a nematode that lodges in veins of the spinal subarachnoid space and causes chronic meningomyelitis in domestic cats of South America. Definitive diagnosis of feline gurltiosis is challenging and only possible after necropsy by detection of adult larvae and based on its morphological characterization. *Gurltia paralyans* share many morphological features with other genus of the family *Angiostrongylidae*, however, no studies have been performed to determine the phylogenetic location of *G. paralyans* in relation with other angiostrongiloids nematodes. The objective of the present study was to develop a PCR technique for molecular detection of feline gurltiosis infection by using the D1-D2 segment of 28S rRNA. Additionally, fragments of RNA (partial sequence of 28s rRNA-gene) from *G. paralyans* were compared with other parasites of the genus *Angiostrongylidae* for taxonomic and phylogenetic analysis. The 28S rRNA D2-D3 region was 717 bp in length and the sequencing was deposited in the GenBank under the accession number JX975484. Phylogenetic analyses revealed that *G. paralyans* is most closely related to *Angiostrongilus vasorum* and *Filaroides martis*. Results indicated that D2-D3 28S region obtained from the parasite can be used as an effective diagnostic method of identification of infected cats.

Acknowledgements:

This research was partially funded by FONDECYT (Grant N° 1120481) from CONICYT, Chile.

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Session Details:	8/27/2013 DOG AND CAT PARASITES 2 1515 - 1630 <i>Meeting Room 3</i>
Oral Presentation Details:	Survey of <i>Aelurostrongylus</i> in cats in the UK – a comparison with <i>Angiostrongylus</i> in dogs
Presentation Time:	1530 -1545
Authors:	Fox M , Brickman K, Lewis B, Guitian J, Stevens K Royal Veterinary College

Recent surveys of catteries for the lungworm, *Aelurostrongylus abstrusus*, and few records seen by a national veterinary diagnostic laboratory, suggest that the parasite is rare in the UK. The aim of this study was to establish the distribution and frequency of infection seen in domestic cats nationwide using an on-line survey of practice veterinarians.

Practices completed a structured questionnaire that sought information on the location of each practice, awareness of the parasite locally, numbers of cases diagnosed (clinical signs only or using additional diagnostic tests) and type of test(s) employed. Choropleth maps were created using Arc GIS 9.2 (ESRI 2006) to visualize the geographic distribution of practices that had seen cases. These represented, for practices located in the same county, the risk of having seen up to or more than five confirmed cases over the previous 12 months. The spatial scan statistic was used to identify significant clusters of practices with a high probability of having at least one or more than five confirmed cases. This was implemented in SaTScan v8.1.1 using a Bernoulli probability model and Monte-Carlo randomisation, clusters for which $P < 0.05$ were considered statistically significant.

One thousand and one practices (40.4% response rate) completed the questionnaire of which 6.1% were aware of the parasite locally, 2% made a diagnosis on clinical grounds alone and 1.2% made a diagnosis confirmed using additional diagnostic test(s); confirmed cases were widely but very thinly distributed. This may reflect the limit of the parasite's distribution in NW Europe, in comparison with higher prevalence figures seen in central and southern Europe.

In contrast, the canine heartworm, *Angiostrongylus vasorum*, is much more widespread (Ashley et al, 2011). Factors that may account for this include a wider intermediate host range, foxes acting as a reservoir of infection and wide movement of dogs within the UK.

Acknowledgements:

Funding provided by Bayer Animal Health for both parasite surveys is gratefully acknowledged.

References:

ASHLEY, L., LIMON, G., GUITIAN, J., HERMOSILLA, C., FOX, M.T. (2011) *Angiostrongylus vasorum* in the United Kingdom – a nationwide postal questionnaire survey. In: *Proceedings of the World Association for the Advancement of Veterinary Parasitology, 21-25 August 2011, Buenos Aires, Argentina*. p.269



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Session Details:	8/27/2013 DOG AND CAT PARASITES 2 1515 - 1630 <i>Meeting Room 3</i>
Oral Presentation Details:	Characterisation of cytokine alterations during experimental <i>Babesia gibsoni</i> infection in dogs
Presentation Time:	1545 -1600
Authors:	Alexa Brown* , Robert Shiel, Susan Bennett, Peter Irwin College of Veterinary Medicine, School of Veterinary and Life Sciences, Murdoch University, Perth, AUSTRALIA

Canine babesiosis is a geographically widespread tick-borne haemoprotozoan disease. The clinical presentation is highly variable and systemic inflammation is considered to be a major feature of the pathophysiology of babesiosis. The host's immune response to infection is mediated via the production of cytokines. Four 139 day old sibling beagles were used in the experiment; two dogs were injected intravenously with *Babesia gibsoni* sourced from a naturally-infected American Bull Terrier. Clinical and haematological parameters were assessed daily in all dogs. Thirteen cytokines (TNF- α , INF- γ , MCP-1, GM-CSF, IL-2, IL-6, IL-7, IL-8, IL-10, IL-15, IL-18, IP-10 and KC-like) were measured in each dog prior to infection, every third day following infection and daily following the development of peripheral parasitaemia. Cytokines were assayed in duplicate using a MILLIPLEX[®] MAP Canine Cytokine Panel read using a Bio-Plex[®] MAGPIX[™] platform. The study ended with euthanasia of infected dogs once peak parasitaemia (>5% of erythrocytes parasitised) was reached. Intra-erythrocytic piroplasms were first observed in peripheral blood 15 days after infection. Infected dogs, but not controls, developed transient pyrexia, anaemia and thrombocytopenia which coincided with the development of peripheral parasitaemia. Marked, persistent, increases in the concentration of multiple cytokines (TNF- α , GM-CSF, IL-2, IL-6, IL-15 and IL-1) and transient increases in the concentration of IL-8, IL-10 and KC-like occurred following, but not prior to, the development of peripheral parasitaemia in infected dogs. The concentration of MCP-1 in infected dogs increased transiently following passage of infected blood and was the only cytokine to increase in infected dogs prior to the development of peripheral parasitaemia. These findings indicate that cytokine-mediated inflammatory responses occur in dogs following experimental infection with *Babesia gibsoni*. However, rather than occurring immediately after infection as expected, the response was delayed and did not occur until peripheral parasitaemia developed coinciding with the development of clinical and haematological abnormalities.



Session Details:	8/27/2013 DOG AND CAT PARASITES 2 1515 - 1630 <i>Meeting Room 3</i>
Oral Presentation Details:	New insights on the biology of <i>Troglostrongylus brevior</i> (Strongylida: Crenosomatidae)
Presentation Time:	1600 -1615
Authors:	Ramos R¹, Giannelli A¹, Brianti E², Dantas-Torres F^{1,3}, Di Cesare A⁴, Traversa D⁴, Otranto D¹ ¹ University of Bari, ITALY, ² University of Messina, ITALY, ³ Centro de Pesquisas Aggeu Magalhães, BRAZIL, ⁴ University of Teramo, ITALY

Respiratory infestations in domestic cats are usually attributed to *Aelurostrongylus abstrusus* (Strongylida: Angiostrongylidae) whereas the reports of *Troglostrongylus* spp. (Strongylida: Crenosomatidae) largely remain anecdotic. *Troglostrongylus brevior* has been recently recognised as an emergent causative agent of broncho-pulmonary nematode infestation in domestic cats. Nonetheless, information on the biology and ecology of this nematode is meagre. The aim of this study was to evaluate the development of *T. brevior* in *Helix aspersa* snails and to assess the survival of *T. brevior* first stage larvae (L1s) in water and in faeces at different controlled temperatures (i.e., 4°, 14° and 26°C). *Helix aspersa* snails were infested with 500 L1 and maintained at a mean temperature of 24°C until being microscopically examined every 3-4 days post-infection, until the retrieval of infectious larvae. Vitality of L1s in water and faeces was assessed every 7 days up to their death. Second and third larval stages of *T. brevior* were detected at 4 and 12 days post-infection, respectively. At 4°C, L1s survived from 56 to 142 days in the faeces and underwater, respectively, whereas, they survived until 7 days either in water or faeces at 26°C. Larvae maintained at 14°C survived from 35 to 63 days in faeces and water, respectively. Data here presented indicate that the survival of *T. brevior* L1s in the environment is dependent of the temperature and provide evidence that *H. aspersa* acts as a suitable intermediate host of *T. brevior*. Moreover, it is suggested that L1s may easily infest mollusks during winter/spring, with a reduction during hot and dry seasons. These data represent the first ground on which building scientific knowledge on the biology of this little known lungworm.

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Taubert A, Pantchev N, Vrhovec MG, Bauer C, Hermosilla C. 2009. Lungworm infections (*Angiostrongylus vasorum*, *Crenosomavulpis*, *Aelurostrongylus abstrusus*) in dogs and cats in Germany and Denmark in 2003–2007. *Vet Parasitol* 159: 175–180.

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Session Details:	8/27/2013 DOG AND CAT PARASITES 2 1515 - 1630 Meeting Room 3
Oral Presentation Details:	Treatment of <i>Dirofilaria repens</i> microfilariaemia with a combination of doxycycline hyclate and ivermectin
Presentation Time:	1615 -1630
Authors:	Alessio Giannelli¹, Rafael Antonio do Nascimento Ramos¹, Donato Traversa², Emanuele Brianti³, Giada Annoscia¹, Francesca Bastelli⁴, Filipe Dantas-Torres^{1,5}, Domenico Otranto¹ ¹University of Bari, Bari, ITALY; ²University of Teramo, Teramo, ITALY; ³ University of Messina, Messina, ITALY; ⁴Private Practitioner, Rome, ITALY; ⁵Fundação Oswaldo Cruz, Recife, BRAZIL;

Dirofilaria repens (Spirurida, Onchocercidae) is among the most widespread mosquito-borne pathogens of dogs, in which it is responsible for nodular and allergic-like skin lesions. Nonetheless, the zoonotic potential of *D. repens* makes the control of this parasitosis of Public health concern, since it has been associated to human cases of dirofilariosis in the Old World.

While control measures for cardio-pulmonary infestation by *Dirofilaria immitis* are well established, little information is currently available on treatment and control of subcutaneous dirofilariosis by *D. repens* in dogs.

The present study aims to evaluate the efficacy of an association of doxycycline hyclate (Ronaxan®, Merial), 10 mg/kg every day for 30 days, and ivermectin (Cardotek 30®, Merial) 6 µg/kg every 15 days for 6 months, in reducing the number of *D. repens* microfilariae in two naturally infested dogs from Italy.

Animals were bled monthly, till the end of the treatment period, and Knott’s modified test and duplex real-time PCR were performed to assess the efficacy of this off-label treatment. Results indicate that the combination used may be effective in treating natural *D. repens* microfilariaemia, since, a reduction of blood circulating microfilariae was observed within 40 days from the beginning of treatment in both dogs. Therefore, given the confirmed zoonotic potential, the frequent subclinical trend of infestation and the controversies in treating *D. repens*, the administration of doxycycline hyclate and ivermectin could be considered an additional option for the therapy of this infestation in dogs living in endemic areas.

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Session Details:	8/27/2013 VACCINES - HAEMONCHUS 1515 - 1630 <i>Meeting Room 5</i>
Oral Presentation Details:	‘Barbervax’, a potential commercial vaccine for Haemonchus contortus: background, mechanism of action and efficacy studies with housed lambs.
Presentation Time:	1515 -1530
Authors:	Julie Fitzpatrick

To our knowledge only one commercial vaccine exists for any helminth parasite of any host, namely Huskvac for the bovine lungworm *Dictyocaulus viviparus*. Dossiers seeking authorisation to sell “Barbervax”, a vaccine for *Haemonchus contortus*, have been submitted to the regulators in Australia and South Africa and the product is expected to reach the market within two years. The vaccine is unusual, partly because its antigens are parasite gut membrane proteins and therefore “hidden”, but also because the antigens are native proteins purified from adult worms. The gut membrane proteins of *Haemonchus* appear to be conserved since the vaccine is effective against all isolates of *H. contortus* tested internationally to date, including against *H. placei*, a different species. It is considered highly unlikely that worms resistant to the vaccine will develop and so the vaccine should offer a more sustainable approach to *Haemonchus* control than anthelmintic drugs. Data from vaccine challenge trials with housed lambs will be presented to illustrate the stability of the vaccine, its efficacy against single or trickle challenge infections and its therapeutic capability in the face of an existing infection. The vaccine has been tested in sheep, goats and calves in several countries and some of that data will be presented by others elsewhere.

Session Details:	8/27/2013 VACCINES - HAEMONCHUS 1515 - 1630 <i>Meeting Room 5</i>
Oral Presentation Details:	“Barbervax”, a potential commercial vaccine for <i>Haemonchus contortus</i>: manufacture and field efficacy trials in Western Australia.
Presentation Time:	1530 -1545
Authors:	Besier B¹, Lyon J¹, Michael D¹, Fitzpatrick J², Michael G², Smith D² ¹ Department Of Agriculture And Food Western Australia, ² Moredun Research Institute

A vaccine against *Haemonchus contortus* was produced from homogenised worms recovered from sheep maintained in a commercial-scale feedlot, prior to slaughter at a local abattoir. The entire procedure operates to stringent accreditation protocols, ensuring optimal sheep health and welfare, and quality control of vaccine production.

The efficacy of different dose rates of vaccine antigen was tested in a field trial over a 4-month period in 2010/11, at a research station near Albany. Groups of 12 lambs were vaccinated on 5 occasions with 2, 5, 10 or 50 micrograms, and run with a non-vaccinated control group of 20 lambs. At weekly intervals, lambs were dosed orally with 3000 infective *H. contortus* larvae. Samples were collected 2-weekly to assess faecal worm egg counts, blood status and serum vaccinal antibodies. Although mean control group *H. contortus* egg counts exceeded 7000 eggs per gram by the last week of the trial (despite salvage treatment of several sheep), comparative counts from groups vaccinated with 50, 10 or 5 µg antigen were reduced by at least 84%.

A further field trial was conducted in 2011/12 at Denmark, west of Albany, using a 5 microgram antigen dose in a group of 40 lambs, with a similar sized control group. A mean protection level of approximately 73% was demonstrated in vaccinated sheep.

The results of the trials confirm that a comparatively small dose of antigen provides a high level of protection from *H. contortus* infection. The effect is expected to be greater when vaccinated sheep run separately, hence avoiding the high levels of pasture larval challenge originating from non-vaccinated sheep.



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Session Details:	8/27/2013 VACCINES - HAEMONCHUS 1515 - 1630 <i>Meeting Room 5</i>
Oral Presentation Details:	“Barbervax”, a potential commercial vaccine for <i>Haemonchus contortus</i>: field efficacy trials with sheep in a high risk region of Australia.
Presentation Time:	1530 -1545
Authors:	W.D. Smith ¹ *, G.F. Newlands ¹ , J.L. Fitzpatrick ¹ , R.B. Besier² ¹ Moredun Research Institute, Bush Loan, Penicuik, Midlothian, EH26 0PZ, UK ² Department of Agriculture and Food Western Australia, Albany, 6330 AUSTRALIA

The vaccine was evaluated in nine trials conducted on 5 different properties within the New England district of New South Wales, a locality in the summer rainfall zone of Australia where *Haemonchus* is endemic and a serious disease of sheep, more especially as drug resistance is widespread. All trials were with Merinos and each ran from November to April, relying on natural infection to provide the challenge.

During 2011-2012 four very similar trials were performed on different farms. Each contained 40 vaccinated and 40 control lambs which grazed together to ensure equal exposure. Each farmer used his own anthelmintic regime for worm control in the ewes. The vaccinated lambs were first immunised when about 6 weeks old. Two more vaccinations followed at 3 or 4 week intervals, thereafter two more were given 6 weeks apart. Faeces and blood were sampled every fortnight for egg counts, haemoglobin concentration and antibody titres. Any lamb with an egg count greater than 15,000 per g or a haemoglobin concentration less than 8.5.g/100ml (equivalent to PCV of 25%) was given a short acting precautionary drench. Over the course of each trial the *Haemonchus* egg counts of the vaccinates were reduced on average by 80% compared to the controls and anaemia was also significantly reduced.

During 2012-2013 two further trials similar to the above were run with lambs, except this time vaccinates and controls grazed separately, each on four replicated plots. Three more trials were conducted with hogget yearlings which had been immunised as lambs during 2011-2012. Here, vaccinates received only four injections over the season, because they had been primed the previous year. These five 2012-2013 trials were not complete at the time of writing, but the preliminary data is very encouraging.

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Session Details:	8/27/2013 VACCINES - HAEMONCHUS 1515 - 1630 Meeting Room 5
Oral Presentation Details:	Field test of MRI Haemonchus vaccine efficacy in Merino lambs.
Presentation Time:	1600 -1615
Authors:	Malcolm Knox ^{1*} , Peter Hunt ¹ , Nick Andronicos ¹ , Jody McNally ¹ , Brian Dennison ¹ , Dominic Niemeyer ¹ George Newlands ² and David Smith ² ¹ CSIRO Animal, Food and Health Sciences, Armidale, NSW 2350 ² The Moredun Group, Pentlands Science Park, Midlothian, Scotland.

Haemonchus contortus is the major nematode pathogen in high rainfall areas of Australia where small ruminants are produced. An effective vaccine against this pathogen is highly desirable, particularly if it is able to protect young animals during the period post-weaning when production loss and mortalities are most frequent. The efficacy of the Moredun Research Institute Haemonchus vaccine was assessed in three types of young Merino lambs in the field during the period post weaning. The first, known as the Elites, had been bred for superfine wool production, whilst the second and third types, the HSF-R and HSF-S lines, had been selected since 1978 to be resistant or susceptible to *H. contortus*, respectively. 80 Elite lambs were divided into 2 equal groups balanced for sex and liveweight and one group was vaccinated at 0, 4, 8, 14 and 20 weeks (vaccinates) while the other group was not vaccinated (control). 20 HSF-R and 20 HSF-S lambs were divided into two groups balanced for sex and allocated to vaccinates and controls as above. All lambs were grazed together as a single flock from weaning at week 4 until the end of the trial. Faecal worm egg counts (FWECS) and blood haemoglobin (Hb) levels were estimated each 2 weeks for 24 weeks and lambs were “salvage” treated with anthelmintic when FWECS exceeded 15,000 eggs/g or Hb fell below 8.5 g/100 mL. The vaccine substantially protected all types of lambs, as measured by reduced *Haemonchus* FWECS and anaemia, compared to unvaccinated controls. Vaccination reduced the requirement for salvage treatment by 73% in the Elite lambs and by 93% in the HSF-S lambs, whilst neither control nor vaccinate HSF-R lambs required salvage treatment.



Session Details:	8/27/2013 VACCINES - HAEMONCHUS 1515 - 1630 <i>Meeting Room 5</i>
Oral Presentation Details:	Simulation study to estimate the minimum vaccine protection required to control <i>Haemonchus contortus</i> in a high risk zone for haemonchosis
Presentation Time:	1615 -1630
Authors:	R.J. Dobson^{1*} , W.D. Smith ² , J.L. Fitzpatrick ² , R.B. Besier ³ ¹ Murdoch University, Murdoch, WA 6150, AUSTRALIA ² Moredun Research Institute, Bush Loan, Penicuik, Midlothian, EH26 0PZ, UK ³ Department of Agriculture and Food Western Australia, Albany, AUSTRALIA

The aim of this study was to estimate the minimum protection required for a vaccine to effectively control *Haemonchus contortus* in a high risk haemonchosis region of Australia; and to evaluate the potential of selecting for anthelmintic resistance by a vaccine in comparison with traditional drenching practices. Parameters that regulate host immunity in the “Worm World” model were modified to simulate vaccine application with protection levels ranging from 50% to 90% in 5% increments. For each protection level a 20 year simulation was run in which all lambs were vaccinated and given a single anthelmintic treatment at lamb marking, their ewes were given two anthelmintic treatments/year but no vaccination. Conventionally managed unvaccinated lambs received five anthelmintic treatments to maintain *Haemonchus* control. The resistance-allele frequencies were set at 1%, 1% and 5% for the three drug classes used to treat stock in the simulations. A vaccine that affords 65% protection was as useful as or better at controlling *H. contortus* than a conventional anthelmintic treatment program. In a high risk area where outbreaks of haemonchosis were expected in 35-50% of years, despite anthelmintic treatments, a vaccine with protection levels of 75% and 80% reduced this to 10% and 0% respectively. By reducing the number of anthelmintic treatments required to control *H. contortus* the use of a vaccine substantially delayed selection for anthelmintic resistance.

Acknowledgements: The *Haemonchus* vaccine simulations were a component of PARAVAC, a multidisciplinary project on veterinary Helminth vaccines funded by the European Union through the 7th EU-Framework Programme for Research and Technological Development.

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Session Details:	8/27/2013 MOLECULAR EPIDEMIOLOGY 1515 - 1630 <i>Meeting Room 6</i>
Oral Presentation Details:	Molecular characterization and phylogenetic analysis of <i>Fasciola hepatica</i> from Cajamarca, Peru
Presentation Time:	1515 -1530
Authors:	Madoka Ichikawa-Seki^{1*} , Pedro Ortiz ² , María Cabrera ² , Tadashi Itagaki ¹ ¹ Iwate University, Morioka, JAPAN ² Universidad Nacional de Cajamarca, Cajamarca, PERU

Fasciola hepatica is widely distributed in the temperate regions. Phylogenetic information of *Fasciola* flukes was not available in South American countries. In this study, we performed molecular characterization and phylogenetic analysis of *F. hepatica* from Cajamarca, Peru.

Fasciola flukes collected from cattle, pigs, and sheep in Cajamarca and Baños del Inca were fixed with 70% ethanol. Self-produced sperm contained in the seminal vesicles were removed from each fluke, stained with Hematoxylin-Carmine and observed by using an optical microscope. Nuclear ribosomal internal transcribed spacer 1 (ITS1) region and mitochondrial NADH dehydrogenase subunit 1 (*nad1*) gene were amplified with DNA extracted from posterior part of the flukes. DNA types of ITS1 were distinguished by using a PCR-RFLP method whereas *nad1* haplotypes were determined by direct sequencing. Phylogenetic analyses were performed on Peruvian *nad1* haplotypes together with those of *F. hepatica* and aspermic *Fasciola* sp. from other countries which were available in GenBank.

All of the *Fasciola* flukes collected in Peru contained abundant mature sperm in their seminal vesicles. Thus, they were thought to have the normal spermatogenetic ability. In addition, all of the *Fasciola* flukes displayed the restriction enzyme fragment pattern which is identical to that of *F. hepatica*. We therefore identified them as *F. hepatica*. The main three *nad1* haplotypes detected in Peruvian *F. hepatica* had the identical nucleotide sequences with *F. hepatica* from Italy, Uruguay, and Iran, respectively. The other *nad1* haplotypes of Peruvian *F. hepatica* had single or few nucleotide substitutions from the main three haplotypes. These findings indicated that *F. hepatica* with the identical *nad1* sequence was widely distributed worldwide. Further study on mitochondrial DNA will reveal the dispersal route of *F. hepatica* from European countries into South American countries.



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Session Details:	8/27/2013 MOLECULAR EPIDEMIOLOGY 1515 - 1630 Meeting Room 6
Oral Presentation Details:	Mitochondrial genome of <i>Angiostrongylus vasorum</i> : comparison with congeners and implications for studying the population genetics and epidemiology of this parasite
Presentation Time:	1530 - 1545
Authors:	Namitha Mohandas ^a , Robin B. Gasser ^a , Abdul Jabbar ^a , Manuela Schnyder ^b , Peter Deplazes ^b , D. Timothy J. Littlewood ^c , Aaron R. Jex ^a ^a Faculty of Veterinary Science, The University of Melbourne, Parkville, Victoria, AUSTRALIA ^b Institute of Parasitology, University of Zurich, CH-8057 Zürich, SWITZERLAND ^c The Natural History Museum, Biomedical Parasitology Department, London, UK

Angiostrongylus vasorum is a strongylid nematode of major clinical relevance in canids, causing angiostrongylosis. In spite of its increasing importance, little is known about the genetics, epidemiology and biology of this parasite. Mitochondrial (mt) DNA can provide useful markers for studies in these areas. Here, the mitochondrial genome was amplified by long-range polymerase chain reaction (long-PCR) from a portion of a single male adult of *A. vasorum*, sequenced using 454 technology, and annotated employing a semi-automated informatic pipeline. This circular mitochondrial genome is 13,422 bp and contains 12 protein-encoding, 22 transfer RNA, and 2 ribosomal RNA genes, consistent with its congeners and other secernentean nematodes. This genome represents a rich source of markers for future investigations of the population genetics and epidemiology of *A. vasorum*. Molecular tools, using these markers, should be useful for explorations into host specificity and for prospecting for cryptic species, and might also underpin the diagnosis of canine angiostrongylosis.





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Session Details:	8/27/2013 MOLECULAR EPIDEMIOLOGY 1515 - 1630 <i>Meeting Room 6</i>
Oral Presentation Details:	Quantitative proteomics in <i>Giardia duodenalis</i>: investigating host origin, assemblage and isolate variation
Presentation Time:	1545 -1600
Authors:	Samantha J Emery^{1*} , Ernest Lacey ² , Paul A Haynes ¹ ¹ Macquarie University, Sydney, AUSTRALIA ² Microbial Screening Technologies Pty. Ltd., Sydney, AUSTRALIA

Giardia duodenalis is a protozoan parasite and major contributor worldwide of diarrhoea and gastroenteritis in vertebrates, including humans. *G. duodenalis* is comprised of discrete subtypes known as assemblages, with assemblage A and B known to be infective for humans. With advances in genetic epidemiology, shotgun quantitative proteomics presents a unique opportunity to analyse global protein expression between strains of the same genetic assemblage, but from different host origins and phenotypes. We have analysed five human or animal strains of *G. duodenalis* from assemblage A to investigate sources of intra-assemblage variation and to identify protein trends associated with host origin. Protein extracts were prepared for analysis using filter assisted separation of proteins (FASP) for digestion and gas-phase fractionation (GPF) for peptide separation. Proteins were identified using LC-MS/MS spectra that were acquired on a LTQ-XL linear ion trap mass spectrometer and peptides were matched individually against the GiardiaDB.org 2.5 [1] release of *G. duodenalis* WB genome for Assemblage A [2]. A non-redundant total of 1310 proteins were identified in *G. duodenalis* across the five strains, with an average of 875 proteins reproducibly identified in each strain. Interestingly, variant surface proteins (VSPs) were both common within, and unique across, isolates, hosts and assemblage in the 5 strains analysed. Additionally, the two strains which expressed > 3-fold higher numbers of VSPs possessed a duplication of chromosome 3, making VSP expression a possible marker of assemblage-independent genetic plasticity [3,4]. In this capacity, we believe that quantitative proteomics is a valuable tool for confirming and exposing the subtleties within strain diversity, complementing current genetic approaches to sub-typing of assemblages.

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Session Details:	8/27/2013 MOLECULAR EPIDEMIOLOGY 1515 - 1630 Meeting Room 6
Oral Presentation Details:	Molecular Epidemiology of <i>Blastocystis</i> isolates from pre-school children and domestic animals
Presentation Time:	1600 -1615
Authors:	Lan P Nguyen ¹ , Cam. D. Phung ² , R.C Andrew Thompson ¹ ¹ Murdoch University, Perth, AUSTRALIA ² National Institute of Hygiene and Epidemiology, Hanoi, VIETNAM

To investigate the molecular epidemiology of *Blastocystis* in pre-school children in Vietnam, a study was conducted in a rural area of Vietnam where the use of untreated animal and human wastes in agriculture is a common practice. Fecal samples and questionnaires were obtained from children under 5 years of age in day care centers. Samples were also collected from their domestic animals including dogs and pigs. Diagnosis was undertaken by conventional PCR, with subsequent genetic characterisation using sequence analysis. Overall, *Blastocystis* was present in 47.9% (125) of human samples. Of their own animals, *Blatocystis* was found in 44.4% (28) and 73% (46) of dog and pig samples, respectively. Most pre-school children in this rural area were harbouring *Blastocystis*. The dominant species of *Blastocystis* detected in human samples was subtype I. In animals the predominant species detected was subtype V. Infections with *Blastoscystis* in humans and animals living within the same household were 21 instances (humans and dogs) and 35 (humans and pigs). Of these, 10 instances are presented of *Blastoscystis* in humans and both their pigs and dogs. Six of the human isolates were identical to the isolates from their animal species.





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Session Details:	8/27/2013 MOLECULAR EPIDEMIOLOGY 1515 - 1630 <i>Meeting Room 6</i>
Oral Presentation Details:	Characterizing population structure and diversity of Australian <i>Eimeria</i>
Presentation Time:	1615 -1630
Authors:	JAT Morgan and RM Godwin(1) Queensland Alliance for Agriculture and Food Innovation (QAAFI), The University of Queensland, St Lucia, Queensland, Australia and (1) Animal Science, Queensland Department of Agriculture, Fisheries and Forestry, The University of Queensland, St Lucia, Queensland, Australia

Poultry coccidiosis is caused by infection with ubiquitous intestinal protozoa of the genus *Eimeria*. The disease impairs growth and is a serious problem under intensive farming conditions where heavy infections can result in death. Australian strains of *Eimeria maxima* and *Eimeria tenella* have been characterised using nuclear DNA microsatellites and mitochondrial DNA mutations. Understanding strain relatedness will give a large scale indication of how coccidiosis spreads. Unstructured diversity would suggest a large panmictic population where outbreak strains sweep the country each year. Strains showing genetic diversity, separated by geographic barriers, may be easier to contain but could differ in cross protective capabilities. Australian strains of *E. maxima* display greater genetic diversity than *E. tenella*. The mitochondrial DNA within both species is largely conserved with the genetic diversity observed not correlating to geographic origin. The nuclear DNA microsatellites detect greater strain variability and show some geographic differentiation. Once strains can be genotyped it will be possible to link characteristics such as pathogenicity, drug resistance and flock performance.

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Session Details:	8/27/2013 VECTOR BORNE DISEASES – GENERAL 1515 - 1630 Meeting Room 7
Oral Presentation Details:	MALDI-TOF mass spectrometry for the identification of insect vectors
Presentation Time:	1515 - 1530
Authors:	Mathis A¹, Kaufmann C¹, Schaffner F¹, Pflüger V² ¹ Institute of Parasitology, University of Zurich, Switzerland, ² Mabritec SA, Riehen, Switzerland

Identification of insect vectors is primarily carried out using morphological features, which can be a time-consuming and difficult task. PCR-based approaches have been developed for the identification of a number of vector species (e.g. for *Culicoides* biting midges [1]). Matrix-assisted laser desorption/ionization time of flight mass spectrometry (MALDI-TOF MS), which has come of age for the high throughput identification of microorganisms, has recently been established to identify imagos [2,3] and larvae [4] of biting midges, and the technique has proven its suitability to accurately identify on a large scale biting midges collected in a field study [5]. We have extended the insect vector reference database to also include culicid mosquito species. Biomarker mass sets, from both imagos and larvae, were determined for the Central European culicids, including all established and presumptive Aedine invasive species such as the Asian tiger mosquito *Aedes albopictus* or the Asian bush mosquito *Ae. japonicus*. Further, biomarker mass sets of eggs were determined for the indigenous and invasive container-breeding Aedine mosquitoes allowing to identify eggs collected in oviposition traps in the framework of surveillance programs. Eggs can be identified by MALDI-TOF MS either singly or in pools of 10 eggs for those species of which at least 3 eggs are present in the sample. Taken together, protein profiling by MALDI-TOF MS can be used as an alternative, quick and inexpensive tool to accurately identify adult and immature stages of insect vectors collected in the field. This approach has the potential to become the method of choice for a centralized, robust and high throughput screening of insect vector populations in connection with surveillance programs.

Acknowledgements:

We acknowledge the financial contribution of the Swiss Federal Veterinary Office (grant 1.08.10 and Reference Centre).

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Session Details:	8/27/2013 VECTOR BORNE DISEASES - GENERAL 1515 - 1630 <i>Meeting Room 7</i>
Oral Presentation Details:	Sugar feeding behaviour and longevity of European <i>Culicoides</i> biting midges
Presentation Time:	1530 -1545
Authors:	Christian Kaufmann ¹ , Alexander Mathis^{1*} , Christoph Vorburger ² ¹ University of Zürich, Institute of Parasitology, Reference Centre for Vector Entomology, Zürich, SWITZERLAND ² Institute of Integrative Biology, ETH Zürich & EAWAG, Dübendorf, SWITZERLAND

Most hematophagous insect vectors can also use sugar as energy source, and the sugar-feeding behaviour influences their longevity and blood-feeding rate and thus their vectorial capacity [1]. For *Culicoides* biting midges, few data considering sugar feeding behaviour is available and none for European species. Are they mere blood feeders or do they access natural sugar sources? We determined the longevity of laboratory-reared *C. nubeculosus* with access to no food, water, 10% sucrose solution, water and blood, 10% sucrose solution and blood, or natural sugar sources (i.e. honey dew and extrafloral nectaries) under constant or fluctuating summer condition. In addition, midges of the *Obsoletus* (n=2243) and *Pulicaris* (n=805) group were caught at a farm site and tested for fructose using the cold anthrone test. In all longevity experiments, the mortality was significantly higher in males than in females. Simulated summer day conditions had a significant positive effect on the longevity. Sugar in the midges' diet significantly boosted their survival. Females with access to water and blood lived, depending on the climatic condition, on average 6.0 and 8.9 days, respectively, which was around one third of their siblings with access to sugar and blood. Access to honey dew significantly increased the midge's longevity whereas extra-floral nectaries had no impact. More than 80% of the field-caught female biting midges within both the *Obsoletus* and *Pulicaris* group were fructose-positive whereas the few males collected (n=83) had a natural sugar feeding rate of 63%. In conclusion, sugar supply extends the midges' longevity and thus increases the vectorial capacity because of the higher number of blood meals taken during the lifespan. The high rate of natural sugar feeding of two most abundant European *Culicoides* groups (*Obsoletus*, *Pulicaris*) offers opportunities for control strategies using toxic sugar baits and for monitoring vector-borne diseases using sugar-treated FTA-cards in the field.

Acknowledgements:

We acknowledge the financial contribution of the Swiss Federal Veterinary Office (grant 1.08.10 and Reference Centre) and the University of Zürich (Forschungskredit of C.K., 4974).

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[1] Foster (1995), Annual Review of Entomology **40**: 443-474.



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Oral Presentation Details:	<i>Trypanosoma cruzi</i> infectivity in triatomines from Brazil may be higher than expected
Presentation Time:	1545 -1600
Authors:	Juciliane Haidamak ¹ , Larissa Reifur ^{1*} , Débora do Rocio Klisiowicz ¹ ¹ Basic Pathology Department, Federal University of Paraná, BRAZIL

In 2006, Brazil received the international certification for elimination of transmission of Chagas disease by its main vector, *Triatoma infestans*. However, other triatomine species have proliferated and some of them are appearing infected with *Trypanosoma cruzi*. Currently, the Secretaries of State for Health (SSH) adopt only the direct exam of fresh triatomine intestinal contents for the diagnosis of *T. cruzi* and in Bahia (the last Brazilian State to receive the certification of transmission elimination) the officials have not found positive results. Considering that the direct method has low sensitivity and specificity, as it relies on the visualization of movements suggestive of a trypanosomatid, this work aimed to detect *T. cruzi* in triatomines, using the polymerase chain reaction (PCR). In addition, the direct fresh method was performed to compare and contrast both tests. The 40 kissing bugs collected around the central north part of Bahia, in May 2012, included *Triatoma brasiliensis* and *Triatoma pseudomaculata*, species that have potential of transmitting *T. cruzi*. With the direct fresh method, only one insect (2.5%) would have been positive for *T. cruzi* following the SSH methodology. On other hand, this number may be much higher than expected by PCR. Our preliminary results show that 8 of the 25 fecal samples (32%) analyzed by PCR were positive for DNA of *T. cruzi*. These results indicate that the real prevalence of infected triatomines may be much higher than the authorities would think. If the PCR cannot be adopted by the SSH due to its high costs, training courses for health professionals who perform the direct test in triatomines are urgently required to obtain more accurate epidemiological data on Chagas disease.

Acknowledgments:

We acknowledge the Coordination of Improvement of Higher Education Personnel (CAPES) for financing.

Session Details:	8/27/2013 VECTOR BORNE DISEASES - GENERAL 1515 - 1630 <i>Meeting Room 7</i>
Oral Presentation Details:	Control of <i>Ixodes holocyclus</i> and <i>Ixodes tasmani</i> on the northern brown bandicoot, <i>Isoodon macrourus</i>
Presentation Time:	1600 -1615
Authors:	Greta Busch^{1*} , Jim Rothwell ² , Stephen Barker ³ ¹ School of Chemistry and Molecular Biosciences, University of Queensland, Brisbane, AUSTRALIA. Currently QAAFI, University of Queensland, Brisbane, AUSTRALIA ² School of Veterinary Science, University of Queensland, Gatton AUSTRALIA. Currently MLA, North Sydney, AUSTRALIA ³ School of Chemistry and Molecular Biosciences, University of Queensland, Brisbane, AUSTRALIA

The Australian paralysis tick *Ixodes holocyclus* causes paralysis and death in many domestic pets and livestock on the eastern coast of Australia. Acaricide treatment of these incidental hosts to prevent *I. holocyclus* infestation is expensive and short lived. The only treatment available for paralysed animals is an anti-serum, which is only effective early in disease progression. Control of ticks (*I. scapularis*) based on treatment of wild hosts has been successful in the United States^{1,2}. A pilot study was conducted to investigate treatment of a wild population of the tick's native host, *Isodon macrourus*, with a topical formulation of fluazuron and ivermectin. Thirty-seven bandicoots at Pinjarra Hills, 15 km west of Brisbane, Queensland, were treated on three occasions between January and July 2010. Tick counts on these animals did not decrease significantly. An increased dose for a fourth treatment of 16 bandicoots between July and September of the same year also had no significant effect on tick counts. Because bandicoots groom with their syndactylous hind foot and not their mouth, and the formulation is effective when ingested following grooming we suggest that inadequate drug was available systemically to kill ticks. We believe that although this pilot study was unsuccessful, host based methods remain a viable alternative for *I. holocyclus* control and the use of oral or injectable acaricides should be investigated.

Data for the seasonal variation of *I. holocyclus* on the control bandicoot population was also collected and presented. Seasonal variation of *I. holocyclus* on a population of wild bandicoots with known individuals has not previously been reported.

Acknowledgements:

Dr. Shan Lloyd and Dr. Ristan Greer.

References:

1. Dolan, M. C., Maupin, G. O., Schneider, B. S., Denatale, C., Hamon, N., Cole, C., et al. (2004) Control of immature *Ixodes scapularis* (Acari : Ixodidae) on rodent reservoirs of *Borrelia burgdorferi* in a residential community of south-eastern Connecticut. J. Med. Entomol. **41**: 1043-1054
2. Miller, N. J., Thomas, W. A. & Mather, T. N. (2009) Evaluating a deer targeted acaricide applicator for area-wide suppression of blacklegged ticks, *Ixodes scapularis* (Acari: Ixodidae), in Rhode Island. Vector-Borne and Zoonotic Diseases **9**: 401-406

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Session Details:	8/27/2013 VECTOR BORNE DISEASES - GENERAL 1515 - 1630 <i>Meeting Room 7</i>
Oral Presentation Details:	Preliminary result of a large-scale field trial to evaluate the efficacy of Waterbuck repellent blend (<i>Kobus ellipsiprymnus</i>) in controlling bovine trypanosomosis in Eastern Africa
Presentation Time:	1615 -1630
Authors:	Norber Mbahin^{1*} , Hippolyte Affognon ¹ , John Andoke ¹ , Moses Makayoto ² , Saini Rajinder ¹ ¹ International Centre of Insect Physiology and Ecology (icipe), Dudu Ville, Nairobi, KENYA ² Kenya Industrial Research and Development Institute (<i>KIRDI</i>), Nairobi, Kenya

Nature has her own defenses against pests and diseases. Tsetse flies avoid many wildlife including the waterbuck (*Kobus ellipsiprymnus*). “The repellents have been identified from odors of animals avoided by tsetse, like the waterbuck, a big antelope species that is common in tsetse-infested areas of eastern Africa but which is rarely fed on by the flies. *icipe* scientists undertook studies to determine why these animals are not attacked by tsetse and have isolated powerful fly repellents from waterbucks which reduce tsetse bites by >90%. But in a bid to help farmers solved this menace, *icipe* has developed a repellent collar that is tied around the animal’s neck and in the process repels tsetse flies. These repellent collars slowly dispense the chemicals in them, thereby protecting the animals and their herders from the flies.

Primary result from a large scale validation field trial with Pastoralists and Agro-pastoralists in Kenya and Uganda show that the disease levels in protected cattle had been reduced by more than 90 percent and that repellent collars performed better than other conventional methods (chemotherapy, targets, pour-on, ...). The annual incidence rate of trypanosomiasis was significantly higher in control (188 cases for 100 animals-years) than that of treatments (66 cases for 100 animals-years) and (P<0.001).

According to a livestock farmer, with the introduction of the repellent collars, weight of animals had significantly increased making them fetch more money as well as enabling those that use bulls ploughing utilize their land effectively. They are saying milk yields had doubled up, a sign that the repellent collars were very effective and their cattle were now more settled when grazing and they were grazing much closer to the park fence than before without being disturbed by tsetse flies.

All this will be discussed in the presentation.

Acknowledgements:

The work was funded by the European Union and thanks to WAAVP AF for the Conference grant.



CONCURRENT SESSION 7

GLOWORM – Impact of global change on ruminant helminths

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Session Details:	8/29/2013 GLOWORM – Impact of global change on ruminant helminths 1015 - 1130 <i>Riverside Theatre</i>
Oral Presentation Details:	Innovative and sustainable strategies to mitigate the impact of global change on helminth infections in ruminants (GLOWORM)
Presentation Time:	1015 -1030
Authors:	Jozef Vercruysse^{1*}, Janina Demeler², Philip Skuce³, Eric Morgan⁴, Jan van Dijk⁵, Laura Rinaldi⁶, Guy Hendrickx⁷, Fiona Kenyon³, Johannes Charlier¹, Theo de Waal⁸ and Georg von Samson-Himmelstjerna² ¹ Ghent University, Merelbeke, BELGIUM ² Free University Berlin, Berlin, GERMANY ³ Moredun Research Institute, Edinbrough, UNITED KINGDOM ⁴ University of Bristol, Bristol, UNITED KINGDOM ⁵ University of Liverpool, Liverpool, UNITED KINGDOM ⁶ University of Naples Federico II, Naples, ITALY ⁷ Avia-GIS, Zoersel, BELGIUM ⁸ University College Dublin, Dublin, IRELAND

Infections with parasitic worms (nematodes and trematodes) represent a significant economic and welfare burden to the European ruminant livestock industry. The increasing prevalence of anthelmintic resistance means that current control programmes are costly and unsustainable in the long term. Recent changes in the epidemiology, seasonality and geographic distribution of helminth infections have been attributed to climate change. However, other changes in environment (e.g. land use) and in livestock farming, such as intensification and altered management practices, will also have an impact on helminth infections. Sustainable control of helminth infections in a changing world requires detailed knowledge of these interactions. GLOWORM (EU funded project 2012 – 2015) is devising new, sustainable strategies for the effective control of ruminant helminthoses in the face of global change. We aim to: (1) optimise diagnosis, by developing novel, high-throughput diagnostic tests for mixed helminth infections, sub-clinical infections and anthelmintic resistance, (2) produce predictive models to identify optimal future intervention strategies, (3) map, monitor and predict the impact of global change on parasite epidemiology, leading to spatial risk maps and improved forecasting of disease, (4) identify and mitigate the economic impacts of infections and (5) involve end-users in the production and dissemination of detailed advice for effective worm control. GLOWORM will develop a panel of innovative technologies and models to monitor and predict changing patterns of infection and disease, optimise the use of anthelmintics to limit the development and spread of drug resistance, and reduce the overall economic impact of helminth infections.

Acknowledgements:

The studies received funding from FP7 GLOWORM project – Grant agreement N° 288975CP-TP-KBBE.2011.1.3-04).



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Oral Presentation Details:	GLOWORM -Novel approaches to improve diagnosis of helminth infection and detection of anthelmintic resistance
Presentation Time:	1030 -1045
Authors:	Demeler J¹, Karanikola S¹, Melville L², Höglund J³, von Samson-Himmelstjerna G¹, Vecruyse J⁴, Charlier J⁴, de Waal T⁵, Morgan E⁶, Kenyon F², Skuce P² ¹ Freie Universität Berlin, ² Moredun Research Institute, ³ Swedish University of Agricultural Science, ⁴ Ghent University, ⁵ University College Dublin, ⁶ University of Bristol

Currently available methods for diagnosis of helminth infections in livestock and detection of anthelmintic resistance are labour-intensive and time-consuming and often only detect single species in single samples. Such tests need to be rapid and robust with multi-species capability and high-throughput capacity to encourage widespread uptake in the field. We have started evaluating the microbead-based Luminex® platform for the simultaneous antibody-mediated detection and quantification of *Dictyocaulus viviparus* and *Fasciola hepatica* in cattle serum samples. Differentiation between positive and negative animals is possible and standard curves have been established for both parasite, showing reliable and repeatable detection in serum samples. Subsequently adaptation for milk samples is envisaged. In parallel, we are evaluating the potential of Luminex® for DNA-based detection and quantification of different sheep and cattle trichostrongylids direct from faecal samples. We have also developed a prototype loop-mediated isothermal amplification (LAMP) assay for the detection of *H. contortus* eggs, which has proved to be more sensitive and rapid than the equivalent PCR and has potential for pen-side applications. We are additionally attempting to develop a pan-trichostrongylid pyrosequencing assay for the quantification of benzimidazole (BZ) resistance alleles in sheep and cattle faecal samples. If successful, these assays will be validated against the standard FECRT and applied to determine species composition and BZ resistance status in field material collected through large-scale spatial sampling of key EU regions. Dairy bulk tank milk samples collected under the same EU sampling regime will be analysed for the presence of the four major nematodes, *Fasciola*, *Dictyocaulus*, *Ostertagia* and *Cooperia* in order to help develop spatial risk maps for the respective infections.

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Session Details:	8/29/2013 GLOWORM – Impact of global change on ruminant helminths 1015 - 1130 <i>Riverside Theatre</i>
Oral Presentation Details:	GLOWORM: Predicting and combating future helminth threats and infection patterns in livestock in Europe
Presentation Time:	1045 -1100
Authors:	Eric Morgan ¹ , Jan van Dijk ² , Hannah Rose¹ , Daniel Smith ² , Tong Wang ¹ , Bashir Bolajoko ¹ , Owen Gethings ¹ , Paul Phelan ³ , Pádraig O’Kiely ³ , Sien Verschave ⁴ , Johannes Charlier ⁴ , Fabien Mavrot ⁵ , Hubertus Hertzberg ⁵ , Friederike Knapp-Lawitzke ⁶ , Janina Demeler ⁶ , Alison Morrison ⁷ , Fiona Kenyon ⁷ , Philip Skuce ⁷ , Giuseppe Cringoli ⁸ , Laura Rinaldi ⁸ ¹ University of Bristol, Bristol, UNITED KINGDOM ² University of Liverpool, Liverpool, UNITED KINGDOM ³ Teagasc, Grange Research Centre, IRELAND ⁴ Ghent University, Merelbeke, BELGIUM ⁵ University of Zürich, SWITZERLAND ⁶ Free University Berlin, Berlin, GERMANY ⁷ Moredun Research Institute, Edinburgh, UNITED KINGDOM ⁸ University of Naples Federico II, Naples, ITALY

Predictive epidemiological models have proven useful in the past for understanding the general dynamics of helminth infection in farmed ruminants, and have in some cases been extended to support management decisions such as the timing of anthelmintic treatment. As part of GLOWORM, predictive models of infection with *Ostertagia ostertagi*, *Haemonchus contortus*, *Nematodirus battus* and *Fasciola hepatica* were developed, with the primary aim of exploring how changes in climate and management are likely to affect the seasonal epidemiology of these parasites in European farming systems. Extensive reviews of the literature revealed some important gaps in parameter estimation, which were addressed by on-going laboratory experiments on the effects of climate on parasite stages outside the definitive hosts. Detail on management factors relevant to transmission was added through surveys of farmers and their advisors in selected regions. Model output was validated qualitatively against published data on seasonal patterns of infection, and used to inform further experiments and longitudinal data collection on study farms. Preliminary results are presented. In the next phase of work, the model framework will be extended to other parasites of importance, including *Teladorsagia* and *Cooperia*, and the potential effects of future environmental change explored explicitly. This will include consideration of parasite adaptation, underpinned by selective studies of regional variation in parasite life history traits, as well as management interventions that could help to combat increased disease risks.

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Session Details:	8/29/2013 GLOWORM – Impact of global change on ruminant helminths 1015 - 1130 <i>Riverside Theatre</i>
Oral Presentation Details:	Spatio-temporal modeling of helminth infections in livestock in Europe
Presentation Time:	1100 -1115
Authors:	Laura Rinaldi ¹ , Koen Mintiens ^{2*} , Els Ducheyne ² , Annibale Biggeri ³ , Dolores Catelan ³ , Vincenzo Musella ¹ , Eric Morgan ⁴ , Diana Williams ⁵ , Johannes Charlier ⁶ , Fabien Mavrot ⁷ , Hubertus Hertzberg ⁷ , Janina Demeler ⁸ , Georg von Samson-Himmelstjerna ⁸ , Theo de Waal ⁹ , Nick Selemetas ⁹ , Jozef Vercruysse ⁶ , Giuseppe Cringoli ¹ , Guy Hendrickx² ¹ University of Naples Federico II, Naples, ITALY ² Avia-GIS, Zoersel, BELGIUM ³ E&P, Milan, ITALY ⁴ University of Bristol, Bristol, UNITED KINGDOM ⁵ University of Liverpool, Liverpool, UNITED KINGDOM ⁶ Ghent University, Merelbeke, BELGIUM ⁷ University of Zürich, Zürich, SWITZERLAND ⁸ Free University Berlin, Berlin, GERMANY ⁹ University College Dublin, Dublin, IRELAND

The application of geo-spatial tools (geographical information systems, global positioning system, satellite-based remote sensing, virtual globes, spatial statistics) to epidemiology in veterinary parasitology has nowadays been firmly established for positioning, collating, exploring, visualizing and analyzing animal health data in a spatially explicit manner. These tools also have a great practical relevance for the standardization of sampling procedures in cross-sectional surveys of animal parasites. As part of the GLOWORM project, a spatial database with parasitological, farm management, environmental and climatic data, was constructed and a standardized cross-sectional sampling was conducted in cattle and sheep farms in pilot regions throughout Europe. Key parameters in the database will be described and the results of a spatial data exploration for the different study regions will be presented and differences between the study regions will be highlighted. The issue of optimal geographical survey sampling will be addressed.

In the next phase, spatio-temporal modeling of parasite distribution and abundance will be developed at local, regional and area-wide scales. This will include multi-scale geo-statistical models, the development of predictive models to assess the impact of future climate trends on prevalence of helminth infection as well as ecological niche models of anthelmintic resistance in domestic ruminants in Europe.

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Session Details:	8/29/2013 GLOWORM - Impact of global change on ruminant helminths 1015 - 1130 Riverside Theatre
Oral Presentation Details:	Novel targeted treatment and targeted selective treatment approaches in sheep and cattle
Presentation Time:	1115 -1130
Authors:	Charlier J¹, Vercruysse J¹, Rinaldi L², Höglund J³, Demeler J⁴, von Samson-Himmelstjerna G⁴, Van Ranst B⁵, Verschave S¹, Melville L⁶, Kenyon F⁶ ¹ Ghent University, ² University of Naples Federico II, ³ Swedish University of Agricultural Sciences, ⁴ Free University Berlin, ⁵ Uniform-Agri, ⁶ Moredun Research Institute

Targeted Treatment (TT) and Targeted Selective Treatment (TST) approaches have been demonstrated as useful approaches to optimize the use of anthelmintic drugs and maintain their efficacy mainly in nematode parasites of ruminants. However, T(S)T approaches have rarely been applied to fluke infections, moreover further assessment of their impact on production and novel concepts is needed to facilitate their integration in routine farm management. In sheep, current TST approaches are applicable for large-scale producers. Therefore, we evaluated optimized timing of treatments based on local epidemiology, production efficiency and use of a sentinel group as an indicator for whole flock treatments. These novel approaches are more suitable for smaller scale enterprises, which are more common throughout the E.U. In cattle, previous work mainly evaluated whole-group treatment approaches but rarely used parasitological or production parameters for targeting treatments to individual animals. We will present the results of field trials evaluating the use of fecal egg counts and mid-season daily weight gains as indicators for treatment in growing cattle and easy-to-use animal (age, body condition scoring) or parasitological parameters (fecal egg counts, milk ELISA) in dairy cows. These results enhance the development of cost-benefit models to assess the economic consequences of the T(S)T approaches and software applications to disseminate optimized anthelmintic usage protocols across the EU member states.

Acknowledgements:

The studies received funding form FP7 GLOWORM project – Grant agreement N° 288975CP-TP-KBBE.2011.1.3-04).



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Session Details:	8/29/2013 RUMINANTS PROTOZOA 1015 - 1130 Meeting Room 1
Oral Presentation Details:	Evaluation of factors contributing to the course of natural cryptosporidiosis in calves in Germany
Presentation Time:	1015 -1030
Authors:	Matthias Lendner ¹ , Franziska Göhring ¹ , Thomas Vahlenkamp ¹ , Monika Krüger ¹ , Peter Möller-Holtkamp ² , Arwid Dauschies ^{1*} ¹ University Leipzig, Leipzig, GERMANY ² MSD Intervet Deutschland GmbH, Unterschleißheim, GERMANY

Cryptosporidium parvum is a widely distributed enteric parasite in calves up to an age of 2 or 3 weeks. Application of halofuginone is suitable to control the disease particularly if combined with proper disinfection. Under conditions of natural exposure the course of the disease and the efficacy of control measures, however, may vary. We therefore investigated a) presence of other enteropathogens in farms with suspected cryptosporidiosis, b) genotypes of *C. parvum* in field isolates, and c) cytotoxicity as a correlate of virulence. In all, 99 farms distributed over Germany participated in the study. 92 % of the farms were positive for *Cryptosporidium* confirming the ubiquitous nature of the parasite. Of 441 individual samples 60.9 % were positive for *C. parvum*, 24.3 % for coronavirus, 20.4 % for rotavirus and 1.5 % for *E. coli* K99. 43 % of the samples positive for cryptosporidiosis represented monoinfections whereas 31 % and 37 % also contained rotavirus or coronavirus, respectively. Bacterial coinfections were only sporadically recorded. Simultaneous infection with virus and *C. parvum* was increasingly observed with increasing severity of disease. 235 field isolates were genotyped based on GP60. 12 subtypes of *C. parvum* were found all belonging to the allele family IIa. The IIaA15G2R1 genotype was representing 70.6 % of the samples, and no particular spatial distribution was noted. Cytotoxicity of field isolates was assessed in HCT-8 monolayers by MTT assay. Out of 39 isolates tested for virulence two displayed distinctly higher cytotoxicity than the reference strain. These two isolates originated from farms with reported incidence of severe cryptosporidiosis. Different properties of field strains and participation of other enteropathogens may explain the variable observations in the field related to the course of cryptosporidiosis and probably influence efficiency of control measures targeted against cryptosporidia.



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Session Details:	8/29/2013 RUMINANTS PROTOZOA 1015 - 1130 Meeting Room 1
Oral Presentation Details:	The prevalence and productivity consequences of <i>Cryptosporidium</i> in sheep in Australia
Presentation Time:	1030 -1045
Authors:	Rongchang Yang*, Una Ryan, Graham Gardner, Andrew Williams, Josephine Ng, Caroline Jacobson School of Veterinary and Life Sciences, Murdoch University, Perth, Australia

Cryptosporidium is an important enteric parasite that causes diarrhoeal disease in humans and animals worldwide. Increased interest in *Cryptosporidium* in livestock has mainly arisen because of the potential public health risks and productivity consequences. An investigation of the prevalence of *Cryptosporidium* and its association with scouring and productivity measures in sheep in Australia was undertaken from January 2011 to March 2013. A total of 3,459 faecal samples were collected from 8 farms across 4 states (3 farms from Western Australia, 2 farms each from Victoria and South Australia and one farm from New South Wales) over 3 sampling periods (weaning, post-weaning and pre-slaughter). The prevalence of *Cryptosporidium* was determined using qPCR analysis and further genotyping was conducted using sequence analysis of the 18S rRNA gene. Data related to scouring (dag score and faecal consistency) and sheep productivity (live weight, carcass weight and dressing percentage) were collected from each farm. Statistical analysis was conducted using Statistical Analysis System (SAS Version 9.2). The prevalence of *Cryptosporidium* ranged from 3.3% to 43.9% on the different farms and during the different sampling periods. The prevalence of zoonotic *Cryptosporidium* species and impact of *Cryptosporidium* on sheep scouring and productivity will be discussed.

Acknowledgements:

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Session Details:	8/29/2013 RUMINANTS PROTOZOA 1015 - 1130 Meeting Room 1
Oral Presentation Details:	The effects of the abortifacient parasite, <i>Neospora caninum</i> on bovine foetuses in early and late gestation
Presentation Time:	1045 -1100
Authors:	Patrick Craig ^{1*} , Diana Williams ¹ , Udo Hetzel ² , Anja Kipar ^{1,2} ¹ University of Liverpool, Liverpool, United Kingdom; ² University of Helsinki, Helsinki, Finland

Background: *Neospora caninum* is an obligate intracellular protozoan parasite, which is the most frequently diagnosed abortifacient in dairy cattle in the UK and is a leading cause of abortion worldwide. How the parasite kills the foetus is not fully understood, but it has been suggested that more mature foetuses are better able to mount a stronger immune response to control parasite multiplication and dissemination.

Aim: To assess the pathological effects of infection with *N. caninum* on bovine foetus and investigate if the foetal immune response contributes to control of parasite dissemination leading to foetal survival.

Methods: Based on the results of the initial histological screening of 35 bovine foetuses from *N. caninum* infected and uninfected dams, five foetuses infected in early gestation, five infected later in gestation and one new-born calf were selected. Haemolymphatic tissues (thymus, spleen, mesenteric lymph node, femoral bone marrow) and major organs (myocardium, *Musculus quadriceps femoris*, liver, lung, brain, spinal cord, *Nervus femoris*, jejunum, kidney and adrenal gland) were subjected to a detailed immunohistological examination, using specific stains to identify parasites, leukocyte subsets and cell turnover.

Results: The most frequently observed lesions in early gestation were multifocal areas of necrosis with *N. caninum* tachyzoites in liver and brain, while the myocardium contained large numbers of parasites without evidence of cell death. In late gestation, histological changes were restricted mainly to the CNS, where non-suppurative inflammation and few tachyzoites were observed. Other non-haemolymphatic tissues exhibited mild mononuclear inflammatory infiltrates.

Conclusion: The results suggest that in early gestation, tachyzoites replicate preferentially in foetal liver, brain and myocardium in the absence of an inflammatory response and cause extensive necrosis in the former. Unlike foetuses in early gestation, those in late gestation exhibited a mononuclear inflammatory infiltrate in various tissues dominated by lymphocytes, plasma cells and fewer macrophages.



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Session Details:	8/29/2013 RUMINANTS PROTOZOA 1015 - 1130 Meeting Room 1
Oral Presentation Details:	Detection and characterisation of <i>Giardia</i> spp. in diarrheic calves in Southern Germany
Presentation Time:	1100 -1115
Authors:	Miriam C. Scheuerle^{*1}, Julia Gillhuber¹, Amanda Ash², Louise Pallant², Andrew Thompson², Kurt Pfister¹ ¹ Comparative Tropical Medicine and Parasitology, Ludwig-Maximilians-Universität, Munich, GERMANY, ² School of Veterinary and Biomedical Sciences, Murdoch University, AUSTRALIA

Neonatal diarrhea poses a massive problem in the rearing of calves. Cryptosporidia and Rotavirus are known to be important in this focus of infection and the treatment management is adjusted accordingly. The influence of *Giardia* is not known. The aim of the study was to get an overview of the current situation in Southern Germany, to estimate the prevalence of *Giardia* spp. and to analyse the zoonotic potential of different Giardia assemblages.

In the course of one year 1749 faecal samples of mostly diarrheic calves of the age between 1 and 369 days (mean 26.6 d) were analysed for *Giardia* spp, *Cryptosporidium* spp and *Eimeria* spp using direct detection methods (smear, MIFC). DNA was extracted from *Giardia*-positive samples and was analysed by PCR and sequencing methods.

155 (8.9%) calves were positive for *Giardia* spp, with a mean age of 50.4 d and a range from 3 to 130 days of age. 293 (16.8%) calves were *Eimeria*-positive, with a mean age of 56.4 d (min = 5, max = 331). 651 (37.2%) samples were *Cryptosporidium*-positive, with a mean age of 11.6 d (min = 1, max = 77). In 75 samples a mixed infection of *Eimeria* and *Giardia*, in 17 of *Cryptosporidium* and *Giardia* and in 5 of *Cryptosporidium* and *Eimeria* was detected. In 747 (42.7%) samples no pathogen was detected.

These results show the potential importance of *Giardia* especially in older calves. The role of *Giardia* and its various assemblages in this focus of infection are presently being investigated. Further studies will investigate the presence of *Giardia* in inapparent infections and in adult cattle.

Acknowledgements:

We thank the veterinarians for sending the samples and the team of the diagnostic lab for the help with processing.



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Session Details:	8/29/2013 RUMINANTS PROTOZOA 1015 - 1130 Meeting Room 1
Oral Presentation Details:	Histologic Lesions in Bubaline and Bovine Foetuses Infected with Different <i>Neospora caninum</i> Strains
Presentation Time:	1115 -1130
Authors:	Andreas L. Chryssafidis^{1,5*}, Germán Cantón^{3,4}, Francesca Chianini³, Elisabeth A. Innes³, Ed H. Madureira², Solange M. Gennari¹ ¹Departamento de Medicina Veterinária Preventiva, Faculdade de Medicina Veterinária e Zootecnia, Universidade de São Paulo, São Paulo-SP, BRAZIL ²Departamento de Reprodução Animal, Faculdade de Medicina Veterinária e Zootecnia, Universidade de São Paulo, Pirassununga-SP, BRAZIL ³Moredun Research Institute, Edinburgh, SCOTLAND ⁴Instituto Nacional de Tecnología Agropecuaria, INTA, ARGENTINE ⁵Present Address: School of Veterinary Medicine, University College Dublin – Belfield, IRELAND

Neospora caninum is a protozoan parasite very important all over the world, being considered the main cause of bovine abortion in some locations (Dubey and Schares, 2006). The objective of this study is to evaluate histologic lesions in foetuses and mothers experimentally infected with *N. caninum* in the first third of pregnancy. Two strains of *N. caninum* were used to infect bubaline and bovine pregnant females. Eight cows and seven buffaloes, seronegative to *N. caninum* and other abortive agents, were selected for the study and protocols for fixed-time artificial insemination were used for greater control of fertilization. At 70 days of gestation, five cows and three buffaloes were inoculated intravenously with 5x10⁸ tachyzoites of Nc-Bahia strain (group 1) and two cows and three buffaloes received Nc-1 strain (group 2) by the same procedures. One animal of each species remained as controls (group 3). Serum samples were collected weekly and all animals from groups 1 and 2 developed specific humoral immune response detected by ELISA. By ultrasound examination, foetal death was detected in only one cow from group 1 at 42 days post infection (d.p.i), while all animals from group 2 presented foetal death at 35 d.p.i.. As soon as abortion was detected, all animals from the same group were slaughtered. Tissue samples were collected from infected mother, fetuses and stained with HE (hematoxilin and eosine) for routine histological analysis. Foetal brains and placentomes were analysed by IHC (immunohistochemistry) as described previously (Maley et al., 2003). Different degrees and frequency of lesions could be seen in samples collected from group 1 and 2 and are presented here. Nc-Bahia strain proved to be less pathogenic than Nc-1, as it caused fewer abortions and less frequent histological lesions with milder severity. The results of this experiment reaffirm the difference of pathogenicity between *N. caninum* strains.



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Session Details:	8/29/2013 GENETIC IMMUNITY NATIVE BREEDS: WHATS OLD IS NEW 1015 - 1130 Meeting Room 2
Oral Presentation Details:	Red Maasai x Dorper resistance to gastrointestinal parasite infections associated to a panel of SNPs
Presentation Time:	1015 -1030
Authors:	Benavides M¹, Sonstegard T², Kemp S³, Mugambi J⁴, Gibson J⁵, Baker L⁶, Van Tassell C² ¹ Embrapa LabEx, BRAZIL, ² Bovine Functional Genomics Laboratory - Beltsville Agricultural Research Center - ARS/USDA, USA, ³ International Livestock Research Institute (ILRI), Nairobi, KENYA, ⁴ Veterinary Research Centre KARI, Muguga, KENYA, ⁵ University of New England, Armidale, NSW, AUSTRALIA, ⁶ Whangamata, NEW ZEALAND

Gastrointestinal (GI) parasitic infection is a main health constraint that affects small ruminant production. Anthelmintic drugs are used to control parasites, however long-term use led to selection pressure, resulting in parasite resistance against all current chemical interventions available in the market. The aim of this study is to identify polymorphisms strongly associated with sheep host resistance against gastrointestinal parasite infections. A double backcross population of Red Maasai and Dorper sheep from the International Livestock Research Institute (ILRI) was genotyped with the OvineSNP50K BeadChip. Data for average faecal egg counts (AVFEC), packed cell volume (AVPCV), and live weight (AVLWT) were adjusted for fixed effects prior to setting the threshold for the tails of the distributions (10% most resistant and 10% most susceptible lambs). Single nucleotide markers were filtered for minor allele frequency, call rates per marker, and Hardy-Weinberg equilibrium criteria using PLINK. Genome-wide significance threshold were defined after 100,000 permutations on EMMAX. Association analyses were calculated using QxPak v5.05 and significant SNPs with -log10 p-values >=4 were observed on 6, 7, and 7 different chromosomes, while 7, 9, and 8 chromosomal regions were detected for AVPCV, AVLWT, and AVFEC, respectively. No SNP was relevant for more than one trait. A set of 7, 10 and 9 SNPs explained 28.6%, 19.4% and 21.8% of the phenotypic variation of those traits. As a practical result, a panel with such markers could be used in Red Maasai x Dorper breeding programmes to select for more resistant sheep. However, to determine the causal mutations that define more resistant Red Maasai x Dorper sheep, further studies will focus on 4, 3, and 3 SNPs that explained 21.8%, 11.2% and 13.4% of the phenotypic variation for AVPCV, AVLWT, and AVFEC, respectively, after a classification tree was used to calculate the best haplotype combination among most significant SNPs.

Acknowledgements:

Embrapa LabEx for funding genotyping analyses.



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Session Details:	8/29/2013 GENETIC IMMUNITY NATIVE BREEDS: WHATS OLD IS NEW 1015 - 1130 Meeting Room 2
Oral Presentation Details:	Immune responses associated with resistance to adult stages of <i>Haemonchus contortus</i> in sheep
Presentation Time:	1030 -1045
Authors:	Gonzalez J ¹ , Piedrafita D ² , Morrison T ³ , Hernandez J ¹ , Millan S ¹ , Rodriguez F ¹ , Meeusen E ² , McNeilly T ³ ¹ University Of Las Palmas De Gran Canaria, ² Monash University, ³ Moredun Research Institute

Protective mechanisms against the worm adult stage instead of larvae, have not been commonly reported in sheep breeds, We have identified sheep indigenous to the Canary Islands, the Canaria Hair Breed sheep (CHB) which mediate resistance to adult stages (González et al, 2008; González et al., 2011). Eosinophils and *gd*/WC1+ T cells were inversely correlated with fecundity at 21 and 28dpi in the resistant CHB, but not susceptible Canaria sheep (CS), suggesting an important role of these cells in immunity to the adult stage. Further immunological analysis reveals that mucus antibodies against adult antigens were negatively correlated with adult length by 28dpi but not at 21dpi in the resistant CHB sheep. Between breed differences in selective cytokine responses were also observed. Before infection there was higher expression of the regulatory T cell associated transcription factor Foxp3 in the abomasal mucosa of susceptible CS sheep. A significant increase in IL-5 gene expression was observed in both abomasal mucosa and abomasal lymph nodes following infection of resistant CHB which was absent in the susceptible CS, and is in agreement with the higher levels of tissue eosinophils, particularly in late stage infection, observed in the CHB sheep. All these parasitological and immunological data suggest differential resistance mechanisms, some affecting the adult parasites. These studies continue to develop our understanding of multi-stage immune responses against infection of small ruminants with *H. contortus* parasites.

Acknowledgements:

This trial was supported by the Agencia Canaria de Investigación, Innovación y Sociedad de la Información Grant (PI2007/036) and through sponsoring Miss Julia N. Hernández. It was also supported by the Ministerio de Economía y Competitividad (Spanish Government) grant (AGL2009/09985).

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González, JF; Hernández, A.; Meeusen, E.N.T., Rodríguez, F.; Molina, J.M.; Jaber, J.R.; Raadsma, H.W.R., Piedrafita, D. (2011a). Fecundity in adult *Haemonchus contortus* parasites is correlated with abomasal tissue eosinophils and gdT cells in resistant Canaria Hair Breed sheep. Vet. Parasitol., 178: 286-292.



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Session Details:	8/29/2013 GENETIC IMMUNITY NATIVE BREEDS: WHATS OLD IS NEW 1015 - 1130 <i>Meeting Room 2</i>
Oral Presentation Details:	Breaking the mould - can resistant animals also be productive
Presentation Time:	1045 -1100
Authors:	A W Greer Faculty of Agriculture and Life Sciences, Lincoln University, Christchurch, New Zealand

Selection of animals genetically resistant to gastrointestinal nematode infections is an approach that has found favour in a number of environments. However, in the predominately temperate environment of New Zealand, enhanced immune capacity is not synonymous with improved animal performance. Lines of animals that have undergone selection for production traits have greater parasitological loadings while genetic indices for animal performance are inversely correlated with indices for resistance. As such, there remain polarised views on the benefits of promoting immune-competence in high performing livestock. Much of the difference in productivity can be attributed to the nutritional cost of the immune response which is absent in very young lambs and has been observed to occur earlier in animals from lines selected for resistance than their resilient counterparts. The possible causes of the apparent trade-off between resistance and productivity will be discussed and it will be proposed that the timing of immune development, and its associated cost, is dependent on relative maturity. The impact on potential growth rate of selecting animals with a greater relative maturity will be outlined leading to the suggestion that a better understanding of the physiology of growth in concert with immunological function is needed to identify resistant animals that are able to bend the growth curve and also be productive animals.



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Session Details:	8/29/2013 GENETIC IMMUNITY NATIVE BREEDS: WHATS OLD IS NEW 1015 - 1130 Meeting Room 2
Oral Presentation Details:	Sustainable animal production by exploiting natural immunity
Presentation Time:	1100 -1115
Authors:	David Piedrafita^{1*}, Els Meeusen¹, Jorge F. González² ¹Monash University, Clayton, AUSTRALIA ²University of Las Palmas de Gran Canaria, Arucas, SPAIN

In many small animal production systems (e.g. sheep, goats), local indigenous breeds are used for major sources of meat, fibre and milk. These breeds are used due to cultural or historical values and more importantly, often have adaptation to the local environment. One of these adaptations includes a natural resilience and/or resistance to worm infection. This ability allows some productivity advantages when compared to commercial breeds requiring high maintenance regimes. However, optimising this productivity still relies on the use of drugs to control worm infection.

Vaccination has long been suggested as an ideal alternative circumventing the many problems of drug based therapeutics. However, there are a few successful vaccines using defined recombinant antigens available currently and their development continues to be a great challenge. Partial protective efficacy has been demonstrated repeatedly by vaccinating animals with native antigen preparations from these worm parasites (e.g. Piedrafita et al. 2012). Such preparations may be easily manufactured locally and if natural antigens are used (as opposed to hidden antigens) can be boosted by natural infection to keep parasite numbers low. Given the natural resistance of many of these indigenous animals, a vaccine with some efficacy may prove highly advantageous and effective in these animals. The use of native antigen preparations may well be a viable long term sustainable method of control against worm infection of small ruminants. This presentation will discuss circumstances in which such a system may provide economically sustainable production increases over the long term.

References:

Piedrafita D, de Veer MJ, Sherrard J, Kraska T, Elhay M, Meeusen EN. (2012). [Field vaccination of sheep with a larval-specific antigen of the gastrointestinal nematode, Haemonchus contortus, confers significant protection against an experimental challenge infection.](#) Vaccine. 30(50):7199-204.



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Session Details:	8/29/2013 ECHINOCOCCUS 1015 - 1130 Meeting Room 3
Oral Presentation Details:	<i>In vitro</i> and <i>in vivo</i> investigations to develop functional imaging by Positron Emission Tomography (PET) for murine and human alveolar echinococcosis
Presentation Time:	1015 -1030
Authors:	Clémence Porot^{1,2}, Junhua Wang^{2,3}, Stéphane Germain⁴, Yann Seimille⁵, Davide Camporese⁶, Jenny Knapp^{1,2}, Dominique A. Vuitton², Oleg Blagosklonov^{1,2}, Bruno Gottstein^{3*} ¹Department of Nuclear Medicine, University of Franche-Comté and University Hospital, & ²WHO Collaborating Centre for Prevention and Treatment of Human Echinococcosis, Besançon, France ³Institute of Parasitology, University of Berne, Switzerland ⁴Center of BioMedical Imaging, University of Geneva, Switzerland, ⁵Department of Medical Imaging and Information Sciences, Division of Nuclear Medicine, University Hospital of Geneva, Switzerland ⁶Advanced Accelerator Applications, Saint Genis-Pouilly, France.

Alveolar echinococcosis (AE) is a severe chronic helminthic disease in humans due to an intrahepatic tumour-like growth of the metacestode of *Echinococcus multilocularis*. Rodents being the natural intermediate host in the parasite life cycle, research in the murine model offers an excellent opportunity to develop new tools for efficient management and treatment of the disease. The present study was designed to develop new functional imaging procedures for the diagnosis, staging and follow-up of AE using Positron Emission Tomography (PET).

[18F]- fluorodeoxyglucose (FDG) is a validated tracer of AE lesions in human patients; however, it does not directly reflect parasite viability but rather peri-parasitic host inflammatory processes. The ideal tracer should be able to assess the course of AE upon direct uptake by the metacestode through its metabolic activity. We designed a radiolabelling protocol which could be assessed for activity in host and parasite cell cultures *in vitro*. We compared the uptake of FDG and of some other PET tracers ([¹⁸F]-fluorotyrosine (FET), [¹⁸F]-fluorothymidine (FLT), [¹⁸F]-fluorometylcholine (FMC), and sodium [¹⁸F]-fluorine (NaF)) by *in vitro* studies on human hepatocytes, human leukocytes and *in vitro*-cultivated metacestode vesicles. Preliminary results showed that leukocytes were the greediest for all fluorinated tracers but mainly for FDG. FLT appeared to be the best promising candidate for AE functional imaging because we observed very high FLT-uptake in parasite vesicles and no FLT-uptake in human leukocytes. In order to confirm FLT potential *in vivo*, we elaborated a PET imaging protocol for appropriate murine AE primary and secondary infection studies. World-wide first PET images of AE in animals were acquired after intraperitoneal metacestode injection; FDG-uptake was studied at advanced infection time points. Experiments confirmed that FDG distribution in PET reflects inflammatory reactions in the peri-parasitic metacestode tumour-like tissue.



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Session Details:	8/29/2013 ECHINOCOCCUS 1015 - 1130 Meeting Room 3
Oral Presentation Details:	Molecular detection of <i>E. granulosus</i> sheep strain (G1) infections in naturally infected dogs in Punjab (India)
Presentation Time:	1030 -1045
Authors:	Dhaliwal B, Sharma R, Sharma J, Gill J Guru Angad Dev Veterinary & Animal Sciences University

Echinococcosis is being considered as a research priority in India. The cestode *E. granulosus* causes significant morbidity and mortality in human beings and huge economic losses in the livestock. Previous studies indicate presence of hydatid cysts due to G1 and G3 strains of *E. granulosus* in food producing animals in this part of the country (Singh et al., 2012). The sheep strain (G1) of *E. granulosus* has been found to be associated with most human infections across the globe (Thompson and McManus, 2002). The recognition of strain variation can prove beneficial for the implementation of disease prevention and control programmes particularly in endemic countries such as India. The faecal samples from 237 pet and stray dogs were collected and analyzed for the presence of eggs of the *Taeniidae* family. A 255 base pair fragment of the mitochondrial 12S rRNA gene was amplified to detect the presence of sheep strain (G1) of *E. granulosus* (Stefanic et al., 2004). The eggs of the *Taeniidae* family were detected in five samples with an overall prevalence of 2.11 per cent. The prevalence was highest in stray dogs (9.52%) living near slaughter shops/post mortem areas. PCR detected DNA of *E. granulosus* sheep strain (G1) in 2 of the 5 egg containing samples. The relative risk for the presence of *Taeniidae* family eggs was found to be 8.19 times high (P=0.056) in stray dogs having access to condemned meat/offal's (living near slaughter shops/post mortem areas) than the stray dogs living in other residential areas. The results reveal the presence of sheep strain of *E. granulosus* and demand implementation of Animal Birth Control programme so as to control the stray dog population of the country.

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24th International Conference of the World Association for the Advancement of Veterinary Parasitology

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Session Details:	8/29/2013 ECHINOCOCCUS 1015 - 1130 Meeting Room 3
Oral Presentation Details:	Emergence of Echinococcus multilocularis in dogs in Canada?
Presentation Time:	1045 -1100
Authors:	Peregrine A¹, Jenkins E², Gesy K², Kerr M³, Scott S², Barnes B⁴, Skelding A¹, Gottstein B⁵ ¹ University of Guelph, Guelph, Ontario, Canada, ² University of Saskatchewan, Saskatoon, Saskatchewan, Canada, ³ 3Prairie Diagnostic Services, Saskatoon, Saskatchewan, Canada, ⁴ West View Veterinary Hospital, Powell River, British Columbia, Canada, ⁵ Universitat Bern, Bern, Switzerland

Until 2009, *Echinococcus multilocularis* was considered to be endemic in wildlife in only two regions of Canada: the northern tundra zone of the western Canadian Arctic, and southern parts of Alberta, Saskatchewan and Manitoba. No cases of this parasite had been described in dogs in Canada. In 2009, hepatic alveolar hydatid disease (AHD) was diagnosed in a 3-year old dog that had lived permanently in British Columbia; *E. multilocularis* was definitively identified on histology, sequence data for the mitochondrial 12S rRNA gene, RFLP analysis of the mitochondrial NADH dehydrogenase 1 and 12S rRNA genes, and direct immunofluorescence of tissue. In 2012, a second case of hepatic AHD was similarly diagnosed in a 2-year old dog that had resided in only two parts of southern Ontario; a third case was diagnosed in a 4-year old dog that lived primarily in Alberta and Manitoba. None of the dogs had ever left Canada. All three dogs died within a few weeks of developing clinical signs. Genetic analysis of tissue from the dog in British Columbia indicated that sequence data for the *cox1*, *cob1* and *nad2* genes grouped with haplotypes from France and Belgium. Tissue from the liver of the Alberta dog similarly grouped with strains of *E. multilocularis* from west-central Europe. Typing of material from the Ontario dog was not possible. Epidemiological studies suggest that all three dogs were most likely infected through contact with eggs in feces of endemic wild canids. The origin of the European-type strains of *E. multilocularis* in these Canadian dogs is unclear, but appears most likely to be associated with either importation of dogs into Canada from Europe, since cestocide treatment at the time of importation is not required, or historic importation of red foxes into North America from Europe for hunting and the fur trade.



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Session Details:	8/29/2013 ECHINOCOCCUS 1015 - 1130 <i>Meeting Room 3</i>
Oral Presentation Details:	Development of a rat model for the study of alveolar echinococcosis and the different factors that influence the success of the infection
Presentation Time:	1100 -1115
Authors:	Armua-Fernandez M , Schweiger A, Eichenberger R, Deplazes P Institute of Parasitology, University Of Zurich

Alveolar echinococcosis is a deadly zoonotic disease caused by the larval stage of *Echinococcus multilocularis*. Foxes are the most important definitive hosts excreting eggs with their feces. Classically, the disease is preceded by a long asymptomatic period of 5-15 years, but, in immunodeficient patients the disease progresses rapidly. In the past, the mouse model for metacestode propagation has been used in numerous studies, however only a little work has been performed concerning the intermediate host specificity. Rats have been shown to be highly resistant to *E. multilocularis* in nature, but could be a suitable rodent model for parasite propagation after intraperitoneal inoculation[1]. The aim of this work was to study the role of different host and parasite factors in the establishment of alveolar echinococcosis in a rat model. Fifty-one Wistar rats were divided into 8 groups according to age (2 month-old or 12 month-old), immunity status (immunocompetent, immunodeficient or iatrogenically immunosuppressed), infection route (oral or intraperitoneal) and type of inoculum (eggs, free oncospheres, or metacestode material). The viability of the eggs was assessed by the sodium hypochlorite resistant test (SHRT) described by Deplazes (2005)[2]. The rats received from 900 to 10000 hypochlorite-resistant eggs/oncospheres depending on each group. The groups were subdivided and euthanized at week 24 and 36. Moreover, 30 immunodeficient nude rats were orally

inoculated with *E. multilocularis* eggs and euthanized on weeks 6, 12, 18 and 24. Intraperitoneal infections with metacestode material were successful independently of the age. In orally inoculated (eggs or free oncospheres) groups there was no macroscopic evidence of *E. multilocularis* development in both immunocompetent and immunodeficient nude rats. However, for the first time, a successful orally infection with eggs was observed in 2 out of 6 rats with iatrogenically induced immunosuppression.

Acknowledgements:

The researchers would like to thanks to all the Institute members for their valuable help throughout the experiment.

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Session Details:	8/29/2013 ECHINOCOCCUS 1015 - 1130 Meeting Room 3
Oral Presentation Details:	Echinococcosis in Khyber Pakhtunkhwa, Pakistan
Presentation Time:	1115 -1130
Authors:	Rehman T², Panni M¹, Ali I¹, Alam M³, Ahmad A⁴, Khan J⁴, Khan S⁴ ¹ Institute of Biotechnology and Genetic Engineering, ² Khyber Medical University, ³ University of Swabi, ⁴ Relief International

Echinococcosis commonly referred to as the Hydated cyst disease affects both humans and animals. The well documented species of the genus *Echinococcus* causing hydated cyst disease in humans include *Echinococcus granulosus* and *Echinococcus multilocularis*. In this study we assessed the prevalence of Echinococcosis and analyzed the efficiency of ELISA based procedures for screening individuals [both animals and humans] for Echinococcosis. Our results indicated that 0.33% of the animal species brought to slaughter houses in Peshawar city were infected with *Echinococcus* species. ELISA based procedures was efficient enough to figure out the state of being infected with Echinococcus species in a significant number of human and animal species. We also carried out species identification and typing of *Echinococcus granulosus* isolated from the cysts of human beings by PCR or PCR-RFLP. Majority of the humans were infected with *E.Granulosis*. The infected individuals with confirmed hydated cysts belonged to various districts of Khyber Pakhtunkhwa, Pakistan and Afghanistan. The genotyping of *E. Granulosis* and screening of individuals groups of people having frequent contacts with animals is currently underway. As imaging techniques could not be applied for screening populations, therefore, so as to know about the actual prevalence of the disease, ELISA seems to be a better option for initial diagnosis of Echinococcosis.



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Session Details:	8/29/2013 VACCINES - GENERAL 2 1015 - 1130 Meeting Room 5
Oral Presentation Details:	Immunization studies in rabbits using gut membrane-bound proteins derived from <i>Rhipicephalus appendiculatus</i> , <i>R. evertsi evertsi</i> and <i>Amblyomma variegatum</i> female ticks
Presentation Time:	1015 -1030
Authors:	Helen Lydia Kutima Jomo Kenyatta University of Agriculture and Technology, Nairobi, Kenya

The objective of this study was to immunize rabbits with Gut Membrane-Bound Proteins (GMBP) derived from partially engorged *Rhipicephalus appendiculatus*, *R. evertsi evertsi* and *Amblyomma variegatum* female ticks and to assess whether the elicited immunity was protective against both homologous and heterologous tick instars and to isolate and identify the protective antigens. Sodium dodecyl sulphate-polyacrylamide gel electrophoresis (SDS-PAGE) of the GMBP antigens demonstrated protein bands with molecular weights ranging from 16 to 140 KDa. Thirty-seven, 45 and 39 protein bands were fractionated from *R. appendiculatus*, *R. Evertsi evertsi* and *A. variegatum* GMBP antigens, respectively, all possessing molecular weights ranging from 14 to 140 KDa. Twenty-two of the isolated proteins were shared among the three tick species. Immunized rabbits acquired resistance to challenge infestation by all instars of the three tick species. Resistance was manifested by prolonged feeding, reduction in engorgement weights, egg mass weights, moulting and percentage hatchability and increased mortality. Immunization of rabbits with GMBP antigens generated protection and cross-protection against challenge infestation with homologous and heterologous instars, respectively. Cross-protection was more pronounced in the homologous than heterologous systems.

Enzyme-Linked Immunosorbent Assay (ELISA) technique detected circulating antibodies in the anti-sera to GMBP from homologous and heterologous systems one week after the primary dose. Ouchterlony double immunodiffusion reactions with anti-tick GMBP sera formed 2 to 3 precipitin lines with homologous GMBP antigens and one to two precipitin line(s) with each heterologous GMBP antigens. A line of complete identity was observed when anti-sera to GMBP antigens reacted with GMBP from homologous and heterologous tick species, suggesting common antigenic epitopes.

Western blot analysis on GMBP of *R. appendiculatus*, *R. evertsi evertsi* and *A. Variegatum* with sera from immunized rabbits detected protein bands specific to the homologous GMBP antigens, and revealed considerable cross-reactions in the heterologous systems. These results suggested further the presence of common antigens. The presence of cross-reacting antigens conferred cross-protection.

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Session Details:	8/29/2013 VACCINES - GENERAL 2 1015 - 1130 Meeting Room 5
Oral Presentation Details:	Evaluation of <i>in silico</i> predicted and expressed anti- <i>Rhipicephalus microplus</i> antigens and their elicited immune responses in rabbits
Presentation Time:	1030 -1045
Authors:	Sabine Richards*, Christine Maritz-Olivier University of Pretoria, Pretoria, SOUTH AFRICA

The impact of ticks on livestock is immense resulting in billions of dollars of losses to the economy annually worldwide¹. Ticks are one of the most important vectors of animal as well as human diseases and transmit more infectious diseases than any other group of arthropods². The most economically important tick species in livestock in tropical and subtropical regions globally is *Rhipicephalus microplus*. Research focusing on the production of improved or even new acaricidal compounds as well as vaccine-based controls is slow³. In the field of vaccine development progress is hindered by the identification of promising candidates. In this study we used a combined functional genomics and reverse vaccinology approach in the identification of promising gut plasma membrane associated antigens. These transcripts were recombinantly expressed and used for the immunization of rabbits to obtain polyclonal antiserum for subsequent localization of the antigens in vivo as well as in BME (embryonic) cells. Evaluation of antibody responses over time and affinity of antibodies towards the antigen have also been monitored. The capillary feeding technique of ticks will be tested using the antiserum obtained to predict possible protective antigens for subsequent cattle vaccine trials.

Acknowledgements:

Red Meat Research Foundation of South Africa
 Technology and Human Resources for Industry Programme (THRIP)
 National Research Foundation (NRF)
 Gauteng Department of Agriculture and Rural Development (GDARD)

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Session Details:	8/29/2013 VACCINES - GENERAL 2 1015 - 1130 Meeting Room 5
Oral Presentation Details:	Antigenic diversity in <i>Theileria parva</i> in vaccine stabilate and African buffalo
Presentation Time:	1045 -1100
Authors:	Johanneke Hemmink^{1*}, Willie Weir², Roger Pelle³, Tatjana Sitt³, Phil Toye³, Nicholas Juleff⁴, Ivan Morrison¹ ¹Roslin Institute & Royal (Dick) school of veterinary science, Edinburgh, UNITED KINGDOM ²University of Glasgow, Glasgow, UNITED KINGDOM ³International Livestock Research Institute, Nairobi, KENYA ⁴The Pirbright Institute, Pirbright, UNITED KINGDOM

Theileria parva is a tick-borne intracellular protozoan parasite which infects cattle and African buffalo (*Syncerus caffer caffer*) in Eastern and Southern Africa. Most buffalo in endemic regions are infected but do not suffer clinical disease. In contrast, cattle infected with buffalo derived parasites develop severe disease, but have low levels of parasitaemia and infection is usually not transmissible by feeding ticks.

The infection and treatment method (ITM) for immunisation of cattle against *Theileria parva* was developed in the 1970s. Animals are infected with live sporozoites and treated simultaneously with oxytetracycline to avoid severe disease reactions. One such ITM vaccine is the Muguga cocktail, which contains a mixture of three parasite stocks - Muguga, Kiambu 5 and Serengeti transformed – originally chosen based on cross-immunity trials. This vaccine has been used with success in the field in several areas in Eastern Africa. However, there is evidence that vaccination using cattle derived parasites does not always provide adequate protection against buffalo-derived *T. parva* (Radley et al., 1979).

A number of *T. parva* antigens recognised by CD8 T cells from cattle immunised by ITM have been identified. Some of these antigens show a high degree of sequence polymorphism. Allelic diversity appears to be much greater in buffalo derived *T. parva* parasites than in cattle-derived parasites (Pelle et al., 2011). To examine in more depth the antigenic diversity in *T. parva*, a multi-locus sequence typing system was established using Roche 454 amplicon sequencing. Antigenic diversity in the *T. parva* parasites that make up the Muguga cocktail was investigated and compared with that of buffalo-derived parasites collected from different geographical locations. The results indicate that the Muguga cocktail vaccine contains limited antigenic diversity, whereas buffalo-derived parasites are highly diverse both at the population level and within individual animals.

Acknowledgements:

We thank the International Livestock Research Institute and the Pirbright Institute for supplying DNA.



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Session Details:	8/29/2013 VACCINES - GENERAL 2 1015 - 1130 Meeting Room 5
Oral Presentation Details:	Characterisation of a new <i>Babesia bovis</i> thrombospondin-related anonymous protein as a novel blood-stage vaccine candidate
Presentation Time:	1100 -1115
Authors:	Mohamad Alaa Terkawi ¹ , Jadsada Ratthanophart ¹ , Mahmoud AbouLaila ² , Akram Salama ^{1,3} , Naoaki Yokoyama ¹ , Yoshifumi Nishikawa ¹ , Xuenan Xuan ¹ and Ikuo Igarashi ^{1*} ¹ National Research Center for Protozoan Diseases, Obihiro University of Agriculture and Veterinary Medicine, Obihiro, JAPAN ² Department of Parasitology, Minoufiya University, Sadat City, EGYPT ³ Department of Animal Medicine and Infectious diseases, Minoufiya University, Sadat City, EGYPT

A cDNA encoding a *Babesia bovis* protein sharing significant homology with thrombospondin-related anonymous protein (TRAP) from other apicomplexan was found in EST database and designated *BbTRAP2*. The full length of *TRAP2* contains an open reading frame of 3084 bp with predicted 1027 amino acids and molecular mass of 110-kDa. *BbTRAP2* has the typical structure of apicomplexan TRAPs as determined by the presence of two VWFA domains. Recombinant protein encoding truncated BbTRAP2 gene (341-920 aa) was expressed as a GST fusion protein in *E. coli* with a 91-kDa molecular mass. Recombinant BbTRAP2 (rBbTRAP2) demonstrated high antigenicity with *B. bovis*-infected sera collected from geographically different regions of the world. Moreover, antiserum against rBbTRAP2 specifically reacted with the corresponding authentic protein by an indirect fluorescent antibody test and Western blot analysis. Confocal laser microscope examination revealed apical localization of BbTRAP2 in the parasite. Three bands corresponding to 104, 76 and 44-kDa were identified on the parasites lysate and the supernatant of cultured parasites revealing that BbTRAP was proteolytically processed into 76- and 44-kDa proteins and shed into the culture. Strikingly, erythrocytes biding assay demonstrated that bovine erythrocytes precipitated BbTRAP2 and its smaller product from the parasites lysate. Furthermore, growth inhibition assay using purified anti-rBbTRAP2 IgG showed the significant growth inhibition of *B. bovis* in a dose dependent manner. Strikingly, anti-rBbTRAP2 serum were the most inhibitive of the parasites growth as compared to anti-sera made against different recombinant proteins including merozoite surface antigen 2c (BbMSA-2c), C-terminal rhoptry-associated protein 1 (BbRAP-1/CT) and spherical body protein 1 (BbSBP-1). Moreover, pre-incubation of free merozoites with 1 mg/ml of anti-rBbTRAP2 serum resulted in 80% inhibition of the invasion into erythrocyte. These results indicated that the new thrombospondin-related anonymous protein, BbTRAP2, might be a promising candidate for development subunit vaccine against *B. bovis* infection.

Session Details:	8/29/2013 VACCINES - GENERAL 2 1015 - 1130 Meeting Room 5
Oral Presentation Details:	In vitro feeding model for cattle tick vaccine candidate and gene function screening
Presentation Time:	1115 -1130
Authors:	Ala Lew-Tabor ^{1*} , Anthea Bruyeres ² , Bing Zhang ² , Manuel Rodriguez Valle ¹ ¹ The University of Queensland, St. Lucia, Brisbane, Queensland, AUSTRALIA ² Queensland Department of Agriculture, Fisheries & Forestry, St. Lucia, Brisbane, Queensland, AUSTRALIA

Rhipicephalus (Boophilus) microplus [Acari:Ixodidae] ticks cause economic losses for cattle industries throughout tropical and sub-tropical regions of the world estimated at \$US2.5b annually. Lack of access to efficacious long lasting vaccination regimes and increases in tick acaricide resistance has led to the investigation of targets for the development of novel anti-tick vaccines and treatments. *In vitro* tick feeding methods have been used for many tick species to study the effect of new acaricides or the transmission of tick borne pathogens. Few studies have reported the use of capillary *in vitro* feeding for functional genomic studies using RNA interference and/or the effect of specific anti-tick antibodies. In particular, *in vitro* feeding reports for the cattle tick are limited due to its relatively short hypostome. Methods were modified (Willadsen et al.) to further optimise tick sizes/weights, feeding using serum (bovine and ovine), blood anti-coagulants, and IgG concentrations for effective antibody delivery. Ticks are fed overnight and monitored for ~5-6 weeks to determine egg output and success of larval emergence using a humidified incubator. Lithium heparin blood tubes (Terumo Venosafe) provided the most reliable anti-coagulant for bovine blood feeding compared with citrated or EDTA blood tubes. Although >30mg semi-engorged ticks fed more reliably, ticks as small as 15 mg also fed to repletion to lay viable eggs. Ticks which gained less than ~10mg during *in vitro* feeding typically did not lay eggs. One mg/ml IgG from TickGARD®^{PLUS} vaccinated cattle produced a potent anti-tick effect *in vitro* (74-83% effectivity) similar to that observed *in vivo*. Alternatively, feeding of dsRNA targeting Bm86 (TickGARD®^{PLUS} antigen) did not demonstrate anti-tick effects (11% effectivity) compared with the potent effects of ubiquitin dsRNA (Lew-Tabor et al. 2010). This is the first study demonstrating tick *in vitro* feeding methods which will impact the development of anti-cattle tick vaccines and treatments.

Acknowledgements:

This research was supported by the CRC for Beef Genetic Technologies and the .Queensland Smart State Innovation Fund (National and International Research Alliance Program). The authors wish to thank Dr. Louise Jackson and Dr Wayne Jorgensen for both tick supply and advice, as well Sandy Jarrett and Catherine Minchin for technical support (Qld Department of Agriculture, Fisheries & Forestry).

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Session Details:	8/29/2013 DRUG RESISTANCE - SMALL RUMINANTS 2 1015 - 1130 Meeting Room 6
Oral Presentation Details:	UK guidelines for worm control – evaluating production, infection and resistance development with use on commercial farms
Presentation Time:	1015 -1030
Authors:	Learmount J AHVLA

UK guidelines on best practice resistance delaying strategies for sustainable control of parasites in sheep (SCOPS) have been produced and regularly updated since 2003 (Abbott et al, 2012). First year results for a 3 year study to evaluate SCOPS guidelines on UK sheep farms are presented. Sixteen farms were selected based on a 2 cube factorial design with 3 factors known to affect worm epidemiology: control regime (Best practice/Traditional) (Leathwick et al, 2006, 2008, Sherrill et al, 2006), farm type (upland/lowland) or climatic region (South West/North East) (van Dijk et al, 2008). Intervention plans, using 7 potential resistance delaying management practices were drawn up for 8 best practice study farms and compared to 8 farms using traditional high risk management. A cohort of 40 lambs were weighed and tagged at birth for identification and effect of the management strategies on parasite infection levels (faecal egg count (FEC)) and performance (live weight gain and finish times) was measured. The number of drug doses used on each farm was recorded. Drug resistance was monitored using Faecal Egg Count Reduction (in vivo) and Larval Development (in vitro) tests. The trial was designed to test for non-inferiority of best practice compared to traditional management strategies. There was no significant effect of control regime, farm type or climatic region on finish weight, time to finish or daily weight gain. With birth weight, there was a positive effect for finish weight (fatter at birth = fatter at slaughter) and time to finish (fatter at birth = quicker to slaughter). Analysis of FEC data showed no effect for farm type, or control regime. However, there was a borderline ($p=0.08$) effect for climatic region, with lower infection in the North East. Fewer drug treatments were carried out with Best Practice compared to Traditional management.

Acknowledgements: This study is funded by the UK Veterinary Medicines Directorate to whom we are grateful. We are also grateful to the private veterinarians involved in the study: Mike Glover, Tim Bebbington, Kate Hovers, Erica Moks, Fiona Lovatt, John Hughes, Debby Brown, Paul Roger and Helen Fielding. Finally thanks are due to Stephane Pietraville for carrying out the statistical analysis.

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Session Details:	8/29/2013 DRUG RESISTANCE - SMALL RUMINANTS 2 1015 - 1130 <i>Meeting Room 6</i>
Oral Presentation Details:	Implementation of resistance management practices on commercial sheep and cattle farms in New Zealand
Presentation Time:	1030 -1045
Authors:	Tony Rhodes^{1*} , Dave Leathwick ² , Bill Pomroy ³ , Tania Waghorn ² ¹ PGG Wrightson, Dannevirke, NEW ZEALAND ² AgResearch Grasslands, Palmerston North, NEW ZEALAND ³ Massey University, Palmerston North, NEW ZEALAND

In 2010 a programme to evaluate Best Practice Parasite Management practices on commercial farms in New Zealand was initiated. Sheep farms were selected on the basis of having significant problems involving resistance to 2 or more anthelmintic classes. The aims were to manage parasitism, maintain or improve on existing production figures, and ensure that the efficacy of anthelmintics did not decline further.

A management programme was designed specifically for each farm by a parasitologist, a farm consultant, a local veterinarian and the farmer. Strategies implemented included minimising unnecessary treatments whilst maintaining a strategic preventive drenching programme, maintaining refugia of susceptibility and the use of combinations of different anthelmintic classes. Regular monitoring included multiple faecal egg counts combined with an annual faecal egg count reduction test.

In each case the farmer has significantly changed parasite management practice. Compared to pre-programme, all now routinely apply at least five additional strategies that are considered best practice. Farmers have quickly understood the rationale and principles that constitute best practice, and have been very adept at identifying practical techniques for applying these that most suit them and their farming system.

On every farm “hot spots” - paddocks, grazing blocks and practices with a high risk of resulting in a population of highly selected resistant worms – were able to be identified. Simple but effective changes in management were able to be identified to reduce or eliminate this risk.

A comprehensive programme of monitoring has assisted farmers to quickly build confidence around changing practice, and reducing the number of treatments. All farms have changed to using combination oral treatment of cattle. Stock performance has been maintained, expenditure on parasite treatment has been decreased, effective products are now administered and the number of treatments has declined compared to pre-programme.

Acknowledgements:

This project was funded by MAF-SFF, Beef+Lamb NZ, AGMARDT and MSD.



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Session Details:	8/29/2013 DRUG RESISTANCE - SMALL RUMINANTS 2 1015 - 1130 <i>Meeting Room 6</i>
Oral Presentation Details:	Efficacy of monepantel against multi-resistant gastro-intestinal nematodes in sheep
Presentation Time:	1045 -1100
Authors:	J. Bailey^{1*} , H. Sager ² , B. Bapst ² , G. Strehlau ² , R. Kaminsky ² ¹ Novartis Animal Health Australasia, North Ryde, 2113, Australia ² Novartis Animal Health, Centre de Recherche, St-Aubin, Switzerland

Drug resistance has become a global phenomenon in gastrointestinal nematodes (GIN) of sheep with widespread resistance against all three older classes of broad-spectrum anthelmintics: the benzimidazoles, levamisole and the macrocyclic lactones. New anthelmintics are important to control infections with multi-resistant nematodes in areas where classical anthelmintics are no longer effective, and to prevent the spread of resistance in areas where the problem is not as severe. Monepantel (*Zolvix®*) **was introduced to the market in 2009 in New Zealand. The high efficacy of this new anthelmintic class against GIN in sheep has been demonstrated in several studies. Still lacking was the proof of efficacy against multi-resistant isolates.**

In order to assess the activity of monepantel against multi-resistant GIN, recent field isolates from farms with documented lack of efficacy were used for experimental infection of sheep. Two *Haemonchus contortus*-isolates from Australia and Switzerland as well as a *Teladorsagia circumcincta*-isolate from Scotland and a *Trichostrongylus colubriformis*-isolate from Australia were included in the studies. The infected sheep were treated orally according to the product labels with 2.5 mg/kg body weight monepantel.

The results demonstrate that monepantel was fully effective against the multi-resistant *H. contortus*-isolates (>99.9%) as well as *T. circumcincta* and *T. colubriformis* (both 99.9%). In contrast, all other anthelmintic classes resulted in efficacies clearly below 90%.

New anthelmintics are valuable tools for the strategic control of GIN in sheep. With monepantel, sheep farmers have a possibility to effectively treat their animals even in the presence of multiple anthelmintic resistance where all other classical drugs do not provide sufficient activity.

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Session Details:	8/29/2013 DRUG RESISTANCE - SMALL RUMINANTS 2 1015 - 1130 Meeting Room 6
Oral Presentation Details:	Combination anthelmintics are not magic bullets – they require knowledge and wise use
Presentation Time:	1100 -1115
Authors:	Barry Hosking^{1*} , Heinz Sager ² , Peter Rolfe ¹ , Ronald Kaminsky ² ¹ Novartis Animal Health Australasia Pty Limited, Kemps Creek, AUSTRALIA ² Novartis Centre de Recherche Santé Animale SA, St-Aubin, SWITZERLAND

The beneficial role of combination anthelmintics has been demonstrated by simulation modeling^{1,2} and was confirmed recently in an empirical study³. However, in a new era of having the luxury of several novel anthelmintics it is appropriate to reflect on some threats and opportunities associated with their use in combination formulations. One of these active ingredients, derquantel, was launched as a combination formulation with abamectin. The second new active, monepantel was launched as a mono-therapy. The rate at which resistance may develop to a combination anthelmintic that contains at least one new active ingredient appears to depend *inter alia* on two key factors, (1) the efficacy of each active ingredient against drug-susceptible and drug-resistant parasites, and (2) the degree that resistant survivors of treatment can be diluted into a pool of susceptible genotypes. Recent modeling studies indicate that moderate-high levels of starting efficacy by one¹ or more² partners in a combination can still have some benefit in slowing the development of resistance but in practice it is difficult to quantify at what point the combination loses this benefit in the presence of drug resistant parasites. Three controlled pen studies are discussed where a combination of abamectin + derquantel has been ineffective against adult and fourth-stage larvae of a multi-resistant *Haemonchus contortus* isolate, and fourth-stage larvae of a macrocyclic-lactone resistant *Teladorsagia* spp. isolate. Efficacy (geometric mean) of the combination was 93.8%, 17.1% and 86.3%, respectively in these experiments.^{4,5,6} It is noteworthy that fourth-stage larvae of *Teladorsagia* spp. and *H. contortus* are some of the less sensitive parasites to derquantel. Monepantel was highly effective against these parasites. These data confirm the importance of understanding the drench resistance status on individual farms – this is an essential principle of parasite control that continues to be poorly adopted around the world.

Acknowledgements:

The abamectin + derquantel studies were undertaken by staff at the Novartis Animal Health international R & D Centres in Australia (Yarrandoo) and Switzerland (Centre de Recherche Santé Animale). Resistance characterization of the isolates was completed at Yarrandoo.



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Session Details:	8/29/2013 DRUG RESISTANCE - SMALL RUMINANTS 2 1015 - 1130 <i>Meeting Room 6</i>	
Oral Presentation Details:	Anthelmintic resistance of sheep gastro-intestinal nematodes in 3 continental European countries	
Presentation Time:	1115 -1130	
Authors:	Thomas Geurden ¹ , Herve Hoste ² , Philippe Jacquiet ² , Donato Traversa ³ , Smaro Sotiraki ⁴ , Antonio Frangipane di Regalbano ⁵ , Annunziata Giangaspero ⁶ , David Bartram¹ ¹ Zoetis ² Institut National de la Recherche Agronomique / UMT Maîtrise de la Santé des Troupeaux de Petits Ruminants/ Ecole Nationale Vétérinaire de Toulouse, France ³ University of Teramo, Department of Comparative Biomedical Sciences, Italy ⁴ Veterinary Research Institute – Hellenic Agricultural Organization-Demeter (former NAGREF), Greece ⁵ University of Padua, Department of Animal Medicine Production and Health, Italy ⁶ University of Foggia, Department of Science of Agriculture, Food and Environment	

This study aimed to evaluate the efficacy of commonly used anthelmintics in Greece, France and Italy. In each country, ten study sites were selected based on a history of frequent use of anthelmintic compounds. On all farms, sheep were naturally infected with gastro-intestinal nematode parasites. Animals were allocated into 4 treatment groups of 10 animals each and were treated either with an oral formulation of moxidectin, ivermectin, albendazole/fenbendazole or levamisole (netobimin in France). One group remained untreated. A modified McMaster technique, with a sensitivity of 15-50 eggs per gram of faeces was used to monitor faecal egg counts (FEC). Assessment of efficacy was based on the arithmetic mean FEC of each treatment group versus the control group 14 days after treatment. The efficacy of MOX and IVM was high at all study sites, except on 1 farm in Greece with a reduced efficacy of both MOX (91%; 95% confidence interval (CI) 53-100%) and IVM (0%; 95% CI 0-100%). After treatment, *Haemonchus* was the most prevalent parasite on this farm. In France, treatment with either fenbendazole or netobimin was not effective on any of the farms, whereas in Greece and Italy reduced efficacy was detected on 2 to 6 out of 10 farms after treatment with albendazole/fenbendazole or levamisole. In these 3 countries, *Teladorsagia*, *Haemonchus*, *Trichostrongylus* and *Oesophagostomum* or a combination of these nematodes was identified on farms with reduced efficacy. The present study demonstrates that (suspected) anthelmintic resistance against albendazole/fenbendazole, netobimin and levamisole is occurring in all countries, although to a varying extent. The efficacy of an oral treatment with MOX or IVM was highly effective, except on one farm in Greece.

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Session Details:	8/29/2013 VECTORS BORNE DISEASES - TICKS 1015 - 1130 Meeting Room 7
Oral Presentation Details:	Morphological and genetic diversity of <i>Rhipicephalus sanguineus</i>
Presentation Time:	1015 -1030
Authors:	Filipe Dantas-Torres^{1,2}, Domenico Otranto² ¹Centro de Pesquisas Aggeu Magalhães, Recife, BRAZIL ²Università degli Studi di Bari, Valenzano, ITALY

The brown dog tick (*Rhipicephalus sanguineus*) is the most widespread tick species infesting dogs and a well-recognised vector of numerous pathogens to dogs and humans worldwide. While considered a valid tick species, the taxonomic status of the *R. sanguineus* is currently under dispute, mainly because the whereabouts of its type specimen is unknown. Recent genetic and crossbreeding studies have shed new light into the discussion, but the morphological variability of ticks found on dogs from different continents has yet to be addressed. We conducted a comprehensive morphological and genetic study on 276 representative tick specimens selected out of over 5,000 brown dog ticks collected from Europe (France, Greece, Italy, Portugal, Spain), Asia (India, Pakistan, Thailand, Vietnam), Africa (Nigeria, South Africa), Americas (Brazil, Costa Rica, Colombia, Guatemala, Honduras), and Oceania (Australia). After detailed morphometric examination, tick specimens were used for genetic analysis based on multiple partial mitochondrial (16S, 12S, and *cox1*) gene sequences. Our results confirmed the presence of *R. sanguineus* (*sensu stricto*) in all continents and revealed the existence of at least four unidentified species belonging to the *R. sanguineus* group. This study will pave the way for the redescription of *R. sanguineus* and *Rhipicephalus turanicus* as well as the description of new species.

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Session Details:	8/29/2013 VECTORS BORNE DISEASES - TICKS 1015 - 1130 <i>Meeting Room 7</i>
Oral Presentation Details:	Identification of ticks (Acari: Ixodidae) and their bacterial communities by PCR-single-strand conformation polymorphism (SSCP) and DNA sequencing
Presentation Time:	1030 -1045
Authors:	Clare A. Anstead^{1*} , Neil B. Chilton ¹ ¹ University of Saskatchewan, Saskatchewan, CANADA

Ticks are important vectors of pathogens to humans, domestic animals, and wildlife. Despite the medical and veterinary significance of ticks as vectors, little is known of the bacterial communities of many tick species in Canada. In the present study, ticks feeding on small mammals from three geographically distant locations in Saskatchewan and British Columbia were identified to the species-level using PCR-SSCP analyses and DNA sequencing of part (~420 bp) of the mitochondrial 16S rRNA gene. Then, the bacterial genera present within each individual tick was determined using SSCP analyses of amplicons (~250 bp) of prokaryotic 16S rDNA derived from the total gDNA of each tick. Individual DNA bands were excised from SSCP gels, purified, re-amplified and subjected to DNA sequencing. The results revealed that the small mammals were parasitised by several tick species of two genera (*Ixodes* and *Dermacentor*), some of which are also known to occur on humans and livestock, and/or are known to be vectors of pathogenic bacteria. Furthermore, individuals of each tick species, irrespective of life cycle stage, could be easily distinguished from each other by their 16S rDNA SSCP profiles. Examination of the bacterial communities of these ticks revealed significant interspecific differences in composition at the genus level, and also confirmed that some genera (e.g., *Rickettsia* and *Rickettsiella*) were found in more than one tick species. However, further investigation using PCR-SSCP and DNA sequencing revealed that each tick species had a different species of *Rickettsia* and *Rickettsiella*, some of which represented new species. The implications of these findings are discussed.

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Session Details:	8/29/2013 VECTORS BORNE DISEASES - TICKS 1015 - 1130 Meeting Room 7
Oral Presentation Details:	Molecular detection of tick-borne pathogens in ticks infesting dogs in south-eastern Romania
Presentation Time:	1045 -1100
Authors:	IONITA M ¹, MITREA I ¹, PFISTER K ², SILAGHI C ¹ ¹ University of Agronomic Sciences and Veterinary Medicine of Bucharest, ² 2Comparative Tropical Medicine and Parasitology, Ludwig-Maximilians-Universität München, GERMANY

Ticks serve as vectors for many pathogens of veterinary but also zoonotic importance. There is limited information on the occurrence of tick borne pathogens in Romania. Therefore, the aim of this study was to use molecular techniques to assess the prevalence of vector borne pathogens in ticks infesting dogs in south-eastern Romania. A total of 314 ticks were collected from 30 stray dogs, in 2011 and 2012, resp. Among them, 253 were identified as *Rhipicephalus sanguineus*, 56 as *Dermacentor reticulatus*, and 5 as *Ixodes ricinus*. Of them, 160 ticks (maximum 10 ticks per dog), including *R. sanguineus* (n=118), *D. reticulatus* (n=37), and *I. ricinus* (n=5), were molecularly screened for tick-borne pathogens by real-time polymerase chain reaction (PCR) for the presence of *Anaplasma phagocytophilum*, *Anaplasma platys*, *Ehrlichia canis*, *Borrelia burgdorferi* sensu latu, and by conventional PCR and subsequent sequencing for *Rickettsia* spp., and *Babesia* spp. Overall, 52 of the 160 ticks (32.5%) were positive for at least one pathogen. *Babesia* spp. was detected in 16.3% of the examined ticks (*D. reticulatus*, n=20, *R. sanguineus*, n=5, and *I. ricinus*, n=1), *E. canis* in 16.1% (*R. sanguineus*, n=19), and *Rickettsia* spp. in 4.4% (*D. reticulatus*, n=5 and *R.sanguineus*, n=2). One *R. sanguineus* and three *D. reticulatus* ticks were co infected: *E. canis* + *Rickettsia* spp. and *Rickettsia* spp. + *Babesia* spp., respectively. Sequencing data revealed the following rickettsial species: *R. raoultii* in *D. reticulatus* and *R. conorii* in *R. sanguineus*. This is the first report of *R. conorii* in ticks in Romania. Preliminary sequencing results of the *Babesia* spp. products revealed sequences identical or closely related to *B. canis* in *D. reticulatus*. The findings of this study indicate that animal and human pathogens are abundant in ticks infesting dogs in south-eastern Romania and emphasize the potentially high risks of exposure to infection with these agents.



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Session Details:	8/29/2013 VECTORS BORNE DISEASES - TICKS 1015 - 1130 Meeting Room 7
Oral Presentation Details:	Insight into success of tick control and prevalence of transmitted pathogens in urban dogs in Berlin, Germany
Presentation Time:	1100 -1115
Authors:	von Samson-Himmelstjerna G¹, Schreiber C¹, Kohn M¹, Beck S¹, Pachnicke S², Krieger K³, Groß M¹, Baldermann C¹, Krücken J¹, Demeler J¹, Kohn B¹ ¹ Freie Universität Berlin, ² Bayer Vital, Leverkusen, Germany, ³ Bayer Animal Health, Monheim, Germany

To establish the current prevalence of both ticks on urban dogs and tick-transmitted pathogens in these ticks, several projects were conducted during the years 2010-2012. Based on a questionnaire survey and the collection of ticks from 251 dogs over a period of 13 months, factors putatively associated with infestation were studied. It was concluded that both body size and length of fur correlated with significantly higher tick infestation. Noteworthy, of all attached ticks collected from dogs treated with licensed acaricidal drugs, 44.2% of the ticks had attached to the dogs within the protection time period. Comparison of drug classes revealed that *I. ricinus* had attached more frequently than *D. reticulatus* (p<0.001) when phenylpyrazols (fipronil, pyriprol) were used. Based on the scutal indices, more than 60% of the *I. ricinus* and 40% of the *D. reticulatus* were found after feeding for a minimum of two days. In addition to the above mentioned species only *Ixodes hexagonus* was found repeatedly on dogs within the study. Using PCR and sequencing or HRM-PCR *Babesia*, *Borrelia*, *Rickettsia*. and *Anaplasmataceae* were detected. Prevalences of *Babesia* in *Ixodes* spp. were found to be approximately 3%. *Rickettsia* spp. infected 61% of *I. ricinus*, 39% of *D. reticulatus* and 44% of *I. hexagonus*. Of all examined *I. ricinus* ticks, 6.5% and 4.3% were infected with *Anaplasma phagocytophilum* and the emerging pathogen *Candidatus* Neoehrlichia mikurensis, respectively. Examined *I. hexagonus* had a prevalence of 3.9% for *A. phagocytophilum* and 5.9% for *Cand.* Neoehrlichia mikurensis. Prevalences for *Borrelia* spp. were found to be as high as 11.6% in *I. ricinus* and 11.2% in *I. hexagonus*. The total prevalence of any infection was 65% in *I. ricinus*, 59% in *I. hexagonus* and 64% in *D. reticulatus*. Similarly high *Rickettsia raoulti* prevalences for the latter host were obtained from questing ticks.



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Oral Presentation Details:	Troublesome Ticks: Emerging and Potentially Zoonotic Vector-Borne Diseases in Australia
Presentation Time:	1115 -1130
Authors:	Peter Irwin , Andrea Paparini, Charlotte Oskam, Mike Bunce and Una Ryan College of Veterinary Medicine, School of Veterinary and Life Sciences, Murdoch University, Perth, AUSTRALIA

Ticks transmit a greater variety of pathogenic microorganisms than any other arthropod group, and are among the most important vectors of diseases affecting humans, livestock and companion animals. In Australia it has been recognized for many years that ticks are responsible for the transmission of rickettsial diseases (Queensland tick typhus and Flinders Island spotted fever) to people, and are the vector for bovine and canine babesiosis (*Babesia bovis* and *B. bigemina*, and *B. (canis) vogeli* respectively), bovine theileriosis (*T. buffeli/sergenti/orientalis* group) and anaplasmosis (*Anaplasma marginale*), and canine cyclic thrombocytopenia (*A. platys*). Tick species such as *Rhipicephalus (Boophilus) microplus*, *Haemaphysalis longicornis*, and *Rhipicephalus sanguineus*, introduced relatively recently to the Australian continent, are the vectors responsible for the transmission of tick fever (in its broadest sense) to cattle and dogs. Whilst Australia is free of more serious forms of some of these diseases (canine ehrlichiosis for example) there is growing concern from recent research and case reports for other tick-borne infectious diseases occurring in Australia, and considerable media attention regarding 'Lyme-like illness' and the possible emergence of potentially zoonotic diseases caused by *Borrelia* spp., *Anaplasma* spp. and *Ehrlichia* spp. In 2012 a case of fatal human babesiosis caused by *B. microti* was reported in a man who lived in southern NSW (Senanayake et al., 2012) and later the same year two cases of tularaemia (caused by *Francisella tularensis*) were detected in Tasmania. Neither organism was known in Australia previously, so what was the origin of these infections? Are there tick species established in ecological niches in Australia that have not yet been identified or have such pathogens always been here, undetected to date with life cycles involving local ticks and native animals? This presentation will review recent evidence and consider new strategies to investigate the potential emergence of tick-borne diseases in Australia.

Reference: Senanayake et al. (2012) First report of human babesiosis in Australia. *Med J Aust* 196(5): 350



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Session Details:	8/29/2013 PARASITES IN THE TROPICS 2 1015 - 1130 Meeting Room 8
Oral Presentation Details:	Helminths epidemiology and prevalence of gastrointestinal nematodes in cattle of Kirinyaga County, Kenya
Presentation Time:	1015 -1030
Authors:	F K Njonge^{1*}, M Mutugi², S M Githiga³ and R Waihenya², P G Kareru². ^{1*}Department of Land Resources and Animal sciences, ²Faculty of science, Jomo Kenyatta University of Agriculture and Technology. P.o Box 62,000, 00200 Nairobi, Kenya. ²Department of Zoology, ²Faculty of science, Jomo Kenyatta University of Agriculture and Technology. ³ Department of Veterinary Pathology, Microbiology and Parasitology, Faculty of Veterinary Medicine, University of Nairobi. PO Box 29053, 00625 Nairobi, Kenya

The gastrointestinal tract (GIT) of animals harbor a variety of parasites particularly helminthes, which causes clinical and sub clinical parasitism. These parasites adversely affect the health status of animals and cause enormous economic losses to the livestock industry. The aim of this study was to determine the prevalence of gastrointestinal nematodes in cattle of Kirinyaga County. Epidemiological data was collected using a questionnaire survey administered to 244 respondents while rectal faecal samples from 261 cattle were collected within a period of four months to determine helminths and protozoa egg counts. Sampling of herbage was carried out from 6 communal grazing sites for analysis of infective nematode larvae levels in the pasture. The cattle were weighed and blood collected by jugular venipuncture to determine the Packed Cell Volume (PCV) and Total Protein (TP). Descriptive statistics were used. The larvae harvested by coproculture of cattle faeces were for *Haemonchus Spp* (59%), *Trichostrongylus Spp* (26%), *Nematodirus Spp* (5%) and *Oesophagostomum Spp* (10%). *Haemonchus Spp* was the most prevalent nematode of cattle in Kirinyaga county. The highest Egg Per Gram (EPG) recorded was 1,800 with a mean of 88.8. *Haemonchus spp* was also the most prevalent nematode infective larvae species in herbage samples. Others were *Trichostrongylus* and *Oesophagostomum*. These nematodes were found in all the pastures samples. This study has shown that the farmers in the study area have a good understanding of GIN and their control methods but there was no defined pattern of GIN control. The study also documents GIN epidemiological profile of cattle infections and the results form the basis for recommending the control strategies of GIN in this area and possibly areas with similar agro ecological zones and farming activities in Kenya.

Key words: Prevalence, gastrointestinal nematodes, helminths, cattle, Kirinyaga,



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Session Details:	8/29/2013 PARASITES IN THE TROPICS 2 1015 - 1130 Meeting Room 8
Oral Presentation Details:	Cattle ticks and tick-borne pathogens, central Nigeria
Presentation Time:	1100 -1115
Authors:	Vincenzo Lorusso*¹, Kim Picozzi¹, Michiel Wijnveld², Ayodele Majekodunmi¹, Gyang Balak³, Charles Dongkum³, Augustine Igweh³, Frans Jongejan², Sue Welburn¹ ¹ The University of Edinburgh, Edinburgh, UNITED KINGDOM ²Utrecht Centre for Tick-borne Diseases, Utrecht University, Utrecht, THE NETHERLANDS ³ Nigerian Institute of Trypanosomiasis Research (NITR), Jos, NIGERIA

Ticks and tick-borne pathogens undermine cattle fitness and productivity in the whole of sub-Saharan Africa, including Nigeria (**Leeflang & Ilemobade, 1977**). This study aimed to assess the occurrence of ticks and tick-borne pathogens in cattle in an area of central Nigeria where no acaricides have historically been employed, in order to help the design of area specific targeted control interventions.

In October 2010, all visible adult ticks were collected from a number of at least 15 cattle in 9 villages in Plateau State. Collected ticks were kept in 70% ethanol and morphologically identified. In addition, a molecular screening by means of polymerase chain reaction and reverse line blot hybridization was carried out on blood samples collected in October 2008 from 712 cattle of the same villages.

5,011 ticks were collected from 228 cattle. Three tick genera and 11 species were identified, being *Rhipicephalus* (*Boophilus*) *decoloratus*, *Rhipicephalus* (*Boophilus*) *annulatus*, *Rhipicephalus* (*Boophilus*) *geigy* the most prevalent species (~65%) followed by *Rhipicephalus guilhoni*, *Hyalomma truncatum*, *Amblyomma variegatum*, *Rhipicephalus simus* Group, *Rhipicephalus turanicus*, *Rhipicephalus sanguineus*, *Hyalomma rufipes*, *Rhipicephalus lunulatus*. No *Rhipicephlaus* (*Boophilus*) *microplus* was retrieved, suggesting that the eastward expansion within West Africa of this tick species has not yet reached central Nigeria. Ten different tick-borne microorganisms were detected, including *Anaplasma marginale*, *Anaplasma centrale*, *Ehrlichia ruminantium*, *Ehrlichia* sp. Omatjenne, *Rickettsia* spp., *Babesia bigemina*, *Babesia bovis*, *Theileria mutans*, *Theileria velifera*, and *Theileria taurotragi*, with high frequency of co-infections with two or more microorganisms. The high prevalence (>30%) found for *A. marginale* and *T. mutans* poses a threat to the introduction of exotic taurine breeds. The lower prevalence recorded for *B. bigemina* (<10%), *A. centrale*, *B. bovis*, and *E. ruminantium* (<5%) suggests their involvement in the episodic outbreaks of disease in the indigenous cattle population.

References:

Leeflang P, Ilemobade A: Tick-borne diseases of domestic animals in Northern Nigeria. Trop Anim Health Prod 1977, 9:211–218



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Acknowledgments:

This study was funded by the UK’s Biotechnology and Biological Sciences Research Council (BBSRC) under the ‘Combating Infectious Diseases in Livestock for International Development’ (CIDLID) scheme, and the 7th Framework Programme of the European Union under the ‘Integrated Control of Neglected Zoonoses (ICONZ)’ project. Authors wish to thank Dr Abraham Goni Dogo (Parasitology Division, Nigerian Veterinary Research Institute) for helping with tick collection; Dr Alan Walker for the assistance with tick identification; Prof Lorenza Beati (Georgia Southern University, U.S.A.) for her valuable suggestions; Albert Mugenyi (The University of Edinburgh) for helping with map design, and all Fulani herders and village heads for their cooperation.



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Session Details:	8/29/2013 PARASITES IN THE TROPICS 2 1015 - 1130 Meeting Room 8
Oral Presentation Details:	High prevalence of <i>Schistosoma japonicum</i> in humans and bovines from Northern Samar, the Philippines
Presentation Time:	1045 -1100
Authors:	C. A. Gordon^{1,2}, A. G. Ross³, L. P. Acosta⁴, M. Jis⁴, G.N. Gobert¹, D.J.Gray², R. M. Olveda⁴, D. P. McManus¹ ¹Molecular Parasitology Laboratory, Infectious Diseases Division, Queensland Institute of Medical Research, Brisbane, Australia ²Infectious Disease Epidemiology Unit, School of Population Health, University of Queensland, Brisbane, Australia ³Griffith Health Institute, Griffith University, Queensland, Australia ⁴Department of Immunology, Research Institute of Tropical Medicine, Manila, Philippines

Schistosoma japonicum is the causative agent of schistosomiasis in the Philippines, China and parts of Indonesia. In the Philippines, 6.7 million people live in endemic areas with 1.8 million having direct exposure through daily water contact activities. As a zoonosis *S. japonicum* infects over 40 mammalian species, including water buffalo which have been shown to be major reservoir hosts in China. In the Philippines, water buffalo (Carabao) have been considered unimportant hosts due to low prevalence and infection intensity found in previous studies.

Six barangays from the Northern Samar municipality of Palapag were surveyed to determine the role of carabao and cattle in the Philippines Bovine samples were examined with an improved microscopy technique (formalin-ethyl acetate sedimentation (FEA-SD) and qPCR analysis, while human samples were examined by KK (Kato-Katz) in addition to qPCR.

High *S. japonicum* prevalence was found in humans when using qPCR (90.36%), while KK showed a much lower prevalence (22.86%). High prevalence was also found in bovines when using FEA-SD (72.00%) and qPCR (81.50%). Intensity of infection varied for bovines with cattle having a higher epg (eggs per gram) (2.23) than carabao (1.49). The Bovine Contamination Index was calculated using the combined carabao and cattle epg (1.74) and showed that each bovine was excreting an average of 42,750 eggs into the environment daily.

Bovines, particularly carabao, due to their high rate of daily water contact, likely play a more substantial role in schistosomiasis transmission in the Philippines than has been reported previously.

Acknowledgements:

We acknowledge the assistance and work of members of the Immunology Laboratory at the Research Institute of Tropical Medicine (RITM), Manila, the regional staff and volunteers from the municipality of Palapag and the Mayor of Palapag. This study received support from the NHMRC of Australia and the UBS Optimus foundation of Switzerland.



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Session Details:	8/29/2013 PARASITES IN THE TROPICS 2 1015 - 1130 Meeting Room 8
Oral Presentation Details:	Trypanosomiasis vs. Tick-borne Diseases: Production constraints in traditionally managed Fulani White Cattle in Nigeria
Presentation Time:	1100 -1115
Authors:	Ayodele Majekodunmi^{1*}; Vincenzo Lorusso,¹ Charles Dongkum², Emmanuel Onovo³, Michael Thrusfield⁴, Kim Picozzi¹, Sue Welburn¹ ¹School of Biomedical Sciences, College of Medicine and Veterinary Medicine, University of Edinburgh, EH16 4SB UK. ²Nigerian Institute for Trypanosomiasis Research, P.M.B. 1303, Vom, Plateau State, Nigeria. ³Parasitology Department, National Veterinary Research Institute, Vom, Plateau State, Nigeria ⁴Veterinary Clinical Sciences, Royal (Dick) School of Veterinary Studies, College of Medicine and Veterinary Medicine, University of Edinburgh, EH25 9RG UK

African animal trypanosomiasis and tick borne diseases are arguably the most important endemic diseases of livestock in Sub Saharan Africa. They are responsible for billion dollar losses in meat and milk production, decreased reproductive capacity, reduced income for poor livestock keepers and high expenditure on treatment and control at state and individual levels (1). However, the relative importance of these diseases differs depending on location, livestock present, ecological setting, husbandry and availability of diagnostic and control methods. Efforts to control these diseases and reduce their economic impacts must be adapted to the specific circumstances (2,3).

The Jos plateau in North-Central Nigeria is an important cattle producing region endemic for tick borne diseases but previously free of tsetse flies and trypanosomiasis. This disease is also now endemic in the area but the extent of its impact on cattle health and productivity is yet to be determined. This study investigates the relative importance and impact of these endemic diseases on the health and productivity of ~10,000 cattle across the Jos Plateau. Longitudinal cluster surveys were conducted to determine the prevalence, distribution and seasonal variation of these diseases and how they interact with each other. Their impacts on productivity and the benefits of strategic integrated control methods were also investigated.

Acknowledgements

Nigerian Institute for Trypanosomiasis Research
National Veterinary Research Institute
University of Edinburgh
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Session Details:	8/29/2013 MSD (GOLD SPONSOR) Chair: Griff Dalglish 1330 - 1445 <i>Riverside Theatre</i>
Oral Presentation Details:	“Research experience on the practical approach of parasite control in livestock in parts of Southern Africa, a changing scenario”
Presentation Time:	1330 -1445
Authors:	Tom Strydom

A major pressure to livestock farming in Southern Africa is the cost of controlling ecto-and endoparasites and the effect they have on production. To cattle farmers the major onslaught is from a variety of tick species (single as well as multi-host species) and the diseases they transmit. On the other hand small stock farmers are more concerned with the devastating effect of internal parasites, especially *Haemonchus* spp.

Over the last 20 years many farmers had to change their approach of parasite control in livestock from an attempt to “eradicate all” to a situation of “management “ of parasites. This is mainly due to the development of resistance of parasites to antiparasitics, particularly in one-host (*Rhipicephalus decoloratus* and *R. microplus*) tick species in cattle and *Haemonchus* spp. in small stock, and the unavailability of new actives to control these parasites. Furthermore the change in the geographic distribution of parasites (in particular tick species) due to uncontrolled livestock movements also played a role in the approach of farmers to control these parasites.

One example of the change in the approach can be seen in the coastal areas of South Africa where farmers previously had been practicing a policy of total tick control by treating their cattle on a weekly basis. Nowadays they rather ensure immunity of their cattle to tick-borne diseases with less or minimal treatments for ticks. On their part small stock farmers had to change their approach to control internal parasites from “deworming programs” where sheep and goats were treated for internal parasites every 6 to 8 weeks to a policy where stock are monitored for the effect of worms as an indication of when to apply targeted selective treatments.

Session Details:	8/29/2013 VACCINES - FLUKES 1330 - 1445 <i>Meeting Room 1</i>
Oral Presentation Details:	Biochemical characterisation of serine protease inhibitors from <i>Schistosoma japonicum</i>
Presentation Time:	1330 -1345
Authors:	Adebayo Molehin^{1,2*} Geoffrey Gobert ¹ and Donald McManus ¹ ¹ Molecular Parasitology Laboratory, Queensland Institute of Medical Research, Herston Queensland AUSTRALIA ² School of Population Health, The University of Queensland, Herston Road, Herston Queensland AUSTRALIA

Schistosomiasis remains a major global public health problem, but despite significant progress in the control of this disease, clear limitations necessitate the development of an effective anti-schistosomal vaccine. Serine protease inhibitors (serpins) are a superfamily of proteins involved in many important biological processes such as blood coagulation, fibrinolysis and inflammation. These inhibitors are known to play central roles in host immune modulation and/or evasion by pathogens. Furthermore it has been suggested that serpins may have evolved specifically in limiting the host immune activation by mediating the inhibition of host immunomodulatory signals. We hypothesise that serpins provide similar functions for schistosomes and their disruption by an effective host immune response by vaccination provides an opportunity to eliminate and control these parasites. Therefore, the aim of this study was to biochemically characterise novel serpins from *Schistosoma japonicum* and investigate the potential of these proteins as suitable anti-schistosomal vaccine candidates. Gene expression results from data mining of previously published microarray findings of our group and subsequent confirmation with quantitative PCR showed that two *S. japonicum* serpins termed *SjB6* and *SjB10* are differentially expressed in different life cycle stages of the parasite. The highest relative gene expression was observed in the egg and cercarial stages for *SjB6* and *SjB10* respectively indicating possible pathological and/or immunological relevance as well as a possible role for *SjB10* in cercarial penetration. Western blot analysis confirmed the expression of the native proteins in the adult worms. Recombinant proteins produced were tested for their inhibitory activity against a panel of serine proteases. *SjB10* was shown to be biochemically active against pancreatic elastase and chymotrypsin while *SjB6* showed no activity against any of the proteases tested. Work is now ongoing for the immunolocalisation of the native proteins using polyclonal antibodies raised in rabbit as well as evaluating their possible anti-schistosomal vaccine efficacies.

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Session Details:	8/29/2013 VACCINES - FLUKES 1330 - 1445 <i>Meeting Room 1</i>
Oral Presentation Details:	RNAi-Based Screening for Vaccine Targets Identification of <i>Schistosoma mansoni</i> Tegument Proteins
Presentation Time:	1345 -1400
Authors:	Leow CY^{1,2,5*} , Willis C ¹ , Loukas A ³ , Hofmann A ⁴ , Jones M ^{1,2} , ¹ Parasite Cell Biology, Queensland Institute of Medical Research, Australia ² School of Veterinary Science, The University of Queensland, Australia ³ Queensland Tropical Health Alliance, James Cook University, Australia ⁴ Structural Chemistry Program, Eskitis Institute for Cell & Molecular Therapies, Griffith University, Australia ⁵ Institute for Research in Molecular Medicine, Universiti Sains Malaysia, Malaysia

Efforts to develop potential vaccines against schistosomes have focused on the identification of parasite surface antigens which can trigger protective immunity in the host. However, the limiting step in schistosome vaccine development is the identification of feasible protective antigens. In this study, a rapid and cost-effective method RNA interference (RNAi) was applied to investigate the gene function of surface-associated annexins in *S. mansoni*. Expression of five annexin genes identified in the adult tegument was found to be up-regulated upon transition from cercariae to schistosomula and adult worms. Silencing of annexins was facilitated by electroporation with target specific dsRNA cultured on three weeks then the isolated RNA was subjected for gene expression quantification. In brief, gene expression for adult parasites treated with annexin-specific-dsRNA resulted in 80 – 96% reduction while in schistosomula there was an 87 – 95% reduction in transcription levels. Fluorescence intensity displayed on the tegument surface of dsAnx-treated schistosomula showed an average of 34.8 % reduction when compared to luciferase dsRNA-treated group. Silencing of each annexin did not affect the parasite survival rate but conversely reduced their growth size as well as motility significantly at both schistosomula and adult stages. Anx(*Sm*)3 was selected for vaccine efficacy study in mice. A chimeric peptide (Chimeric-AT) harbouring the linker region of Anx(*Sm*)3 was engineered fused with *Sm*-TSP-2. Sera from mice infected with *S. mansoni* reacted strongly with both synthetic Anx(*Sm*)3 linker peptide and Chimeric-AT, showing that they are both immunogenic. Chimeric-AT delivered in alum induced high IgG1/IgG2a ratio, implying Th2 type response was dominant. Mice vaccinated with Chimeric-AT adjuvated with alum showed 40.4% significant reduction in intestinal egg burden as compared to the control group. Taken together, our results show that Chimeric-AT conferred a high level of antibody production and suggests this multi-antigen construct would be a potential vaccine candidate against schistosomiasis.

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Session Details:	8/29/2013 VACCINES - FLUKES 1330 - 1445 <i>Meeting Room 1</i>
Oral Presentation Details:	Immunomics-based identification of schistosomiasis vaccine antigens: an integrated discovery and validation approach
Presentation Time:	1400 -1415
Authors:	Gaze S ¹ , Pearson M ¹ , Driguez P ² , Mendez T ³ , Doolan D ² , Trieu A ² , McManus D ² , Cardoso F ² , Sasaki R ⁴ , Felgner P ⁴ , Bethony J ⁵ , Loukas A ¹ ¹ James Cook University, Cairns, AUSTRALIA, ² Queensland Institute of Medical Research, Brisbane, AUSTRALIA, ³ Federal University of Minas Gerais, Belo Horizonte, BRAZIL, ⁴ University of California Irvine, Irvine, USA, ⁵ George Washington University, Washington DC, USA

Schistosomiasis is a neglected tropical disease affecting >230 million people and causes over 200,000 deaths annually. To identify new vaccine antigens and assess their potential protective efficacy and safety, we used an immunomics approach with sera from putatively resistant (PR) and chronically infected (CI; stratified by infection intensity) people in a high transmission area for schistosomiasis in Brazil. We selected mostly tegumental *Schistosoma mansoni* and *S. japonicum* proteins, produced them using an *in vitro* rapid translation system (RTS) and printed them to generate the first protein microarray for a multi-cellular pathogen. Arrays were screened to detect IgG subclass and IgE responses; antigens which showed preferential/unique recognition by IgG1/3 from PR individuals were up-selected, and those that were the target of potentially deleterious IgE responses (in terms of vaccine-induced hypersensitivity) were down-selected. We detected strong correlations between the number of antigens recognized and infection intensity for all antibody subclasses, most notably IgE. Surprisingly, PR individuals produced little IgE but instead made robust IgG1/3 responses to a small number of antigens exposed on the parasite surface, highlighting their potential as vaccine antigens. Cluster analysis was performed to identify antigen clusters based on their antibody recognition profiles. Two clusters contained antigens that were preferentially recognized by IgG1/3 of PR individuals but were not major targets of IgE; these clusters included the previously described vaccine candidates Sm-TSP-2 and Sm29, as well as a panel of new antigens that have not been previously described. We have shown here the use of a high throughput immunomics approach to profile antibody responses from PR and CI individuals that has unearthed a suite of novel potentially protective and safe schistosomiasis vaccine antigens. To complement our human subjects-oriented antigen discovery approach, we are also probing arrays with sera from non-human primates that have been vaccinated with irradiated schistosome cercariae.



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Session Details:	8/29/2013 VACCINES - FLUKES 1330 - 1445 <i>Meeting Room 1</i>
Oral Presentation Details:	Molecular Characterization of Annexin (Anx) and Tetraspanin (TSP) Gene Families from <i>Fasciola hepatica</i>
Presentation Time:	1415 -1430
Authors:	Rathinasamy V¹, Toet H¹, David Young N², Beat Gasser R², Spithill T¹ ¹ Latrobe University, ² University of Melbourne

Liver fluke infection in livestock is an increasingly serious threat on animal production resulting in decreased milk, meat and wool production. An efficient vaccine is needed to combat this disease due to the emergence of fluke drug resistance. The tegument of the parasite is exposed to the host immune system and has been shown to be a target for antibody-dependent cell mediated cytotoxicity killing of juvenile parasites *in vitro*. We propose that tegument proteins of *Fasciola hepatica* could serve as potential vaccine candidates. Proteomic analysis of the adult fluke tegument identified proteins with homology to Annexins (FhAnx) and Tetraspanins (FhTSP) of *Schistosoma*. In this study, FhAnx and FhTSP protein sequences expressed in adult *F. hepatica* have been identified and selected for molecular characterization to identify potential vaccine candidates. Eight sequences predicted to encode proteins from each family have been identified and annotated as FhAnx1-8 and FhTSP1-8, respectively. The identified FhAnx proteins contain predicted conserved Annexin and calcium binding domains and share 45-66% identity with *Schistosoma* Annexins. All the FhTSP proteins contain predicted transmembrane and extra cellular domains and share 42-72% identity with *Schistosoma* TSPs. Transcript profiling using RNAseq data revealed that all identified FhAnx and FhTSP proteins were upregulated in immature flukes, with the exception of FhTSP1. Quantitative PCR (qPCR) was performed for FhAnx1, -2, -8 and FhTSP2, -5 in juvenile and adult stages. FhAnx1, -2 and FhTSP2, -5 were expressed at significantly higher levels in juveniles than adult flukes, whereas FhAnx8 was expressed at significantly higher levels in adult flukes compared with juveniles. FhAnx1, -2, -3, -8 and FhTSP2, -3, -5, -8 were predicted to be surface-expressed based on identity to known surface-expressed orthologs from other trematodes and were selected for recombinant expression and RNA interference analysis. Functional characterization of these proteins is currently underway.



Session Details:	8/29/2013 VACCINES - FLUKES 1330 - 1445 Meeting Room 1
Oral Presentation Details:	Field Trial in Commercial Irish Farms with Experimental Vaccine Using Recombinant Mutant <i>Fasciola hepatica</i> Cathepsin L1 in Cattle
Presentation Time:	1430 -1445
Authors:	Andreas L. Chryssafidis^{1*}, Yan Fu¹, Silvia T. Talavera-Arce¹, Andrés García-Campos¹, John P. Dalton², Grace Mulcahy¹ ¹ School of Veterinary Medicine, University College Dublin – Belfield, IRELAND ² Institute of Parasitology, McGill University, CANADA

Cathepsin L1 (CL1) is a proteinase secreted by *Fasciola hepatica* that is involved in host invasion, nutrition, immune modulation and was indicated as good option for vaccination (Dalton et al., 2003). A recombinant mutant CL1 (rmFhCL1) was used in an experimental vaccination protocol, where protective immune response against liver fluke infection could be detected, as there was a decrease in fluke burden and impaired helminth development in vaccinated animals (Golden et al., 2010). That experimental protocol is now being tested in a large scale field trial and results are presented here. For this field trial, 210 bovines were selected from three different farms with previous reports of *F. hepatica* infection, in the Republic of Ireland. Animals were grouped according to age, gender and location. The vaccine consists of 200µg of rmFhCL1 in 2ml of adjuvant (Montanide 70VG®, Seppic). Vaccinated animals were dosed twice by SC route, three weeks apart and kept in commercial field conditions, naturally exposed to the infection. Blood and faecal samples are collected periodically from each animal for serologic (ELISA), haematological (lymphocytes and eosinophils), biochemical (GLDH and γGT) evaluation and faecal egg counting (sedimentation) assay. Productivity data is recorded for further analysis. All routine treatments are provided to the animals as usual, with exception of flukicide treatment. As these are commercial animals, eventually slaughtered ones will have their livers collected for fluke burden analysis and *F. hepatica* eggs viability assay. Cattle from different ages, vaccinated with rmFhCL1, showed high and persistent levels of specific humoral immune response anti-*F. hepatica*. Natural exposure of the animals was confirmed by seroconversion and detection of liver fluke eggs in faeces of controls. Analysis of egg counts, egg viability and fluke burdens, all of which are relevant to the protective effect of a vaccine, are on-going.

Acknowledgements:

This work is funded by the EU commission under Framework 7 Programme. The authors are grateful to the staff of Teagasc Research Centre for the support with the animals.



Session Details:	8/29/2013 CONSERVATION AND WILDLIFE TAXONOMY 1330 - 1445 Meeting Room 2
Oral Presentation Details:	Morphological Features and Molecular Characteristics of Piroplasms infecting the Platypus (<i>Ornithorhynchus anatinus</i>)
Presentation Time:	1330 -1345
Authors:	Andrea Paparini ¹ , James Macgregor ¹ , Brittani Lea ¹ , Charlotte Oskam ¹ , Kris Warren ¹ , Una Ryan ¹ , Peter Irwin ¹ ¹ College of Veterinary Medicine, School of Veterinary and Life Sciences, Murdoch University, Perth, AUSTRALIA

Piroplasms belonging to genera *Theileria* and *Babesia* (Phylum: Apicomplexa) are vector-borne protozoan haemoparasites with similar phenotype that infect erythrocytes of domesticated mammals and wildlife including birds. In addition, piroplasms of *Theileria* have an exoerythrocytic life cycle stage within the host's white blood cells. Observations of intraerythrocytic piroplasms have been made sporadically in peripheral blood films of Australian native mammals since the first report was made nearly a Century ago and the advent of PCR has stimulated renewed research interest and descriptions of the molecular phylogeny of these organisms in a variety of marsupial hosts. A piroplasm (*Theileria ornithorhynchi*) has been described in previous studies of the platypus (*Ornithorhynchus anatinus*). As part of a study into the health and ecology of this iconic monotreme, blood samples were collected for haematological and biochemical analysis from wild-trapped platypuses in Tasmania. A subset of these samples, together with their ectoparasites, was evaluated for piroplasm infections by blood film microscopy and molecular analysis of the 18S ribosomal RNA gene, and phylogenetic analysis was performed with NJ trees using BIONJ. Estimates of evolutionary divergence between sequences were calculated by MEGA 5. A total of 27 blood samples and eight ectoparasites (seven ticks, one leech) were examined from 27 platypuses. All ticks were identified as *Ixodes ornithorhynchi*. Piroplasm infections were highly prevalent in the population studied (27/27; 100% infected); organisms were pleomorphic with infrequent tetrads and intra-leukocytic forms, thought to be *Theileria* schizonts, were occasionally observed. Anaemia was not detected. Many platypuses were co-infected with trypanosomes. All blood samples and three ectoparasites were positive for piroplasm DNA and phylogenetic analysis suggested the presence of more than one piroplasm species. This study emphasises the importance of combining traditional parasitological techniques (e.g. microscopy and tick examination) with molecular techniques if the life cycle of organism is to be understood.



Session Details:	8/29/2013 CONSERVATION AND WILDLIFE TAXONOMY 1330 - 1445 Meeting Room 2
Oral Presentation Details:	Novel parabasalid flagellates endosymbiotic in native Australian subterranean termites
Presentation Time:	1345 -1400
Authors:	Ly L University of Queensland

Termites are vital for recycling plant material through digestive processes involving endosymbiotic micro-organisms. Little is known about the protozoan taxa occurring in lower termites native to Australia. A survey was conducted on 125 termite colonies in north-eastern Australia and interim results are presented for parabasalid flagellate communities found in 25 colonies of the subterranean termites *Schedorhinotermes intermedius* and *S. seclusus*. Individual workers were found to have up to several thousand individual flagellates in their hindguts. A total of ten flagellate species were identified belonging to three different orders: eight spirotrichonymphid species from the genera *Holomastigotoides*, *Microjoenia* and *Spirotrichonympha* (basal bodies arranged in spiral patterns), one trichomonad species from the genus *Pseudotrypanosoma* (four anterior flagella and one recurrent flagellum with undulating membrane) and one trichonymphid species from the genus *Pseudotrichonympha* (with a radially symmetrical flagellated rostrum). Five flagellate species had previously been described, albeit in other termite host species. The remaining five flagellate species (from the genera *Holomastigotoides*, *Microjoenia* and *Pseudotrypanosoma*) were unique in structure as evidenced by silver impregnation of cytoskeletal features (and supported by transmission electron microscopy of cell and organelle ultrastructure). The discovery of many novel flagellate species in this small subsample of termite hosts suggests the presence of a rich and diverse endemic fauna of endosymbiotic protozoa in native Australian termites.



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Session Details:	8/29/2013 CONSERVATION AND WILDLIFE TAXONOMY 1330 - 1445 <i>Meeting Room 2</i>
Oral Presentation Details:	The micromorphological specializations of the sucking louse <i>Linognathus euchore</i> from the springbok <i>Antidorcas marsupialis</i>.
Presentation Time:	1400 -1415
Authors:	Green E Dept. of Anatomy, (Medsunsa campus), University of Limpopo

Linognathus euchore is an obligate bloodsucking parasite of springbok which may cause anemia. The five species of *Linognathus* described from springbok to date are morphologically very similar. The males are particularly difficult to identify due to their sexual dimorphism and a lack of diagrammatic descriptions in the literature. In this study the functional micromorphology of both sexes of *L. euchore* was investigated by scanning electron microscopy (SEM) as well as additional features of taxonomic importance.

The lice collected live from springbok that had been brought to the state veterinary laboratories at Bloemfontein for *post mortum*, were fixed in 70% ethanol. The lice were cleaned by ultrasonication before being routinely processed for SEM and viewed in a Leica stereoscan 420 at 5 to 10 kV.

The elongated conical head tapered from the enlarged ocular prominences to the haustellum at the anterior tip. Three pairs of hooked stylets for piercing the skin were observed protruding from the cone-shaped haustellum. The two large pore organs each contained a tuft organ and together with their associated plate organs were borne on antennal segments IV and V. The thorax was deeply cleaved and bore a pair of long setae and mesothoracic spiracles. Legs I each bore a slender claw while the claw of II and III were extremely robust with well-developed scaled tibial pads for attachment. Abdominal segments III to IV bore single long marginal setae while VI to VII were characterized by pairs of long marginal setae. The female gonopods IX were curved medially each bearing a terminal tuft of setae while gonopods X had a fringe of short setae. The male had a very large genital plate that reached from segment VII posteriorly and terminated in a single bulbous process. The pseudopenis and parameres of the everted male genitalia were also described.

Session Details:	8/29/2013 CONSERVATION AND WILDLIFE TAXONOMY 1330 - 1445 Meeting Room 2
Oral Presentation Details:	A novel <i>Babesia</i> spp. associated with morbidity and mortality in eastern grey kangaroos
Presentation Time:	1415 -1430
Authors:	Donohoe S ¹ , Peacock C ² , Choo A ² , O'Donoghue P ³ , Cook R ⁴ , Srivastava M ⁵ , Vogelnest L ¹ , Gordon A ⁶ , Kirkland P ⁵ , Rose K ¹ ¹ Taronga Conservation Society Australia, ² University Of Western Australia, ³ The University of Queensland, ⁴ Former Regional Veterinary Laboratory, ⁵ Elizabeth Macarthur Agricultural Institute, ⁶ Department of Agriculture, Fisheries and Forestry

The agent associated with a syndrome of anaemia and debility in eastern grey kangaroos (*Macropus giganteus giganteus*) on the north coast of New South Wales (NSW) and in south-eastern Queensland (QLD) is herein characterised as a novel *Babesia* spp. We present the detailed investigation of 12 cases from two outbreaks of this disease during 2012 in NSW and QLD, and review archival material from cases recognised since 1994 at the former Regional Veterinary Laboratory Wollongbar in NSW. Affected animals have marked anaemia, lethargy, weight loss, variable neurological signs (altered mentation, vision deficits and loss of pupillary light reflexes) and an increased blood clotting time. At necropsy, the blood is watery and there is generalised tissue pallor and oedema and splenomegaly.

In anaemic animals, typical intraerythrocytic *Babesia* organisms are detected in less than 2% of erythrocytes in peripheral blood smears. However, examination of histological sections (and impression smears) of a range of organs including kidney, brain, spleen, and heart reveals parasitised erythrocytes and extraerythrocytic aggregates of zoites within vessels. These changes are most prominent within capillaries of the renal glomerular tufts and brain. Phylogenetic analysis of 18s RNA and HSP70 genes extracted, amplified and sequenced from samples of kidney, brain and blood from affected animals clearly indicates that the organism resides within the genus *Babesia*, and has greatest similarity to an unnamed *Babesia* spp. recently detected in a woylie (*Bettongia penicillata ogilbyi*) in Western Australia.

Based on historical records and recent reports, the spectrum of clinical findings and geographic range of infection appear to be expanding. Further studies are required to characterise the transmission and pathogenesis of disease associated with this novel species of *Babesia*.



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Session Details:	8/29/2013 CONSERVATION AND WILDLIFE TAXONOMY 1330 - 1445 <i>Meeting Room 2</i>
Oral Presentation Details:	Presence of cryptic species within the nematode genus <i>Cloacina</i>
Presentation Time:	1430 -1445
Authors:	Shuttleworth M¹, Jabbar A^{1, 2}, Chilton N³, Gasser R¹, Beveridge I² ¹ Faculty of Veterinary Science, The University of Melbourne, Parkville, Victoria, AUSTRALIA, ² Faculty of Veterinary Science, The University of Melbourne, Werribee, Victoria, AUSTRALIA, ³ The Department of Biology, the University of Saskatchewan, Saskatoon, Saskatchewan, CANADA

The swamp wallaby, Wallabia bicolor, is a macropodid marsupial, distributed along Australia's eastern coast and harbours a variety of parasites throughout its range. It is believed that the wide distribution of the host in different ecological zones has led to the speciation of various parasites. This study investigated several nematode species of the genus *Cloacina* found throughout the host's distribution to investigate the presence of cryptic species using morphological and molecular methods. Specimens were collected from a number of localities along the eastern coast of Australia and a number of *Cloacina* species (n = 9) were identified based on their morphologic characteristics. Genetic variation was assessed by subjecting specimens to PCR-based mutation scanning and sequence analyses of the first (ITS-1) and second internal transcribed spacers (ITS-2) of the nuclear ribosomal DNA. PCR amplicons were screened for the genetic variation between and within species using single-strand conformation polymorphism analysis, followed by the targeted sequencing of PCR amplicons. Phylogenetic analyses of both the ITS-1 and ITS-2 data were used to examine the sister-species relationships within and between species, and to reveal the evolutionary relationships of the species of *Cloacina*. Further investigations will focus on determining the presence of cryptic species in other widely distributed parasite species found in this host, as well as analyse the co-evolutionary relationship between *Wallabia bicolor* and the genus *Cloacina*.



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Session Details:	8/29/2013 DIAGNOSTICS - MOLECULAR 1330 - 1445 <i>Meeting Room 3</i>
Oral Presentation Details:	A high-throughput diagnostic platform for gastrointestinal nematode infections in small ruminants
Presentation Time:	1330 -1345
Authors:	Florian Roeber^{1,2*} , Aaron R. Jex ¹ and Robin B. Gasser ¹ ¹ <i>Faculty of Veterinary Science, The University of Melbourne, Parkville, Victoria 3010, AUSTRALIA</i> ² <i>AusDiagnostics Pty Ltd., Beaconsfield, New South Wales 2015, AUSTRALIA</i>

Compounded by drug resistance problems, parasites of livestock cause diseases that have a major economic impact, costing billions of dollars in losses, worldwide. In particular for gastrointestinal parasites, the accurate diagnosis of infections and the detection of drug resistance are central to their effective control, but can be challenging by routine diagnostic methods. Current methods used for the *ante mortem* diagnosis in ruminants, such as sheep and goats, are time-consuming and laborious to perform, and are of limited sensitivity and specificity. To overcome these problems, we have developed an advanced molecular method for the specific diagnosis of key strongylid infections in sheep. This assay is based on the isolation of nematode eggs from faecal samples, the purification of genomic DNA, followed by real-time PCR of a nuclear DNA spacer region and melting-curve analysis. Using this assay, specific and semi-quantitative amplification is consistently achieved from picogram amounts of genomic DNA from eggs of *Haemonchus contortus*, *Teladorsagia circumcincta*, *Trichostrongylus* spp., *Oesophagostomum venulosum* or *Chabertia ovina*. Multiple studies undertaken in the last three years [1-3] demonstrate that the diagnostic performance of this assay is superior to existing methods. The assay, which has now been adapted to a robotic platform, can replace antiquated methods for species- or genus-specific diagnosis in live sheep and is ready for commercial application in a service laboratory setting. The development of this advanced assay has major implications for epidemiological and ecological investigations as well as for integration into parasite monitoring, drug resistance (i.e., faecal egg count reduction) testing, and parasite management and control programs.

Acknowledgements:

Funding from the Australian Research Council is gratefully acknowledged (RBG). FR is the recipient of scholarships from The University of Melbourne, Australia.

References:

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- [3] Roeber F, Larsen JWA, Anderson N, Campbell AJD, Anderson GA, Gasser RB, et al. A Molecular Diagnostic Tool to Replace Larval Culture in Conventional Faecal Egg Count Reduction Testing in Sheep. *PLoS ONE.* 2012a;7:e37327.



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Session Details:	8/29/2013 DIAGNOSTICS - MOLECULAR 1330 - 1445 Meeting Room 3
Oral Presentation Details:	Molecular Diagnosis and Therapeutic Trials on Fasciolosis in Sheep
Presentation Time:	1345 -1400
Authors:	Khalid Mehmood^{1*}, Muhammad Ijaz², Ahmad Jawad Sabir³, Muhammad Sarwar Khan², Aneela Zameer Durrani² ^{1*}University College of Veterinary and Animal Sciences, Islamia University of Bahawalpur (IUB) Punjab, PAKISTAN, Email: khalid.mehmood@iub.edu.pk ²Department of Medicine and Surgery, University College of Veterinary and Animal Sciences, Lahore, PAKISTAN ³Institute of Continuing Education and Extension, University of Veterinary and Animal Sciences, PAKISTAN

The present study was conducted to establish polymerase chain reaction (PCR), compare the faecal sedimentation test and PCR for the diagnosis of fasciolosis and to evaluate the efficacy of various anthelmintics under field conditions in sheep. For accurate diagnosis of Fasciolosis, 300 samples (n= 150 fecal; n= 150 bile) of sheep were collected from different private and public slaughter houses of districts Okara, Sahiwal and Lahore. Ova of *Fasciola spp.* were identified by microscopic examination while molecular conformation was done by using PCR. The species of *F. hepatica* were identified by PCR. Overall prevalence of fasciolosis in fecal and bile samples of sheep in various districts of Punjab on the basis of microscopic examinations and PCR was 12% and 14.33% respectively. The district wise prevalence was 11, 12 and 13% through microscopic examination and by PCR it was 13, 14 and 16% in Lahore, Okara and Sahiwal respectively. The Prevalence rate of *F. hepatica* was more by PCR than microscopic examination. For therapeutic trials, 30 sheep positive for Fasciolosis were randomly divided into group A, B and C. The animals of group A were given Zaniil (Oxyclozanide) orally @ 1ml per 3kg body weight; the animals of group B were given Albendazole orally @ 1ml per 3kg body weight while the animals of group C were given the grounded powder of Neem leaves (*Azadirachta indica*) @ 5-6 teaspoon (25-30gm) orally. The eggs per gram (EPG) values and efficacy of Oxyclozanide (Zaniil), Albendazole and Neem leaves against fasciolosis in 30 positive sheep were recorded at 3, 7 and 14 days after the treatment. The efficacy of oxyclozanide and albendazole was significantly higher (p= 0.000) than Neem leaves. In sheep against the fasciolosis Oxyclozanide has significant effect on EPG followed by albendazole and Neem leaves.

Acknowledgements:

The author is thankful to Dr. Rashid Ahmad, Director Livestock Production Research Institute, Bahadurnagar for providing necessary research facilities.

Key words: PCR, Microscopic, Prevalence, Oxyclozanide, Efficacy.



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Session Details:	8/29/2013 DIAGNOSTICS - MOLECULAR 1330 - 1445 Meeting Room 3
Oral Presentation Details:	High prevalence of <i>Taenia saginata</i> cysticercus infection in slaughtered dairy cows in Central Europe: a multi-test analysis
Presentation Time:	1400 -1415
Authors:	Eichenberger R ¹ , Lewis F ² , Gabri��l S ³ , Dorny P ³ , Torgerson P ² , Deplazes P ¹ ¹ Institute of Parasitology, University of Zurich, Switzerland, ² Section of Veterinary Epidemiology, University of Zurich, Switzerland, ³ Departement of Biomedical Sciences, Institute of Tropical Medicine, Antwerp, Belgium

The diagnostic values of seven serological tests, and the obligatory routine meat inspection for the detection of *Taenia saginata* infection in animals with typically low parasite burdens was investigated. A total of 793 slaughtered cows were randomly selected in three EU approved abattoirs in Switzerland, known to be an endemic area for *T. saginata* cysticercosis. Serological tests (ELISAs) based on a somatic larval antigen, isoelectric focused somatic larval antigen, larval excretory/secretory (ES) antigen, synthetic peptides HP6-2, Ts45S-10, pooled peptides, and a monoclonal antibody (mAb) based antigen capture assay were initially evaluated by classical methods. As there is no perfect diagnostic gold standard reference test, the obligatory meat inspection and four of the serological tests were further analysed using Bayesian inference to estimate the prevalence and the diagnostic test sensitivities and specificities. The best performing test for the identification of *T. saginata* exposure was an ELISA based on larval ES antigen with a sensitivity and specificity of 81.6% (95% credibility intervals; 70.1-92.0%) and 96.3% (93.5-99.0%), respectively. An ELISA based on a commercial obtainable synthetic peptide Ts45S-10 had estimated values of 55.2% (45.9-65.1%) and 84.7% (81.6-87.6%), respectively. An ELISA based on mAb, which was designed for antigen detection in viable infections, had estimates of 14.3% (8.7-23.3%) and 93.7% (91.5-95.5%), respectively. The diagnostic sensitivity of the obligatory standard EU meat inspection procedure for the detection of *T. saginata* cysticercosis at the abattoir was 15.6% (10.0-23.3%). Based on these data, the prevalence of cysticercosis in dairy cows presented at abattoirs in Switzerland was estimated at 16.5% (12.5-21.2%), in the observed population with high prevalence of *Dicrocoelium dendriticum* (60.8%) and *Fasciola hepatica* (13.5%). These results demonstrate that the contact rate of dairy cows with *Taenia saginata* eggs is higher than previously indicated by abattoir reports (0.6-1.8%).



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Session Details:	8/29/2013 DIAGNOSTICS - MOLECULAR 1330 - 1445 <i>Meeting Room 3</i>
Oral Presentation Details:	Genetic characterization of selected parasites from people with histories of gastrointestinal disorders
Presentation Time:	1415 -1430
Authors:	Koehler A¹, Bradbury R^{2,3}, Stevens M⁴, Haydon S⁴, Jex A¹, Gasser R¹ ¹ University Of Melbourne, ² Medical Research Council International Nutrition Group, ³ School of Medicine, University of Tasmania, ⁴ Melbourne Water Corporation

Mutation scanning analysis and targeted sequencing were used for the genetic characterization of some key parasites from a cohort of 227 people with histories of gastrointestinal disorders in Australia. Genomic DNAs from faecal samples were subjected to PCR-amplification of regions in the genes 60-kDa glycoprotein (*gp60*) for *Cryptosporidium*, triose phosphate isomerase (*tpi*) for *Giardia* and in the second internal transcribed spacer region (ITS-2) for strongylid nematodes. *Cryptosporidium*, *Giardia* and strongylid nematodes were detected in 94, 132 and 12 samples, respectively. *Cryptosporidium hominis* subgenotypes IbA10G2, IdA15G1, IgA17, IgA18 and IfA13G1 were identified in 74.6, 16.9, 5.6, 1.4 and 1.4% of 71 samples, respectively. For *C. parvum*, subgenotypes IIaA17G2R1 (47.6%) and IIaA18G3R1 (23.8%) were found in 23 samples. *Giardia* assemblage B (78%) was more common than assemblage A (22%). In addition, the nematodes *Ancylostoma ceylanicum* (n = 2), *Ancylostoma duodenale* (4), *Necator americanus* (5) and *Haemonchus contortus* (1) were detected. This appears to be the first genetic identification of *A. ceylanicum* from humans in Australia, and we provide molecular evidence of *H. contortus* in a child. Implications from this study will be discussed.



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Session Details:	8/29/2013 DIAGNOSTICS - MOLECULAR 1330 - 1445 <i>Meeting Room 3</i>
Oral Presentation Details:	No more confusion: it is <i>Tritrichomonas foetus</i> based on comparative analysis of <i>Tritrichomonas foetus</i> cat and cattle genotype, and <i>Tritrichomonas suis</i> at ten DNA loci
Presentation Time:	1430 -1445
Authors:	Jan Šlapeta ^{1,*} , Norbert Müller ² , Colin Stack ³ , Giselle Walker ⁴ , Ala Lew-Tabor ⁵ , Jan Tachezy ⁶ , Caroline F. Frey ² ¹ Faculty of Veterinary Science, University of Sydney, New South Wales 2006, Australia ² Institute of Parasitology, Vetsuisse Faculty, University of Berne, Berne, Switzerland ³ School of Science and Health, University of Western Sydney, Penrith, New South Wales, Australia ⁴ Department of Botany, University of Otago, Dunedin, New Zealand ⁵ Centre for Animal Science, Queensland Alliance for Agriculture and Food Innovation, The University of Queensland, Queensland, Australia ⁶ Department of Parasitology, Faculty of Science, Charles University in Prague, Czech Republic

The parasitic flagellate *Tritrichomonas foetus* causes significant disease in domestic cattle and cats. On the other hand, parasitological dilemma revolving around *T. foetus* has been haunting the field for over 50 years, because a very similar - if not identical – flagellate, called *T. suis*, was isolated from pigs. In 1960, Charles Hibler reviewed flagellates in pigs and wrote that if tritrichomonads from cattle and pigs were to be placed in a single species, the name *T. suis* would have priority over *T. foetus*. Later, Normal Levine in 1973 stated that “... it might still be worthwhile to retain both names simply as matter of convenience”. And then Bronislaw Honigberg in 1978 concludes that “... because much confusion would be created among parasitologists and veterinarians if the taxonomic status of especially *T. foetus* were changed, it seems advisable to postpone the implementation of such changes”. To date the “status quo” was not resolved based on objective data. We have selected 10 genes including 8 belonging to the cysteine protease gene family relevant to pathogenesis. A worldwide collection of isolates (bovine, feline and porcine) was screened to determine their genetic identity. To our surprise, there was no intra-feline-strain variability or intra-bovine/porcine-variability; however there was strong in-between feline and bovine/porcine difference. On the basis of this data we judge *T. suis* and *T. foetus* to be subjective synonyms. For the first time, on objective nomenclatural grounds, the authority of *T. suis* is given to Davaine, 1875, rather than the commonly cited Gruby and Delafond, 1843. To maintain prevailing usage of *T. foetus*, we are suppressing the senior synonym *Trichomonas suis* Davaine, 1875 according to Article 23.9, because it has never been used as a valid name after 1899 and *T. foetus* is widely discussed as the cause of bovine trichomonosis. We conclude that bovine, feline and porcine isolates fall within the single species *T. foetus*. This promotes the stability of *T. foetus* for the veterinary and economically significant venereal parasite causing bovine trichomonosis.

Reference:

Šlapeta J, Müller N, Stack C, Walker G, Lew-Tabor A, Tachezy J and Frey CF (2012). Comparative analysis of *Tritrichomonas foetus* (Riedmüller, 1928) cat genotype, *T. foetus* (Riedmüller, 1928) cattle genotype and *Tritrichomonas suis* (Davaine, 1875) at ten DNA loci. *International Journal for Parasitology* 42(13-14): 1143-1149 [<http://dx.doi.org/10.1016/j.ijpara.2012.10.004>]



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Session Details:	8/29/2013 HOST PARASITE INTERACTIONS 1330 - 1445 Meeting Room 5
Oral Presentation Details:	Effect of repeated antigen administration on hypersensitivity and faecal moisture content in sheep following infection with <i>Trichostrongylus</i> spp
Presentation Time:	1330 -1345
Authors:	Lauren Staveley, Lucy Woolford, Phil Hynd, Ryan O’Handley* ¹ School of Animal and Veterinary Sciences, University of Adelaide, Roseworthy, South Australia University,

Diarrhoea leading to breach soiling remains an important problem in Australian sheep production. There is evidence this condition may be the result of a hypersensitive inflammatory condition within the small intestine of sheep following exposure to infectious nematode larvae. In this study, we examined if a repeated exposure to parasite antigen could prevent the development of a hypersensitive inflammatory condition in sheep following a sudden challenge with *Trichostrongylus* L3s after an extended period without exposure to nematodes. Methods : Merino wethers (N=24) were randomly divided into 3 groups and housed individually indoors. Sheep in group 1 received a preparation of *Trichostongylus* antigen 3 times per week for 13 weeks while sheep in groups 2 and 3 remained unexposed. On day 94, sheep in groups 1 and 2 were challenged with 7000 *Trichostrongylus* L3s with group 3 sheep serving as uninfected controls. Complete blood counts, mast cell tryptase activity, histamine levels and total IGE levels were measured pre and post-challenge. Faecal moisture was measured in faecal samples collected pre-challenge and every second day following challenge. On day 27 post-challenge, sheep were euthanized. Intestinal worm counts were performed and standardised representative intestinal samples were collected from each animal to compare histological changes between each group and to look for markers of hypersensitivity (eoisinophils, mast cells, goblet cells). Results: Faecal moisture content did not differ significantly between groups and was not affected by challenge. Group 2 sheep had elevated peripheral blood eosinophils compared to group 1 sheep 4 days following challenge. Interestingly, peripheral basophil levels were elevated at a number of time points following challenge in group 1. Further work is required to validate this novel approach to reducing nematode hypersensitivity.

Acknowledgements:

This work was supported by Meat and Livestock Australia



Session Details:	8/29/2013 HOST PARASITE INTERACTIONS 1330 - 1445 <i>Meeting Room 5</i>
Oral Presentation Details:	Do gastro-intestinal nematode infections induce pain in their sheep hosts?
Presentation Time:	1345 -1400
Authors:	Chylinski C , Cortet J, Crochet D, Cabaret J INRA,

Pain as a consequence of gastro-intestinal nematode (GIN) infection is a new concept to sheep health and welfare, yet there is good reason to suspect it may occur. The *Haemonchus contortus* GIN penetrates the sheep abomasal mucosa twice during their development causing substantial tissue damage and lesions to the HCl acid glands. Other abomasal disturbances such as torsion or ulcers are already established sources of pain in ruminants. Based on the scale used by French ethical committees to quantify pain (0 = no pain to 3 = intense long lasting pain), we hypothesized sheep infested with an *H. contortus* infection would experience a 1 (light pain of short duration) or 2 (pain accompanied by symptoms of health deterioration i.e. anaemia, weight loss) degree of pain. The study incorporated a comprehensive collection of physiological and behavioural variables which taken together could provide an indication of pain from 0 - 3. The variables include pepsinogen (direct measure of abomasal lesions), cortisol (stress), eosinophil counts (response to infection), body temperature (homeostatic stability and potential direct indicator of pain and/or inflammation), anaemia and weight fluctuations (general health), clinical examinations and behavioural analysis. The variables were expected to be negatively affected by greater intensities of infection and compared in the presence and absence of analgesic pain relief. Preliminary analyses of all variables (except cortisol) have shown this not to be the case. The variables were not affected in a consistent way that would be indicative of a pain response greater than 1. Additionally, the variables were not always reversed in the presence of analgesics which instead had an unexpected modulatory effect on the sheep response. Body temperature emerged as a new and promising variable. It was significantly altered in the presence of infection, and differed substantially again in the presence of analgesics and may thereby be associated with pain.

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Session Details:	8/29/2013 HOST PARASITE INTERACTIONS 1330 - 1445 <i>Meeting Room 5</i>
Oral Presentation Details:	Molecular characterisation of host-pathogen immune mechanisms - Lectin Pathway inhibition by parasitic scabies mites.
Presentation Time:	1400 -1415
Authors:	Simone Reynolds^{1*} , Angela Mika ¹ , Robert Pike ² , Anna Blom ³ , Dave Kemp ¹ and Katja Fischer ¹ ¹ Infectious Diseases Division, Queensland Institute of Medical Research, Brisbane, Australia ² Biochemistry and Molecular Biology, Monash University, Melbourne, Australia ³ Department of Clinical Chemistry, University Hospital Malmö, Lund University, Malmö, Sweden

Scabies is a parasitic skin infestation caused by the mite *Sarcoptes scabiei*. Common worldwide, it remains a major public health problem in socially disadvantaged populations, including Australian Indigenous communities. Scabies lesions are commonly co-infected with opportunistic bacteria, particularly Group A streptococci (GAS). In Australian Indigenous communities the increased streptococcal burden has been associated with extreme levels of Rheumatic Heart Disease and Rheumatic Fever. Mass scabies treatment programs have resulted in reduced scabies prevalence coinciding with significantly reduced rates of bacterial infections. Hence scabies eradication may result in improved health outcomes. Recent reports of mite resistance to current scabicides, emphasises the need to identify novel targets for protective intervention.

We have identified two scabies mite protease paralogues which facilitate host immune evasion by inhibiting the Lectin pathway, a component of human innate immunity. These two proteases are members of a multigene family that are catalytically inactive due to structural restraints and mutations in the catalytic triad. They have been named Scabies Mite Inactive Serine Protease Paralogues (SMIPP-Ss). Employing site-directed mutagenesis we are identifying the complement binding site(s) in the two SMIPP-Ss to determine the binding mechanism. Initial studies suggest inhibition is through binding to the collagen region of Mannan Binding Lectin (MBL), the initiator molecule of the Lectin pathway. Studies are currently determining if displacement of MBL associated serine proteases (MASPs) is also a factor. The role of the anti-complement activity of scabies mites in the development of secondary bacterial infections has also become an area of interest with *in vitro* studies indicating that SMIPP-Ss enhance GAS survival. We anticipate that this research may lead to the development of novel parasitic therapeutics influencing rates of scabies and associated secondary infections. It may also lead to the identification of anti-complement compounds suitable for complement-associated disease therapy.





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Session Details:	8/29/2013 HOST PARASITE INTERACTIONS 1330 - 1445 <i>Meeting Room 5</i>
Oral Presentation Details:	Scabies mites give bacteria a helping hand - <i>Staphylococcus aureus</i> co-infections of mite infected skin are promoted by mite complement inhibitors
Presentation Time:	1415 -1430
Authors:	Pearl M Swe , David J Kemp, Katja Fischer Infectious Diseases Program, Biology Department, Queensland Institute of Medical Research, Brisbane, Australia

Scabies is a contagious superficial skin infection caused by the parasitic mite *Sarcoptes scabiei*. Although scabies infection alone is not life-threatening, it is complicated by secondary bacterial infections. It has been suggested that mites contribute to the transmission of staphylococci and reports exist of scabies patients co-infected with *Staphylococcus aureus*¹ and MRSA². Scabies mites cause mechanical infringement by burrowing into the upper epidermis and colonisation of *S. aureus* in these skin burrows has been reported. The human complement system is an immediate defence against the invading pathogen. As a successful pathogen, *S. aureus* produces an array of complement evading molecules. Interestingly, scabies mites also produce several families of different protein classes that interfere with various host complement molecules. They are secreted into the mite gut and excreted into the epidermal burrows with the faeces. We hypothesise that scabies mite complement inhibitors create a microenvironment that promotes bacterial survival. Such scabies mite complement inhibitors have been reported to increase the growth of *Streptococcus pyogenes in vitro*³. Here we investigate the effect of recombinant scabies mite complement inhibitors on staphylococcal *in vitro* survival. Firstly, we addressed this in whole blood bactericidal assays and showed that mite complement inhibitors increased the survival and growth of *S. aureus* in a concentration dependent manner. We will present data signifying that these complement inhibitors reduce the opsonisation of *S. aureus*. Reduced opsonisation resulted in reduced phagocytosis of *S. aureus* by neutrophils. *In vivo* data monitoring *S. aureus* survival on porcine skin in the presence or absence of recombinant mite complement inhibitors is currently underway. We postulate that comprehending the interactions between mite complement inhibitors, bacteria and the host immune factors will foster the development of novel interventions.

Acknowledgements:

We acknowledge the National Health and Medical Research Council and the Cooperative Research Centre for Aboriginal and Torres Strait Islander Health for financial support of this work.

References:

1. Whitehall, J., *et al.* 2013. J Paediatr Child Health. 49(2): p. 141-3.
2. Lin, S., *et al.* 2009. J Am Geriatr Soc. 57, 1713-1714
3. Mika, A. *et al.* 2012. PloS NDT. 6, e1563



Session Details:	8/29/2013 HOST PARASITE INTERACTIONS 1330 - 1445 Meeting Room 5
Oral Presentation Details:	<i>Eimeria bovis</i> modulates endothelial host cell cholesterol metabolism
Presentation Time:	1430 -1445
Authors:	Hamid P, Hermosilla C , Kleinertz S, Hirzmann J, Lochnit G, Taubert A Justus Liebig University Giessen, Germany

During first merogony *Eimeria bovis* forms large macromeronts of up to 400 µm size containing >120,000 merozoites. As the sporozoite stage cannot provide all components necessary for this nutrient and energy demanding process, the parasite needs to scavenge molecules from the endothelial host cell. Especially for the offspring’s membrane production, large amounts of cholesterol are indispensable for a successful replication process. We here analyse the parasite’s influence on cholesterol and lipid contents of the host cell and estimate several molecules being involved in both host cell derived *de novo* synthesis of cholesterol and receptor-mediated uptake of low density lipoproteins (LDL) from the extracellular compartment.

Kinetic analyses on developing *E. bovis* meronts I revealed esterified cholesterol and fatty acid accumulation in form of lipid bodies deposition in infected host cells as detected by Nile Red staining. Furthermore, cholesterol tracer (filipin) showed strong fluorescent signals in infected bovine endothelial cells confirming high levels of cholesterol within developing intracellular stages. Several gene transcripts of molecules being involved in cellular cholesterol *de novo* synthesis via the mevalonate biosynthesis pathway (e. g. HMG-CoA synthase, HMG-CoA-reductase and squalenepoxidase) were found up-regulated towards the end of macromeront formation. Simultaneously, gene transcripts of the LDL-receptor and the oxidised LDL receptor 1, which both play an important role in receptor-mediated cholesterol acquisition via LDL uptake from the extracellular compartment, were found induced during *E. bovis* infection of endothelial host cells. Furthermore, cellular cholesterol processing appeared enhanced as key molecules, such as cholesterol-25-hydroxylase and acetyl-CoA acetyltransferase were significantly up-regulated in infected cells, the latter of which promotes cellular cholesteryl ester synthesis and lipid droplet biogenesis.

Overall, these results indicate that *E. bovis* massively exploits the host cell cholesterol metabolism to guarantee its intracellular growth and replication.

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Session Details:	8/29/2013 DRUG RESISTANCE - MOLECULAR 1330 - 1445 <i>Meeting Room 6</i>
Oral Presentation Details:	Ivermectin-aglycone: A novel P-gp inhibitor to reverse macrocyclic lactone resistance
Presentation Time:	1330 -1345
Authors:	Lespine A ^{1,2} , Sutra J ^{1,2} , Prichard R ³ , Ménez C ^{1,2} ¹ INRA, UMR1331, Toxalim, Research Centre in Food Toxicology, F-31027 Toulouse, France, ² Université de Toulouse, INP, UMR1331, Toxalim, F- 31000 Toulouse, France, ³ Institute of Parasitology, McGill University, Montreal, Canada

Anthelmintic macrocyclic lactone (ML) resistance severally threatens nematode control in livestock and humans. Resistance to MLs in nematodes is associated with overexpression of efflux ATP Binding-Cassette (ATP) transporters (Lespine et al., 2012). This leads to therapy failure by decreasing drug concentration in the target organism. Identification of safe and effective inhibitors of efflux transporters to increase treatment efficiency is of interest. In this context, we have tested ivermectin-aglycone, and found that it is an excellent P-gp inhibitor with little neurotoxicity.

Ivermectin-aglycone was synthesised from ivermectin, purified by HPLC and characterized by mass spectrometry. Its ability to inhibit ABC transporter activity was tested in cells overexpressing human P-glycoprotein. Its neurotoxicity was evaluated *in vitro* by measuring its capacity to open rat GABA-gated chloride channels expressed in recombinant *Xenopus laevis* oocytes and *in vivo* in P-gp deficient mice. The ability to reverse P-gp mediated drug resistance was assayed in human lymphoma vinblastine resistant CEM/VLB cells and in ivermectin-resistant *Caenorhabditis elegans*.

Ivermectin-aglycone inhibits human P-gp transport activity with a similar efficiency as ivermectin and with lower potency (EC₅₀=10 and 1 µM for ivermectin-aglycone and ivermectin, respectively). Unlike ivermectin, ivermectin-aglycone had low affinity for the rat GABA receptor and had no observable neurotoxicity in P-gp-deficient mice. When co-incubated with vinblastin, ivermectin-aglycone restored drug sensitivity in vinblastin-resistant cells overexpressing P-gp with a similar degree of reversal potency as ivermectin. Ivermectin-aglycone by itself had little effect on ivermectin-resistant *C. elegans* but in combination with ivermectin, it restored sensitivity to ivermectin.

Its ability to reverse P-gp-mediated drug resistance in mammalian cells and in nematodes and its very low neurotoxicity make ivermectin-aglycone an interesting P-gp reversing agent to be used *in vivo*. Combining ivermectin-aglycone with MLs to increase drug efficacy, and to reverse ML resistance opens a new approach for sustaining anthelmintic control after ML resistance has arisen.

Acknowledgements:

Kathy Keller

References:

A Lespine, C Ménez, C Bourguinat, R Prichard. 2012; P-glycoproteins and other ABC transporters in the pharmacology of anthelmintics: prospects for reversing transport-dependent anthelmintic resistance. IJP-Drug and Drug Resistance.2, 58-75



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Session Details:	8/29/2013 DRUG RESISTANCE - MOLECULAR 1330 - 1445 <i>Meeting Room 6</i>
Oral Presentation Details:	Using next generation sequencing to identify ivermectin resistance loci in <i>Haemonchus contortus</i>.
Presentation Time:	1345 -1400
Authors:	Peter Hunt^{1*} , Tom Walsh ² , Bryce Little ³ , Rowan Bunch ³ , Sean McWilliam ³ , Blair Harrison ³ , Aaron Ingham ³ , Andrew Kotze ³ ¹ Commonwealth (of Australia) Scientific and Industrial Research Organisation (CSIRO) Armidale, NSW, AUSTRALIA. ² CSIRO, Acton, ACT, AUSTRALIA. ³ CSIRO, St Lucia, QLD, AUSTRALIA.

Genetic recombination during gametogenesis results in the re-sorting of parental genome segments. Individuals from different populations may differ because of various factors including genetic selection. When individuals from two populations mate and produce F1 offspring, genome segments deriving from each population are re-combined in F1 gametes. F2, derived from crosses amongst the F1, therefore have a re-combined genome; each chromosome contains segments derived from each of the grandparent populations. We took *H. contortus* from an ivermectin resistant population and mated them with nematodes from an ivermectin sensitive population (Hunt et al., 2010). We used larval F2 nematodes to infect sheep, and subsequently treated some sheep with ivermectin, leaving others untreated. We sequenced the DNA of adult male F2 nematodes derived from either ivermectin treated sheep (survivors of ivermectin treatment – F2IVM) or F2 nematodes which had not been exposed to ivermectin (F2UNS). When drug resistance is observed in parasitic nematodes, the resistance alleles have become more frequent due to selective sweeps. We have used three different strategies to identify the hallmarks of these selective sweeps through analysis of short read DNA sequences. We sorted through the DNA sequences from F2IVM and F2UNS looking for instances where variants occurred in very different frequencies, based on read numbers, between the two samples. Initially we did this with a reduced representation library produced by sequencing DNA restriction fragments. The fragments contained in this data set were assembled into 18,009 putative loci at which 39,128 alleles (variants of reads) were observed. For each locus, F2UNS and F2IVM were compared for allelic diversity, differences in allele frequency and Wright’s FST. When ranked using these three methods, an overlapping set of 184 loci were investigated further. Additional genome sequencing and comparative genomic location analysis of these loci will be presented.

Acknowledgements:

Thanks to Andre Rickers and others at GeneWorks South Australia for taking on a slightly non-standard project.

References:

Hunt, PW, Kotze, AC, Knox, MR, Anderson, LJ, McNally, J, Le Jambre, LF. 2010. The use of DNA markers to map anthelmintic drug resistance loci in an intraspecific cross of *Haemonchus contortus*. *Parasitology*, 137, 705-717.





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Session Details:	8/29/2013 DRUG RESISTANCE - MOLECULAR 1330 - 1445 <i>Meeting Room 6</i>
Oral Presentation Details:	Macrocyclic lactone resistance in nematodes: Molecular marker for resistance detection
Presentation Time:	1400 -1415
Authors:	Urdaneta-Marquez L ¹ , Dent J ² , Janukavicius P ² , Beech R ¹ , Prichard R ¹ ¹ McGill University, Institute of Parasitology, ² McGill University, Department of Biology

Macrocyclic lactone (ML) resistance has become a serious problem for parasite control in livestock in many parts of the world. The detection of ML resistance currently relies primarily on the faecal egg count reduction test (FECRT) which requires faecal samples from animals before and 10 – 18 days after ML treatment and microscopic estimation of faecal egg counts. Furthermore, if a resistant genus is to be identified, the FECRT usually needs to be coupled to larval cultures. These tests are slow, laborious, insensitive and expensive. In vitro tests, such as larval motility tests and larval development assays, are not sensitive for detecting low-moderate levels of resistance, are slow and are inconsistent. The identification of genetic changes implicated in the mechanism of resistance offers the possibility of developing rapid and inexpensive DNA based assays for ML resistance and would allow the detection of low level resistance. We have analyzed ML resistant and susceptible strains and isolates of *Caenorhabditis elegans* and *Haemonchus contortus*, for genetic differences, including using Next Generation sequencing. Similar genetic changes were revealed in strains of the free-living nematode and the parasite that had been selected with MLs. These changes have been confirmed in field isolates of the parasite from Africa, Australia, Europe and North and South America. Rescue studies with a gene implicated in ML resistance have been conducted in *C. elegans*, confirming the involvement of these genetic changes in ML resistance. These findings represent significant advances in the understanding of the mechanism of ML resistance and the ability to use a DNA based assay to detect ML resistance in nematodes.

Acknowledgements:

This research was supported by funding from NSERC, Canada; FRQNT, Québec; MDEIE-PSR-SIIRI, Québec and the Québec Centre for Host-Parasite Interactions. We are also grateful to many colleagues from around the world who have provided us with ML sensitive and resistant isolates of *H. contortus* worms, larvae or DNA, and to Dr Catherine James who provided us with an ivermectin selected strain of *C. elegans*.

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Session Details:	8/29/2013 DRUG RESISTANCE - MOLECULAR 1330 - 1445 Meeting Room 6
Oral Presentation Details:	Whole genome analysis for macrocyclic lactone resistance markers in <i>Dirofilaria immitis</i>
Presentation Time:	1415 -1430
Authors:	Bourguinat C ¹ , Geary T ¹ , Keller K ¹ , Blagburn B ² , Bowman D ³ , Malone J ⁴ , Pulaski C ⁴ , Kaminsky R ⁵ , Prichard R ¹ ¹ Institute Of Parasitology, McGill University, CANADA, ² Auburn University, Auburn, USA, ³ Cornell University, Ithaca, USA, ⁴ Louisiana State University, Baton Rouge, USA, ⁵ Novartis Animal Health, St Aubin, SWITZERLAND

Macrocyclic lactone (ML) endectocides are used, mostly at monthly intervals, during the transmission season for chemoprophylaxis for heartworm (*Dirofilaria immitis*) in dogs and cats. There are increasing reports of apparent loss of efficacy (LOE) of ML heartworm preventatives in some locations in recent years. ML resistance is widely recognized in nematode gastrointestinal parasites of ruminants and horses and in the human filarial nematode *Onchocerca volvulus*. Previously a correlation between a P-glycoprotein genotype and ivermectin efficacy had been established (Bourguinat et al., 2011). The goal of our project was to find markers that could predict ML resistance in *D. immitis*. We used a whole genome approach on phenotypically well characterized pool samples to address this issue. Using Illumina technology, we sequenced the genomes of 8 well characterized pools of *D. immitis*. We used bioinformatic tools to identify loci that may be predictive for ML resistance in *D. immitis*. Over 90Mbp loci on the genome, around 200 loci showing differences between susceptible and LOE pools were found. This was followed by multiplex PCR with Sequenom technology on 186 of these loci in 612 individual parasites (adult worms and microfilaria) that were well characterized with regard to the phenotypic response to treatment in the dog. Ideally a DNA marker should be present in worms in all true LOE dogs and nearly absent in susceptible samples. From those 186 possible markers, 5 markers met these criteria and seem to be extremely promising for the detection of ML resistance. These markers should be valuable tools to detect and monitor for ML resistance in *D. immitis*.

Acknowledgements:

This research was supported by Novartis Animal Health, NSERC, Canada, and the Centre for Host-Parasite Interactions/FRQNT, Québec. We thank the following persons for parasite samples: Tara Paterson (School of Veterinary Medicine, St. George’s University, Grenada), Elena Carreton Gomez (University of Las Palmas de Gran Canaria, Spain), Hubert Smith (Haywood Animal Hospital, Brownsville, TN, USA), Aaron Bhan (Main West Animal Hospital, Welland, Ontario, Canada), Andrew Peregrine (Ontario Veterinary College, University of Guelph, Guelph, ON, Canada), Claudio Genchi (Dipartimento di Patologia Animale,Igiene e Sanità Pubblica Veterinaria, Italy).

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Correlation between loss of efficacy of macrocyclic lactone heartworm anthelmintics and P-glycoprotein genotype. Bourguinat C, Keller K, Blagburn B, Schenker R, Geary TG, Prichard RK. Vet Parasitol. 2011; 176:374-81.





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Session Details:	8/29/2013 DRUG RESISTANCE - MOLECULAR 1330 - 1445 <i>Meeting Room 6</i>
Oral Presentation Details:	Drug-efflux and target-site gene expression patterns in levamisole-resistant <i>Haemonchus contortus</i>.
Presentation Time:	1430 -1445
Authors:	Sarai R^{1,2}, Kopp S², Coleman G², Kotze A¹ ¹ CSIRO Animal, Food And Health Sciences, ² School of Veterinary Science, University of Queensland

Levamisole-resistance is a serious issue impacting on the control of a number of parasitic nematodes of small ruminants. Implicated in the observed resistance are the nicotinic acetylcholine receptor (nAChR) subunits which make up the target of the drug. In addition there is some evidence that receptor ancillary proteins and P-glycoproteins (Pgps) may play a role. In the present study we have taken two approaches to study the molecular basis of levamisole resistance in *Haemonchus contortus*: firstly, measuring gene expression differences between highly resistant subpopulations within a field-derived isolate compared to the bulk of the population, and secondly, following changes in gene expression patterns and resistance levels during the imposition of drug selection pressure on larval life stages over a number of generations. We focused on nAChR subunits, receptor ancillary proteins and Pgps. The first study highlighted the roles of ancillary proteins (decreases in *Hco-unc-74*, *Hco-unc-50*, *Hco-ric-3*), receptor subunits (decreases in *Hco-unc-63*, *-unc-29*) and Pgps (increases in *Hco-pgp-3*, *-4*, *-10* and *-14*) within resistant fractions compared to the whole population. The second study showed decreased expression of receptor subunit genes in larvae exposed to selection pressure with levamisole over nine generations, as well as changes in Pgp expression. Additionally, the levamisole-pressured worms showed increasing levels of resistance to other compounds (bephenium and ivermectin). Together, these two studies provide a greater understanding of the molecular mechanisms of levamisole resistance and the role of nAChRs, Pgps and ancillary proteins.

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Session Details:	8/29/2013 DRUG EFFICACY - SHEEP 1330 - 1445 <i>Meeting Room 7</i>
Oral Presentation Details:	Production responses in ewes treated pre-lambing with controlled release capsules containing both anthelmintic and minerals
Presentation Time:	1330 -1345
Authors:	Chris Miller^{1*} and Dave Leathwick ¹ ¹ AgResearch Grasslands, Palmerston North, NEW ZEALAND

In New Zealand the use of controlled release (100 day) anthelmintic capsules in ewes over lactation has been popular with farmers for many years. This is despite evidence that their use accelerates the development of anthelmintic resistance (Leathwick et al. 2006). Surprisingly, there is little reliable data on the production benefits of their use, or on which to make decisions regarding targeted use. In response to farmer requests for more information an industry-funded project was initiated in 2011.

There were 3 trial designs, each addressing a different question raised by the farmers. However, common to all trials was treatment with a combination capsule (albendazole + abamectin + selenium + cobalt) administered approximately 2 weeks prior to lambing, an untreated control group and a mineral supplemented group. Ewes in the latter group were administered both selenium and cobalt by injection at rates calculated to approximate the release rates of the capsule. Trials were conducted on 8 farms in year 1 and 6 of these repeated the same trial in year 2.

Exceptional conditions for pasture growth in year 1 were contrasted by a cold spring and drought in year 2. Ewe liveweight response to the capsule varied between farms and years, but the difference between years was not as great as might be expected based on the seasons. Measureable liveweight responses were attributable to both the anthelmintic and to the minerals, although the pattern of these responses varied between farms. Hence, the response to capsule use that farmers observe often involves a significant response to the minerals. The average response measured at weaning was reduced by mating time indicating compensatory growth in the untreated animals after weaning. Overall the response to the capsule was not influenced by ewe condition score indicating that targeted treatment of thin ewes had little advantage.

Acknowledgements:

This project was funded by MAF-SFF, Beef+LambNZ, AgMardt, Landcorp Farming, PGG Wrightson, Keinzley AqVet and Ravensdown.

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Session Details:	8/29/2013 DRUG EFFICACY - SHEEP 1330 - 1445 <i>Meeting Room 7</i>
Oral Presentation Details:	Effects Of Protein Supplementation On Gastrointestinal Nematode Infestation In Lambs
Presentation Time:	1345 -1400
Authors:	Farhana Riaz Chaudhary^{1*} , Muhammad. Rafiq ² , Muhammad. Fatah Ullah. Khan ² ¹ Department of Zoology, Pir Mehr Ali Shah-Arid Agriculture University, Rawalpindi. ² Small Ruminant Research Program, Animal Sciences Institute, National Agricultural Research Centre, Park Road, Islamabad

In Pakistan sheep productivity is low due to factors including poor genetic potential, malnutrition and harsh climatic conditions. Among these, nutritional factors are the main determinants in the ruminants by making animals more susceptible to parasitic diseases mainly nematode infestation which reduces growth and reproductive performance. Therefore, said study was designed to see the effects of dietary crude protein levels on the gastrointestinal nematode parasites load in weaned Bulkhi lambs. For this purpose twenty seven lambs of four months age were dewormed then divided randomly into three groups (n=9). Group-1 (G-I) served as the control group and maintained under the farm practices. Group-II grazed along with protein supplementation at a rate of 0.3% of their body weight which was 300 g/day/lamb. Lambs in Group- III received supplementation at the rate of double doze (600 g/day/lamb) of that given to the lambs in G-II. Data obtained from a trial of 12 weeks revealed that G-1 gained significantly ($P \leq 0.05$) less body weight (26.7 ± 1.07) with higher faecal egg counts (1853 ± 23) and had lower packed cell volume (15.99 ± 1.9), haemoglobin (21 ± 2.4), red blood cells (7.0 ± 0.2) and total protein level (37 ± 2.8) followed by G-III (epg: 1380 ± 28) and G-II (epg: 303 ± 11), respectively. However, in G-II lower GIN faecal egg counts numbers, higher values of haematological parameters, growth rate and wool quality were largely affected by protein supply ($P \leq 0.05$) than other groups. It is concluded that supplementary feeding with protein feed substantially reduced the production losses attributable to nematode infections in young grazing lambs. This study would not only help to develop integrated approach for controlling GIN (generally in winter season due to scarcity of pasture) but also help to conserve the efficacy of anthelmintics in naive form.

Acknowledgements:

We would like to thank the Department of Zoology, Pir Mehr Ali Shah Arid Agriculture University Rawalpindi for funding this research.



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Session Details:	8/29/2013 DRUG EFFICACY - SHEEP 1330 - 1445 <i>Meeting Room 7</i>
Oral Presentation Details:	Efficacy of a combination of monepantel and abamectin against naturally acquired gastrointestinal parasites in sheep
Presentation Time:	1400 -1415
Authors:	Rolfe P¹ , Pathiaux V ¹ , Griffiths T ¹ , Nottingham R ² ¹ Novartis Animal Health, ² Pharmvet Solutions

Combinations of anthelmintic classes with different modes of action have been used to slow the development of resistance, particularly to new chemical classes, and to manage resistance once it has occurred. In this study, the efficacy of a combination of monepantel (25 g/L) and abamectin (2 g/L) given orally to sheep under typical field conditions (minimum 2.5 mg/kg monepantel and 0.2 mg/kg abamectin) was assessed. The study was conducted on 19 sites in France (3), United Kingdom (4), Australia (6) and New Zealand (6) and included a wide range of ages and breeds of sheep. In France and the United Kingdom, a total of 274 sheep were treated, in Australia and New Zealand 340 and 300 sheep respectively were treated. The sites were selected to represent the range of climatic regions and production systems and where common parasite genera were present. Efficacy was expressed as the percentage reduction in geometric mean faecal egg counts (FEC) after treatment compared to untreated controls and to those treated with macrocyclic lactones (ML), benzimidazoles (BZ), imidazothiazoles (LEV) and 2 or 3 way combinations of these classes.

In the European study, the FEC reduction 12 days after treatment (“strongyle” type eggs) was >99.4% (one site>98.9%). ML resistance was confirmed on 4/7 sites, BZ resistance on 7/7 sites and LEV resistance on 2/5 sites. In Australia, the reduction in FEC was >99.9% on all sites. Resistance to MLs was confirmed (ivermectin 5/6 sites; moxidectin 2/4 sites), as well as to combinations of BZ/LEV (3/5 sites) and to combinations of BZ/LEV/ML (2/4 sites). In New Zealand the combination formulation was highly effective. The parasite genera that were present were *Teladorsagia* spp, *Haemonchus* spp, *Trichostrongylus* spp, *Nematodirus* spp *Cooperia* spp and *Chabertia/Oesophagostomum* spp. No treatment related adverse events were observed on any site.

A combination formulation of abamectin and monepantel was safe and highly effective against the major gastrointestinal parasites present in sheep.

Session Details:	8/29/2013 DRUG EFFICACY - SHEEP 1330 - 1445 <i>Meeting Room 7</i>
Oral Presentation Details:	Assessment of monepantel and monepantel sulphone gastrointestinal concentration profiles in sheep:-relevance of the kinetics/efficacy relationship-
Presentation Time:	1415 -1430
Authors:	Lifschitz A , Ballent M, Virkel G, Sallovitz J, Viviani P, Mate L, Lanusse C Facultad Ciencias Veterinarias, UNCPBA

Monepantel (MNP) is a novel amino-acetonitrile derivative anthelmintic drug. Based on a distinctive mode of action, MNP is active against a variety of multidrug resistant gastrointestinal (GI) nematodes (Kaminsky *et al.* 2008). The plasma pharmacokinetics of MNP and its main sulphone metabolite (MNPSO₂) has been described in sheep (Karadzovska *et al.*, 2009). The anthelmintic efficacy greatly depends on the active drug concentrations attained at the sites of nematode location (Lanusse and Prichard, 1993). Thus, data on MNP concentration profiles reached in target tissues is needed to optimize its therapeutic use. The goal of the current study was to assess the relationship between the plasma disposition kinetics of MNP and MNPSO₂ and their concentration profiles attained in GI tissues of parasite location in sheep. Twenty two healthy lambs received MNP (Zolvix®, Novartis) orally at 2.5 mg/kg. Blood samples were collected from six animals between 0 and 14 days post-treatment (plasma disposition study). Additionally, four lambs were sacrificed at 8, 24, 48 and 96 hours post-administration to measure the drug/metabolite concentrations at the mucosa and luminal contents from abomasum and duodenum. Drug concentrations were measured by HPLC. MNP concentrations in plasma were significantly lower compared to its sulphone metabolite. The peak plasma concentrations were 15.1 (MNP) and 61.3 ng/ml (MNPSO₂). MNP and MNPSO₂ levels measured in GI contents and mucosal tissue were considerably higher than those recovered in the bloodstream. At 24 hours post-treatment, mean MNP (3943 ng/ml) and MNPSO₂ (204 ng/ml) concentrations in abomasal content were markedly higher than those recovered in plasma, which ranged between 10.8 (MNP) and 60.3 (MNPSO₂) ng/ml. Although MNP is efficiently metabolized to MNPSO₂ in the liver, the large concentration profiles of both anthelmintically active molecules recovered from the abomasum and small intestine may greatly contribute to the broad spectrum efficacy against GI nematodes.

Acknowdgements

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Session Details:	8/29/2013 DRUG EFFICACY - SHEEP 1330 - 1445 <i>Meeting Room 7</i>
Oral Presentation Details:	Ewe but not lamb worm control increases weaning weight of prime lambs
Presentation Time:	1430 -1415
Authors:	Dever M , Kahn L, Bowers S University Of New England

This experiment determined the effect of ewe and lamb worm control on prime lamb production at weaning. The core of the experiment was a 2 X 2 factorial design conducted with two mobs of 120 twin-bearing Border Leicester x Merino ewes on each of three farms. From within each mob, half were randomly allocated to be worm-suppressed (CAP) and the remaining to a proposed regional best practice (BP) strategy. Eight weeks post lambing, lambs were randomly allocated from within ewe worm control treatment to receive CAP or BP strategy. CAP ewes were serially treated with persistent anthelmintics and an effective short-acting drench at 80–90 day intervals. CAP lambs received the same treatment at eight and 12 weeks of age. BP strategy had low worm-risk lambing paddocks and effective anthelmintic treatment of ewes at 2 weeks pre-lambing and 8 weeks post lambing: BP lambs remained untreated. Both CAP and BP ewes and their lambs grazed together. The period from 2 weeks pre-lambing to weaning (at 14 weeks post lambing) is reported.

Mean worm egg count (WEC) pre-lambing ranged between 290–3000 epg. At 8 and 14 weeks post lambing, mean ewe WEC ranged from 400–2500 epg and 1000–3700 epg, respectively. Predominant infective worms at weaning were *Haemonchus contortus* (45%) and *Trichostrongylus* spp. (45%). Lamb WEC at weaning ranged from 1000–4500 epg with *H. contortus* (70%) and *T. spp.* (25%) dominant. Live weights of lambs at weaning were higher (P=0.029) when reared by CAP ewes (31.6 ± 0.25 kg v's 30.8 ± 0.25 kg). In contrast, live weight of lambs at weaning was unaffected by lamb treatment.

The importance of controlling worm infections in ewes has been highlighted. These findings are significant for developing strategies that reduce the cost of worms on prime lamb production in Australia.

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Session Details:	8/29/2013 ONE HEALTH - ANIMAL PRODUCTION 1330 - 1445 <i>Meeting Room 8</i>
Oral Presentation Details:	The microbiome of scabies mite infected porcine skin.
Presentation Time:	1330 -1345
Authors:	Swe P ¹ , Zakrzewski M ² , Krause L ² , Kemp D ¹ , Fischer K¹ ¹ Infectious Diseases Program, Biology Department, Queensland Institute of Medical Research, ² Genetics & Computational Biology Department, Queensland Institute of Medical Research

Scabies mite skin infection involves complex interactions between host, mites and bacteria. Scabies mites interfere with human complement protection^{1,2}, thereby promoting growth of *Streptococcus pyogenes*^{3,4} and *Staphylococcus aureus* (unpublished). This likely applies to other bacteria within the mite infested skin. However, the diversity of bacteria associated with *S. scabiei* has not been investigated and it is unknown whether *S. scabiei* relies on obligatory endosymbionts for survival. We hypothesize that scabies alters the bacterial skin microbiome and promotes the growth of opportunistic pathogens.

Pigs develop a manifestation of scabies closely resembling human crusted scabies and the porcine innate immunity is very comparable to humans. We have developed a tractable experimental porcine scabies model⁵. We have completed a 16 week trial to examine changes in the microbial communities on pig skin due to scabies infection, prior to, during, after scab formation and after treatment with acaricide. Scraping and swab samples were collected from affected skin sites in 2 week increments throughout the trial. Mites were isolated from scabs and washed to remove external bacteria. At week 14 pigs were treated with acaricide and infections cleared within ten days. Final sampling was done 4 weeks after treatment, when recovery of the skin was visible. DNA was extracted from scrapings and isolated mites followed by pyrosequencing of 16S rRNA genes.

High throughput sequencing circumvents the challenges involved in isolation and cultivation of many cutaneous pathogens. Following the study in pigs, we will assess human clinical samples. While we expect that the pig and human scabies associated microbiomes are different, we propose that scabies alters the healthy microflora in both hosts and that the range of associated pathogenic and possibly mite symbiotic organisms can be identified. Knowledge of the microbiota associated with *S. scabiei* will offer new perspectives for developing new prophylactic and therapeutic measures.

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Session Details:	8/29/2013 ONE HEALTH - ANIMAL PRODUCTION 1330 - 1445 <i>Meeting Room 8</i>
Oral Presentation Details:	<i>Echinococcus canadensis</i> in slaughtered farmed elk in Southern Alberta, Canada
Presentation Time:	1345 -1400
Authors:	Ralston B¹, Thompson A², Olson M³ ¹ Alberta Agriculture And Rural Development, ² World Health Organization Collaborating Centre for the Molecular Epidemiology of Parasitic Infections, School of Veterinary and Biomedical Sciences, Murdoch University, Murdoch, AUSTRALIA, ³ Bow Valley Research, Alberta, CANADA

Echinococcus granulosus is a concern in the transmission of hydatid disease through canines' consumption of infected material. Lungs from 1190 head of southern Alberta farmed elk were obtained from area abattoirs and were examined for the presence of hydatid cysts over a two year period. During this period an approximate total of 13,642 head of elk were slaughtered at abattoirs in Alberta. Hydatid cysts were present in 29 (2.4%) of examined animals with a total of 54 cysts being recovered. Two animals had six large cysts in each of one lung. DNA was extracted from protoscoleces recovered from cysts in 16 separate lungs and all were genotyped as *E. canadensis*. The presence of cysts in elk lungs highlights the importance of proper disposal of offal to avoid consumption by wild/tame canines and the potential transmission of the disease to humans.

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Session Details:	8/29/2013 ONE HEALTH - ANIMAL PRODUCTION 1330 - 1445 <i>Meeting Room 8</i>
Oral Presentation Details:	Migratory pattern of <i>Toxocara cati</i> and <i>Toxocara canis</i> in pigs
Presentation Time:	1400 -1415
Authors:	Yoshida A ¹ , Poulsen C ² , Skallerup P ² , Maruyama H ¹ , Thamsborg S ² , Nejsum P² ¹ University of Miyazaki, ² University Of Copenhagen

In man infections with *Toxocara cati* and *T. canis* may cause visceral larva migrans (VLM). The relative contribution of the two species in VLM as well as the predilection sites of *T. cati* in the human host is largely unknown. We used the pig as a model for human infection and conducted two studies to explore the migratory patterns of *T. cati* as compared to *T. canis*. Four groups of 5-7 pigs were inoculated with 50,000 (study A) or 10,000 (study B) embryonated eggs of either *T. cati* or *T. canis*. Larvae were recovered from liver, lungs, mesenterial lymph nodes, heart, brain, eyes, diaphragm, tongue and skeletal muscles at day 14 post infection (p.i.)(study A) or day 30-32 p.i. (study B) by HCl/pepsin digestion. A higher, but not significantly so, mean larval burden was found in lymph nodes of *T. cati* than *T. canis*, both on day 14 p.i. (134.0 vs. 99.9) and day 30-32 p.i. (3.6 vs. 1.3). The opposite trend was found in the lungs, both on day 14 p.i. (57.4 vs. 95.7; NS) and on day 30-32 p.i. (1.9 vs. 11.0; *P*=0.08). In addition, we recovered larvae from the liver of three *T. canis* infected pigs (10, 65 and 83 larvae) on day 14 p.i. and 1 out of 7 on day 30-32 p.i. (11 larvae) whereas no larvae were found in livers of *T. cati* infected pigs. Gross pathology of livers from *T. canis* infected pigs on day 14 p.i. was more severe than *T. cati* even though numbers of white spots were similar. Our data suggest a different tissue distribution of *T. cati* and *T. canis* which may reflect different migratory patterns in VLM and perhaps different pathogenicity.





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Session Details:	8/29/2013 ONE HEALTH - ANIMAL PRODUCTION 1330 - 1445 <i>Meeting Room 8</i>
Oral Presentation Details:	Oxfendazole treatment trial to control porcine cysticercosis in Angónia District, Mozambique
Presentation Time:	1415 -1430
Authors:	Pondja, A. ¹ , Neves, L. ¹ , Mlangwa, J. ² , Afonso, S. ¹ , Fafetine, J. ¹ , Willingham III, A.L. ³ , <u>Thamsborg, S.M.</u> ³ , Johansen, M.V. ³ ¹ Eduardo Mondlane University, Mozambique; ² Sokoine University of Agriculture, Tanzania; ³ University of Copenhagen, Denmark

A randomized controlled field trial to evaluate the effectiveness of a single oral dose of 30 mg/kg of oxfendazole (OFZ) treatment for control of porcine cysticercosis was conducted in 4 rural villages of Angónia district, north-western Mozambique. Two hundred and sixteen piglets aged 4 months were recruited and assigned randomly to OFZ treatment or control groups. Fifty four piglets were treated at 4 months of age (T1), other 54 piglets treated at 9 months of age (T2) and matched with 108 controls from the same litters and raised under same conditions. Baseline data were collected on the prevalence of porcine cysticercosis based on Ag-ELISA, and knowledge and practices related to *Taenia solium* transmission based on questionnaire interviews and observations. All animals were followed and re-tested for porcine cysticercosis by Ag-ELISA at 9 and 12 months of age where the study was terminated. Overall prevalence at baseline was 5.1% with no significant difference between groups. At the end of the study, infections were found in 66.7% of the controls, 21.4% of the T1 and 9.1% of the T2 pigs. There was a significant reduction in the prevalence of *T. solium* cysticercosis if pigs were treated with OFZ either at 4 months (OR = 0.14; 95% CI: 0.05, 0.36) or at 9 months of age (OR = 0.05; 95% CI: 0.02, 0.16). Strategic treatment of pigs in endemic areas should be further explored as a means to control *T. solium* cysticercosis/taeniosis.



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Session Details:	8/29/2013 ONE HEALTH - ANIMAL PRODUCTION 1330 - 1445 <i>Meeting Room 8</i>
Oral Presentation Details:	Control of <i>Taenia solium</i>: calculation of the minimum number of vaccination/ chemotherapy interventions required in pigs per year to achieve control
Presentation Time:	1430 -1445
Authors:	Lightowlers M University of Melbourne

The TSOL18 vaccine and oxfendazole chemotherapy provide new opportunities for prevention of *Taenia solium* infection in pigs and, thereby, reduce the global burden of neurocysticercosis. Despite the extraordinary effectiveness of these new interventions, many challenges remain in implementing *T. solium* control. One of these challenges is the lack of a defined breeding season for pigs in *T. solium* endemic areas, leading to the introduction of new susceptible animals into the population constantly. This presentation will consider the various logistic limitations that apply to both vaccination and chemotherapy in pigs and estimates the minimum number of interventions that would be required annually to achieve an effective control scenario. A program involving implementing vaccination plus chemotherapy in pigs 2-9 months of age at 4-monthly intervals per year was determined to provide the minimum but effective control scenario.

Session Details:	8/29/2013 COMMERCIAL LIVESTOCK - SHEEP 1515 - 1630 <i>Riverside Theatre</i>
Oral Presentation Details:	Total tract digestibility is reduced in anorexic parasitized ewes
Presentation Time:	1515 -1530
Authors:	Jos Houdijk* , Bert J. Tolkamp, Mike R. Hutchings SRUC, Edinburgh, UNITED KINGDOM

Diet formulation for livestock is largely based on data from digestibility studies where disease is carefully excluded, e.g. for sheep in AFRC (1993). Here, we assess effects of parasitism on feed total tract digestibility and performance in lactating ewes. Twin-bearing individually housed Mule ewes were drenched to remove existing worm burdens and divided into three groups of 16 ewes with similar mean body weight (68.2 ± 1.1 kg) on day₋₃₉ approximately (day₀ is parturition). From day₋₃₂ until day₃₆, two groups of ewes were fed pelleted lucerne *ad libitum* and either dosed with 10,000 infective *Teladorsagia circumcincta* larvae every Mon-Wed-Fri (PAR) or sham-infected with water (CON). A third group of ewes (RES) were treated as CON during pregnancy but fed restrictedly at 80% of achieved intake by CON ewes during lactation. Apparent total tract dry matter (DM), nitrogen (N) and organic matter (OM) digestibility was determined through DM, N, OM and acid-insoluble-ash determination in feed and faeces, collected from day₂₇ to day₂₉. Ewe DM intake was measured twice weekly, and ewes and litters were weighed weekly. Apparent total tract digestibility in CON, PAR and RES ewes averaged 53.8, 45.6 and 55.3% for DM (sed 3.4%; $P=0.013$), 58.8, 53.4 and 61.9% for N (sed 3.1%, $P=0.029$) and 54.6, 46.4 and 55.8% for OM (sed 3.4%; $P=0.014$), respectively. Treatment did not interact with time for daily DM intake ($P>0.20$), which averaged 4.44, 4.16 and 3.45 kg for lactating CON, PAR and RES ewes, respectively (sed 0.12 kg/day; $P<0.001$). Their body weight loss averaged 69, 162 and 252 g/day (sed 37 g/day; $P<0.001$) and their litters gained 718, 669 and 654 g/day (sed 24 g/day; $P=0.033$), respectively. These results show that periparturient parasitism may reduce nutrient digestibility, which implies decreased feedstuff nutritive values and an increased environmental footprint arising from increased N excretion during nematode infection.

Acknowledgements:

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Session Details:	8/29/2013 COMMERCIAL LIVESTOCK - SHEEP 1515 - 1630 <i>Riverside Theatre</i>
Oral Presentation Details:	Lower worm egg counts associated with higher ewe body condition score
Presentation Time:	1530 -1545
Authors:	Kahn L , Dever M, Bowers S University Of New England

Managing breeding ewes to ensure they meet or exceed minimum body condition score (CS) targets (typically > 3) is a critical issue for improving reproductive success. Higher CS is associated with more body protein and fat and this may be of benefit to host resistance against gastrointestinal nematode parasites (GIN). CS was estimated and faeces collected to determine worm egg counts (WEC) from 120 Border Leicester x Merino ewes on each of three farms on three occasions (prelambing, 8 and 14 weeks post lambing) in 2012-13. Ewe CS (1-5 scale) was categorised into 0.5 unit bands, from a low of 2-2.5 to a high of 4-4.5. Mean WEC was negatively associated with CS and backtransformed values, separated ($p < 0.01$) using a nonparametric multiple comparison test (Wilcoxon method), for the various CS bands were: 2-2.5 = 1520^a ep μ ; 2.5-3 = 1771^a ep μ ; 3-3.5 = 830^b ep μ ; 3.5-4 = 358^c ep μ ; and 4-4.5 = 262^c ep μ . The predominant GIN were *Haemonchus contortus* (53%) and *Trichostrongylus colubriformis* (42%). These results indicate that managing ewes to achieve CS targets for reproductive success will attract further benefit for host resistance to GIN. Higher CS (> CS=3) was associated with further reductions in mean WEC but the additional benefit may be offset when considered in conjunction with other issues such as whole-farm stocking rates.

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Session Details:	8/29/2013 COMMERCIAL LIVESTOCK - SHEEP 1515 - 1630 Riverside Theatre
Oral Presentation Details:	Effect of lambing season on the periparturient egg rise of gastrointestinal nematodes
Presentation Time:	1545 -1600
Authors:	Laura C. Falzon¹, Paula I. Menzies¹, Krishna P. Shakya², Andria Jones-Bitton¹, John VanLeeuwen³, Jacob Avula², Jocelyn T. Jansen⁴, Andrew S. Peregrine^{2*} ¹Department of Population Medicine, Ontario Veterinary College, University of Guelph, Guelph, Ontario, Canada; ²Department of Pathobiology, Ontario Veterinary College, University of Guelph, Guelph, Ontario, Canada; ³Department of Health Management, Atlantic Veterinary College, University of Prince Edward Island, Charlottetown, Prince Edward Island, Canada; ⁴Ontario Ministry of Agriculture, Food and Rural Affairs, Elora, Ontario, Canada

The epidemiology of the periparturient egg rise (PPER) of gastrointestinal nematodes (GINs) in sheep remains unclear. Earlier studies have suggested that the PPER may be influenced by the lambing season. This study was performed to determine the effect of lambing season on the PPER in sheep in Ontario, Canada. Six farms that practiced out-of-season lambing were sampled for three consecutive lambing seasons (winter, spring, autumn). For each lambing season, all farms were visited five times, following a specific schedule that was determined around the predicted 50% lambing date for that season; on the first visit for each farm, 20 pregnant ewes and 20 non-pregnant/early gestation ewes were randomly selected. On each visit, fecal samples were collected from selected animals and processed individually to measure the GIN fecal egg count (FEC); blood samples were collected on 3 visits and the packed cell volume (PCV) determined. Ewes were classified into 5 different production stages (maintenance, early/late gestation, early/late lactation) based on information collected during farm visits and lambing dates. Descriptive statistics were performed, followed by the creation of a mixed linear model of the logarithmic-transformed outcome FEC. During the winter and spring lambing seasons, the FECs increased gradually over the gestation period and peaked during lactation, with these increases being larger in ewes with a low PCV (three-way interaction in the final model). In the autumn lambing season, the FECs started off higher in early gestation, and increased rapidly to peak in late gestation, particularly for animals with a low PCV. The PPER occurred during all three lambing seasons, but its magnitude and distribution varied with the lambing season and PCV, suggesting that the PPER in ewes depends on both environmental and physiological factors, an important consideration when implementing preventive parasite control strategies on sheep farms that practice out-of-season lambing.

Acknowledgements: This research was supported by the Ontario Ministry of Agriculture, Food and Rural Affairs – New Directions Research Program, with additional financial assistance from the Ontario Sheep Marketing Agency, the Nova Scotia Agricultural College – Organic Science Cluster, and the University of Guelph.



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Session Details:	8/29/2013 COMMERCIAL LIVESTOCK - SHEEP 1515 - 1630 Riverside Theatre
Oral Presentation Details:	Gastrointestinal nematode control in sheep under three grazing management systems and factors influencing faecal worm egg count
Presentation Time:	1600 -1615
Authors:	Walkden-Brown S ¹ , Colvin A ² , Hall E ³ , Knox M ⁴ , Mackay D ⁵ , Scott J ⁶ ¹ School of Environmental and Rural Science, University of New England, Armidale 2351, Australia, ² School of Environmental and Rural Science, University of New England, Armidale 2351, Australia, ³ 111 Margaret Street, Launceston, Tasmania 7250, Australia, ⁴ CSIRO Livestock Industries, Armidale 2350, Australia, ⁵ 3 Jayne Cl, Armidale, NSW 2350, Australia, ⁶ School of Environmental and Rural Science, University of New England, Armidale 2351, Australia

A six-year study on 50 ha farmlets on the northern tablelands of NSW compared control of gastrointestinal nematode (GIN) infection of sheep under typical (TYP), high input (HI) or intensive rotational grazing (IRG) management systems. The major sources of variation in faecal worm egg count (WEC) were also examined. The data set comprised 5644 faecal worm egg count (WEC) records and 322 larval differentiation tests.

Worm infections in ewes, lambs, hoggets and wethers were, with some exceptions, adequately controlled through a combination of regular monitoring of WEC, anthelmintics and grazing management. The IRG farmlet had lower mean WEC (444 epg) and annual anthelmintic treatment frequency (3.1 treatments/yr) over the whole experimental period than TYP (1122 epg, 4.3 treatments/yr) or HI (1374 epg, 4.7 treatments/yr). The main factors influencing WEC were the time since the last anthelmintic treatment, and the anthelmintic used at that treatment. The magnitude of these effects dwarfed those climatic and management factors that might be expected to influence the epidemiology of GIN infections via environmental or host-mediated mechanisms. Nevertheless management factors associated with stocking rate and grazed proportion (proportion of each farmlet grazed at any one time), and climatic indicators of both temperature and moisture availability had significant effects on WEC.

The results show that in a region with *Haemonchus contortus* as the major GIN, improved host nutrition under the HI system did not provide more effective control of GIN than typical management, while IRG did provide considerably better control. Tactical worm control based on WEC monitoring provided adequate control of worms on all three farmlets for much of the experimental period but failed to prevent significant spikes in WEC on the TYP and HI farmlets to values associated with significant production loss on multiple occasions, and mortality on one occasion.

Acknowledgements:

The Cicerone farmlet experiment was generously funded by Australian Wool Innovation. The support and practical assistance of the Cicerone Farm Manager, Mr Justin Hoad and the Cicerone Executive Office, Ms Caroline Gaden, are gratefully acknowledged.





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Session Details:	8/29/2013 COMMERCIAL LIVESTOCK - SHEEP 1515 - 1630 <i>Riverside Theatre</i>
Oral Presentation Details:	The influence of farmer autonomy on gastrointestinal nematode infection in semi-extensive meat sheep farms
Presentation Time:	1615 -1630
Authors:	Cabaret J¹ , Chylinski C ¹ , Meradi S ² , Leignel G ³ , Nicourt C ⁴ , Bentounsi B ⁵ , Benoit M ³ ¹ INRA and François Rabelais University, ² Biological Sciences, University, ³ INRA, URH, ⁴ INRA, RiTME,, ⁵ Veterinary Département, Parasitology, Mentouri University

Integration in farming can be applied at two different levels: 1) General integration of a production system such as in poultry and pig industries where a private integrator provides young animals, food and sometimes housing and therapeutics; 2) Local integration at farm level where the farmer decides on the complementarity of agriculture and husbandry, the animals to be bred, food management, housing and therapeutics. Local integration is seen at various degrees in organic and conventional semi-extensive meat sheep farms. The aim of this research was to relate the level of integration on sheep farms to the control of gastrointestinal nematode (GIN) infection. Sixteen French (F) (conventional and organic) and 20 Algerian (A) (conventional) meat sheep farms were studied. Questionnaires and interviews were used to obtain information on farming characteristics. Faecal egg counts (FEC) were used to estimate the level of infection in ewes. The following integration variables were recorded and coded from 0 (absence of autonomy) to 3 (largest autonomy=absence of integration): 1) mixture of agriculture and husbandry, 2) housing, 3) feeding diversity, 4) therapeutics, 5) commercialisation of their animal products. Both regions had a GIN fauna which included *Ostertagiinae* and *Trichostrongylus* with a very low prevalence of *Haemonchus*. The FEC were on average 314 vs 113 (F and A respectively). Spearman correlations with FEC and autonomy were only found to be significant with the therapeutics variable: -0.63 vs -0.41 (F and A respectively). The therapeutics variable was a combination of the number of synthetic anthelmintic treatments, the use of alternative dewormers, and whether or not the farmer was the decision maker for anthelmintic treatments. This means that a greater autonomy in therapeutics is associated with greater worm control as estimated from FEC. Thus, if dependable control information is available to the farmer he can perhaps be relied upon to take control decisions into his own hands.

Acknowledgements:

The INRA-CIAB and EU Parasol project funded the sheep surveys. C. Chylinski is a grateful recipient of a PhD grant from Nematode System Health EU Marie Curie project.

Session Details:	8/29/2013 HOST PARASITE RELATIONSHIPS 2 1515 - 1630 <i>Meeting Room 1</i>
Oral Presentation Details:	<i>Opisthorchis viverrini</i> exosomes, a molecular mechanism for host-parasite interactions
Presentation Time:	1515 -1530
Authors:	Sotillo Gallego J¹, Chaiyadet S², Smout M¹, Jones M³, Mulvenna J⁴, Sripan B², Loukas A¹ ¹ Centre for Biodiscovery and Molecular Development of Therapeutics, James Cook University, Cairns, Queensland, Australia, ² Department of Parasitology, Khon Kaen University, Khon Kaen, Thailand, ³ School of Veterinary Sciences, The University of Queensland, Gatton, QLD, Australia, ⁴ Division of Infectious Diseases, Queensland Institute of Medical Research, Brisbane, QLD, Australia

Opisthorchis viverrini is a liver fluke trematode that causes major health problems in several Southeast Asian countries such as Thailand, Cambodia and Laos. The importance of *O. viverrini* is related to its infection-associated morbidity, which often culminates in bile duct cancer, or cholangiocarcinoma (CCA). The excretory/secretory products (ESP) of *O. viverrini* have been characterised using proteomic approaches, but substantially less is known about the mechanisms by which these ESP interact with the host and promote tumourigenesis. Herein, we show that *O. viverrini* secretes extracellular vesicles of endocytic origin, known as exosomes. These exosomes contain parasite-specific proteins already identified as components of the ESP in previous studies (Mulvenna *et al.*, 2010). Also, we show that these extracellular vesicles are internalized by human biliary epithelial cells and induce significant changes in cellular morphology and gene/protein expression. Exosomes have already been described in other helminths (Marcilla *et al.*, 2012) and protozoa such as *Leishmania* spp. and *Trypanosoma* spp. (Silverman *et al.*, 2010; Clayton and Estevez, 2011), and have been demonstrated to play a role in the modulation of the host immune response. The presence of exosomes in *O. viverrini* ESP may explain how proteins with no classical secretory signal motif are released into the extracellular environment by the parasite, and may play a significant role in host-parasite interactions and disease pathogenesis.

Acknowledgements:

This work was supported by project and program grants from the National Health and Medical Research Council of Australia (NHMRC). AL is supported by a NHMRC principal research fellowship.

References:

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Session Details:	8/29/2013 HOST PARASITE RELATIONSHIPS 2 1515 - 1630 Meeting Room 1
Oral Presentation Details:	A granulin growth factor secreted by the carcinogenic liver fluke, <i>Opisthorchis viverrini</i> , and its role in carcinogenesis
Presentation Time:	1530 -1545
Authors:	Smout M ¹ , Sotillo J ¹ , Laha T ² , Sripa B ² , Mulvenna J ³ , Chan L ⁴ , Brindley P ⁵ , Loukas A ¹ ¹ Queensland Tropical Health Alliance and Centre for Biodiscovery & Molecular Development of Therapeutics, James Cook University, Cairns, QLD, Australia, ² Department of Parasitology, Khon Kaen University, Khon Kaen, Thailand, ³ Queensland institute of Medical Research, Brisbane, QLD, Australia, ⁴ Institute of Molecular Bioscience, Brisbane, QLD, Australia, ⁵ George Washington University, Washington DC, USA

The human liver fluke, *Opisthorchis viverrini*, infects 9 million people throughout South-East-Asia and is a major cause of cholangiocarcinoma (bile duct liver cancer). In fact, as many as one-sixth of infected patients will develop liver cancer. The mechanisms by which the parasite causes cancer are multi-factorial, but one process is the secretion of mitogenic parasite proteins into the bile ducts, driving cell proliferation and creating a tumourigenic environment. Using proteomics and transcriptomics to characterise the *O. viverrini* secretome, we identified Ov-GRN-1, a homologue of the human growth factor, granulin. Previously we demonstrated potent growth factor activity (nanomolar) of recombinant Ov-GRN-1 on human biliary cells. Here we show that Ov-GRN-1 induces wound closure *in vitro* and results from *in vivo* wound healing experiments are ongoing and will be presented. Ov-GRN-1 stimulated angiogenesis (blood vessel formation) *in vivo*, a process critical for cancer development. Binding of recombinant Ov-GRN-1 to biliary epithelial cells induced dramatic changes in protein expression. Indeed, and in support of our hypothesis, many of the cellular proteins that were upregulated in response to Ov-GRN-1 were associated with cell growth and cancer, whereas the downregulated proteins were associated with tumour/proliferation suppression. Finally, silencing of *Ov-grn-1* gene expression using RNA interference resulted in reduced mitogenicity of biliary cells by *O. viverrini* excretory/secretory products. Our novel findings contribute to the understanding of host-parasite interactions, and begin to address the mechanisms by which this parasite causes such a devastating form of cancer.

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Session Details:	8/29/2013 HOST PARASITE RELATIONSHIPS 2 1515 - 1630 <i>Meeting Room 1</i>
Oral Presentation Details:	Membrane biogenesis and renewal of the <i>Schistosoma mansoni</i> tegument
Presentation Time:	1545 -1600
Authors:	Leigh Schulte ^{*(1, 2)} , Jason Mulvenna ⁽¹⁾ , Geoffrey Gobert ⁽¹⁾ and Malcolm Jones ^(1, 2) ⁽¹⁾ Queensland Institute of Medical Research, Brisbane ⁽²⁾ School of Veterinary Sciences, The University of Queensland, Brisbane

The tegument of *Schistosoma mansoni* serves a variety of critical biological roles for the parasite, including nutrition, osmoregulation, immune evasion and immuno-modulation. Dynein light chains (DLCs) and tetraspanins (TSPs) are prominent proteins in the tegument and appear to be intimately linked with other molecules present in the apical, host-interactive, membrane of the parasites. In other eukaryotic cells, cytoplasmic DLCs are a subunit of motor complexes involved in diverse cellular translocation events as protein trafficking, mitosis and ciliary beating. DLCs of the schistosome tegument likely have similar roles and are likely to be important in the development and renewal of the tegument membrane, thereby contributing to parasite survival in its host. TSPs are membrane-spanning proteins that act as scaffolds for the formation of membrane-associated protein complexes comprising a wide variety of proteins. These tetraspanin-enriched microdomains are known to play a wide range of roles within human cells, including maintenance of cell morphology and cell signalling. As an anti-schistosomal vaccine SmTSP-2 has shown high protection, however its biological role in the tegument remains unknown.

To explore protein interactions within the tegument we have used multiple methods, including Blue Native polyacrylamide gel electrophoresis and protein crosslinkers, coupled with in-line liquid chromatography-tandem mass spectrometry. To functionally characterise selected tegumental proteins, RNA interference has been used to knock down the gene of interest, and phenotypic changes will be visualised by electron microscopy. This study provides insights into the molecular complexes associated with the host-interactive surface of schistosomes and will highlight, which molecules are associated with the surface membranes, but how these molecules functionally contribute to the maintenance of the parasite host-parasite interface. This is a critical biological function for the survival of the parasite within the mammalian host and may lead to the identification of novel targets for vaccination or drug therapy for schistosomiasis.



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Session Details:	8/29/2013 HOST PARASITE RELATIONSHIPS 2 1515 - 1630 <i>Meeting Room 1</i>
Oral Presentation Details:	To serve or to protect? Functional analysis of <i>Fasciola hepatica</i> type 2 cystatin.
Presentation Time:	1600 -1615
Authors:	Saša Štefanić^{1*} , Zuzana Kovarova ² , Michael Mares ² , Peter Deplazes ¹ ¹ Institute of Parasitology, Vetsuisse Faculty, University of Zurich, Winterthurerstr. 266a 8057 Zurich, Switzerland ² Institute of Organic Chemistry and Biochemistry ASCR, Flemingovo namesti 2, Prague 16610, Czech Republic

Cystatins are reversible tight-binding inhibitors of cysteine proteases of the papain (C1) and legumain (C13) enzyme families [1]. They are found in a large variety of organisms ranging from protozoans to vertebrates, localizing both intracellularly and extracellularly, and assume important physiological roles such as protecting cells from uncontrolled activities of endogenous cysteine proteases [2]. In addition, parasite cystatins have an important role in the invasion process by regulating the activity of host proteases. Substantial immunomodulatory effects of filarial and tick cystatins have been demonstrated [3-5], but less is known about the function of cystatins in trematodes [6, 7]. We investigate functional aspects of *Fasciola hepatica* type 2 cystatin (FheCY2) in juvenile and adult stages using several complimentary approaches. The change in global proteolytic activity (particularly the role in regulation of the activity of gut proteases, cathepsins B and L) and the effect on worm survival *in vitro* and *in vivo* is assessed using RNAi based approach. The approach is validated by *in vitro* protease activity assays and complemented by confocal microscopy to investigate the tissue localization of FheCY2. The FheCY2 was expressed in the yeast *Pichia pastoris* in its active form, and the recombinant protein inhibited typical members of the C1 cysteine protease family (papain). Blood serum from cattle infected with *F. hepatica* reacted positive against the recombinant molecule, and the presence of FheCY2 in the supernatant of cultivated parasites was demonstrated by using specific antibodies. Furthermore, we obtained knockdown of FheCY2 in cultured worms, but no obvious phenotypic alterations were observed. Confocal microscopy demonstrated that FheCY2 is localized to the secretory system of adult parasites. The role of FheCY2 in the establishment of the infection is being investigated in a sheep model to assess the vaccine potential of FheCY2, its role during the infection and migration phase of *F. hepatica* and involvement in immunomodulation.

Session Details:	8/29/2013 HOST PARASITE RELATIONSHIPS 2 1515 - 1630 Meeting Room 1
Oral Presentation Details:	Expression and functional characterization of the <i>R. microplus</i> serpin (RMS-4), a specific Thrombin inhibitor
Presentation Time:	1615 -1630
Authors:	Xu T ¹ , Rodriguez-Valle M ¹ , Lew-Tabor A ^{1,2} ¹ The University Of Queensland, ² Murdoch University, Centre for Comparative Genomics

Rhipicephalus (Boophilus) microplus is a one-host bovine ectoparasite, widely distributed in tropical and subtropical areas of the world. The current Australian industry annual loss due to ticks and TBDs is estimated over 175 million AUS\$ (1). Studies have found that *R. microplus* is able to circumvent the host’s haemostatic system using specific serine protease inhibitors (serpins) (2). Additionally, serpins are considered as potential target proteins for vaccine and drug development (3). RMS-4 is one of fourteen novel serpins identified from Australian *R. microplus* transcriptome libraries. The full coding sequence of RMS-4 was attained by RACE, which deduces 404 amino acids consisting of three β-sheets, eight α-helices and a reactive centre loop. Bioinformatics analysis predicted RMS-4 as a putatively inhibitory and secretory serpin. The results of gene expression analysis showed that RMS-4 is expressed in eggs, nymphs, female salivary glands, ovaries and female guts. The recombinant RMS-4 (rRMS-4) was expressed in the methylotrophic yeast *Pichia pastoris*. rRMS-4 was purified by nickel affinity chromatography and gel filtration chromatography. An array of serine proteases was used to characterise the inhibitory activity of rRMS4. Data obtained from these assays showed that rRMS-4 is a Thrombin specific inhibitor with the second-order association rate constant (k_{ass}) of $9.2 \times 10^4 \text{ M}^{-1}\text{s}^{-1}$. Thrombin was inhibited at a ratio of 1:4 molecules of rRMS-4. This research shows for the first time, a recombinant serpin from *R. microplus* with highly significant Thrombin inhibition. The results obtained contribute to the understanding of the role of *R. microplus* serpins during tick-host interactions.

Acknowledgements

This research has been supported by the Beef CRC and Meat & Livestock Australia.

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Session Details:	8/29/2013 DIAGNOSTICS - NEMATODES 1515 - 1630 <i>Meeting Room 2</i>
Oral Presentation Details:	Surprising Results for the Distribution of and Short Term Variation in Cattle Faecal Worm Egg Counts
Presentation Time:	1515 -1530
Authors:	Van Burgel A Department Of Agriculture And Food Western Australia

The data from a recent series of faecal egg count reduction tests on young cattle from 19 farms in the south west of Western Australia showed some unexpected results in the distribution of and short term variation in cattle faecal worm egg counts.

The distribution was much less over dispersed than expected with only a small proportion of animals having zero counts. A negative binomial distribution was fitted to each dataset and the overdispersion (k) parameter was 1.7 on average across the farms, higher than typically experienced in sheep in the same region. The consequences of this for the method of faecal worm egg count reduction tests is discussed as well as comparisons to older cattle and sheep.

It was also surprising to observe how frequently the faecal worm egg counts of animals in the control group (no drench) varied considerably over two weeks. On some farms a large and significant increase was observed in some animals while other animals in the same group had a large and significant decrease. This insight came about as a consequence of counting extra chambers for some control animals such that the conversion factor was four eggs per gram for each egg counted rather than the usual 12.5. The results for cattle are compared to those observed in sheep and also comparisons to other research findings in the literature are discussed.



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Session Details:	8/29/2013 DIAGNOSTICS - NEMATODES 1515 - 1630 <i>Meeting Room 2</i>
Oral Presentation Details:	Prevalence of <i>Strongyloides stercoralis</i> infection in a remote Indigenous community as determined by ELISA testing from dried blood spot for antibodies to the recombinant antigen NIE
Presentation Time:	1530 -1545
Authors:	Mounsey K ^{1,2} , Rampton M ^{1,2} , Llewlyn S ² , Pasay C ² , King M ² , Holt D ³ , Currie B ³ , Kearns T ³ , Andrews R ³ , Nutman T ⁴ , McCarthy J ² ¹ University Of The Sunshine Coast, ² Queensland Institute of Medical Research, ³ Menzies School of Health Research, ⁴ National Institutes of Health

Parasitologic diagnosis of infection with the intestinal nematode *Strongyloides stercoralis stercoralis* is relatively insensitive and logistically challenging. Serologic assays based on detection of antibodies to crude larval antigen offer increased sensitivity, but specificity is hampered by cross-reactive antibodies and persistence after cure. Further, standardization of antigen for assays is problematic. The use of recombinant antigen can potentially overcome these problems, and the NIE antigen from *S. stercoralis* has been used widely with good diagnostic sensitivity and specificity.

Detection of antibody eluted from dried blood spots has shown utility in large-scale seroepidemiologic studies, and is appealing in children where venipuncture or stool collection is problematic. We adapted an existing NIE-ELISA protocol for the testing of anti-strongyloides antibody response on dried blood spots collected as part of an ivermectin mass drug administration conducted in a Northern Territory community. The NIE ELISA was first validated using representative positive, negative, and equivocal time-matched serum samples previously tested using *S. ratti* antigen ELISA. Optimal assay and storage conditions were determined using positive control blood spots, and samples screened with the adapted NIE-DBS-ELISA. Blood spots were stable for several days at 37°C, or following longer-term storage at 4°C, -20°C or -80°C.

The sensitivity of the NIE-DBS-ELISA was determined by ROC analysis to be 82%. Of the 219 blood spots tested, 18% were positive for *S. stercoralis*, a similar prevalence to that documented by standard *S. ratti* serology. In representative samples positive for *S. ratti*-specific antibodies, a significant decline in NIE optical density was observed at 6 and 12 months following ivermectin MDA ($p < 0.0001$). No time-associated differences were seen in negative or equivocal samples. This further confirms the high seroprevalence of *S. stercoralis* in remote Australian Indigenous communities, and suggests that collection of dried blood spots may be useful approach for field-friendly diagnosis of strongyloidiasis.

Session Details:	8/29/2013 DIAGNOSTICS - NEMATODES 1515 - 1630 <i>Meeting Room 2</i>
Oral Presentation Details:	P-Glycoproteins in macrocyclic lactone resistance of equine parasitic nematodes: Functional analysis of putative resistance markers using a yeast expression system
Presentation Time:	1545 -1600
Authors:	Janssen J ¹ , Kaschny M ¹ , Demeler J ¹ , Ramünke S ¹ , Burton T ² , Besognet B ³ , Kanellos T ³ , Kerboeuf D ⁴ , von Samson-Himmelstjerna G ¹ , Krücken J¹ ¹ Freie Universität Berlin, ² Colorado State University, ³ Zoetis, ⁴ INRA

Macrocyclic lactone (ML) resistance is widespread in the horse roundworm *Parascaris equorum* and is beginning to arise in small strongyles (cyathostomins). Although the mode of ML action in nematodes is well known, mechanisms of ML resistance are not yet understood. Mammalian P-glycoproteins (Pgps) have been shown to transport MLs and nematode Pgps were frequently postulated to be involved in ML resistance. In a recent study three single nucleotide polymorphisms (SNPs) in the *P. equorum pgp-11* gene were identified which correlated with reduced ML efficacy on German horse farms. Here, pyrosequencing assays were developed to rapidly and precisely quantify the alleles present in a particular population. Very high correlation between actual and observed allele frequencies were observed for all three assays ($p>0.95$). This will allow comparing SNP frequencies with faecal egg count reduction test data for a larger number of farms from different regions in order to systematically address the importance of the SNPs in ML resistance. In addition, functional assays are currently used to determine whether these SNPs influence transport of MLs by *PeqPgp-11*. A yeast growth assay was established using *Cylicocyclus elongatus* Pgp-9 and a *Saccharomyces cerevisiae* strain deficient in 6 ABC transporters. Recombinant expression of this transporter slightly decreases susceptibility of yeast cells to the fungicide ketoconazole. In yeasts expressing *C. elongatus* Pgp-9, at a ketoconazole concentration where they still show normal growth, addition of increasing amounts of verapamil and the MLs ivermectin, eprinomectin or moxidectin decreased yeast growth. These data strongly suggest that MLs sensitise the recombinant yeast strain by competitive inhibition of ketoconazole extrusion mediated by a parasitic nematode Pgp.

References

Genetic Variants and Increased Expression of *Parascaris equorum* P-glycoprotein-11 in Populations with Decreased Ivermectin Susceptibility (2013) Jana Janssen, Jürgen Krücken, Janina Demeler, Marta Basiaga, Sławomir Kornaś, Georg von Samson Himmelstjerna. PLoS One <http://dx.plos.org/10.1371/journal.pone.0061635>



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Session Details:	8/29/2013 DIAGNOSTICS - NEMATODES 1515 - 1630 <i>Meeting Room 2</i>
Oral Presentation Details:	Evaluation of resistance in a selected field strain of <i>Haemonchus contortus</i> to ivermectin and moxidectin using the Larval Migration on Agar Test
Presentation Time:	1600 -1615
Authors:	Fortes F ¹ , Kloster F ¹ , Schafer A ² , Bier D ¹ , Buzatti A ¹ , Yoshitani U ¹ , Molento M ¹ ¹ Universidade Federal do Parana, ² Universidade Federal de Santa Maria

Haemonchus contortus is one of the most common and economically significant causes of disease in small ruminant farms worldwide. Parasite control programs - including *H. contortus* - rely mostly on the use of anthelmintic drugs - ATH. The consequence of using ATH as the sole sanitary strategy to avoid parasite infection has reduced the efficacy of all chemotherapeutic products heavily selecting for ATH-resistance populations. The widespread of ATH-r and the difficulty of its early diagnosis has been a major concern for the sustainable parasite management on farms. The objective of this research was to determine and compare the ivermectin (IVM) and moxidectin (MOX) effect in a selected field strain of *H. contortus* with a known ATH-r status, using the *in vitro* larval migration on agar test (LMAT). Third stage larvae of the selected isolate were obtained from faecal cultures of experimentally infected sheep and incubated with 11 concentrations of IVM or MOX: 6, 12, 24, 48, 96, 192, 384, 768, 1536, 3072 and 6144 µg/ml. The dose-response curves were obtained with R^2 value above 0.9 and the 50% lethal concentration (LC_{50}) dose for the tested anthelmintic drugs used a four-parameter logistic model. The LC_{50} value for MOX was significantly lower than IVM (1.253 µg/ml and 91.06 µg/ml), identifying the *H. contortus* isolate as considerably less susceptible to IVM compared to MOX. Furthermore, the LMAT showed a high consistency ($p < 0.0001$) and provided to be a useful diagnostic tool for monitoring the resistance status of IVM and MOX in *H. contortus* field isolate. The LMAT technique may be used on official routine drug monitoring programs under the Ministry of Agriculture guidance.

Acknowledgements:

The authors are grateful to Conselho Nacional de Desenvolvimento Científico e Tecnológico for the financial support - Process 559614/2009-8 and to Coordenação de Aperfeiçoamento de Pessoal de Nível Superior, CAPES/REUNI for providing a doctoral degree scholarship to Fernanda S. Fortes.



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Session Details:	8/29/2013 DIAGNOSTICS - NEMATODES 1515 - 1630 <i>Meeting Room 2</i>
Oral Presentation Details:	Coprophagy interferes with coproscopical diagnosis of helminth infections in dogs.
Presentation Time:	1615 -1630
Authors:	Nijse R , Wagenaar J, Ploeger H Utrecht University

Coprophagial behaviour is common amongst dogs. Parasite eggs shed by other animals can pass the digestive tract of dogs what may result into a false positive diagnosis of infection with gastro-intestinal parasites.

As part of an ongoing longitudinal study in which dog owners submit fecal samples monthly for 2 years to detect the presence of enteropathogens in dogs, we were able to observe how often coprophagy occurs in dogs resulting in false positive samples.

Feces was collected between January and June 2013 and examined using the CSF-technique with a sugar flotation solution (density 1.3 g.cm⁻³). If a sample tested positive for helminth eggs, the owner was asked to collect another sample 3 days after keeping the dog from eating anything from the environment. If the samples were tested positive again it was considered a patent infection, if negative the first was considered to be false positive due to coprophagy.

So far, 102 of 1576 (6,4 %) samples tested positive. Of these, 44 (43%) tested negative in the repeated sample and consequently were considered false positive. Several of the samples considered to be false positive, were found to contain eggs in varying stages of development, including moving larvae in strongyle-type eggs. There were no differences in percentages of observed false positives between months.

286 of 567 (50%) dog owners mention that their dogs eat feces. 36% of 925 dogs actually have been observed to eat feces by their owners. Nonetheless, the percentage of dogs eating feces is likely an underestimation. 27.5% of *Eimeria* oocyst positive samples originated from dogs that do not eat feces according to their owner.

Results indicate that coprophagy may result in a serious overestimation of the prevalence of patent helminth infections in dogs. Further, dogs might act as transport hosts due to their coprophagic behaviour.



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Session Details:	8/29/2013 DRUG EFFICACY - ECTOPARASITES 1515 - 1630 <i>Meeting Room 3</i>
Oral Presentation Details:	Tea tree (<i>Melaleuca alternifolia</i>) oil for the control of sheep lice and myiasis
Presentation Time:	1515 -1530
Authors:	James P , Callander J University Of Queensland

Tea tree oil (TTO) derived from the Australian native plant *Melaleuca alternifolia* has wide ranging antimicrobial properties and has been used since the first Australians to treat a range of cutaneous ailments. In our studies the effect of TTO (Terpinen-4-ol chemotype) was tested against sheep ectoparasites in a series of laboratory and animal experiments. In laboratory tests against the sheep myiasis fly *Lucilia cuprina*, TTO demonstrated ovicidal and larvicidal activity and repelled both adult flies and larvae. In laboratory assays with sheep lice (*Bovicola ovis*), immersion of wool containing lice in 1% TTO formulations for 30–60 s consistently gave 100% kill of adult and nymphal lice and 70–100% mortality of lice eggs. Fumigant activity was apparent against both lice and eggs. In animal studies, immersion dipping of sheep with moderate to heavy *B. ovis* infestations in 1% and 2% TTO formulations eradicated lice from all animals. Tea tree oil composition is regulated under International Organization for Standardization standard 4370, helping to counter difficulties with variable quality and efficacy often encountered with botanical compounds. Our results, together with the antimicrobial and wound healing properties of TTO, suggest significant potential for the development of ectoparasiticides incorporating TTO for treating pediculosis in sheep and cutaneous myiasis.

Session Details:	8/29/2013 DRUG EFFICACY - ECTOPARASITES 1515 - 1630 <i>Meeting Room 3</i>
Oral Presentation Details:	Acaricidal effect of extracts of fruits of <i>Piper tuberculatum</i> against the cattle tick <i>Rhipicephalus microplus</i>
Presentation Time:	1530 -1545
Authors:	Lima A, Sousa-Filho J, Pereira S, Costa-Junior L Federal University Of Maranhão, Brazil

Rhipicephalus microplus is the main problem of cattle livestock. Plant bioactive Molecules can be an alternative to control of this ectoparasite. Thus, the purpose of this study was to evaluate the in vitro efficacy of fruits extracts of *Piper tuberculatum* obtained with different solvents on larvae and engorged females of *R. microplus*. Hexane, ethyl ether, ethanolic and methanolic extracts of *P. tuberculatum* fruits was performed. After extraction all extracts were dried and obtained Hexane, ethyl ether, ethanolic and methanolic extracts to use in the tests. Adult Imersion Tests and Larval Packet Tests were performed with all extracts using five different concentrations. Hexane extracts of *P. tuberculatum* showed high larvicidal activity against *R. microplus* (LC 50 = 0.04 mg/mL), followed by ethyl ether (LC50 = 0.08 mg/mL), ethanolic (LC 50 = 2.73 mg/mL) and methanolic (LC 50 = 4.49 mg/mL) extract. Fruits extracts of *P. tuberculatum* were efficient against engorged females of *R. microplus*. Ethyl acetate extracts showed high efficiency (LC 50 = 18.4 mg/mL), followed by methanolic (LC 50 = 105.6 mg/mL), ethanolic (LC 50 = 140.0 mg/mL) and Hexane (LC 50 = 297.4 mg/mL) extract. All extracts showed similar chromatographic profile, with 24% of piperine. Mammalian toxicity tests need to be conducted to further acaricidal *in vivo* tests against *R. microplus*.

Acknowledgements:

FAPEMA, CAPES, and CNPq.

Session Details:	8/29/2013 DRUG EFFICACY - ECTOPARASITES 1515 - 1630 <i>Meeting Room 3</i>
Oral Presentation Details:	A multi-site randomised controlled trial to evaluate the efficacy of plastic clips to prevent flystrike in Australian sheep
Presentation Time:	1545 -1600
Authors:	Playford M¹ , Rabiee A ² , Lean I ² , Evans I ³ ¹ Dawbuts Pty Ltd, ² SBScibus Pty Ltd, ³ Australian Wool Innovation

Aim: Flystrike (cutaneous myiasis) is a common disease of Australian sheep, with major welfare and economic impacts. Preventive measures in the past have relied on chemicals and surgical modification of the breech area. This trial was conducted to evaluate the efficacy of plastic clips applied to the breech area and tail to alter the susceptibility of sheep to flystrike.

Methods: Male and female lambs on 208 properties across Australia were assessed for parameters predisposing to flystrike (bodyweight, skin type and thickness, breech bare area measurement and scores, urine and faecal stain scores), then randomly assigned to treatment (2 breech and 2 tail clips applied at lamb marking, n=80) and control (no treatment, n=80) groups. Farm (area, rainfall, size) and flock (breed, wool diameter) features were also recorded. Clips were applied by 35 trained operators. Lambs were assessed at day 14 for healing and at day 55, when the measurements and scores were again conducted. Changes in flystrike predisposition parameters were assessed and correlated with lamb, flock and farm features using a multivariate analysis.

Results: Treated male and female lambs had 16% and 21% greater horizontal bare area measurements, and 31.7% and 32.7% higher bare area scores than control lambs, respectively at 55 days post-treatment. Scores for wrinkle (6.8% and 5.8% respectively), dag (12% and 12.25% respectively) and urine stain (18.75%) were lower in treated male and female lambs. Bodyweights were slightly lower in treated lambs compared to controls; 0.320kg (1.24%) and 0.430kg (1.58%) for ewes and wethers, respectively.

Conclusion: This trial showed that when assessed on 32,028 lambs across climate and geographical zones of Australia, polypropylene clip treatment improved parameters closely associated with flystrike susceptibility.

Acknowledgements: Operators, Regional Coordinators, property owners, AWI staff and contractors who made this study possible.

References:

Playford, M., I. Evans, J. Lloyd, P. Lawton, A. Rabiee, and I. Lean. 2012. Multisite randomised controlled trial to evaluate polypropylene clips applied to the breech of lambs as an alternative to mulesing. I: effects on body weight, breech bare area measurements and scores, wrinkle scores and faecal and urine staining. Aust Vet J 90(11):415-422.

Rabeee, A., M. Playford, I. Evans, G. Lindon, M. Stevenson, and I. Lean. 2012. Multisite randomised controlled trial to evaluate polypropylene clips applied to the breech of lambs as an alternative to mulesing. II: multivariate analysis of relationships between clip treatment and operator, sheep, farm and environmental factors. *Aust Vet J* 90(11):423-432.

Session Details:	8/29/2013 DRUG EFFICACY - ECTOPARASITES 1515 - 1630 Meeting Room 3
Oral Presentation Details:	Treatment and control of bovine mange infestation with ivermectin long-acting injection (IVOMEC® GOLD)
Presentation Time:	1600 -1615
Authors:	Hamel D ¹ , Silaghi C ² , Joachim A ³ , Löwenstein M ³ , Visser M ¹ , Winter R ¹ , Yoon S ⁴ , Cramer L ⁴ , Rehbein S ¹ ¹ Merial GmbH, Kathrinenhof Research Center, Rohrdorf, Germany, ² Comparative Tropical Medicine and Parasitology, Ludwig-Maximilians-Universität, Munich, Germany, ³ Parasitology and Zoology, University of Veterinary Medicine, Vienna, Austria, ⁴ Merial Limited, Duluth, GA, USA

The efficacy of ivermectin long-acting injection (IVM LAI; IVOMEC® GOLD, Merial; 3.15% ivermectin w/v) was evaluated in cattle with induced *Sarcoptes scabiei* var. *bovis* or *Psoroptes ovis* infestations in four similar studies (two per parasite) conducted in Germany and Austria. Sixteen Fleckvieh cattle were included in each study. Approximately 8 weeks following induced infestation using recent field isolates (~4,700 *Sarcoptes* or ~2,100 *Psoroptes* mites per animal), cattle in each study were formed into replicates of two animals each based on pre-treatment bodyweights. Within replicates, animals were allocated randomly to one of two groups: saline (control) or IVM LAI. Both treatments were administered by subcutaneous injection in front of the right shoulder on Day 0 at 1 mL/50 kg bodyweight. For evaluation of efficacy, skin scrapings taken prior to treatment and at intervals of 7±1 days for 8 weeks were examined to determine the number of live mites, and size and character of skin lesions were scored.

Following treatment, mite counts of the IVM LAI-treated cattle were significantly lower than those of the controls at each evaluation. IVM LAI-treated cattle were free of *Sarcoptes* mites from Day 14 or free of *Psoroptes* mites from Days 13 or 28 and remained mite-free until study end. Mange lesions regressed accordingly, starting on Day 21 in the *Sarcoptes* infested cattle or on Days 28 or 34 in the *Psoroptes* studies.

Over the post-treatment period, IVM LAI treated cattle gained significantly more weight than the saline-treated controls: *Sarcoptes* studies, 64.1 kg vs. 46.9 kg and 68.6 kg vs. 48.6 kg; *Psoroptes* studies, 43.0 kg vs. 20.8 kg and 43.4 kg vs. 34.9 kg.

These studies demonstrated a high efficacy of IVOMEC GOLD against bovine mange mite infestations with associated improved weight gain.

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Session Details:	8/29/2013 DRUG EFFICACY - ECTOPARASITES 1515 - 1630 <i>Meeting Room 3</i>
Oral Presentation Details:	Canine generalized demodicosis treated with varying doses of Advocate® (moxidectin 2.5% + imidacloprid 10%) (Bayer Animal Health) and oral ivermectin: parasitocidal effects and long-term treatment outcomes
Presentation Time:	1615 -1630
Authors:	Paterson T ¹ , Halliwell R ¹ , Fields P ² , Lanza Louw M ¹ , Ball G ¹ , Louw J ¹ , Macpherson C ³ , Pinckney R ⁴ , McKibben J ¹ ¹ St. George's University, Small Animal Clinic, ² Brigham Young University, ³ St. George's University, WINDREF, ⁴ St. George's University, Department of Pathobiology

Fifty-eight dogs suffering from generalized demodicosis were included in this blind, randomized clinical trial which compared the efficacy of Advocate® (moxidectin 2.5%+imidacloprid 10%)(Bayer Animal Health, Leverkusen, Germany) at varying intervals with ivermectin. They were randomly assigned to one of four treatment groups: Advocate® applied once monthly (ADV1), biweekly (ADV2), weekly (ADV4) or ivermectin 500µg/kg orally once daily (IVR). Dogs were evaluated at four week intervals until parasitological cure (two series of deep skin scrapings undertaken at monthly intervals that were negative). Forty dogs completed the 16-week efficacy phase, with 5 cases achieving parasitological cure. Five dogs were judged treatment failures and subsequently treated with ivermectin. The treatment protocol was changed for the remaining dogs during an eight-week cross-over phase which resulted in 9 more dogs achieving parasitological cure. Thereafter, all remaining animals were treated with ivermectin until cured. A total of 26 dogs achieved parasitological cure during the course of the study. Twenty-three remained disease-free for >12 months while two were lost to follow-up and one died of unrelated causes. Parasitocidal efficacy was assessed during the efficacy phase by changes in mite counts (live adult, juvenile and egg) and skin lesion extent & severity scores. Statistical significance among treatment groups was assessed using ANCOVA. Planned pair wise comparisons were then used to identify differences between specific treatment groups. The efficacy of Advocate® increased with its rate of application across all measures of efficacy and although ivermectin was shown to be more effective than Advocate® applied once weekly, both treatment protocols produced clinically satisfactory results. Three dogs developed ivermectin toxicity but no adverse effects were attributable to the use of Advocate®. It was concluded that weekly application of Advocate® can be recommended as effective for the treatment of canine generalized demodicosis without the associated risk of toxicity.

Acknowledgement:

I would like to acknowledge Bayer Animal Health for supporting this research through the provision of a grant and investigational product.

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Session Details:	8/29/2013 FUNCTIONAL GENOMICS 3 1515 - 1630 Meeting Room 5
Oral Presentation Details:	Sequencing and characterization of <i>Leishmania australiensis</i> .
Presentation Time:	1515 -1530
Authors:	Lu W ¹ , Choo A ¹ , Santos C ^{1,2} , Jackson A ³ , Rogers M ⁴ , Peacock C ^{1,2} ¹ University Of Western Australia, ² Telethon Institute for Child Health Research, ³ University of Liverpool, ⁴ The Wellcome Trust Sanger Institute

The recent identification of a unique species of *Leishmania* endemic to Australia that causes cutaneous disease in macropods provides an ideal comparator to the human pathogenic species¹. While capable of infecting human and murine macrophages and neutrophils, it is considered not to be pathogenic in humans. In addition it is the only *Leishmania* species that is transmitted by a vector that is not a sand fly. We have sequenced and annotated the entire genome of two isolates of this species from the Northern Territory using next generation sequence technology. We have used a novel approach for whole genome shotgun sequencing using multiple libraries of differing insert size to generate a *de-novo* assembly of this novel species and report on the genetic differences between this mammalian pathogen and the human pathogenic species previously sequenced². Sequence analysis of the genome has demonstrated a very high similarity to other sequenced *Leishmania* species that cause disease in humans with a high degree of conservation in both synteny and gene content. As expected there are a small number of genes restricted to either human or mammalian *Leishmania* genomes providing an insight into the possible mechanisms of pathogenicity. The availability of two isolates, one derived from the original source of a red kangaroo reported in 2004¹ and the other from the vector, provides some indication of the genetic diversity within this novel species. In addition we have undertaken immune response assays in both mouse and human macrophages and compared the response to human pathogenic species.

References

1) Rose K, Curtis J, Baldwin T, Mathis A, Kumar B, Sakthianandeswaren A, et al. Cutaneous leishmaniasis in red kangaroos: isolation and characterisation of the causative organisms. Int J Parasitol. 2004; 34:655-64.

2) Peacock CS, Seeger K, Harris D, Murphy L, Ruiz JC, Quail MA, et al. Comparative genomic analysis of three Leishmania species that cause diverse human disease. Nat Genet. 2007; 39:839-47.



Session Details:	8/29/2013 FUNCTIONAL GENOMICS 3 1515 - 1630 <i>Meeting Room 5</i>
Oral Presentation Details:	Transcriptional and functional characterization of cysteine proteases of the bovine lungworm <i>Dictyocaulus viviparus</i>
Presentation Time:	1530 -1545
Authors:	Strube C , Korrell J, Haake C Institute For Parasitology, University Of Veterinary Medicine Hannover

Cysteine proteases of helminth parasites are proposed to play important roles on host invasion, cuticle molting, food digestion, and defence against the host's immune response, making them a potential target for new immunotherapeutic and immunodiagnosics strategies. Probe-based quantitative real time PCR investigations on the transcription pattern of different *D. viviparus* cathepsins and legumains during the parasite's life cycle revealed that cathepsin Bs (cat-B1, B2 and B3) and legumains (leg-1 and 2) were almost exclusively expressed in parasitic stages. By contrast, cat-L2 showed the highest transcription pattern in early free-living larval stages of the bovine lungworm, whereas cat-F and Z were transcribed in both, early free-living and parasitic stages. Interestingly, cat-F appears to be primarily female-associated. To characterize the enzymatic activity and biological function of cat-L2, B3 and leg-1, they were recombinantly expressed in the yeast *Pichia pastoris*. Specific synthetic substrates were tested in vitro to estimate the possible functions in vivo followed by analysis of the preferred pH range and temperature optima. Furthermore, the enzyme's inhibitor profiles were created and possible interactions between cathepsins and legumain were analysed. Interestingly, the cathepsins appeared to work best at pH 4.5-5.0 and a temperature of 45 °C, which may be reached in the environment but does not occur in the cattle lung. Similarly, leg-1 worked best at pH 5.5 and 40 °C. The cathepsins were capable of self activation, while leg-1 showed only very low activity when assayed alone. The activity increased significantly through addition of cat-L2, suggesting that leg-1 is trans-activated by cat-L2. Furthermore, trans-activation of cat-B3 by cat-L was found, but the effect was weaker than observed for leg-1. Functional characterization of further cysteine proteases and evaluation of possible natural substrates such as haemoglobin and collagen is currently in progress.

Acknowledgements:

The study is funded by the German Research Foundation (DFG) under Grant STR 1171/2.



Session Details:	8/29/2013 FUNCTIONAL GENOMICS 3 1515 - 1630 Meeting Room 5
Oral Presentation Details:	Transcriptome of <i>Cryptosporidium parvum</i> (bovine genotype) in vitro and in vivo stages: New insights into the biology of an intestinal parasite
Presentation Time:	1545 -1600
Authors:	Lippuner C ^{1,3}, Basso W ¹, Okoniewski M ², Brugmann R ², Künzli M ², Hässig M, Hehl A, Deplazes P ¹ Institute of Parasitology, University of Zürich, Zürich, Switzerland, ² Department of Farm Animals, University of Zürich, Zürich, Switzerland, ³ FGCZ, University / ETH of Zürich, Zürich, Switzerland

Cryptosporidium spp. are important zoonotic pathogens causing severe diarrhea in young animals. So far, effective prevention and treatment protocols are missing and relatively little is known about the biology of this apicomplexan parasite.

The *C. parvum* genome has been sequenced and is available through EuPathDB. However, transcriptome data from oocysts or sporozoites are scarce, and generation of datasets from cultured parasites has been hampered by technical difficulties. In particular cultivation of parasites in vitro on a large-scale and efficient separation of intracellular parasites from host cell material remains a challenge. Furthermore, isolation of merozoites and gametocytes stages from infected calves in sufficient amounts and purity for RNA-sequencing is inherently difficult.

Here, we present an analysis of the first semi-quantitative transcriptome dataset from intestinal stages isolated from newborn calves experimentally infected with oocysts of a local *C. parvum* (bovine genotype) isolate. At 47 or 93 h post infection, calves were euthanatized and parasite stages were isolated from the mucosa of the small intestine and separated from host enterocytes. Furthermore, material of in vitro cultures and of excysted sporozoites was produced. Purified polyA⁺RNA was sequenced on a SOLiD platform to generate a gene expression dataset of in vitro and in vivo life cycle stages. Millions of raw reads could be mapped to the *C. parvum* genome allowing identification of transcripts from most predicted open reading frames in the *Cryptosporidium* genome database. Comparative analysis of expression profiles shows that regulation of several functional gene clusters is stage specific. More importantly, our data provides an opportunity for comparison with datasets from in vitro cultivated parasites to identify key factors for sustained development and formation of oocysts.

Acknowledgements:

The Functional Genomic Center Zürich gave constant support and Hanspeter Müller supported the animal experiments. C.L. was founded by grants of the University of Zürich.





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Session Details:	8/29/2013 FUNCTIONAL GENOMICS 3 1515 - 1630 <i>Meeting Room 5</i>
Oral Presentation Details:	In silico analysis of <i>Dermanyssus gallinae</i> transmembrane and excretory/secretory proteins
Presentation Time:	1600 -1615
Authors:	Schicht S¹, Qi W², Poveda L², Strube C¹ ¹ Institute For Parasitology, University Of Veterinary Medicine Hannover, ² Functional Genomics Center Zurich

The poultry red mite *Dermanyssus gallinae* (De Geer, 1778) is a hematophagous ectoparasite which affects chicken worldwide leading to high economic losses in poultry farming. Control of the mite is extremely difficult even though 35 acaricide compounds are proven to be effective against the parasite. Treatment failures in terms of repeated or long term chemical control may lead to acaricide resistance as it was shown for several substances or drug classes like pyrethroids or organophosphates. Besides, acaricide residues may remain in animal products leading to long withdrawal times after treatment or prohibition of use in utilised poultry houses due to food safety regulations. Therefore, the development of new control methods by identification of new drug targets or development of a vaccine against this poultry pest is required. Computational tools for analysis of *D. gallinae* next generation sequencing transcriptomic data were used to identify putative transmembrane (pTM) and excretory/secretory (pES) proteins as these proteins represent a favoured group of antigens for development of new control measures. The predicted 7,361 pTM and 3,091 pES proteins were analysed for their function by Gene Ontology mapping, InterProScan and KEGG pathway mapping leading to a variety of proteins proposed to be involved in important developmental processes, the neuronal network and metabolic pathways like blood digestion. Identified pTM and pES proteins represent a repertoire of possible target molecules for future intervention strategies.



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Session Details:	8/29/2013 FUNCTIONAL GENOMICS 3 1515 - 1630 <i>Meeting Room 5</i>
Oral Presentation Details:	<i>Proteins of the Toxoplasma secretome influence the host epigenome: an in-silico approach</i>
Presentation Time:	1615 -1630
Authors:	Syn G , Blackwell J, Jamieson S, Francis R Telethon Institute For Child Health Research

The ubiquitous eukaryotic protozoan parasite *Toxoplasma gondii* can impair chromatin remodeling in mammalian host cells and susceptibility to congenital toxoplasmosis has been shown to be associated with variants in host genes that are under epigenetic regulation. We therefore questioned whether *T. gondii* secretes proteins that localize to the host cell nucleus that can directly modulate the host epigenome. We used an *in silico* pipeline to identify *T. gondii* secreted proteins as candidates for translocation to the host cell nucleus and infer function from their domain architecture. Using ToxoDB, we derived 334 proteins experimentally shown to be part of the *T. gondii* secretome, or which were known dense granule, microneme and rhoptry proteins. Proteins shown to contain a transmembrane domain were excluded from further analysis. Prediction of nuclear localisation for the remaining 288 proteins was carried out using three separate methods: 1) PredictNLS in conjunction with ACCpro which predicts exposed nuclear localisation signals; 2) NucPred which predicts whether a protein spends any time spent in the nucleus; and 3) InterProScan combined with a custom developed filter of Gene Ontology (GO) terms which searches for domain terms with nuclear associated functions. This method identified 35 proteins from the *T. gondii* secretome predicted to have a nuclear localisation by all 3 methods. Of these, 24 proteins are also predicted to have a putative epigenetic function based on GO terms, including proteins capable of modifying or interacting with histones and methylated DNA. These results suggest that several proteins within the *T. gondii* secretome are trafficked to the host cell nucleus and have the potential to modify the host epigenome. These proteins are currently being experimentally verified.

Session Details:	8/29/2013 DRUG RESISTANCE - SMALL RUMINANTS 3 1515 - 1630 <i>Meeting Room 6</i>
Oral Presentation Details:	A population genetics approach to ivermectin resistance in the parasitic nematode <i>Haemonchus contortus</i>
Presentation Time:	1515 -1530
Authors:	Roz Laing³ , Burgess C ¹ , Morrison A ¹ , Bartley D ¹ , Redman E ² , Rezansoff A ² , Tait A ³ , Skuce P ¹ , Gilleard J ² , Devaney E ³ ¹ Moredun Research Institute, ² University of Calgary, ³ University of Glasgow

Anthelmintic resistance is a major constraint to the sheep industry worldwide and is an emerging concern for parasite control in other species. Little is known about the mechanisms underlying resistance in parasitic nematodes and current recommendations for sustainable parasite control are based largely on theory. *Haemonchus contortus*, an intestinal parasitic nematode of small ruminants, is unsurpassed in its ability to develop resistance to anthelmintics and is a valuable parasitic nematode model.

We are investigating genetic changes in UK field populations of *H. contortus* using both candidate gene and whole genome approaches. We aim to identify genetic loci associated with ivermectin resistance to improve our understanding of how resistance arises and spreads. SNPs and/or altered expression levels of number of ligand-gated chloride channels and P-glycoproteins in the *H. contortus* genome have been associated with ivermectin resistance in laboratory isolates but the importance of these mutations in field isolates remains unclear.

Firstly, we are using a population genetics approach to genotype individual worms in field populations of *H. contortus* from farms throughout the UK in respect to three ligand-gated chloride channel loci (*glc-5*, *gbr-2* and *hg1*) and three P-glycoprotein loci (*pgp-A*, *pgp-1* and *pgp-9*), all of which have been previously associated with ivermectin resistance. Farmers were asked to complete a questionnaire describing flock management and anthelmintic regime to allow *H. contortus* populations from farms with differing histories of ivermectin use to be compared for evidence of selection at candidate gene loci.

Our second, global approach is to use RAD-seq to genotype individual worms from farm populations with differing anthelmintic regimes to identify markers associated with resistance. This approach is unbiased (does not rely on prior assumptions as to the mechanism of anthelmintic resistance) and provides genome-wide coverage of markers, which will be used to identify regions of the genome under selection.

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Session Details:	8/29/2013 DRUG RESISTANCE - SMALL RUMINANTS 3 1515 - 1630 <i>Meeting Room 6</i>
Oral Presentation Details:	The in vitro and in vivo response of Haemonchus contortus to benzimidazole treatment: sheep versus goats
Presentation Time:	1530 -1545
Authors:	Varady M , Konigova A, Dolinska M, Skolnikova E Institute Of Parasitology SAS, Kosice, Slovakia

Anthelmintic resistance among parasites of sheep and goats has been known to occur for at least four decades. Both species of host have similar genera of nematodes, but the nematodes in goat herds usually develop anthelmintic resistance more rapidly. The emergence and rapid spread of anthelmintic resistance worldwide have forced the development of several *in vitro* and *in vivo* techniques for the detection of resistance. The present study was designed to compare two *in vitro* methods as tools for detection of benzimidazole and ivermectin resistance in *Haemonchus contortus* in sheep and goats. Additionally, *in vivo* anthelmintic treatments with benzimidazole drug in the same dosage (sheep recommended dose) have been carried out. In this study 14 goat kids and 14 lambs, were each infected with 3000 L3 larvae of one resistant (benzimidazole, closantel, rafoxanide and ivermectin resistant) and one susceptible isolate of *H. contortus*. The differences between values of ED50/ED99 in Egg hatch test and LD50/LD99 in Micro agar larval development test in goats and sheep were not statistically different which pointed out on a fact that identical parasite infection gave identical *in vitro* response in detection of anthelmintic resistance. The results of *in vivo* FECR test showed that albendazole treatment reduced susceptible isolate by 100 % and resistant isolate by > 99 % in both animal species. Genotyping of both isolates revealed 10 % and 26 % of benzimidazole resistant alleles in susceptible and resistant isolates respectively.

Acknowledgements: *The study was supported by Grant Agency VEGA, Grant No. 2/0151/13 of the Scientific Agency of the Slovak Academy of Sciences and Slovak Research and Development Agency Project No. 0539-10.*



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Session Details:	8/29/2013 DRUG RESISTANCE - SMALL RUMINANTS 3 1515 - 1630 <i>Meeting Room 6</i>
Oral Presentation Details:	The use of a stochastic model to predict the role of monepantel in combination anthelmintics
Presentation Time:	1545 -1600
Authors:	Hosking B¹, Dobson R² ¹ Novartis Animal Health, ² Murdoch University

The evolution of anthelmintic resistance in sheep grazing systems is determined by the extent that survivors of drug treatment contribute their genes to future generations. This is influenced by a complex array of factors such as anthelmintic exposure, efficacy, parasite biology, host immunity, grazing management, refugia and climate. Mathematical models are therefore used to bring such factors into a structured framework that allows the testing of treatment scenarios in timeframes not achievable if biological studies were undertaken. A new multi-species stochastic model (Risk Management Model for Nematodes™; RMMN™) for sheep in Australian grazing systems was used to examine the potential for monepantel to be used in combination anthelmintics. RMMN predicts, over 20-year simulation periods, the effect that the treatment regimens will have on mixed nematode burdens (*Haemonchus contortus*, *Teladorsagia circumcincta*, *Trichostrongylus colubriformis* and *T. vitrinus*), and the production/cost-benefits associated with control. In the scenarios simulated, the resistance-allele frequency for monepantel in the target parasites was purposely set to force resistance to occur within 5–10 relative years. From this baseline, combination anthelmintics could be modeled. A strategy for providing refugia by deliberately leaving some adult sheep untreated was also explored. Using *T. circumcincta* and *T. colubriformis* in Western Australia as an example, resistance to monepantel was set up to occur in six relative years. When combined with abamectin (resistance allele frequency set at 3%), the relative years to resistance was >20 years to both active ingredients. There was an associated 3.5-fold increase in the averaged annual income from the ‘treated flock’ when using the combination anthelmintic vs. the mono-product. In Western Australia, providing a refugia strategy can greatly reduce the risk of selecting for drug resistance.

Session Details:	8/29/2013 DRUG RESISTANCE - SMALL RUMINANTS 3 1515 - 1630 <i>Meeting Room 6</i>
Oral Presentation Details:	Monepantel resistance selection studies in <i>Teladorsagia circumcincta</i>
Presentation Time:	1600 -1615
Authors:	Bartley D , Devin L, Morrison A Moredun Research Institute

Anthelmintic resistance (AR) in nematode parasites of small ruminants is a global problem. Two new compounds have recently been introduced on to the UK market (monepantel (MPTL) and derquante). In order to preserve the efficacy of these compounds it is essential to understand both a) the mechanisms involved in the selection of resistance and b) how the parasites evolve to deal with these compounds.

To answer these questions a MPTL-resistant *Teladorsagia circumcincta* isolate has been artificially selected *in vivo* from a phenotypically characterised isolate (MTci7). Basically, eggs from surviving worms from sheep administered sub-optimal dose rates (Zolvix®) were cultured to provide infective larvae to infect further sheep until a resistant isolate was generated (~7 rounds of selection). A controlled efficacy test was conducted using the original parental isolate and the newly generated MPTL resistant isolate (MTci7_MPTL-R) both under anthelmintic stress (Zolvix®, 2.5 mg/kg bodyweight) and at rest (untreated, n=5 per group). Phenotypic characteristics e.g. pre-patent period, fecundity, eggs *in utero*, establishment rates, adult-worm length and morphology were examined.

Faecal egg count rose earlier in MTci7_MPTL-R than in MTci7 (d14 compared to d17 for initial rise). Establishment rates were 28% and 56% for MTci7 and MTci7_MPTL-R respectively (1980 and 3920 respectively) at rest. The resistance status of the MTci7_MPTL-R isolate was confirmed with 0% efficacy in both faecal egg count and worm burden at 7-days post zolvix® **administration**. **Egg in utero** counts were 27% higher in MTci7_MPTL-R compared to MTci7 (31v22 eggs respectively).

The trial results suggest that anthelmintic selection in *T. circumcincta*, albeit under experimental conditions, can select for more prolific/fecund and quicker maturing populations. These populations are currently being investigated for presence/absence of the MPTL-1 gene which is associated with resistance in *Haemonchus*¹. These data provide an insight in to how parasites evolve in response to anthelmintic pressure.

Acknowledgements:

The authors gratefully acknowledge the Scottish Government RESAS for funding this work

and our colleagues in Bioservices and Disease Control at Moredun for their technical assistance with the Controlled Efficacy Test.

References:

1 Kaminsky R, Ducray P, Jung M, Clover R, Rufener L, et al. (2008) A new class of anthelmintics effective against drug-resistant nematodes. *Nature* 452: 176–180.

Session Details:	8/29/2013 DRUG RESISTANCE - SMALL RUMINANTS 3 1515 - 1630 <i>Meeting Room 6</i>
Oral Presentation Details:	Molecular genetic analysis of interspecies hybridization between <i>Haemonchus contortus</i> and <i>Haemonchus placei</i> and its implications for the spread of benzimidazole resistance mutations
Presentation Time:	1615 -1630
Authors:	Chaudhry U¹, Redman E², Muthusamy R³, Abbas M⁴, Gilleard J⁵ ¹ Faculty Of Veterinary Medicine, University Of Calgary, CANADA, ² Faculty of Veterinary Medicine, University of Calgary, CANADA, ³ Department of Parasitology, Veterinary Collage Chennai Tamil Nadu, INDIA, ⁴ Veterinary Research Institute (VRI) Lahore Punjab, PAKISTAN, ⁵ Faculty of Veterinary Medicine, University of Calgary, CANADA

Resistance to the all class of anthelmintic has been observed in parasitic nematodes of livestock. There are many aspects of the genetics of anthelmintic resistance that remain poorly understood. It is still unclear how resistance mutations originate and spread in parasite populations in the field. Resistance is widespread in the highly pathogenic small ruminant parasitic nematode *H. contortus* and this parasite provides us a valuable model system in which to study such questions. For this parasite, three different mutations (P200, P198 and P167) in the isotype-1 β -tubulin gene have been associated with benzimidazole (BZ) resistance [1, 2]. We are studying these mutations to investigate whether one parasite species can serve as a source of resistance mutations for another species by virtue of interspecies hybridization and genetic introgression. Although, *H. contortus* and the related species *H. placei* have strong host preferences, they can infect multiple host species and co-infections occur. *H. contortus* is commonly found in sheep and goats, whereas *H. placei* is common in cattle. In contrast, the extent of anthelmintic resistance in *H. placei* is currently unknown. The two parasite species are phylogenetically close and experimental co-transplantation of adult parasites can result in hybridization between two species. *H. contortus* and *H. placei* are sympatric in many regions of the world especially where large and small ruminants share the same pasture. In the present study, we have shown that co-infection of sheep and goats are common in some regions. We use a number of genetic markers to demonstrate interspecies hybridization does occur in field populations suggesting the potential for introgression of BZ resistance mutations between these species. This has major implications for the spread of anthelmintic resistance from small ruminants to large ruminants and for the potential emergence of anthelmintic resistance in the important cattle parasite *H. placei*.

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- (1) Silvestre, A. and J. F. Humbert (2002). "Diversity of benzimidazole-resistance alleles in populations of small ruminant parasites." *Int J Parasitol* 32(7): 921-8.
- (2) De Lourdes Mottier, M. and R. K. Prichard (2008). "Genetic analysis of a relationship between macrocyclic lactone & benzimidazole anthelmintic selection on *H. contortus*." *Pharmacogenet Genomics* 18(2): 129-40.

Acknowledgements: Natural Sciences and Engineering Research Council of Canada, Biotechnology and Biological Sciences Research Council of United Kingdom

CONCURRENT SESSION 9

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Session Details:	8/29/2013 APICOMPLEXAN BIOLOGY 2 1515 - 1630 <i>Meeting Room 7</i>
Oral Presentation Details:	Next-generation anti-parasitic agents from Nature
Presentation Time:	1515 -1530
Authors:	Skinner-Adams T¹ , Gardiner D ² , Trenholme K ² , Piggott A ³ , Capon R ³ ¹ Griffith University, ² Queensland Institute of Medical Research, ³ University of Queensland

Unlike their synthetic cousins, natural products (NPs) have evolved through millions of years of selection in biological systems to interact with biological processes and to have pre-optimized drug-like properties. For these reasons nature has long been recognized as a valuable source of active compounds that can be used to combat man's most lethal parasitic diseases. Quinine, from the bark of the cinchona tree, has been used as an anti-malarial since the 15th century. Artemisinin, from the Chinese wormwood *Artemisia annua*, has been used by the Chinese to treat malaria for thousands of years and is now a component of many first-line anti-malarial treatment regimens (Artemisinin Combination Therapies). While these natural products have been highly successful in reducing infection and mortality many are now associated with resistant parasites. To ensure that cheap and effective anti-parasitic treatments remain available new biologically active compounds need to be identified. To identify compounds with potentially useful anti-parasitic activity we have screened a unique library of NPs for compounds with anti-malarial activity. This library, assembled from marine and microbial sources contains molecules not available in other compound collections. Our studies have identified several structural classes of compounds with potent activity against asexual (pM and nM IC₅₀ values) and sexual stage malaria parasites which may pave the way to the development of new anti-parasitic drugs.



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Session Details:	8/29/2013 APICOMPLEXAN BIOLOGY 2 1515 - 1630 <i>Meeting Room 7</i>
Oral Presentation Details:	Targeting post-translational modification enzymes for malaria therapy
Presentation Time:	1530 -1545
Authors:	Katherine Andrews^{1, 2*} , Katharine Trenholme ² , Ishani Sahama ¹ , Fabian de Labastida Rivera ² , Chris Engwerda ² , Ashraf Haque ² ¹ Eskitis Institute for Cell and Molecular Therapies, Griffith University, Queensland, AUSTRALIA; ² Queensland Institute of Medical Research, Queensland, AUSTRALIA;

Malaria parasites have a complex life cycle involving functionally distinct forms in two different host species. This requires rapid transition between morphological states and tightly regulated gene expression. Posttranslational modification (PTM) enzymes involved in regulating gene expression and stage-specific conversion are therefore promising targets for the development of novel antimalarial inhibitors. Approaches targeting proteins involved in PTMs have been successfully used to control other human diseases. Two drugs that target histone deacetylase (HDAC) enzymes are now clinically approved for treatment of cancer. Several HDAC inhibitors have also been shown to have promising antimalarial profiles.

We have shown that hydroxamate-based HDAC inhibitors can have potent *in vitro* activity against asexual blood stages of the two major human malaria parasite species, *Plasmodium falciparum* and *P. vivax* (IC₅₀ ~20-300nM). In this stage of the parasites lifecycle, the compounds have been shown to act by causing histone protein hyperacetylation and de-regulation of normal parasite transcriptional control. Our studies on the effect of HDAC inhibitors on other life cycle stages have also shown that the development of exo-erythrocytic stage *P. berghei* sporozoites infecting human liver cells is potently inhibited by these compounds (IC₅₀ ~150nM). Here, we present new data to show that these HDAC inhibitors have activity against the gametocyte stage of the parasite, making HDACs potential new targets for development of transmission blocking drugs. Furthermore, preliminary studies show that one clinically approved anti-cancer HDAC inhibitor, SAHA, protects mice from severe symptoms in an experimental cerebral malaria (ECM) mouse model. This effect is associated with host serum cytokine changes, notably an increase in IL-10 levels. Studies are now underway to confirm these findings in an ECM rescue model. Results of this work may lead to development of a new approach for adjunctive treatment of cerebral malaria.



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Session Details:	8/29/2013 APICOMPLEXAN BIOLOGY 2 1515 - 1630 <i>Meeting Room 7</i>
Oral Presentation Details:	A Humanized Mouse Model for Transmission Blocking Antimalarial Assessment and Discovery.
Presentation Time:	1545 -1600
Authors:	Butterworth A ^{1, 2} , Apte S ¹ , Skinner-Adams T ³ , Trenholme K ^{1, 2} , Gardiner D ^{1, 2} ¹ Queensland Institute Of Medical Research, ² School of Medicine, University of Queensland, ³ Eskitis Institute for Drug Discovery, Griffith University

Antimalarial drugs that effectively kill the transmission stage of the malaria parasite lifecycle, the gametocyte, are recognized as key tools required for the global elimination of malaria. Currently only one drug, primaquine, is clinically available for the clearance of *Plasmodium falciparum* gametocyte stages, however the use of this drug is limited by toxicity. Therefore, the search for new antimalarials that can clear gametocytes is an important priority in malaria research. Unfortunately methods that enable the identification of potential anti-gametocyte agents in *in vivo* animal studies are limited. Animal studies are important as they enable the activity of metabolites to be assessed. *In vivo* methods for examining the activity of compounds against gametocytes rely on mouse models and murine *Plasmodium* species. While these models are useful, their relevance to human disease, particularly *falciparum* malaria is questionable due to significant differences in gametocyte development. To improve the current position we have developed a mouse model that enables *P. falciparum* gametocytes to be studied *in vivo*. Maintenance of the gametocytes within mice requires manipulation of the mouse immune system. Infection is established in SCID mice (deficient in B and T lymphocytes) that are administered liposomal clodronate to deplete macrophages. Clearance of parasites is also limited by removing the host's spleen and overwhelming the immune system with human erythrocytes prior to infection. Pure gametocyte cultures are FITC stained before injection and the kinetics of gametocyte clearance assessed by fluorescence activated cell sorting. Humanized mouse models provide a novel and accessible means of anti-gametocyte antimalarial assessment and enable the important step of *in vivo* analysis prior to human trials in the drug development pipeline. The steps involved in the development of the model and data from the validation of the model using currently available antimalarials will be presented.

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Session Details:	8/29/2013 APICOMPLEXAN BIOLOGY 2 1515 -1630 Meeting Room 7
Oral Presentation Details:	In vitro and in vivo studies of fenofibric acid-based drug combinations for treatment of malaria
Presentation Time:	1600 - 1615
Authors:	Rina P. M. Wong^{1*}, Justine G. W. Wong¹, Alison Rose², Madhu Page-Sharp¹, Kevin T. Batty³, Brioni R. Moore¹, Timothy M. E. Davis ¹ ¹School of Medicine and Pharmacology, University of Western Australia, Fremantle Unit, AUSTRALIA ²Cell Biology Research Unit, Fremantle Hospital, Fremantle, WESTERN AUSTRALIA ³School of Pharmacy, Curtin University, Bentley, WESTERN AUSTRALIA

Because *Plasmodium falciparum* has developed resistance to most available therapies, new antimalarial agents are urgently needed¹. Fenofibric acid (FA) is a lipid-modifying drug shown to inhibit *P.falciparum* *in vitro* with additive activity when combined with dihydroartemisinin (DHA)². The present study extended these observations to *in vitro* interactions between FA and other antimalarials. Additionally, we investigated the pharmacokinetics and pharmacodynamics of FA in a murine malaria model.

In vitro isobolographic studies revealed additive interactions between FA and pyronaridine against 3D7 (chloroquine (CQ)-sensitive) and W2mef (CQ-resistant) strains of *P.falciparum*. Similarly, there were additive interactions between FA and piperazine against W2mef. Antagonistic interactions were observed between FA and lumefantrine, desbutyl-lumefantrine and quinine against both W2mef and 3D7, and between FA and piperazine against 3D7. In all cases, the interactions were mild.

We conducted a three-part *in vivo* investigation, comprising (i) pharmacodynamic assessment of FA monotherapy and of FA in combination with DHA in *P.berghei*- infected mice, (ii) pharmacokinetic studies of single dose FA (1000mg/kg) in healthy and malaria-infected mice, (iii) 4-day suppressive studies of single dose FA (300mg/kg and 1000mg/kg). In study (i), three daily doses of 1000mg/kg FA showed no effect on parasitaemia or survival relative to infected untreated animals, and no additive effect with DHA. In study (ii), the elimination half-life and apparent clearance of FA were 6.5h and 0.8L/h/kg in controls and 4.0h and 0.3L/h/kg in malaria-infected mice. In study (iii), FA exhibited no suppressive effects on early parasitaemia development.

Despite initial *in vitro* data suggesting a possible role for FA in the treatment of malaria, the present detailed additional *in vitro* and *in vivo* studies were negative. The generally mild interactions between FA and a range of antimalarial drugs suggest that humans treated with FA for dyslipidaemia and who contract malaria will respond normally to conventional combination antimalarial treatment.

Acknowledgements:

Dr Jean-Claude Ansquer, Dr Olivier Lacombe, Inventiva, Daix, France.
Haematology Department, PathWest Laboratory Medicine, Fremantle Hospital.



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1. Sibley, C. H., Guerin, P. J. And Ringwald, P. (2010). Monitoring antimalarial resistance: launching a cooperative effort. *Trends Parasitol* 26(5) 221-224.
2. Wong, R. P. M. and Davis, T. M. E. (2012). *In vitro* antimalarial activity and drug interactions of fenofibric acid. *Antimicrob Agents Chemother* 56(6) 2814-2818.

Session Details:	8/29/2013 APICOMPLEXAN BIOLOGY 2 1515 -1630 <i>Meeting Room 7</i>
Oral Presentation Details:	Potent ex vivo activity of pyronaridine, naphthoquine and methylene blue against chloroquine resistant field isolates of Plasmodium falciparum and P. vivax
Presentation Time:	1615 - 1630
Authors:	Grennady Wirjanata ¹ , Boni Sebayang ² , Ferryanto Chalfein ³ , Pak Prayoga ³ , Leily Trianty ² , Enny Kenangalem ^{3,4} , Rintis Noviyanti ² , Julie Lotharius ⁵ , Jörg Möhrle ⁵ , Nicholas Anstey ¹ , Ric Price ^{1,6} , Jutta Marfurt ¹ ¹ Menzies School of Health Research and Charles Darwin University, Darwin, Australia ² Eijkman Institute for Molecular Biology, Jakarta, Indonesia ³ Papuan Health and Community Development Foundation, Timika, Papua, Indonesia ⁴ District Ministry of Health, Timika, Papua, Indonesia ⁵ Medicines for Malaria Venture, Geneva, Switzerland ⁶ Centre for Tropical Medicine, University of Oxford, United Kingdom

In vitro drug susceptibility testing of *P. falciparum* is used routinely to screen for antimalarial drug activity free from confounding effects of host immunity and drug pharmacokinetics. Despite the lack of a continuous *ex vivo* culture system for *P. vivax*, the revised, field-based schizont maturation test has proven utility in measuring the comparative *ex vivo* schizonticidal activity of novel and standard antimalarials against field isolates to help prioritise the development of new therapies which retain efficacy to both species of malaria. The 4-aminoquinolines naphthoquine (NQ) and pyronaridine (PYR) have been introduced recently as a partner drugs for anti-malarial combination therapy (ACT). Methylene blue (MB) is an old antimalarial, but was abandoned because of its side effects.

We assessed the anti-malarial *ex vivo* activity of NQ, PYR and MB against multidrug-resistant *P. vivax* field isolates and showed good *ex vivo* efficacy (median IC₅₀, [range]) for NQ (3.6 nM [1.5-34.2]), PYR (2.4 nM [0.7-11.4]), and MB (1.2 nM [0.7-1.6]). Correlation patterns between NQ, PYR and other quinoline-based compounds chloroquine, amodiaquine, piperazine, and mefloquine were different between the two malaria species. Studies investigating the stage-specific activity of these compounds are still ongoing.

The potent *ex vivo* activity of NQ, PYR and MB against both *P. falciparum* and *P. vivax* highlights a promising role as partner drugs in ACTs in geographical locations where both species are endemic. In addition, these *ex vivo* data provide essential phenotypic information for complementary molecular studies elucidating the genetic basis of resistance in *P. vivax*.

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Session Details:	8/27/2013 A walk on the wild side 1140 - 1240 <i>Riverside Theatre</i>
Poster with 2 minute Oral Presentation Details:	Description and taxonomy of three species of Acanthocephala in Australia
Authors:	Leah Brunt ^{1*} ; Shokoofeh Shamsi ¹ , John Harper ² , Lesley Warner ³ ¹ School of Animal and Veterinary Sciences/Graham Centre for Agricultural Innovations, Charles Sturt University, Wagga Wagga, Australia; ² School of Agricultural and Wine Sciences/Graham Centre for Agricultural Innovations, Charles Sturt University, Wagga Wagga, Australia; ³ South Australian Museum, Adelaide, Australia
Poster Number:	26

The Acanthocephala are intestinal parasites with vertebrate being definitive hosts. They are important parasites of wild and captive animals. Epizootics of acanthocephalans have been known to kill a great number of individuals in a short time. In the present study, we examined two species of marlins: black marlin, *Makaira indica* and striped marlin, *Tetrapturus audax* from Nelson Bay (south eastern coast of Australia) for infection with internal parasites. Several species of nematodes, cestodes and acanthocephalans were found in the intestine of both black and striped marlins. The focus of this paper, however, is on acanthocephalan parasite in black marlins only. Parasite specimens were kept frozen after collection in the field. In the lab they were thawed at room temperature and placed in lactophenol for light microscopy. Examination of key morphological characteristic features, such as proboscis armature, the lemnisci, proboscis receptacle and ligament sacs suggested (Edmonds 1989) they can be placed into three distinct species however they cannot be placed within any known described species. We provide a full description of these species, their nomenclature and details on how to differentiate them from closely related species.

Acknowledgements:

We would like to thank Dr Julian Pepperell for his help to have access to marlin specimens, fishermen in 2010 Nelson bay fishing tournament who provided us with fish specimens and Graham Centre for Agricultural Innovations and Australian society for Parasitology for travel assistance.

References:

Edmonds, S.J., *A LIST OF AUSTRALIAN ACANTHOCEPHALA AND THEIR HOSTS*. Records of the South Australian Museum (Adelaide), 1989. **23**(2): p. 127-134.



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Session Details:	8/27/2013 A walk on the wild side 1140 - 1240 Riverside Theatre
Poster with 2 minute Oral Presentation Details:	<i>Paradiscogaster flindersi</i> and <i>P. oxleyi</i> n. sp. (Digenea: Faustulidae): overlapping host and geographical distributions in corallivore chaetodontid fishes in the tropical Indo-west Pacific.
Authors:	Pablo Diaz ^{1*} , Rod Bray ² , Thomas Cribb ¹ (presenting author asterisked) ¹ The University of Queensland, Brisbane, AUSTRALIA ² Natural History Museum, London, UNITED KINDOM
Poster Number:	200

A total of 2868 individuals of 47 species of chaetodontids fishes were examined for faustulids at 7 major localities in the Tropical Indo-West Pacific (TIWP). Combined morphological and molecular analyses allow us to describe *Paradiscogaster oxleyi* n. sp. from three localities in the TIWP: off Lizard Island, off Palau and Swain Reefs; in three host species: *Chaetodon lunulatus* (type-host), *C. ornatissimus* and *C. meyeri*. Molecular analysis of samples from two host species and three localities supports the morphology-based conclusion that *P. oxleyi* n. sp. is the same species at the three localities. *Paradiscogaster flindersi* is reported from three new localities in the TIWP (off New Caledonia, Ningaloo Reefs and Swain Reefs) plus the original type-locality from Heron Island (Bray, Cribb & Barker, 1994), and is now known from 13 chaetodontid species. Sequences of the ITS2 rDNA region from samples consistent with *P. flindersi* differed from those from *P. oxleyi* n. sp. in 11-12 base pairs. The host ranges of the two species overlap broadly. Neither species was found in French Polynesia but both were found at Swain Reefs on the Great Barrier Reef. Only one of the two species was found at each of the five other sites. Both species occur almost exclusively in specialist corallivores allowing the inference that the metacercariae occur in corals.

Acknowledgements:

This work was supported by Australian Research Council and Australian Biological Resources Study funding to Cribb. Collecting in French Polynesia was supported by the BioCode, Coral Spot program (financially supported by the French Polynesian Territory and the French Government) and Pakaihi ite Moana in Marquesas (financially supported by AAMP, by the French Polynesian Territory and the French Government). We thank Drs Rob Adlard, Lee Barnett, Janet Hunter, Tim Littlewood, Marissa McNamara, Terry Miller, Matt Nolan, Peter Olson and Pierre Sasal for assistance with collection and dissection of fishes. Dr Scott Cutmore helped with molecular analyses. We appreciate the support of staff of the Heron Island and Lizard Island research stations.

References:

Bray, R. A., Cribb, T. H. and Barker, S. C. (1994). Fellodistomidae and Lepocreadiidae (Platyhelminthes: Digenea) from chaetodontid fishes (Perciformes) from Heron Island, southern Great Barrier Reef, Queensland, Australia. Invertebrate Taxonomy, 8, 545-581.



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Session Details:	8/27/2013 A walk on the wild side 1140 - 1240 Riverside Theatre
Poster with 2 minute Oral Presentation Details:	Checklist of parasites of labrid fishes (Pisces: Labridae) around the world, including unpublished data from Lizard Island, Australia, and Robinson Crusoe Island, Chile
Authors:	Gabriela Muñoz ¹ , Pablo Diaz ^{2*} (presenting author asterisked) ¹ Valparaiso University, Valparaiso, CHILE ² The University of Queensland, Brisbane, AUSTRALIA
Poster Number:	201

Labrid fishes are one of the most widespread groups with approximately 580 species which are mostly dispersed in tropical and subtropical marine waters (Choat & Bellwood 1998). Diverse habitats also mean diverse parasite-fauna, due the complex life cycles that most endoparasites have, which include several hosts species to develop their larval and adult stages. In this regard, labrid fishes have great parasite richness, although few studies have focused on their whole parasite communities (Campos & Carbonell 1994; Muñoz & Cribb 2005; Muñoz & Cribb 2006; Muñoz *et al.* 2007) and as result of this, most of the information is spread out over many publications. The most known parasites of labrids are from Australia in the Great Barrier Reef, New Caledonian and Indonesian reefs. However, labrids are present in many other habitats in which they are surprisingly unknown.

This study aims to know the parasites of a labrid fish, *Malapterus reticulatus*, endemic species from Robinson Crusoe Island in Chile, and 16 species from the Great Barrier Reef, Australia. This study also provides a list of the parasite species reported from labrids around the world based on references published in different sources. *Malapterus reticulatus* had only one parasite species, the copepod *Lepeophtheirus* sp., whereas in the 16 labrid fishes from the coral reef we found at least 34 parasite species, although most of them were already recorded in previous studies. In total, we enlisted 214 parasites identified at the species level, and at least 130 parasites identified at the order, family or genus level, in 125 labrid species from different countries. Trematode contains more species than other parasite groups which was due the great number of taxonomical studies focused and published on trematodes.

Acknowledgements:

We thank Paulo Lagos for his help in the collection of the fishes in Robinson Crusoe Island, the staff of Lizard Island Research Station, Dr Thomas Cribb for their support on the filed trips, and Nadia Santini for her suggestions to the manuscript.

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Session Details:	8/27/2013 A walk on the wild side 1140 - 1240 Riverside Theatre
Poster with 2 minute Oral Presentation Details:	Gastrointestinal parasites of the Common Eider (<i>Somateria mollissima</i>) – Seasonal, geographical and host related variations in the parasite burdens of two distinct Danish populations
Authors:	Marie S Jensen ¹ , Mariann Chriél ¹ , Mohammad NS Al-Sabi ¹ , Ole R Therkildsen ² , Heidi L Enemark ^{1*} ¹ National Veterinary Institute, Technical University of Denmark, Frederiksberg, DENMARK ² Department of Bioscience – Wildlife Ecology and Biodiversity, Aarhus University, Aarhus, DENMARK
Poster Number:	69

Due to a recent decline in the number of Common Eiders (*Somateria mollissima*) in Denmark, prevalence, intensity and composition of the gastrointestinal helminth fauna of Common Eiders were examined to establish reference data of the helminth fauna of apparently healthy birds. Furthermore, seasonal, geographical and host related variations in helminth composition were studied. The birds (*N*=157) were collected through November 2010 to January 2012 from two distinct colonies, Jutland (*N*=103) and Zealand (*N*=54), comprising 54 males and 102 females of which 20 were gathered during the nesting period. The study is ongoing, and so far most parasites have only been identified to the family level. Eight trematode families, two nematode families, one acanthocephala and one cestode family were identified. For the gizzard nematode *Amidostomum acutum*, significantly higher intensities (*p*<0.05) were seen in adults (max. intensity 245). For all other helminths, the intensity of infection was significantly higher in juveniles compared to adults. Prevalence and intensity of acanthocephala and *A. acutum* were significantly influenced by geography (*p*=0.004 & 0.03 respectively). Higher prevalence of acanthocephala was found in Jutland (83%) compared to 52% in Zealand; whereas *A. acutum* was more prevalent in Zealand (88%) compared to Jutland (66%). Significant seasonal variations in intensities were observed for acanthocephala, *A. acutum* and cestodes. *A. acutum* intensity was highest in spring (max. intensity 245), whereas acanthocephala and cestode intensities were higher during fall (max. intensities: 1153 & 10480 respectively). While acanthocephala and cestodes were almost absent in nesting females, infections with *A. acutum* remained high during the incubation period, and most notably, a significant (*p*<0.001) increase in both intensity and prevalence (100%) of trematodes of the family Notocotylidae was observed in nesting females. Ongoing analyses will determine correlation between parasite burden and body condition.

Acknowledgements:

The Danish Hunters Association is thanked for supplying birds for the study; and Cynthia D Juel and Leif B Eiersted are acknowledged for skilled technical assistance. The study was financed by the Danish Nature Agency, Aarhus University and the Technical University of Denmark.



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Session Details:	8/27/2013 A walk on the wild side 1140 - 1240 Riverside Theatre
Poster with 2 minute Oral Presentation Details:	Gastrointestinal endoparasite fauna of wild wolf (<i>Canis lupus</i>) populations in Croatia
Authors:	Carlos Hermosilla* ¹ , Sonja Kleinertz ¹ , Liliana M. R. Silva ^{1,2} , Jörg Hirzmann ¹ , Djuro Huber ³ , Josip Kusak ³ , Anja Taubert ¹ ¹ Justus Liebig University Giessen, Giessen, GERMANY ² University of Evora, Evora, PORTUGAL ³ University of Zagreb, Zabreb, CROATIA
Poster Number:	65

The European wolf (*Canis lupus*) is a large carnivore species inhabiting limited areas of Europe with several small populations still being considered as endangered. Wolves can be affected by a wide range of protozoan and metazoan parasites. Parasitic diseases are increasingly recognized for their profound influences on individual, population and ecosystem health. Furthermore, a number of parasitic diseases have gained importance in recent years as agents of opportunistic infections. We here report on the gastrointestinal endoparasite fauna of wolves from the mountainous areas of the Gorski Kotar region, Croatia. In total, 400 individual wolf faecal samples were collected during field studies on wolf ecology in the years 2002-2011. Parasite eggs, larvae, oocysts/sporocysts and cysts were identified by using standard flotation techniques and morphological analyses, faecal smear techniques and *Giardia*/*Cryptosporidium* copro-ELISAs. A subset of samples was analyzed by PCR and consecutive sequencing to identify taeniid eggs ($n=7$) on the *Echinococcus granulosus*/*E. multilocularis* species level. Overall, more than 16 taxa were detected in the wolf samples. Sporocysts of *Sarcocystis* spp. occurred most frequently (19.1%), followed by *Capillaria* spp. eggs (16%), *Ancylostoma*/*Unicinaria* eggs (13.1%), *Crenosoma vulpis* larvae (4.6%), *Angiostrongylus vasorum* larvae (3.1%), *Toxocara canis* (2.8%), *Hammondia*/*Neospora*-like oocysts (2.6%), *Cystoisospora ohioensis* oocysts (2.1%), *Giardia* spp. cysts (2.1%), *C. canis* oocysts (1.8%), *Trichuris vulpis* eggs (1.5%), *Taenia* spp. eggs (1.5%), *Diphyllobotrium latum* eggs (1.5%), *Strongyloides planiceps* eggs (0.5%), *Opisthorchis felineus* eggs (0.5%), *Toxascaris leonina* eggs (0.3%) and *Alaria alata* eggs (0.3%). PCR analyses reveal the presence of *E. granulosus* eggs in one animal. The here identified parasite fauna of wolves in Croatia consists of several protozoan and metazoan parasites with not only pathogenic potential for the wolves but further with anthroponozoonotic potential in the Gorski Kotar region.

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Session Details:	8/27/2013 A walk on the wild side 1140 - 1240 Riverside Theatre
Poster with 2 minute Oral Presentation Details:	Endoparasite fauna of German red foxes (<i>Vulpes vulpes</i>) with emphasis on <i>Angiostrongylus vasorum</i>
Authors:	Kathrin Schug ¹ , Carlos Hermosilla* ¹ , Jörg Hirzmann ¹ , Roland Schaper ² , Anja Taubert ¹ ¹ Justus Liebig University Giessen, Giessen, GERMANY ² Bayer Animal Health GmbH, Leverkusen, GERMANY
Poster Number:	68

In Germany, the spread of foxes (*Vulpes vulpes*) from sylvatic to urban areas is a well-known feature. With their urbanization foxes import infectious parasitic stages in close proximity to man and pets. Especially life-threatening parasites, such as *Echinococcus multilocularis* for humans or *Angiostrongylus vasorum* for dogs, may be of major concern. So far, data on the latter parasite in foxes in Germany are scarce. Therefore we conducted a study on fox parasites covering the period of one year. Overall, pluck (heart and lung) and faecal samples of 569 foxes were collected from three regions of Germany (Hesse, Thuringia, Rhineland-Palatinate). Lungs, hearts and adjacent vessels were processed for adult nematode detection. Parasitological diagnoses of faecal samples were performed by SAF technique, *Giardia*- and *Cryptosporidium*-Coproantigen-ELISAs.

Foxes proved heavily infected with lungworms: 69.2 % of the foxes carried adult *Eucoleus aerophila*, in 32.3% of the samples *Crenosoma vulpis* were found. Overall, adult *A. vasorum* were detected in 14.1% of the samples. Significant regional differences concerning *A. vasorum* infections became evident with highest prevalences in Rhineland-Palatinate (27.3%), followed by Hesse (19.1%) and Thuringia (8.4%).

In faecal samples, *Capillaria/Eucoleus* spp. eggs occurred most frequently (51.2%), followed by *Toxascaris leonina* (35.4%), *Toxocara canis* (14.7%), *Isospora* spp. (13.6%) Ancylostomatids (13.3%), taeniids (8.1%), *Trichuris vulpis* (4.6%), *Sarcocystis* spp. (2.5%), *Alaria alata* (0.9 %) and *Physaloptera* spp. (0.5 %). Coproantigen-ELISAs revealed prevalences of 10.2 % and 2.1% for *Cryptosporidium* spp. and *Giardia* spp. infections, respectively.

These results indicate that German red foxes have to be considered as eminent reservoir hosts for *A. vasorum* which causes a severe cardiopulmonary disease in dogs. Furthermore, the spectrum of parasites reveals both pathogenic parasitoses for dogs and infections with an anthroponozoonotic potential for humans.



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Session Details:	8/27/2013 A walk on the wild side 1140 - 1240 Riverside Theatre
Poster with 2 minute Oral Presentation Details:	Wild rodents as intermediate and paratenic hosts of canine and feline parasites in Berlin
Authors:	Julia Blümle ¹ , Jürgen Krücken ¹ , Denny Maaz ¹ , Janina Demeler ¹ , Daniela Antolová ² , Roland Schaper ³ , Georg von Samson-Himmelstjerna ¹ ¹ Freie Universität Berlin, Berlin, Germany ² Slovak Academy of Sciences, Košice, Slovak Republic ³ Bayer Animal Health GmbH, Monheim, Germany
Poster Number:	50

Wild rodents are important intermediate or paratenic hosts for many parasites infecting canids and felids. In this study, rodents (257) were trapped in two urban (backyard and city park) and two peri-urban (forests) locations in Berlin between November 2010 and November 2011. DNA was isolated from striated muscle and brain tissue and analysed for the presence of ascarids and coccidian by PCR. In 4.3% of the samples ascarid DNA was detected – including *Toxocara canis* and *Toxocara cati* but also species without paratenic hosts such as *Parascaris equorum*. A *T. canis* ELISA was positive in 13.6% of the serum samples – the majority of these samples were from *Apodemus agrarius*. The coccidian parasite most often identified using a pan-coccidian PCR followed by Sanger sequencing of the PCR product was *Frenkelia glareoli*, a parasite found in bank vole that does not use canids or felids as definitive hosts but different buzzard species. Due to its high zoonotic potential, a *Toxoplasma gondii* specific PCR was performed which is more sensitive than the coccidian PCR since it targets a *T. gondii* specific repetitive element. This analysis revealed a *T. gondii* prevalence of 4.3%. In addition, *Mesocostoides litteratus* metacestodes were found in the abdominal cavity as identified by PCR targeting the ITS region of the rDNA genes. This cestode species uses both canids and felids as definitive hosts. Considering the short live time of small rodents there is apparently a high infectious pressure of both zoonotic parasites with canid and feline definitive hosts but also with parasites of birds of prey.



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Session Details:	8/27/2013 A walk on the wild side 1140 - 1240 Riverside Theatre
Poster with 2 minute Oral Presentation Details:	The prevalence of intestinal and ecto-parasites of <i>Apodemus agrarius</i> in Korea
Authors:	Yong Suk Lim1, Ju-Ha Song1, Tamer Said Abdelkader2, Hong-Shik Oh3, Jong-Taek Kim4, Jeong-Hwa Shin4, Jung-Hyun Kim4, Jong-Min Kim 4, Jae-Hak Park2, Hee-Jeong Youn1* Joon-Seok Chae 1department of Veterinary Parasitology, College of Veterinary Medicine, Seoul National University, Seoul, 151-742, Korea, 2 Department of Laboratory Animal Medicine, College of Veterinary Medicine, Seoul national University, Seoul, Korea, 3 Department of Science Education, Jeju National University, Jeju, Korea, 4 College of Veterinary Medicine, Kangwon National University, Chuncheon, Korea, 5 Biosafety Research Team, Environmental Health Research Department, National Institute of Environmental Research, Incheon, Korea
Poster Number:	66

In order to investigate the internal and ecto-parasites from *Apodemus agrarius*, Ninety three *Apodemus agrarius* were captured from 11 provinces of Korea. A kind of louse were detected on the back of 29 (31.2%) mice anus of 50 (53.8%) mice. Another kind of louse and its' eggs were detected on the back of 17 (18.3%) mice anus of 10 (10.8%) mice. A kind of mites were detected on the back of 8 (8.6%) mice anus of 15 (16.1%) mice. Unidentified nematodes were detected in intestinal contents of 20 (21.5%) mice and coccidia were detected in intestinal contents of 5 (5.4%) mice. Nematode and coccidia were detected in the feces of 1 (1.1%) mice. Regional incidences were 50% in Yongyang, 50.0% in Jeju, 33.3% in Mungyong, 31.8% in Chuncheon, 26.7% in Yangyang, and 16.7% in Gwangju.

All kind of parasites will be identified by PCR and sequencing.

Keywords : intestinal parasites, ecto-parasites, *Apodemus agrarius*, louse, mite, coccidia

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Session Details:	8/27/2013 A walk on the wild side 1140 - 1240 Riverside Theatre
Poster with 2 minute Oral Presentation Details:	Gastro-intestinal parasites of Korean Water Deer (<i>Hydropotes inermis argyropus</i>)
Authors:	Yong Suk Lim, Kyong Hee Kim, Baek-Jun Kim, Hee-Jeong Youn, Joon-Seok Chae 1College of Veterinary Medicine, Seoul National University, Seoul, 151-742, Korea
Poster Number:	2

Korean water deer is a major species of deer in Korea. They live in mountain and plain areas. Their feces were collected from mountain and plain in Korea. The intestinal parasites were surveyed from the feces of Korean water deers by use of sedimentation and floatation methods. Oocysts of coccidia (12.28%), cysts of ciliates (3.51%), eggs of *Trichuris spp* (5.26), *Nematodirus* (4.39%), *Capillaria* (0.88), and unidentified nematode (2.63), mite (0.88) and it's egg (1.75) were detected from the feces of 114 water deer. Any kinds of parasites were detected from 36 (31.8%) per 114 fecal samples. The fecal samples collected from mountain in winter season were highest prevalence (57.9%) of parasites. That from field in autumn was second higher pre valence (50.0) than the other fecal samples from mountains and field at the other seasons (20.7-33.3%)

The isolated parasitic eggs will be identified by PCR and sequencing.

Keywords : Water deer, intestinal parasites, coccidian, Trichuris spp

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Session Details:	8/27/2013 A walk on the wild side 1140 - 1240 Riverside Theatre
Poster with 2 minute Oral Presentation Details:	Circulation of helminthozoonoses in protected area of Tatra National Park, Slovakia
Authors:	Martina Miterpáková*, Zuzana Hurníková, Adriana Iglódyová Institute of Parasitology, Slovak Academy of Sciences, Košice, Slovakia
Poster Number:	261

Tatra National Park (TANAP) has been in the long term most favourite tourist area in Slovakia. From a public health perspective, greatly important is monitoring of serious parasitic diseases transmissible to humans (alveolar echinococcosis, trichinelosis and dirofilariosis) in their natural reservoir, wild carnivores, especially red fox (*Vulpes vulpes*).

More than 200 wild carnivores originated from various recreational areas of TANAP were examined for the presence of *Echinococcus multilocularis*, *Trichinella* spp. and *Dirofilaria* spp. All samples came from the death animals and were collected by TANAP workers.

E. multilocularis was detected in more than 40.0 % of foxes originated from recreational settlements of TANAP. The tapeworm was also diagnosed in 3 racoon dogs, wild and domestic cats, and juvenile stages in polecat and badger.

Trichinella larvae were found in muscles of 18.8% red foxes. In addition, beech and pine martens, racoon dogs, polecats, wolf, otter, brown bear, lynx and domestic cat were found to be infected. In all infected animals, the sylvatic species *T. brittovi* was identified.

In total 41 samples from free living carnivores were examined for *Dirofilaria* presence. *D. repens*, zoonotic agent of subcutaneous dirofilariosis, was diagnosed in 3 red foxes and 1 beech marten.

Long-term parasitological research confirmed a high prevalence of alveolar echinococcosis and trichinellosis in the territory of Tatra National Park. Zoonotic nature of the diseases and the fact that the TANAP is most visited tourist areas in Slovakia, greatly increase the risk of transmission to humans. The first finding of *D. repens* in carnivores from northern mountainous part of Slovakia confirmed that environmental circumstances in this area are also favourable for the presence of both, parasite and vector.

Acknowledgements:

This study has been realized thanks to the financial support of the Research & Development Operational Programme funded by the ERDF: Environmental protection against parasitozoonoses under the influence of global climate and social changes (code ITMS: 26220220116).



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Poster with 2 minute Oral Presentation Details:	Morphometric characterisation of enteric coccidia from native Australian mammals
Authors:	Peter O'Donoghue*, Michelle Chin Ying Chan The University of Queensland, Brisbane, AUSTRALIA
Poster Number:	64

Numerous coccidian parasites have been described from mammals throughout the world, but information on infections in native Australian animals is sparse and fragmentary. An opportunistic survey was conducted on faecal samples collected from wild and captive populations of rodents, bandicoots, possums and echidnas from southern and eastern Australia. Sporulated oocysts were harvested and identified by morphometric characterisation. Coccidial infections were detected in 44 of 294 animals (prevalence of 16%). All findings represented new records of infection and a total of 22 novel oocyst morphotypes were discovered. Fifteen novel *Eimeria* morphotypes were detected: 11 from native rodents (*Hydromys chrysogaster*, *Melomys cervinipes*, *Uromys caudimaculatus*, *Rattus fuscipes*, *R. leucopus* and *R. lutreolus*), two from bandicoots (*Isodon macrourus*, *I. obesulus*, *Perameles gunnii* and *P. nasuta*), one from possums (*Trichosurus vulpecula*) and one from echidnas (*Tachyglossus aculeatus*). Two novel *Isospora* morphotypes were detected from rodents (*R. fuscipes* and *R. leucopus*), and two novel *Octosporella* morphotypes were found: one from rodents (*R. leucopus*) and one from bandicoots (*I. obesulus*). Most morphotypes were specific for individual host species (oioxenous) although several were found in closely-related hosts (stenoxenous). The intensities of infection were generally low and none were associated with any apparent clinical signs of disease. Possible pseudoparasites detected included a novel *Monocystis* morphotype in rodents (*R. fuscipes* and *R. leucopus*), a novel *Zygocystis* morphotype in a rodent (*R. leucopus*), and a novel *Adelina* morphotype in a bandicoot (*P. nasuta*) [similar coccidia occur in earthworms and insects]. Collectively, the results indicate high parasite endemicity in native Australian mammals, suggesting their coevolution in long geographic isolation.



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Session Details:	8/27/2013 A walk on the wild side 1140 - 1240 Riverside Theatre
Poster with 2 minute Oral Presentation Details:	Parasites of cormorants from Riverina region
Authors:	Tom O'Brien ¹ , Matthew McLellan ² , Nigel Urwin ¹ , Rob Woodgate ¹ , Shokoofeh Shamsi ^{1*} ¹ School of Animal and Veterinary Sciences, Graham Centre for Agricultural Innovation, Charles Sturt University, Wagga Wagga, Australia; ² NSW Department of Primary Industries, Narrandera Fisheries Centre, Narrandera Australia
Poster Number:	67

Cormorants are a common predator in fish farms across NSW. They have been responsible for causing almost total depredation of fish in a fish farm. Narrandera Fisheries Centre runs programs to help recover populations of endangered native species such as trout cod and provides fingerlings of three other Australian native fish species to improve freshwater recreational fisheries and conservation initiatives. The Centre is permitted under The National Parks and Wildlife Act to remove cormorants from its farms in order to effectively run these programs. This provided opportunity for us to examine internal and external parasites of cormorants. The aims of the current study were to determine the parasites present and to assess the risk of these parasites to the health of native farmed freshwater fish species in the region. A total of 17 cormorants, *Phalacrocorax carbo* were shot by staff in the Narranderra Fisheries Centre from December 2012 to January 2013. Internal and external parasites, including nematodes, cestodes and lice, of 17 cormorants were collected and identified using morphological tools. We discuss the importance of parasites found in cormorants for both the aquaculture industry and fish health.

Acknowledgement:

Tom O'Brien is a grateful recipient of the summer research scholarship from Graham Centre for Agricultural Innovation. We would like to thank Dr David Reed from Wagga Wagga City Council for his contribution to this research. We acknowledge, School of Animal and Veterinary Science, Charles Sturt University and Graham Centre for Agricultural Innovation for financial support to attend the conference



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Session Details:	8/27/2013 A walk on the wild side 1140 - 1240 Riverside Theatre
Poster with 2 minute Oral Presentation Details:	First report of <i>Ancylostoma ceylanicum</i> in wild canids.
Authors:	Felicity A. Smout ^{1*} , R.C. Andrew Thompson ² , Lee F. Skerratt ¹ ¹ James Cook University, Townsville, AUSTRALIA ² Murdoch University, Perth, AUSTRALIA
Poster Number:	205

The parasitic nematode *Ancylostoma ceylanicum* is common in dogs, cats and humans throughout Asia, inhabiting the small intestine and possibly leading to iron-deficient anaemia in those infected. It has previously been discovered in domestic dogs in Australia and this is the first report of *A. ceylanicum* in wild canids. Wild dogs (dingoes and dingo hybrids) killed in council control operations (n=26) and wild dog scats (n= 89) were collected from the Wet Tropics region around Cairns, Far North Queensland. All of the carcasses (100%) were infected with *A. caninum* and three (11.5%) had dual infections with *A. ceylanicum*. Scats, positively sequenced for hookworm, contained *A. ceylanicum*, *A. caninum* and *A. braziliense*, with *A. ceylanicum* the dominant species in Mount Windsor National Park, with a prevalence of 100%, but decreasing to 68% and 30.8% in scats collected from northern and southern rural suburbs of Cairns, respectively. Due to the ability of *A. ceylanicum* to cause a patent infection in humans, the zoonotic risk arising from this wild dog reservoir to communities in the Wet Tropics should be determined.

Acknowledgements:

The authors would like to thank CSIRO Atherton, Cairns Council and Damian Marrant for assistance with sample collection. Felicity Smout received funding assistance from the Australian Society of Parasitology researcher exchange training and travel award. We would also like to thank Aileen Elliott, Louise Pallant and Angela Reeves for their advice and expertise with microscopic and PCR analysis.

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Session Details:	8/27/2013 All about tapeworms 1140 - 1240 Meeting Room 1
Poster with 2 minute Oral Presentation Details:	Cystic echinococcosis in an Uruguayan domestic cat caused by <i>Echinococcus granulosus sensu stricto</i> (genotype 1)
Authors:	Maria Teresa Armua-Fernandez ¹ , Oscar F. Castro ² , Alejandro Crampet ³ , Álvaro Bartzabal ⁴ , Regina Hofmann-Lehmann ⁵ , Felix Grim ¹ , Peter Deplazes ¹ ¹ Institute of Parasitology, University of Zurich, Zurich, Switzerland; ² Departamento de Parasitología y Enfermedades Parasitarias, Facultad de Veterinaria, Universidad de la Republica, Montevideo, Uruguay; ³ Departamento de Anatomía Patológica, Facultad de Veterinaria Universidad de la República, Montevideo, Uruguay; ⁴ Liberal professional, Rocha, Uruguay; ⁵ Laboratory Medicine, University of Zurich, Zurich, Switzerland.
Poster Number:	212

Echinococcus species require two mammalian hosts to complete their life cycle. The species most frequently found in most continents is *E. granulosus sensu stricto* (genotype 1). It is a zoonotic agent and causes a significant burden of disease worldwide. Dogs or other canids are the definitive hosts while domestic and wild ungulates are typically the main intermediate hosts. Felids are considered relatively resistant to intestinal *Echinococcus* infections. Exceptions are *E. felidis* in Africa and *E. oligarthrus* in South America which both rely on wild felids as definitive hosts, and *E. multilocularis* which occasionally develops to gravid stages with low egg production rates in cats. On the other hand, several cases of cystic echinococcosis (CE) in domestic cats have been reported from different regions of the world [1, 2]. In this work a new case of CE associated with a feline immunodeficiency virus infection (FIV) in an Uruguayan cat is reported. The cat was taken to a veterinary clinic in Rocha city, Uruguay due to dyspnea, constipation and abdominal enlargement. During surgery a large quantity of cysts was retrieved from the abdominal cavity. The cysts were 0.29 cm to 5.31 cm in diameter, fluid filled and showed the typical characteristics of hydatid larval stages, i. e. a laminar and a germinal layer with brood capsules and protoscoleces. The species was identified as *E. granulosus sensu stricto* (genotype 1) by molecular tools using cytochrome oxidase subunit 1 as target gene[3]. FIV-induced decreased immunity could be a determining factor in the development of cystic echinococcosis in cats.

Acknowledgements:

The researchers would like to thanks to Alicia von Gehlen (Facultad de Veterinaria, Universidad de la Republica, Montevideo, Uruguay) and Iskenderali Ziadinov (University of Zurich) for their kind translation assistance as well as Luis Rista (Zoonosis Committee, Uruguay), and Diogo Guerra (University of Zurich) for their valuable contributions to this manuscript.

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Session Details:	8/27/2013 All about tapeworms 1140 - 1240 Meeting Room 1
Poster with 2 minute Oral Presentation Details:	The decline in equine <i>Echinococcus granulosus</i> in south-west England.
Authors:	Gerald.Coles* and Helen Jones School of Clinical Veterinary Sciences, University of Bristol, Langford House, Bristol BS40 5DU, UK.
Poster Number:	155

Introduction: In the 1970s equine *E.granulosus*, believed to be non-infective to humans, was very common in horse livers (60%) (1) due to feeding of raw horse meat to fox hounds and the lack of a really effective cestode. How far the incidence had declined with the introduction of praziquantel was unknown.

Methods: Numbers of infected livers were counted in 2002 and ten years later. Questionnaires were sent out to hunt kennels.

Results: Of 921 horses inspected in 2002 17.4% had *E.granulosus* cysts in their livers. Most livers had 1-2 cysts 1-10 cm in diameter. By 2012 this figure had declined to 5.2% (1205 horses). In 2002 of 18 kennels 18% said they fed horse meat regularly and 59% occasionally. In 2012 out of 21 kennels 48% said they fed raw horse meat regularly and 33% occasionally. Praziquantel was used on average 1.76 X per year in all kennels in 2012. Where horse meat was fed regularly the average number of doses per year was 1.4 with 3 kennels using no products containing praziquantel.

Discussion: The decline in infection rates is encouraging. Since most horses taken to the abattoir are about 20 years old, the infection rate in younger horses should now be lower. However to ensure eradication of equine *E.granulosus* more treatment of dogs with praziquantel is required.

Reference: (1) Thompson, R.C.A. and Smyth, J.D. Veterinary Parasitology 1975; 1:107.



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Session Details:	8/27/2013 All about tapeworms 1140 - 1240 Meeting Room 1
Poster with 2 minute Oral Presentation Details:	Counting of <i>Anoplocephala</i> eggs in equine faecal samples.
Authors:	Jon Cima and Gerald Coles* School of Veterinary Sciences, University of Bristol, Langford House, Bristol BS40 5DU, UK
Poster Number:	81

Introduction: Previous attempts at counting eggs of *Anoplocephala perfoliata* have not been very successful [1,2]. With the introduction of a novel egg counting technique sensitive to 1 e.p.g., FLOTAC [3], the possibility of using this technique to count cestode eggs in horse faecal samples was examined.

Methods: Adult *A.perfoliata* and faeces from horses with known numbers of worms were collected from a li-censed horse abattoir. A known number of eggs from mature segments were re-suspended and added to 10 g of faeces from uninfected horses and counted with the FLOTAC chamber.

Results: When eggs were added directly to the FLOTAC cell the recovery was 100%. Recovery rates using 5% Tween 20 and saturated solutions were sucrose 81%, sodium chloride 79% and zinc sulphate 74%. Best results (72%) with 10 gr faeces were with 10% Tween 20 and 50% sucrose. When eggs were added to differ-ent egg free faeces, eggs were always found in the sample, but the results were variable. Egg loss occurred when the faeces were filtered. The repeatability of counts from naturally infected faecal samples from horses with heavy worm burdens was low, varying from horse to horse, suggesting eggs were not evenly distributed in the faeces. By contrast 88% recovery of eggs was obtained when added to cattle faeces.

Discussion: The coarse nature of the fibres in horse faeces traps *A.perfoliata* eggs making faecal egg counts unreliable. Novel methods of estimating *A.perfoliata* burdens in horses are required

Acknowledgements: Jon Cima was supported by a Wellcome student summer grant.

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Poster with 2 minute Oral Presentation Details:	Bovine cysticercosis control at a feedlot farm
Authors:	Samuel Carvalho de Aragão ^{1*} , Silvana de Cássia Paulan ¹ , Diego Pacheco dos Santos ¹ , Píer Kenji Rauschkolb Katsuda Ito ¹ , José Pavan Neto ^{2*} ; José Henrique Hildebrand Grisi-Filho ³ , Cáris Maroni Nunes ¹ ¹ UNESP – University Estadual Paulista, Faculty of Veterinary Medicine, Araçatuba, SP, Brazil ² Floresta Farm Zoothechnician ³ USP – University of São Paulo, Faculty of Veterinary Medicine and Zootechny, São Paulo, SP, Brazil
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Control of the taeniasis-cysticercosis complex in Brazil is based on *post-mortem* inspection at slaughterhouses, basic sanitation and health education. Bovine cysticercosis is responsible for economic losses in the meat chain and one of the factors that difficult its control is that ranches that supplies slaughterhouses do not breed the cattle. These are purchased by the feedlot owner from many different ranches at about 3-6 months of age without any testing and then spend 12-15 months on pasture before entering the feedlot. This makes traceability and environment sanitation very difficult. Albendazole sulfoxide has been the preferred drug for beef cattle treatment but many producers don't follow the proper treatment schedule and dosing. In this study, from 2010 to 1012 we managed a beef cattle farm located in Três Lagoas, MS, Brazil (S 20°20,98 5' W 052°07,49 7') presenting 25% of cysticercosis incidence (185/742). Management consisted of i) chemotherapy by four subcutaneous doses of albendazole sulfoxide (7mg/kg) every 30 days, ii) farm workers coproparasitological testing, and iii) the identification of the farm network of commercial trades. We identified a positive human *Taenia saginata* carrier that was properly treated with niclosamide and remained to be negative after one year. Besides, a network consisting of eight farms was identified as the main responsible for cysticercosis incidence at the feedlot. Association of a proper chemotherapy and network changes progressively decreased cysticercosis prevalence to 3.7% (31/837) in 2011 and to 1.80% (39/2142) in 2012. These results confirm that a proper management by chemotherapy and ranches network analysis can aid the bovine cysticercosis control, minimizing economic losses as well as preventing human taeniasis.

Acknowledgements:

CNPq – 485406/2011-0



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Session Details:	8/27/2013 All about tapeworms 1140 - 1240 <i>Meeting Room 1</i>
Poster with 2 minute Oral Presentation Details:	Infection Rates, Cyst Fertility and Larval Viability of Hydatid Disease in Camels (<i>Camelus dromedarius</i>) from Borena, Kereyu and Harar Areas of Ethiopia
Authors:	<i>Muskin Salih¹, Hailu Degefu ¹ and Moti Yohannes ¹</i> ¹ Jimma University, College of Agriculture and Veterinary Medicine, P.O.Box: 307, Jimma, Ethiopia
Poster Number:	273

The study was conducted from October 2009 to March 2010 at Akaki sub city municipal abattoir in Addis Ababa to determine the prevalence of hydatidosis in camel slaughtered for human consumption. Out of a total of 460 camels slaughtered 104 (22.6%) were found harboring hydatid cysts. The degree of prevalence between males (19.01%) and females (49.09%) was statistically significant ($\chi^2=25.4$, $p < 0.05$). The highest rate of infection (27.77%) was observed in camel from Harar while the lowest (20.62%) was found in animal from Kereyu. The infection rate were significantly different among the three age groups ($\chi^2 =8.8$, $DF=2$, $p<0.05$). The prevalence was found to be high (28.63%) in animal greater than 10 years. The organ distributions of the cysts were 67.3% in lung alone, 25% both liver and lungs, 6.73% in liver only and 0.96% in heart. The mean intensity of hydatid cyst among affected camels was found to be 3.1 ± 5.8 . The majority (74.5%) of the cysts identified in this study were non calcified cysts. The fertility of the cysts was 57.24% and 40% in lung and liver, respectively, out of these fertile cyst 66.6% of them were found to be viable in both organs. Therefore, an effort should be made to control the transmission of cystic echinococcosis from slaughter house by safe disposal of infected offal.

Key words: Prevalence, Camel , Hydatidosis , Abattoir, Ethiopia



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Session Details:	8/27/2013 All about tapeworms 1140 - 1240 Meeting Room 1
Poster with 2 minute Oral Presentation Details:	Modulation of fibrosis and inflammation via anthelmintic praziquantel and flavonoid silymarin during larval cestode infection in mice
Authors:	Emilia Vendelová, Gabriela Hrčková, Samuel Velebný, Michaela Dolinská* Institute of Parasitology, Slovak Academy of Sciences, Košice, SLOVAK REPUBLIC
Poster Number:	185

Larval stage of tapeworms cause neglected diseases that can be fatal and are difficult to treat. Anthelmintics (praziquantel, albendazole) represent inefficient drugs and no therapy is presently available that reliably kills the dangerous tapeworm larvae. Larval tapeworms maintain long-term survival due to hosts immune-suppression and often parasite fibrous encapsulation. Infection-associated Th2 type of immune response and fibrosis along with low availability of drugs contribute to reduced effectiveness of treatment. Derived from a variety of sources, natural compounds are increasingly exploited for drug development, and secondary plant metabolites have a great potential in antiparasitic therapy with possible immunomodulatory effect. In the present study on experimental parasitic infection caused by the larval stage of model cestode *Mesocostoides vogae* in mice we examined the immunomodulatory effects of flavonoid silymarin (SIL) alone and its effect in combination with drug praziquantel (PZQ). Peritoneal exudate cells from infected and treated mice were evaluated for the modulation of non-specific effector functions (respiratory burst, phagocytic activity), relative gene expression of transcription factor NF-KB and cytokines IFN-γ, TNF-α, IL-4, IL-5. In addition, mode of action of PZQ and SIL involved analysis of expression of genes for collagens, TGF-β and cytokines of Th1/Th2 type in the livers samples. Parallel administration of natural substance with drug significantly elevated efficacy of the treatment. The effects on ROS production, cells distribution and the degree of fibrosis differed between treated groups. Our finding showed that during the chronic inflammatory disease caused by parasitic cestodes, flavonoid silymarin has multiple positive effects. Combined therapy with drug and natural compound silymarin showed several benefits compared with classical treatment, in terms of increased efficacy and improved immunopathology of hosts.

Acknowledgements: Support was given by Grant Agency VEGA, project no. 2/0150/13.



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Session Details:	8/27/2013 All about tapeworms 1140 - 1240 Meeting Room 1
Poster with 2 minute Oral Presentation Details:	Risk factor-based management of <i>Taenia saginata</i> cysticercosis outbreaks on farm level: a risk assessment chart as a tool for veterinarians
Authors:	Ramon M. Eichenberger ¹ , Peter Deplazes ¹ ¹ Institute of Parasitology, University of Zurich, Zurich, SWITZERLAND
Poster Number:	4

Taenia saginata cysticercus infection in cattle is an important parasitosis for the livestock industry. Infected cattle are detected during the obligatory meat inspection at abattoirs which represents the only control measure in many countries. Bovine cysticercosis may generate substantial financial loss by severe downgrading or even condemnation of infected carcasses. Here, we present a risk factor-based approach for the management of affected farms, summarised in a risk assessment chart devised for veterinarians in Switzerland. The chart is based on known risk factors for bovine cysticercosis including factors concerning sanitary conditions, food and feeding management, and environmental conditions (flooding of pastures, risky water sources, grazing areas located close to railways or parking lots, leisure activities around these areas, and organised public activities) [1; 2; 3; 4]. The variables of each factor are classified to one of the risk groups (high-, medium-, and low infection risk) on the chart. The case management consists of 1) personal interview with the farmer addressing the risk factors, 2) stool examination of the persons on the farm, and 3) serological investigation of the cattle. The scheme was evaluated by follow-up investigations of three severely affected farms in collaboration with veterinarians. Three stool samples from all people on the farms were coproscopically analysed for the presence of taeniid eggs by standard flotation technique, copro-antigen ELISA [5] and a sensitive flotation and sieving method [6], followed by molecular verification [7]. The infection status of animals was controlled by repeated serological tests [8]. The situation of the farms resolved by adhering to the recommendations, and no new infections were recorded on these farms as evidenced by abattoir reports and serological follow up investigations (up to two years), respectively. This risk assessment chart represents an effective tool for veterinarians to identify and eliminate risk factors of farms which experienced cysticercosis cases.

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Session Details:	8/27/2013 All about tapeworms 1140 - 1240 Meeting Room 1
Poster with 2 minute Oral Presentation Details:	Identification and characterization of Kunitz type protease inhibitor in <i>Echinococcus granulosus</i>
Authors:	Shiwanthi Ranasinghe ^{1, 2*} , Katja Fischer ¹ , Geoffrey Gobert ¹ , Darren Gray ² , Don McManus ¹ ¹ Queensland Institute of Medical Research, Brisbane, Queensland, Australia ² University of Queensland, Brisbane, Australia
Poster Number:	184

Cystic echinococcosis caused by larval stages of *Echinococcus granulosus* is a near cosmopolitan zoonotic disease which accounts for more than 90% of clinical cases of hydatid disease and causes substantial morbidity and mortality globally. The Kunitz type proteins belong to the I2 family of protease inhibitors and are involved in a diverse range of biological processes in invertebrates [1]. In parasitic helminths these proteins have been shown to provide protection from host enzyme digestion. Using data from a recent genomic study of *E. granulosus*, we have identified secretory type gene sequence with similarity to single domain Kunitz type serine protease inhibitors (EgKI). Recombinant form of the EgKI protein (rEgKI9) was produced using the *E. coli* expression system and purified with Nickel affinity chromatography. Real time PCR results indicated that EgKI9 is highly expressed in adult worms. Immunolocalization, using antibodies produced in mice, showed that EgKI9 is present along the tegument of the adult worm indicating a likely role in providing protection from host digestive enzymes. Serine protease inhibitory assays were performed using trypsin, chymotrypsin and neutrophil elastase. rEgKI9 inhibit trypsin in femtomolar range but no inhibition was detected for latter two proteases. As a potent inhibitor of mammalian intestinal proteases, this EgKI protein may play a key role in the survival of adult *E. granulosus* within the host. We consider the rEgKI9 may be a useful candidate as novel drug target to control cystic echinococcosis.

Acknowledgements: NHMRC Program grant, UQI scholarship

Reference: 1. Ranasinghe S, McManus DP: **Structure and function of invertebrate Kunitz serine protease inhibitors.** *Dev Comp Immunol* 2013, **39**(3):219-227.



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Session Details:	8/27/2013 All about tapeworms 1140 - 1240 Meeting Room 1
Poster with 2 minute Oral Presentation Details:	Extra-cerebral coenurosis – location of cysts in goat carcasses
Authors:	Rolf K. Schuster ^{1*} , Saritha Sivakumar ¹ , Tadeus Wieckowsky ² ¹ Central Veterinary Research Laboratory, Dubai, U.A.E. ² Nad Al Sheba Palace Veterinary Clinic, Dubai, U.A.E
Poster Number:	32

Coenurosis is a disease caused by the larval stage of taeniid cestodes of the genus *Multiceps*. *Multiceps multiceps* and *M. serialis* are the best known species larval stages of which occur predominantly in the central nervous system of small ruminants and subcutaneous tissues of leporids, respectively. Further species of veterinary significance, *M. gaigeri* in goats and *M. skrjabini* in sheep were synonymised with *M. multiceps* due to the morphology of their bladderworms. However, recent molecular examination of intramuscular coenuri from goat carcasses revealed differences in the genome. Thirty-two goat carcasses of animals aged between 5 and 6 months were objected at meat inspection due to the presence of bladderworms in an abattoir in Dubai between August 2012 and March 2013. The majority showed single cyst that were cut out but 7 bodies had to be discharged due to generalised coenurosis of carcass and offal with a maximum number of 41 coenuri. In the majority of goats, cysts were located in the left (n=14) and right (n=12) legs followed by loin (n=7), rack (n=6), left (n=5) and right (n=4) shoulder and breast (n=2). Diaphragm, abdominal muscles, kidneys and heart of 10, 10, 4 and 3 animals, respectively, were also affected. A swelling on the right masseter of one goat turned out also to be a coenurus. The size of the parasitic cysts ranged from corn grain with 15 scolexes arranged in 4 clusters found in the heart to goose egg with 375 scolices in 13 clusters attached to the thoracal part of diaphragm.

All goats were healthy prior slaughter and did not show any clinical symptoms of gid.



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Session Details:	8/27/2013 All about tapeworms 1140 - 1240 Meeting Room 1
Poster with 2 minute Oral Presentation Details:	Artemia as intermediate host for bird cestodes
Authors:	R.Schuster ¹ , Saritha Sivakumar ¹ , Kevin Hyland ² ¹ Central Veterinary Research Laboratory, Dubai, U.A.E. ² Wildlife Protection Office, Dubai, U.A.E.
Poster Number:	156

Artemia is a genus of aquatic crustaceans known as brine shrimps. They are the staple food for a variety of aquatic birds and also act as intermediate host for parasites. A total of 4,892 specimens (1,737 males and 3,154 females) brine shrimps, *Artemia salina* from an artificial pond in Dubai, were examined in monthly intervalls between February 2010 and January 2013 for the presence of larval cestode infections. The pond is home to a permanent population of around 50 greater flamingos (*Phoenicopterus roseus*). Cysticercoides were found in 45% of brine shrimps and 7 cestode species were recorded (Table). The maximum number of 16 cysts of 4 different species was isolated from one crustacean. There was always an increase in percentage of infection from October/November to May (because of optimum temperature and influx of migratory birds) and a drastic decline in the number of brine shrimps when the outside temperatures becomes too hot in June/July. The brine shrimps regain life when the temperature lowers down to optimum and water is filled in October-November.

Table 1: Cestode larval stages found in *Artemia salina* in a pond in Dubai

Species	Prevalence (%)	Mean intensity	Final hosts
Flamingolepis liguloides	32.5	1.9	flamingos
F. flamingo	13.5	1.3	flamingos
Wardium stellorae	3.4	1.1	gulls
Eurycetes avoceti	5.2	1.1	waders, flamingos
Gynandrotaenia stammeri	1.9	1.1	flamingos
Anomotaenia spp.	0.8	1.2	waders
Confluaria sp.	0.2	1.1	grebes

Acknowledgements:

The authors are grateful to Mr. B. Srinivas for his participation in the collection of brine shrimps.



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Session Details:	8/27/2013 All about tapeworms 1140 - 1240 Meeting Room 1
Poster with 2 minute Oral Presentation Details:	Bovine cysticercosis – development of a real-time PCR to enhance classification of suspect cysts identified at meat inspection
Authors:	Leigh Cuttell ¹ , Helen Owen ¹ , Alicja E. Lew-Tabor ² , Rebecca J. Traub ^{1*} (presenting author asterisked) ¹ The University of Queensland, Gatton, AUSTRALIA ² Queensland Alliance for Agriculture and Food Innovation, St. Lucia, AUSTRALIA
Poster Number:	33

Laboratory confirmation methods are important in bovine cysticercosis diagnosis as other pathologies can result in morphologically similar lesions resulting in false identifications. We developed the first real-time PCR assay to identify *T. saginata* in suspect cysts encountered at meat inspection and compared its use with the traditional method of identification, histology, as well as a published nested PCR (Chiesa et al., 2010; Cuttell et al., 2013). The assay simultaneously detects *T. saginata* DNA and a bovine internal control using the cytochrome c oxidase subunit 1 gene of each species and shows specificity against parasites causing lesions morphologically similar to those of *T. saginata*. The assay was sufficiently sensitive to detect 1 fg (Ct 35.09 ± 0.95) of target DNA using serially-diluted plasmid DNA in reactions spiked with bovine DNA, as well as identify all viable and caseated positive control cysts. A loss in PCR sensitivity was observed with increasing cyst degeneration as seen in other molecular methods. In comparison to histology, the assay offered greater sensitivity and accuracy with 10/19 (53%) *T. saginata* positives detected by real-time PCR and none by histology. When the results were compared with the reference PCR, the assay was less sensitive but offered advantages of faster turnaround times and reduced contamination risk. Estimates of the assay's repeatability and reproducibility showed the assay is highly reliable with reliability coefficients greater than 0.94.

Acknowledgements:
Project funded by Meat and Livestock Australia (MLA). We thank David Jordan (NSWDPI) and Baden Pearse (DAFF) for assistance and advice. Thanks to Jan Slapeta and Luzia Rast (USyd), John Ellis (USyd), Asma Latif (University of Punjab, Pakistan) and Tamsin Barnes (UQ) who supplied DNA or specimens of non-target parasites. Catherine Minchin (DAFF) performed the inter-laboratory assay reliability testing, Laercio Porto (UQ) assisted in statistical analysis and Jess Morgan (UQ) advised on assay design. We are extremely grateful to the on-plant veterinarians for their help in forwarding suspect cysts identified at meat inspection.

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Cuttell, L., Owen, H., Lew-Tabor, A.E., Traub, R.J., 2013, Bovine cysticercosis–development of a real-time PCR to enhance classification of suspect cysts identified at meat inspection. Veterinary Parasitology. In press, accepted manuscript. <http://dx.doi.org/10.1016/j.vetpar.2013.02.018>.

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Poster with 2 minute Oral Presentation Details:	Molecular study of tapeworms infecting wild canids in NSW and WA
Authors:	Thomas Williams*, Kate Mitchell, Nigel Urwin, David Jenkins School of Animal and Veterinary Sciences, Charles Sturt University, Locked Bag 588, Wagga Wagga NSW 2678 Australia
Poster Number:	

Taenia ovis has been identified as a major source of economic loss to the Australian sheepmeat industry. Infection in sheep is widespread and common in all sheep rearing areas of Australia. This study, funded by Meat and Livestock Australia, is revisiting the transmission pathway of this parasite in wildlife, through an investigation of foxes (*Vulpes vulpes*) and wild dogs (*Canis lupus dingo* and hybrids (*Canis lupus dingo* x *Canis lupus familiaris*)). Wild dogs and foxes shot in the course of on farm control programs were examined for the presence of taeniid tapeworms. DNA was extracted from these and the mitochondrial small subunit ribosomal RNA (*rrnS*) gene was amplified by PCR. Sequence of analysis was used to determine the species present. The species found, their genetic diversity and the implications for mode of transmission will be discussed.



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Session Details:	8/27/2013 Bite me! - ectos as parasites 1140 - 1240 Meeting Room 2
Poster with 2 minute Oral Presentation Details:	Persistent Canine Demodicosis in a Local Bred Mongrel Bitch following Prolonged treatment with Ivermectin and Oxytetracycline LA with Topical application of Cypermethrin
Authors:	George B.D.J. Ahmadu Bello University, Zaria, NIGERIA
Poster Number:	186

An eight year old mongrel bitch locally bred in Zaria, Nigeria has persistently suffered from a generalized, squamous demodicosis in the last one year despite regimented parenteral and topical treatment with ivermectin (Promectine LA, 10mg/ml, Invesa), Oxytetracycline dihydrate (oxy-200 LA,20%, VETINDIA Pharmaceuticals Ltd) and Cypermethrin (Cypermil pour-on, 5mg/ml, Ouro Fino). Treatments were carried out initially at monthly intervals but later changed to two-week intervals. The bitch littered seven puppies during this time which have remained apparently uninfected three months later. Low immunological competence due to age and stress of pregnancy may be immediately responsible for treatment failure but the efficacy and authenticity of the drugs/chemicals used may not be guaranteed considering the existing proliferation of adulterated/fake medication imported/manufactured in and outside Nigeria. Alternatively, more recent and efficient therapeutic combinations needs be tried.

Acknowledgements:

I wish to thank the authorities and staff of the Department of Veterinary Parasitology and Entomology Ahmadu Bello University, Zaria, Nigeria for the provision of facilities that enabled me to carry out this work.

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Session Details:	8/27/2013 Bite me! - ectos as parasites 1140 - 1240 Meeting Room 2
Poster with 2 minute Oral Presentation Details:	A SEM study of the micromorphology of the sucking louse <i>Linognathus angasi</i> from the Nyala <i>Tragelaphus angasi</i> from South Africa.
Authors:	E.D.Green Dept of Anatomy, University of Limpopo, Box 232, MEDUNSA, 0204, South Africa. Edward.Green@ul.ac.za
Poster Number:	71

Sucking lice collected from wild nyala in the Ndumu Game Reserve in Kwazulu-Natal, South Africa were identified by light microscopy as *Linognathus angasi* Weisser & Ledger 1977. As the four *Linognathus* species found on the related bushbuck, nyala and greater kudu are morphologically very similar and difficult to distinguish, it was decided to do a scanning electron microscope (SEM) study to investigate the micromorphological characteristics of *L. angasi*. The lice were ultrasonically cleaned and routinely prepared for SEM and viewed in a Zeiss SUPRA55VP FE-SEM.

Small scale-like setae covered the head, thorax and membranous abdomen. The post-antennal conical head bearing five pairs of setae, tapered to join the thorax while the short rounded pre-antennal part enclosed the flaps of the haustellum at the anterior tip. The antennal segments IV and V each bore a large pore organ with its sensory tufts, and two plate organs. The robust thorax bore a pair of large lateral spiracles and a pair of long setae on the mesothorax, and ventrally a linear sternal plate which is a distinguishing feature of *L. angasi*. Legs I each bore a slender claw while the claws of legs II and III were extremely robust closing against scaled distotibial pads for attachment. Abdominal segments II to VII bore large lateral spiracles while VI to VII were characterized by pairs of long marginal setae. The female gonopods VIII were curved medially each bearing a terminal fringe of setae while gonopods IX had a medial fringe of short setae. The abdomen of the male had a large genital plate that reached from segment VII posteriorly and terminated in a single bulbous process. The everted pseudopenis had a longitudinal keel-like ridge.

These micromorphological observations on *L. angasi* may contribute to the comparative taxonomy of the *Linognathus* species of the related *Tragelaphus* antelope.



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Session Details:	8/27/2013 Bite me! - ectos as parasites 1140 - 1240 Meeting Room 2
Poster with 2 minute Oral Presentation Details:	In vitro validation of Ethiopian medicinal plant extracts against ticks and mites
Authors:	Spiridoula Athanasiadou ¹ , Etana Debela ² , Aduugna Tolera ³ , Ketema Tolossa ⁴ , Stewart Burgess ⁵ , Tim Connelley ⁶ , Sandra Terry ¹ and Jos GM Houdijk ^{1*} ¹ Scotland's Rural College (SRUC), Edinburgh, UNITED KINGDOM ² School of Veterinary Medicine, Hawassa University, Hawassa, ETHIOPIA ³ School of Animal and Range Science, Hawassa University, Hawassa, ETHIOPIA ⁴ Department of Chemistry, Hawassa University, Hawassa, ETHIOPIA ⁵ Moredun Research Institute, Edinburgh, UNITED KINGDOM ⁶ University of Edinburgh, Edinburgh, UNITED KINGDOM
Poster Number:	206

Although medicinal plants play an important role for parasite control in developing countries, scientific evidence on plant efficacy and side effects is scarce, hampering the establishment of phytomedicine as a reliable parasite control strategy. Here, we present the validation on the medicinal properties of plant preparations originating from Ethiopia, against the ovine mite *Psoroptes ovis*, and the bovine tick *Rhipicephalus appendiculatus* *in vitro*. The selection of plants was based on an ethno-botanical survey (Tolossa et al., 2013), which consisted of a detailed review of existing, anecdotal information on medicinal plants use for parasite control in Ethiopia. Mite and tick larval immersion tests (n=3) were adapted from Borges et al. (2003). In total 90 plant extracts were tested from 30 plants; dried plant matter was extracted by three solvents, methanol, 70% methanol and H₂O. From the 30 plants, five were routinely used by the traditional healers against ecto-parasites. For four of these five plants, this activity was demonstrated here either against ticks, mites or both. At a concentration of 50 g/L, efficacy varied between 55-95%; mortality rates of ecto-parasites in these extracts were significantly different from controls. Furthermore, extracts from plants that have not been previously associated with activity against ecto-parasites showed an *in vitro* efficacy ranging from 50 to 80%. The study shows the importance of validating ethnoveterinary knowledge with controlled experiments. Although the possibility that procedures used here did not result in the extraction of the active compounds in the unvalidated plant can not be excluded at this stage, it is more likely that these are just not present. *In vitro* validations as presented here will be followed by *in vivo* testing of active and selected inactive extracts to confirm biological activity.

Acknowledgements:
The authors gratefully acknowledge funding from the DFID/BBSRC/SG CIDLID program (BB/H009299/1).

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Tolossa K, Debela E, Athanasiadou S, Tolera A, Houdijk JGM (2013) Assessment of ethno-medicinal plants used for treatment of livestock ailments by traditional healers in southern Ethiopia. Proceedings of the 24th International Conference of the World Association for the Advancement of Veterinary Parasitology (submitted)
Borges L.M.F, Ferri P.H., Silva W.J., Silva W.C., Silva J.G. 2003. Medical and Veterinary Entomology 17, 228-231.



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Session Details:	8/27/2013 Bite me! - ectos as parasites 1140 - 1240 Meeting Room 2
Poster with 2 minute Oral Presentation Details:	Effectiveness of Ivermectin Long-acting Injection (IVOMEC® GOLD) on Infestations of Sucking Lice on Cattle
Authors:	James S. Hunter III ¹ , Steffen Rehbein ² , Stephen Yoon ³ , Martin Visser ² , Gregory Johnson ⁴ , Tom Yazwinski ⁵ , Kevin Syvrud ⁶ , Maureen Grubbs ⁷ , Luiz Cramer ³ ¹ Merial Limited, Fulton, MO USA, ² Merial GmbH, Kathrinenhof Research Center, Rohrdorf, Germany, ³ Merial Limited, Duluth, GA, USA, ⁴ Montana State University, Bozeman, MT, USA, ⁵ University of Arkansas, Fayetteville, AR, USA, ⁶ Summit Research, 2020 E. Sierra Road, Helena MT, USA, ⁷ 1402 Buffalo Creek Rd, Upton, WY, USA
Poster Number:	44

The efficacy of ivermectin long-acting injection (IVM LAI; IVOMEC® GOLD, Merial; 3.15% ivermectin w/v) was evaluated in cattle naturally infested with *Linognathus vituli* or *Solenopotes capillatus* in six similar studies conducted in Germany (1 study) and in the USA in Arkansas, Montana and Wyoming (5 studies). Sixteen or 18 Charolais, Hereford, Hereford cross, Fleckvieh, or crossbred cattle were included in the studies. The studies were conducted according to WAAPV guidelines (Holdsworth et al., 2006) using a randomized block design with animals ranked by decreasing lice counts (Day -3 to Day -1) and formed into 8 or 9 replicates of 2 animals each. Within replicates, animals were allocated randomly to one of two groups: saline (control) or IVM LAI. Both treatments were administered by subcutaneous injection in front of the right or left shoulder on Day 0 at 1 mL/50 kg bodyweight. For evaluation of efficacy lice counts from eight documented predilection sites per animal were made at intervals of 7±1 days for 8 weeks.

Following treatment, lice counts of the IVM LAI-treated cattle were significantly lower than those of the controls at each time point in all studies. Efficacy for IVM LAI treated cattle one week after treatment ranged from 99.3% to 100%. For all subsequent time points in the 6 studies (Days 14 – 56) efficacy was 100%. All saline-treated animals remained infested with lice throughout the duration of the studies.

These studies demonstrated a high efficacy of IVOMEC GOLD against naturally occurring sucking lice populations on cattle.

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Session Details:	8/27/2013 Bite me! - ectos as parasites 1140 - 1240 Meeting Room 2
Poster with 2 minute Oral Presentation Details:	Laboratory rearing of buffalo fly, <i>Haematobia (irritans) exigua</i>
Authors:	Peter James ¹ , Geoff Brown ² , Wayne Jorgensen ² and Jim Rothwell ^{3,4} ¹ Queensland Alliance for Agriculture and Food Innovation (QAAFI), University of Queensland, Brisbane, Australia ² Department of Agriculture Fisheries and Forestry, Brisbane, Australia ³ Department of Veterinary Science, Gatton, Australia ⁴ Current address; Meat and Livestock Australia, Sydney, Australia
Poster Number:	43

Buffalo flies are one of the main health issues for extensive beef and dairy production in northern Australia. They cause irritation to cattle, reducing weight gains and milk production and raising welfare concerns. They also vector a filarial nematode *Stephanofilaria* sp. that causes a high prevalence of skin lesions in northern cattle, downgrading skin quality and providing focus for screwworm breeding in the event of an incursion. In recent years buffalo flies have dispersed southwards and westwards into cattle producing areas where infestations have not previously been seen and their range is projected to extend significantly with climate change.

Research into new methods of buffalo fly control is limited by the need to maintain live cattle hosts. This is expensive, severely restricts the type of research that can be conducted and is problematic from an animal ethics standpoint. We have recently developed methods enabling the establishment of a persisting colony of buffalo flies that can be reared through all life stages in the laboratory. Availability of this colony will facilitate the screening of new chemical actives, enable improved monitoring for insecticide resistance through the provision of a reference strain and aid investigation of new biological controls and other novel approaches. It will also avoid the animal welfare issues and expense associated with maintaining live animal hosts for buffalo fly research.



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Session Details:	8/27/2013 Bite me! - ectos as parasites 1140 - 1240 Meeting Room 2
Poster with 2 minute Oral Presentation Details:	Treatment and Control of Natural Infestations of <i>Hypoderma</i> spp. on Cattle with a Single Subcutaneous Injection of Ivermectin Long-acting Injection (IVOMEC® GOLD)
Authors:	James S. Hunter III ¹ , Steffen Rehbein ² , Domenico Otranto ³ , Gregory Johnson ⁴ , Kevin Syvrud ⁵ , Stephen Yoon ⁶ , Luiz Cramer ⁶ ¹ Merial Limited, Fulton, MO USA; ² Merial GmbH, Kathrinenhof Research Center, Rohrdorf, Germany; ³ Università degli Studi di Bari, Italy; ⁴ Department of Animal and Range Sciences, Montana State University, Bozeman, MT, USA; ⁵ Summit Research, Helena MT, USA; ⁶ Merial Limited, Duluth, GA, USA
Poster Number:	45

The efficacy of ivermectin long-acting injection (IVM LAI; IVOMEC® GOLD, Merial; 3.15% ivermectin w/v) was evaluated in cattle naturally infested with *Hypoderma* spp. in three similar studies conducted in Germany, Italy and Montana (USA). Thirty animals were included at site 1 (crossbred beef), 33 cattle at site 2 (Podolica pugliese, Romagnola and Podolica Cross), and 16 animals at site 3 (Angus cross, Hereford cross).

Animals were ranked from highest to lowest on the basis of pre-treatment ELISA antibody test values (positive serology) which indicated exposure to *Hypoderma* spp.

Cattle in sites 1 and 2 were formed into replicates of three animals each. Within replicates, cattle were allocated randomly to one of three treatments: Group 1 – saline (control) at 1 mL/50 kg body weight; Group 2 – IVM LAI at 1 mL/50 kg body weight; Group 3 – IVM LAI at 1 mL/50 kg body weight. Cattle in site 3 were formed into eight replicates of two animals each and randomly allocated to Group 1 or Group 2. Treatments were administered once by subcutaneous injection in front of the shoulders to Group 1 and 2 animals on Day 0 at all 3 sites (when *Hypoderma* spp. were expected to be first instars) and to Group 3 animals when warbles were visible, i.e., *Hypoderma* spp. were expected to be second and/or third instars.

Live *Hypoderma* larvae were recovered from 7/10 control animals at site 1 (1-8 *H. bovis*), from 9/11 control animals at site 2 (1-17 *H. lineatum*) and from 6/8 control animals at site 3 (2-22 *H. bovis*). No live *Hypoderma* larvae were recorded on any treated animal demonstrating 100% efficacy (p<0.01) of IVM LAI against first- and second/third-stage larvae of both *H. bovis* and *H. lineatum*.

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Session Details:	8/27/2013 Bite me! - ectos as parasites 1140 - 1240 Meeting Room 2
Poster with 2 minute Oral Presentation Details:	Monitoring Field Susceptibility to Imidacloprid in the Cat Flea: A World-First Initiative Twelve Years On
Authors:	Steven Kopp ^{1*} , Byron Blagburn ² , Glen Coleman ¹ , Wendell Davis ³ , Ian Denholm ⁴ , Chris Field ⁵ , Joe Hostetler ³ , Norbert Mencke ⁶ , Bob Rees ⁷ , Michael Rust ⁸ , Iris Schroeder ⁶ , Kathrin Tetzner ⁶ , Martin Williamson ⁴ ¹ University of Queensland, Gatton, Queensland, AUSTRALIA ² Auburn University, Auburn, Alabama, USA ³ Bayer Health Care, Shawnee Mission, Kansas, USA ⁴ Rothamsted Research, Hertfordshire, UNITED KINGDOM ⁵ Bayer plc Animal Health Division, Newbury, UNITED KINGDOM ⁶ Bayer Health Care, Monheim, GERMANY ⁷ Bayer Health Care, Brisbane, Queensland, AUSTRALIA ⁸ University of California, Riverside, Riverside, California, USA
Poster Number:	118

In 2001, Bayer Animal Health established an international Flea Susceptibility Monitoring (FSM) initiative, utilising a validated larval development inhibition assay to track the susceptibility of cat flea isolates to imidacloprid. In 2009, an Australian node was incorporated into the program, joining laboratories in the United States and Europe. Field isolates of *Ctenocephalides felis* eggs were submitted to participating laboratories and, where egg quantity and quality was sufficient, were placed in the imidacloprid discriminating dose bioassay for evaluation. In the twelve year period to the end of 2012, a total of 2547 cat flea isolates were received across all sites; 1848 submissions (72.6%) were suitable for placement into the bioassay. In the Northern Hemisphere, isolate submission rate was influenced by season, with highest numbers submitted between June and October. In Australia, heavy flea infestations were observed year-round, and submission rate was largely influenced by program factors and not climate. A total of 1367 valid assays were performed between 2002 and 2012 (assay validity data was not recorded in 2001); adult flea emergence 5% or greater at 3ppm imidacloprid was observed in 38 of these assays (2.8%). For these isolates that reached the threshold for further investigation, re-conduct of the assay using either a repeat challenge dose of 3ppm of imidacloprid or a dose response Probit analysis confirmed their susceptibility to imidacloprid. From 2009-2012, the Australian node performed valid assays on 97 field isolates from a total of 136 submissions, with no adult emergence observed at the 3ppm imidacloprid discriminating dose. In addition to reviewing the data generated by this twelve-year initiative, this paper discusses lessons learned from the coordination and evolution of a complex project across geographically dispersed laboratories on three continents.

Acknowledgements:

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Session Details:	8/27/2013 Bite me! - ectos as parasites 1140 - 1240 Meeting Room 2
Poster with 2 minute Oral Presentation Details:	Dog biting lice (<i>Trichodectes canis</i>) found on Japanese raccoon dogs (<i>Nyctereutes procyonoides viverrinus</i>) in Japan
Authors:	Masaaki Oi ^{1*} , Hisashi Tsuchiya ^{1,2} , Teruyo Tsuchiya ² , Mari Takizawa ² , Tadayoshi Konno ^{1,3} , Ken Okabayashi ¹ , Takanori Narita ¹ , Jun Matsumoto ¹ , Hiroshi Sugiyama ¹ , Sadao Nogami ¹ ¹ Department of Veterinary Medicine, Nihon University, Fujisawa, JAPAN ² Tsuchiya Veterinary Medical Hospital, Matsumoto, JAPAN ³ Hatazawa Animal Hospital, Kisarazu, JAPAN
Poster Number:	70

Dog biting lice (*Trichodectes canis*; De Geer, 1778) have been found on Japanese raccoon dogs (*Nyctereutes procyonoides viverrinus*) in Japan. The lice are common ectoparasites on domestic dogs and have occasionally been found on wild canids (González-Acuña et al., 2007). The raccoon dog belongs to the Canidae family and is native to some Far East Asian countries including Japan. Two separate groups (A and B) of raccoon dogs in a wildlife park in Matsumoto, Japan, were observed. In group A, all 12 raccoon dogs were heavily infested with *T. canis*. In group B, 1 of 4 dogs was slightly infested with the lice. Itching, alopecia, and weight loss were observed in heavily infested raccoon dogs. No other ectoparasites were detected on these raccoon dogs. All the lice-infested raccoon dogs were treated with ivermectin injections and/or fipronil-(S)-methoprene spot-on formulations. In general, biting lice are considered to be parasitic insects that have high host specificity; however, dog biting lice are known to show low host specificity within the Canidae family. In the present case, it can be concluded that the louse life cycle occurs on raccoon dogs because of the infection of the herd with a large number of lice and the presence of various parasite life stages (i.e., eggs, nymphs, and adult males and females). This suggests that the raccoon dog is a definitive host of *T. canis*. This study also confirms the pathogenic role of dog biting lice in the raccoon dog and the efficacy of ivermectin and fipronil-based formulations in the treatment of biting lice-infected raccoon dogs. This is the first report of the infestation of raccoon dogs with dog biting lice in Japan. It is also uncommon in the world (Bádr et al., 2005).

References:

Bádr, V., Štefan, P., Preisler, J. 2005. *Trichodectes canis* (De Geer, 1778) (Phthiraptera, Ischnocera), a new ectoparasite of the raccoon dog (*Nyctereutes Procyonoides*) in the Czech Republic. European Journal of Wildlife Research 51, 133–135.

González-Acuña, D., Briceño, C., Cicchino, A., Funk, S. M., Jiménez, J. 2007. First records of *Trichodectes canis* (Insecta: Phthiraptera: Trichodectidae) from Darwin's fox, *Pseudalopex fulvipes* (Mammalia: Carnivora: Canidae). European Journal of Wildlife Research 53, 76–79.



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Poster with 2 minute Oral Presentation Details:	Expression and Characterization of Cathepsin L from Tsetse (<i>Glossina morsitans morsitans</i>)
Authors:	Ngasaman Ruttayaporn ^{1*} , Mo Zhou ¹ , Keisuke Saganuma ¹ , Shino Yamasaki ¹ , Shin-ichiro Kawazu ¹ , Noboru Inoue ¹ ¹ National Research Center for protozoan Diseases, Obihiro University of Agriculture and Veterinary Medicine, Obihiro, Japan
Poster Number:	249

A cDNA encoding a cysteine protease named TC 31 cathepsin L-like protease, which was previously identified in the fat body of adult tsetse, was cloned from a midgut of adult male tsetse flies (48 h post blood meal). The cDNA encoded 516 amino acid sequence having the highest identity to cathepsin L of *S. peregrina* (81%). The amino acid sequence contained conserved amino acid residues, namely Cys335-His478-Asn498 and Gln329, forming the catalytic triad of an active site of C1A cysteine protease family. Recombinant TC 31 cathepsin L-like protease (rGmcathL) was expressed by using *P. pastoris* expression system as a molecular mass of 69 kDa. The rGmcathL was successfully activated in presence of DTT (2.5 mM) and cysteine (10 mM). Proteolytic activity of the rGmcathL was the highest at pH 6.0 with broad temperature range from 25 to 37 °C. The catalytic efficiency of rGmcathL was determined using synthetic specific substrates, Z-Phe-Arg-MCA and Z-Arg-Arg-MCA. The k_{cat}/K_M values were 10.9 M⁻¹s⁻¹ and 9.1 M⁻¹s⁻¹, respectively. The results indicated the rGmcathL exhibited hydrolysis preference for amino acid that has aromatic ring and hydrophobic side chain (Phe) at P2 position. Moreover, the rGmcathL was capable of degrading both hemoglobin (Hb) and bovine serum albumin (BSA), but it preferred to cleave BSA as compared to Hb. The proteolytic activity of rGmcathL was completely inhibited by broad spectrum cysteine protease inhibitor (E-64, 10 μM). As a future plan, biological significance of the GmcathL in tsetse, such as cellular functions, blood meal digestion, and tsetse –trypanosome interaction, will be clarified.

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Poster with 2 minute Oral Presentation Details:	<i>Pholetiscus dodukgei</i> sp. nov. (Copepoda: Harpacticoida) parasite of <i>Chiromantes haematocheir</i> (Crustacea: Brachyura) from South Korea
Authors:	Sung Joon Song*, Jong Seong Khim School of Earth and Environmental Sciences, and Research Institute of Oceanography, Seoul National University, Seoul 151-742, Republic of Korea
Poster Number:	202

A sesarmid crab, *Chiromantes haematocheir* (De Haan, 1833) inhabits from mudflat on intertidal zone to forest streams, even in mountain, and distribute on coastal areas in the East Asia: Korea, Japan and China. Many kinds of parasitic animals such as barnacle, isopod and copepod were observed between gill chambers of the crab.

Up to date 23 species of harpacticoid copepods belonging to 12 genera of 4 families have been recorded from brachyuran crabs, of which three species of genus *Pholetiscus* in family Canthocamptidae [*P. wilsoni* (Pearse, 1930), *P. orientalis* Humes, 1947 and *P. rectiseta* Humes, 1956) were described from gill chambers of sarsamid crabs. During an investigation of the parasitic harpacticoids of crab, a new species was collected from the crab, *Chiromantes haematocheir* in Korea, and herein described as *Pholetiscus dodukgei* sp. nov. The new species is the first member of parasitic copepod of crab in the Yellow Sea since original description of *P. wilsoni*.

Differential features of the new species are: (1) elongate rostrum reaching end of second antennular segment, (2) antennule 7-segmented, (3) much longer distal endopodal segment of P1, (4) much longer second endopodal segments of swimming legs P2-P4, (5) distal endopodal segment of male P3, second endopod with 2 setules on its surface and distal segment short, and (6) male P5 with 1 endopodal seta and 3 exopodal setae, respectively.

In addition, it should be also noted that the most resemble species, *Pholetiscus wilsoni* (Pearse, 1930) was figured and described inadequately in original report, even in Humes (1947)'s thus further detail re-description is required to clarify the species.

Acknowledgements:

We thank Dr. Jinsoon Park of Seoul National University and Mr. Seungjic Seo of Korea National Park Service for collecting samples from Taean and Daebudo Island. This research was financially supported by the Discovery of Korean Indigenous Species Project, NIBR (National Institute of Biological Resources) given to first author.



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Session Details:	8/27/2013 Divide and Conquer 1140 - 1240 Meeting Room 3
Poster with 2 minute Oral Presentation Details:	Prevalence of Antibodies to <i>Toxoplasma gondii</i> in Horses in Riyadh Province, Saudi Arabia
Authors:	Abdulah D. Alanazi ^{1*} , Mohammed S. Alyousif ² ¹ Department of Biological Sciences, Faculty of Science and Human Studies , Shaqra University,P.O. Box 1040 Ad-Dawadimi 11911 Saudi Arabia.E-mail: aalanazi@su.edu.au.sa . ² Department of Zoology, College of Science, King Saud University. P.O. Box 2455, Riyadh 11451 Saudi Arabia E-mail: myousif@ksu.edu.sa
Poster Number:	217

The aim of the present study was to determine the seroprevalence of *Toxoplasma gondii* in horses used for sporting purposes in the Province of Riyadh, Saudi Arabia. In total, 266 serum samples from clinically healthy horses were analyzed for anti-*T. gondii* antibodies using the Sabin-Feldman dye test. Antibodies to *T. gondii* were found in 84 (31.6%) horses, with specific titers of 1:16 (78 with a prevalence of 29.3%), 1:64 (4 with a prevalence of 1.5%), and 1:256 (2 with a prevalence of 0.8%). The number of seropositive horses in Shaqra (43.7%) was considerably higher than in other regions, with the lowest occurring in Al-Majmaah (11.0%). However, the differences in seroprevalence between the 6 locations were not statistically significant ($P>0.05$). In contrast, the overall seroprevalence in Riyadh province was higher than that reported in other countries. Horses are not a direct source of infection for human toxoplasmosis in this region. Usually human infection is facilitated via cats, which are the reservoir hosts for this parasite.

Acknowledgements:

Aauthors would like to thank the Staff Members Department of Zoology, Faculty of Science, King Saud University for kind technical support.

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Session Details:	8/27/2013 Divide and Conquer 1140 - 1240 Meeting Room 3
Poster with 2 minute Oral Presentation Details:	Polymerase chain reaction vis-a-vis parasitological techniques for diagnosis of <i>Trypanosoma evansi</i> infection in bovines
Authors:	Mandeep Singh Bal ^{1*} , L. D. Singla ² , Ashuma ^{2*} , P. Kaur ² , V. Mahajan ¹ , G. Filia ¹ and M. P. Gupta ¹ ¹ Animal Disease Research Centre, ² Department of Veterinary Parasitology, Guru Angad Dev Veterinary and Animal Sciences University, Ludhiana, Punjab, India.
Poster Number:	84

Trypanosoma evansi a vector borne haemoflagellate, causes ‘Surra’, a highly fatal widely distributed disease in bovines. The outbreaks of the disease usually occur during and after rainy season due to breeding season of Tabanid flies. A total of five hundred six (300 from apparently healthy and 206 from animals with fever) blood samples were collected from dairy animals (cattle = 344; buffaloes = 162) in Punjab State, India. Presence of *T. evansi* in the blood samples was seen by parasitological techniques (PT) including wet blood film (WBF), buffy coat (BC) and thin blood smear (TBS). Polymerase chain reaction (PCR) was performed using 21/22mer primers to get a specific 227 bp band in positive samples. The parasitological prevalence was 1.19% by WBF and 2.38 % by TBS and BC examination. The overall prevalence based on PCR was 4.15%. The sensitivity of WBF, BC and TBS were found to be 28.57%, 57.14% and 57.14%, respectively assuming sensitivity of PCR to be 100 %. More prevalence (4.94 %) of *T. evansi* was observed in case of cattle as compare to buffaloes (2.47 %). Sex wise more prevalence was seen in males as compare to females by both molecular and PT methods. Results obtained with different age groups showed that there was more prevalence of *T. evansi* in heifers, followed by adults and calves by both PT and PCR. More prevalence of surra was seen in animals with history of fever, both by PT (5.34%) and PCR (7.77%) as compare to apparently healthy animals (0.33 % and 1.67 % respectively). There was significant association in animals with the history of fever and detection by PT and PCR. It was concluded PCR should be employed in detection of latent carrier status which is not feasible by parasitological techniques.



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Session Details:	8/27/2013 Divide and Conquer 1140 - 1240 Meeting Room 3
Poster with 2 minute Oral Presentation Details:	Trypanosomiasis Outbreak in Pigs,Deer and Cattle - A Severe Loss Due to Mortality
Authors:	Premaalatha Bathmananban* ¹ ,Chandrawathani Panchadcharam ¹ ,Nurulaini Raimy ¹ ,Zaini Che Mamat ¹ ,Erwanas Asmar Ismail ¹ ,Ernie Aryanti Asat ² & Ramlan Mohamed ¹ ¹ Veterinary Research Institute, Department of Veterinary Services, 31400 Ipoh, Perak ² Ladang Infoternak Sungai Siput (U) , Perak
Poster Number:	242

Trypanosoma evansi is a widely distributed pathogenic species of protozoa transmitted mechanically by tabanid flies. Trypanosomes live in the blood . and tissue fluids of vertebrate hosts such as cattle, horse, dog and camel. Trypanosomiasis is endemic in Malaysia and outbreaks in deer and cattle cause morbidity and mortality. An outbreak of trypanosomiasis was diagnosed by the Parasitology Section of the Veterinary Research Institute (VRI) Malaysia in early 2012. A total of 86 whole blood samples from deer, cattle and buffaloes from a government farm near Sungai Siput, Perak and 16 whole blood samples from a commercial pig farm in Jalong, Perak were submitted for analysis. Sixty three samples were found to be positive for the *Trypanosoma* sp. A detailed epidemiological investigation was conducted to prevent further outbreaks.

Acknowledgements:

The author would like to thank the Director of Veterinary Research Institute (VRI), Ipoh Malaysia for supporting the study. A special thanks to all Parasitology and Haematology staff in VRI for their hardwork and determination and also to the staff of Ladang Inforternak Sungai Siput (U) for their help in collecting samples for this study.

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Session Details:	8/27/2013 Divide and Conquer 1140 - 1240 Meeting Room 3
Poster with 2 minute Oral Presentation Details:	Toxoplasma gondii vaccination in lambs reduces tissue cysts formation in muscles of commercial value after experimental inoculation
Authors:	Germán Cantón^{1,2*}, Alison Burrells¹, Paul Bartley¹, Yvonne Pang¹, Francesca Chianini¹, Elisabeth Innes¹, Julio Benavides³, Frank Katzer¹ ¹ Moredun Research Institute, Edinburgh, UNITED KINGDOM ² Instituto Nacional de Tecnología Agropecuaria (INTA), Balcarce, ARGENTINA ³ Instituto de Ganadería de Montaña (CSIC-ULE), León, SPAIN
Poster Number:	7

Toxoplasmosis is an important zoonoses and humans may acquire infection via consumption of undercooked meat containing tissue cysts. Vaccination has been proposed to reduce parasite burden in meat from animals. The aim of this work is to evaluate the efficiency of a commercially available vaccine on tissue infection following *Toxoplasma gondii* experimental inoculation. Thirty-two *T. gondii*-seronegative Suffolk lambs were examined daily and blood samples taken. Twelve (group B) and 5 (group C) lambs were vaccinated with Toxovax® at day 0. Lambs from group A and B were orally inoculated with 500,000 *T. gondii* oocysts 28 days post-vaccination; group C and D lambs remained un-challenged. Lambs were culled at 14, 28 and 42 days post-inoculation (dpi), and tissue samples including central nervous system (CNS) and skeletal muscle with high commercial value were taken. Serum *T. gondii* antibodies were detected by ELISA and seroconversion was observed in group B and C lambs after vaccination confirming immunization of the lambs. Group A and B animals showed increase in antibody titers after challenge. *T. gondii* DNA was detected by PCR in 65.9% and 75.0% of CNS and heart samples from Group A lambs, while Group B, C and D samples were negative. Parasite DNA was detected in 87.9% of skeletal muscular samples from group A, while only 5.9, 3.1 and 0.0% samples were positive in groups B, C and D, respectively. Genotype I (present in the vaccine) and III *T. gondii* (not included in the vaccine neither inocula) were confirmed after sequencing in muscular samples from group B and C lambs. Vaccination was proven to be effective in significantly reducing formation of tissue cysts in lambs infected with a high dose of *T. gondii* oocysts, and its use could be recommended to reduce meat contamination.

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Session Details:	8/27/2013 Divide and Conquer 1140 - 1240 Meeting Room 3
Poster with 2 minute Oral Presentation Details:	Protozoan encephalitis with Neospora caninum and Sarcocystis tenella co-infection in an adult dog from the UK
Authors:	Stephen Cahalan ¹ , Germán Cantón ^{2,3*} , Paul Bartley ² , Frank Katzer ² , Francesca Chianini ² ¹ Royal Veterinary College, London, UNITED KINGDOM ² Moredun Research Institute, Edinburgh, UNITED KINGDOM ³ Instituto Nacional de Tecnología Agropecuaria (INTA), Balcarce, ARGENTINA
Poster Number:	51

Dogs are the definitive host of the protozoan parasites *Neospora caninum* and *Sarcocystis tenella*. Both organisms are capable of infecting different farm livestock species. Protozoan-associated disease is uncommon in adult dogs although *Neospora* encephalitis, radiculitis and myositis have been reported in puppies. The aim of this work is to describe protozoan encephalitis affecting a 9.9 years-old Greyhound dog. Progressive generalized ataxia and hypermetria affecting all limbs was observed for a period of 2 months with signs of multifocal left forebrain, brainstem and cerebellar lesions. Magnetic resonance imaging demonstrated multifocal white/grey matter cerebral lesions. Serology detected *N. caninum* (1/800) and *Toxoplasma gondii* (1/200). After clindamycin treatment no improvement of clinical signs were observed; further deterioration was noted following treatment with corticosteroids. Elective euthanasia was performed. Histopathological analysis revealed severe multifocal to coalescing non-suppurative necrotizing encephalitis with glial foci in the white and grey matter of the cerebrum and cerebellum, with intralesional protozoan structures, interpreted as tissue cysts and free tachyzoites/merozoites. Immunohistochemistry (IHC) using 2 polyclonal antibodies, raised against *N. caninum* and *Sarcocystis spp* identified morphologically different tissue cysts and free tachyzoites/merozoites with different intensity of labelling. PCR detected *N. caninum* and *S. tenella* in brain tissue. These results confirmed the definitive diagnosis of protozoan encephalitis due to *N. caninum* and *S. tenella*. Although antimicrobials such as clindamycin are reported as effective in treating *Neospora*-encephalitis in puppies, it was unsuccessful in this case. Corticosteroid treatment is likely to have facilitated protozoal proliferation and so increased the severity of the lesions in this dog. Protozoan co-infections are not commonly recognized and IHC is a common ancillary technique used in their diagnosis. Cross-reaction of the antibodies has been reported; therefore the use of this technique on its own may not be enough to achieve a definitive etiological diagnosis.

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Session Details:	8/27/2013 Divide and Conquer 1140 - 1240 Meeting Room 3
Poster with 2 minute Oral Presentation Details:	Differential Gene Expression in the Tachyzoite-Stage of the Apicomplexan Parasites <i>Neospora caninum</i> and <i>Toxoplasma gondii</i>
Authors:	Stephen Daniels ^{1*} , John Ellis ¹ , Stephen Bush ² ¹ School of Medical and Molecular Biosciences and the I3 Institute, University of Technology, Sydney (UTS), Sydney, AUSTRALIA ² School of Mathematics, University of Technology, Sydney (UTS), Sydney, AUSTRALIA
Poster Number:	169

RNA sequencing (RNA-Seq) is a revolutionary high-throughput procedure that sequences the transcriptome of an organism to unprecedented depth and resolution. One of the most popular applications of RNA-Seq is the ability to detect the variance of gene expression or transcript abundance between different life-cycle stages or between biologically relevant samples, which is known as differential expression (DE). *Toxoplasma gondii* and *Neospora caninum* are closely related Apicomplexan parasites that share many biological similarities. *T. gondii* has an extensive host range including a felid definitive host and actively infects a significant proportion of the human population. Transmission is predominately by post natal infection. In contrast *N. caninum* has a life-cycle that involves a canid definitive host, it is not recognised as a human pathogen and transmission is predominately transplacental in cattle. We used the data from the study by Reid et al. (2012) to compare the differential expression of *Neospora* and *Toxoplasma* genes expressed in the tachyzoite using three different algorithms: edgeR, DESeq and baySeq; which helps to reduce false positives and eliminate analytical limitations. Our studies showed that amongst the top 10 orthologous groups ranked by p-value across the three algorithms, there was relative consistency in the composition but variance in the ranking. Taking the top 5 p-value ranked genes in the rhostry, microneme, dense granule and AP2 transcription factor groups, the variance and composition across the three algorithms is much more pronounced. Our results emulate those of the Reid et al. (2012) study, however it has revealed variance in the differential expression data between the algorithm methods highlighting the importance of using a variety of analytical techniques to ensure valid conclusions are made from RNA-Seq experiments. We also emphasise the need for efficient experimental design.

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Reid, A. J., S. J. Vermont, et al. (2012). "Comparative genomics of the apicomplexan parasites *Toxoplasma gondii* and *Neospora caninum*: Coccidia differing in host range and transmission strategy." *PLoS Pathog* 8(3): e1002567.



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Session Details:	8/27/2013 Divide and Conquer 1140 - 1240 Meeting Room 3
Poster with 2 minute Oral Presentation Details:	Identification and characterization of a <i>Trypanosoma congolense</i> 46 kDa protein as a potential serodiagnostic antigen
Authors:	Mo Zhou ¹ , Keisuke Suganuma ¹ , Ngasaman Ruttayaporn ¹ , Nguyen Thu Thuy ¹ , Shino Yamasaki ¹ , Ikuo Igarashi ¹ , Shin-ichiro Kawazu ¹ , Noboru Inoue ^{1*} 1 National Research Center for Protozoan Diseases, Obihiro University of Agriculture and Veterinary Medicine, Inada-cho, Obihiro, Hokkaido, Japan
Poster Number:	82

Trypanosoma congolense is a major livestock pathogen in Africa, causing large economic losses with serious effects on animal welfare. Therefore, reliable serodiagnostic tests are urgently needed for control of *T. congolense* infection. In this study, we have identified a hypothetical protein of *T. congolense* as a new candidate serodiagnostic antigen. The gene encoding a 46.4 kDa protein was cloned and was designated as the TcP46 gene. The complete nucleotide sequence of TcP46 contained an open reading frame of 1,218 bp. Southern blot analysis indicated that at least two copies of the TcP46 gene were tandemly-arranged in the *T. congolense* genome. The recombinant TcP46 (rTcP46) was expressed in *Escherichia coli* as glutathione S-transferase (GST) fusion protein. Western blot analysis and confocal laser scanning microscopy revealed that the native TcP46 protein was expressed in cytoplasm of all the life-cycle stages of the parasite. Moreover, an enzyme-linked immunosorbent assay (ELISA) based on the r-TcP46 detected the specific antibodies as early as 8 days post-infection from mice experimentally infected with *T. congolense*. No cross-reactivity was observed in the rTcP46-ELISA against serum samples from cattle experimentally infected with *Babesia bigemina*, *B. bovis*, and *Anasplama marginale*. These results suggest that the rTcP46 could be used as a serodiagnostic antigen for *T. congolense* infection.

Acknowledgements:

This work was funded by The Graduate School of Agriculture and Veterinary Medicine of Obihiro University, Japan.



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Session Details:	8/27/2013 Divide and Conquer 1140 - 1240 Meeting Room 3
Poster with 2 minute Oral Presentation Details:	Experimental and natural <i>Besnoitia besnoiti</i> infections in cattle
Authors:	Liénard E. ^{1, 2} , Fonclara E. ^{1, 2} , Grisez C. ^{1, 2} , Prévot F. ^{1, 2} , Trumel C. ³ , Salem A. ^{1, 2} , Franc M. ^{1, 2} , Blanchard B. ⁴ , Bouhsira E. ^{1, 2} , Jacquet P. ^{1, 2} 1: INRA, UMR 1225, Ecole Nationale Vétérinaire de Toulouse, 23 Chemin des Capelles, F-31076 Toulouse cedex 3, France 2: Université de Toulouse, INP-ENVT, UMR 1225, Ecole Nationale Vétérinaire de Toulouse, 23 Chemin des Capelles, F-31076 Toulouse cedex 3, France 3: Département des Sciences Cliniques des Petits Animaux, Biologie Médicale, Ecole Nationale Vétérinaire de Toulouse, 23 Chemin des Capelles, F-31076 Toulouse cedex 3, France 4: Adiagene Company, 38, rue de Paris, 22000 Saint Brieuc, France.
Poster Number:	187

Bovine besnoitiosis, due to *Besnoitia besnoiti*, is an emerging cattle disease in Europe. In the acute phase of the disease, cattle may present pyrexia, nasal and ocular discharges and oedema. The subsequent chronic phase is characterized by the formation of numerous tissue cysts in skin, upper respiratory tract and sclera conjunctiva. In the past, several attempts to reproduce experimentally the disease have provided contradictory and non-conclusive results. The aim of this study was to compare the distribution of parasites between experimentally and naturally infected cattle by using real-time PCR on blood and tissue biopsies. Two heifers were experimentally infected with *in vitro* cultured tachyzoites from a strain isolated in the South of France (20 passages culture level at the time of inoculation). In parallel, seventeen animals in the acute phase and three others in severe chronic phase were recruited from the field (natural infections). Eight out of these 17 natural acute cases showed strong positive signals in blood by real-time PCR suggesting that this molecular tool could be of interest in the early diagnosis of bovine besnoitiosis. In contrast, transient positive signals were recorded in the blood of experimentally infected heifers in the first week post-inoculation only. After necropsy, the three severe chronic cases showed high quantifications of parasite DNA in all tissue biopsies including skin, upper respiratory tract and reproductive tract. Despite a serological conversion assessed by Western Blot and ELISA, no parasite DNA was retrieved in experimentally infected heifers at necropsy time (16 weeks post-inoculation). The mild and transient infection observed after inoculation could be explained by the high passage level of the inoculated strain. In contrast, severe chronic cases could have a great importance in epidemiology of besnoitiosis since they represent an abundant source of parasites for biting flies involved in the mechanical transmission of this disease.



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Poster with 2 minute Oral Presentation Details:	Record of <i>Trypanosoma striati</i> Qadri, 1962 in sand goby (<i>Oxyeleotris marmorata</i> , (Bleeker, 1852) from Thailand
Authors:	Worawit Maneepitaksanti, Varinee Panyawachira and Supranee Chinabut Inland Aquatic Animal Health Research Institute, Department of Fisheries, Bangkok 10900 Thailand. E-mail: worawitm@yahoo.com
Poster Number:	28

Trypanosomiasis is a fish disease causing by hemoflagellate protozoa such as *Trypanosoma* sp.. In order to clarify the species of this blood parasite, this study was conducted. Twenty-eight sand goby were collected from three provinces (Suphan Buri, Phra Nakhon Si Ayutthaya, Nakhon Pathom), central part of Thailand for blood parasite examination. The result showed that, fish samples were infected with *T. striati*, the overall prevalence was 96.43%. This finding provides new host and locality record in Thailand.



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Session Details:	8/27/2013 Divide and Conquer 1140 - 1240 Meeting Room 3
Poster with 2 minute Oral Presentation Details:	Comparative studies of the indirect immunofluoresence (IFAT) and immunoenzymatic (ELISA) tests for detecting <i>Neospora caninum</i> antibodies and cross-reactions with <i>Toxoplasma gondii</i> in dogs in southern Romania
Authors:	Violeta Enachescu (Ionescu) ¹ , Mariana Ionita ¹ , Ioan Liviu Mitrea ^{1*} ¹ Department of Parasitology and Parasitic Diseases, Faculty of Veterinary Medicine, University of Agronomic Sciences and Veterinary Medicine of Bucharest, Romania
Poster Number:	85

Dogs can act as reservoirs or indicators of high environmental contamination for *Neospora caninum* and *Toxoplasma gondii*, pathogens with large economic impact. *N. caninum* and *T. gondii* are very closely related protozoans, therefore cross-reactions in immunological assays cannot be excluded. A comparative study of indirect immunofluoresence (IFAT) and immunoenzymatic (ELISA) tests was carried out to determine the seropositivity of *N. caninum* in dogs, considering the possible cross-reactions due to *T. gondii*. A total of 53 dog sera were analyzed for the presence of IgG antibodies against *N. caninum* (by ELISA and IFAT) and against *T. gondii* (by ELISA). The agreement between ELISA and IFAT results for *N. caninum* infection was expressed by kappa value. *N. caninum* antibodies were detected in 23 dogs by IFAT (43.4%), but only 8 dogs were positive by ELISA (15.1%). The agreement between IFAT and ELISA for detecting *N. caninum* antibodies was $k=0.373$. For *T. gondii*, a number of 31 dogs were positive (58.5%). IFAT positive samples were divided into two categories: true positive (negative for *T. gondii* or positive for both *N. caninum* and *T. gondii* by ELISA) and false positive (negative for *N. caninum* and positive for *T. gondii* by ELISA). A total of 11 false positive results (47.8%) and 12 true positive results (52.2%) were registered. The corrected prevalence for *N. caninum* was based on IFAT true positive results and had a value of 22.6%. Correlation between corrected IFAT results and ELISA results for *N. caninum* infection was $k=0.755$. In conclusion, both ELISA and IFAT can be used to distinguish between *N. caninum* infected and noninfected dogs, but a combination of these serological tests (IFAT and ELISA) and identification of possible cross-reactions due to *T. gondii* may reveal a more accurate estimation of *N. caninum* seroprevalence than using of a single diagnostic test.



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Session Details:	8/27/2013 Divide and Conquer 1140 - 1240 Meeting Room 3
Poster with 2 minute Oral Presentation Details:	Expression, immunolocalization and serodiagnostic value of TcIL3000.0.38630 protein from <i>Trypanosoma congolense</i>
Authors:	Kennedy Miyoro Mochabo ^{1, 2*} , Zhou Mo ¹ , Keisuke Suganuma ¹ , Shin-ichiro Kawazu ¹ , Noboru Inoue ¹ ¹ National Research Center for Protozoan Diseases, Obihiro University of Agriculture and Veterinary Medicine, Obihiro, Hokkaido, JAPAN ² Kenya Agricultural Research Institute, Trypanosomiasis Research Centre (KARI-TRC) Kikuyu, KENYA
Poster Number:	83

Animal African trypanosomosis (AAT) or nagana is a serious constraint to livestock sector development in sub-Saharan Africa. The disease, mainly caused by *Trypanosoma congolense*, has a limitation in its diagnosis and treatment. Therefore, there is need for a simple, rapid detection technique to replace the few available serological ones that are of variable sensitivity and specificity. Currently, there is a promising use of recombinant antigens to improve on the trypanosome lysate to detect trypanosome specific antibodies. In this respect, we identified through *T. congolense* whole life-cycle EST data base, a gene that is relatively highly expressed in metacyclic (MCF) and bloodstream (BSF) stages of *T. congolense*. The gene, TcIL3000.0.38630 (1,236 bp) among others, is expressed more in MCF than procyclic forms (PCF) / epimastigote form (EMF) by 8.5 times. We amplified, cloned and sequenced the gene. The recombinant TcIL3000.0.38630 protein was expressed and purified. We further localized the protein in cytosol and on cell surface with signals in MCF and BSF stages. A similar result was obtained in Western blot analysis. As a result of Southern blot analysis, we found that the TcIL3000.0.38630 existed as a single copy gene with probable allelic polymorphism at the *Nar* I restriction site. Through bioinformatics, putative conserved domains for amino acids sequence were found similar to BSF of *T. brucei* invariant surface glycoprotein (ISG) suggesting that the protein may be a potential diagnostic antigen. This was confirmed through ELISA results that the protein is antigenic with mouse experimental sera. The next plan is to test field samples to evaluate practical use of the recombinant TcIL3000.0.38630-based ELISA as an alternative serodiagnostic method for nagana.

Acknowledgements:

This study was financially supported by the Ministry of Education, Culture, Sports, Science and Technology (MEXT) of Japan.



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Session Details:	8/27/2013 Divide and Conquer 1140 - 1240 Meeting Room 3
Poster with 2 minute Oral Presentation Details:	Quantification of <i>Toxoplasma gondii</i> in tissues of experimentally infected rabbits (<i>Oryctolagus cuniculus</i>)
Authors:	Helena Neumayerová ^{1*} , Jana Juránková ¹ , Anita Frencová, Vojtech Baláž ¹ , Břetislav Koudela ¹ (presenting author asterisked) ¹ Veterinary and Pharmaceutical University Brno, Brno, CZECH REPUBLIC
Poster Number:	8

Domestic rabbit (*Oryctolagus cuniculus*) farming belongs to a small-scale industry but the demand on rabbit meat and other rabbit products is increasing mainly in countries such as China, France, New Zeland, Australia, Denmark, Netherlands and many others. From the protection of public health point of view, *Toxoplasma gondii* represents one of the most important zoonotic parasites which are necessary to be controlled, because the meat of infected animals could be a potential source of toxoplasmosis for human. Despite of rabbits are susceptible to *T. gondii* infection, it is usually not manifested except few clinical cases.

The aim of this study was to aces distribution and quantification of *T. gondii* in different tissues after experimental per oral infection with a dose of 8000 oocysts.

A sequence-specific magnetic capture method was used for isolation of DNA from sixteen experimentally infected rabbits euthanized after 2, 4, 7 and 9 weeks post infection. For detection and quantification of *T. gondii* parasites in tissues a real-time PCR for the 529 bp repeat element was used. The preliminary results show that the highest *T. gondii* parasite burdens were detected in lung tissue, lower parasite counts were found in other internal organs and muscles. In spite of organs of rabbits are not commonly used for human consumption, they are offered to some domestic animals (e.g. cats, dogs or chickens) which could be an important way of *T. gondii* transmission in domestic animals.

Acknowledgements:

We would like to thank to “Rabbit Thrhový Štěpánov s.r.o” for opportunity to collect samples in slaughterhouse Kasejovice. Also we are grateful to all people from rabbit farms, especially for their kind cooperation on this project. We also thanks to Jana Skladanyiová for help with preparation of the samples. This project was supported by Ministry of Education of Czech Republic MSM62115712402 MŠMT.

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Session Details:	8/27/2013 Divide and Conquer 1140 - 1240 Meeting Room 3
Poster with 2 minute Oral Presentation Details:	Analysis of the <i>cis</i> -element for gene expression regulation in <i>congolense</i> epimastigote specific protein (CESP)
Authors:	Keiske Suganuma ^{1*} , Mochabo Kennedy Miyoro ¹ , Hassan Hakimi ¹ , Shino Yamasaki ¹ , Junya Yamagishi ² , Masahito Asada ³ , Shin-ichirou Kawazu ¹ and Noboru inoue ¹ ¹ National Research Center for Protozoan Diseases, Obihiro Univ. of Agricult. and Vet. Med., JAPAN ² Tohoku Medical Megabank Organization, Tohoku Univ., JAPAN ³ Department of Protozoology, Institute of Tropical Medicine (NEKKEN), Nagasaki Univ., JAPAN
Poster Number:	37

African trypanosomes are hemoflagellate protozoan parasites responsible for debilitating diseases in humans and animals in sub-Saharan countries. *Trypanosoma congolense*, *T. brucei brucei* and *T. vivax* cause animal African trypanosomosis also known as Nagana. African trypanosomes are transmitted by tsetse flies (*Glossina* spp.) and undergo cell differentiation events during their life cycle. It is known that gene expression in kinetoplastida is regulated post-transcriptionally. Several previous studies have shown that stage-specific gene expression in trypanosomes is regulated by *cis*-elements located in the 3' untranslated region (UTR) of each mRNA and also by RNA binding proteins (RBPs). Lack of *in vitro* culture systems for epimastigote (EMF) and metacyclic stages of *T. brucei* makes the study of these two stages very difficult. On the other hand, all the developmental stages of *T. congolense* IL3000 can be cultivated to study mechanisms of life cycle development of African trypanosome. Our previous study revealed that the *congolense* epimastigote specific protein (*cesp*) gene expression was regulated by *cis*-elements located in its 3'UTR. In the present study, we identified the adenosine and uridine rich region in *cesp* 3'UTR. Using transgenic trypanosome cell lines having different *egfp* expression cassettes, we showed that this adenosine and uridine rich region regulates EMF stage specific gene expression as the regulatory *cis*-element of eukaryotic AU rich element (ARE). Therefore this essential element in *cesp* 3'UTR was designated as *T. congolense* ARE, which might selectively stabilize mRNA in the EMF stage and destabilize mRNA in other stages. RNA electro mobility shift assay revealed that life-cycle stage and RNA sequence specific RBPs interacted with the *T. congolense* ARE. These results indicate that the EMF stage specific *cis*-element (*T. congolense* ARE) and RBPs complexes might specifically stabilize *cesp* mRNA in EMF.

Acknowledgements:

This study was financially supported by the Ministry of Education, Culture, Sports, Science and Technology (MEXT) of Japan.

References:

“The epimastigote stage-specific gene expression of CESP is tightly regulated by its 3'UTR” Suganuma *et al.*, 2012, *Mol. Biochem. Parasitol.* 186(1):77-80.



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Session Details:	8/27/2013 Divide and Conquer 1140 - 1240 Meeting Room 3
Poster with 2 minute Oral Presentation Details:	Profiling compound activity against the life cycle stages of <i>Trypanosoma cruzi</i> .
Authors:	Melissa Sykes ^{1*} , Vicky Avery ¹ ¹ The Eskitis Institute for Drug Discovery, Griffith University, AUSTRALIA
Poster Number:	119

Chagas disease (CD) is caused by the protozoan parasite, *Trypanosoma cruzi*. The disease is endemic to South America, is estimated to cause 14 000 deaths per year [1,2] and has been recognized by WHO as one of the world's 13 most neglected tropical diseases [3]. There are only two drugs available for the treatment of CD, the nitroderivatives nifurtimox and benznidazole. Both have a number of severe side effects which have often forced patients to stop treatment and include nausea, vomiting, severe weight loss, insomnia, depression, vertigo, convulsions and disorientation [4]. Benznidazole treated patients have presented with liver profile abnormalities and gastro intestinal disturbances [5]. Although the use of these drugs to treat the acute phase of the disease is widely accepted, treatment for the chronic disease is not conclusive and there has been recent evidence to show that the efficacy of these drugs at this stage is doubtful [4, 5]. To discover new active compounds against the parasite we have developed an imaging- based assay to enumerate *T. cruzi* intracellular life cycle forms (amastigotes) following exposure of *T.cruzi* infected 3T3 host cells to compounds or known control drugs. The assay technology utilises nuclear and cytoplasmic markers to fluorescently stain both the parasite and host cells, detected with a High Content imaging system and analysed with a developed script. With the use of 3T3 fibroblasts as the host cell, of which growth is not effected by *T. cruzi* early stage infection [3], host cell survival can also be estimated as a primary determination of compound mediated cytotoxicity in the one assay. A trypomastigote imaging-based assay has also been developed to further profile compound activity in relation to the parasite. Although trypomastigotes are not the most clinically relevant form in consideration of the disease state, activity against this motile infective form would be favourable. These assays, along with live cell compound dosing, were utilised to profile the activity of a compound library comprised of FDA approved and biologically active compounds and a separate library comprised of compounds with previously identified anti-malarial activity. Currently the most successful chemical candidate is under evaluation using an *in vivo* mouse model and the preliminary results of these studies will be outlined.

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Dr Agatha Garavelas for isolating Nifurtimox from Lampit tablets.
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Session Details:	8/27/2013 Divide and Conquer 1140 - 1240 Meeting Room 3
Poster with 2 minute Oral Presentation Details:	Are <i>Toxoplasma gondii</i> -infected rodents really more prone to predation by cats?
Authors:	Amanda R. Worth*, Alan J. Lymbery, R.C. Andrew Thompson Murdoch University, Western Australia
Poster Number:	41

It is widely believed that *Toxoplasma gondii* alters the behaviour of rodent hosts to make them more susceptible to predation by cats and to therefore enhance transmission of the parasite to its definitive host. This story is entrenched in the literature, as indirect evidence from experimental behavioural studies suggests that *T. gondii* alters behaviours related to predation risk (eg. activity level, response to novelty, response to predator odour, anxiety level). However, results from past studies are inconclusive due to inconsistencies, and there is no direct evidence that rodents infected by *T. gondii* actually get caught by cats more often than uninfected rodents. This evidence is difficult to obtain as classic predation experiments are not feasible on ethical grounds. Instead, we have used a novel approach to the question of whether rodents infected by *T. gondii* are more likely than uninfected rodents to be caught by cats. Samples included donations of wild rats and mice that were either (1) caught by cats (and returned to the cat owner by their pet) or (2) killed by some other method (eg. poison, trap). The prevalence of *T. gondii* in the samples “caught by cats” was compared to the prevalence in samples from the same location that were “not caught by cats”. If *T. gondii* specifically makes rodents more susceptible to predation by cats it would be expected that the prevalence of the parasite in the “cat-caught” sample would be higher than the “non cat-caught” sample. Preliminary results and limitations of this methodology are discussed.



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Session Details:	8/27/2013 The Joe Boray Session - What's new and wonderful in Parasitology 1140 - 1240 Meeting Room 5
Poster with 2 minute Oral Presentation Details:	Beneficial effects of probiotic bacteria on <i>Trichinella spiralis</i> infection in mice
Authors:	Lýdia Hermanovská ¹ , Emília Dvorožňáková ^{1*} , Zuzana Hurníková ¹ , Viera Revajová ² , Andrea Lauková ³ ¹ Institute of Parasitology, Slovak Academy of Sciences, Kosice, Slovak Republic ² University of Veterinary Medicine and Pharmacy in Kosice, Kosice, Slovak Republic ³ Institute of Animal Physiology, Slovak Academy of Sciences, Kosice, Slovak Republic
Poster Number:	229

Probiotic bacteria are defined as live organisms, which confer benefits to the host. In general, their efficiency was demonstrated to prevent and partially to treat gastrointestinal disorders, respiratory infections, and/or allergic symptoms. Probiotic bacteria have also a potential to control parasite infections, but molecular mechanisms mediating beneficial effects on the parasite infection have not been clear yet. This study was focused on the effect of selected probiotic (bacteriocinogenic) strains of different origin (*Enterococcus faecium* EF55, *E. faecium* AL41, *E. faecium* 2019-CCM7420, *Lactobacillus fermentum* AD1-CCM7421, *Lactobacillus plantarum* L17/1) on parasite reduction and cellular immunity in mice infected with *Trichinella spiralis*. *T. spiralis* is the intestinal nematode with worldwide distribution which causes trichinellosis – a serious zoonosis. The complete life cycle of *T. spiralis* occurs in one host, which means that the host can exert its immune attack at several points in the life cycle. Adult worms reproduce in the small intestine, new born larvae migrate through the blood and lymphatics to the skeletal muscle cells and encapsulated larvae represent the infective stage of the parasite. Probiotic strains were administered daily in dose of 10⁹cfu/100 ml and mice were infected with *T. spiralis* on 7th day of treatment. A protective effect against parasite worm burden in the intestine was observed only in mice treated with probiotic strains of *E. faecium* (reduction cca 40 %). Stimulation of the host immune response (proliferative activity of T cells, CD4 subpopulation, metabolic activity of macrophages) resulted in reduction of muscle larvae with the highest efficacy in mice treated with *E. faecium* AL41, followed by *L. fermentum* AD1-CCM7421 and *L. plantarum* L17/1 treatment. The results indicate that examined probiotic strains might provide a strain-specific protection against parasites not only in the gut, but also in host tissues. Immunological interactions between probiotic strains, parasite and host cells need to be investigated more in details.

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Session Details:	8/27/2013 The Joe Boray Session - What's new and wonderful in Parasitology 1140 - 1240 Meeting Room 5
Poster with 2 minute Oral Presentation Details:	Dot Immunogold Filtration Assay (DIGFA) for the Rapid Detection of Specific Antibody against the Rat Lungworm <i>Angiostrongylus cantonensis</i> (Nematoda: Metastrongyloidea)
Authors:	Prapathip Eamsobhana ¹ *, Xiao-Xian Gan ² , An Ma ² , Yue Wang ² , Darawan Wanachiwanawin ¹ , Hoi-Sen Yong ¹ Department of Parasitology, Faculty of Medicine Siriraj Hospital, Mahidol University, Bangkok, THAILAND ² Institute of Parasitic Diseases, Zhejiang Academy of Medical Sciences, Hangzhou, PR CHINA ³ Institute of Biological Sciences, University of Malaya, Kuala Lumpur, MALAYSIA
Poster Number:	86

A rapid dot immunogold filtration assay (DIGFA) was adopted for specific immunodiagnosis of human cerebral angiostrongyliasis using purified 31-kDa glycoprotein specific to *Angiostrongylus cantonensis* as diagnostic antigen and protein A colloidal gold conjugate as antigen-antibody detector. A total of 59 serum samples were assayed – 11 samples from clinically diagnosed patients with detectable *A. cantonensis*-specific antibody in immunoblotting; 23 samples from patients with other related parasitic diseases, i.e. gnathostomiasis (n=8), cysticercosis (n=5), toxocariasis (n=2), filariasis (n=4), paragonimiasis (n=2) and malaria (n=2); and 25 samples from normal healthy subjects. The sensitivity and specificity of DIGFA to detect anti-*A. cantonensis* specific antibody in serologically confirmed angiostrongyliasis cases, were both 100%. No positive DIGFA was observed in cases with other parasitic diseases, and the healthy control subjects. The 3-min DIGFA is as sensitive and specific as the 3-hr immunoblot test in angiostrongyliasis confirmed cases which revealed a 31-kDa reactive band.

The gold-based DIGFA is more rapid and easier to perform than the traditional enzyme-coupled ELISA. The test utilizing purified *A. cantonensis* antigen is reliable and reproducible for specific immunodiagnosis of human infection with *A. cantonensis* – thus can be applied as an additional routine test for clinical diagnostic support. Large-scale sero-epidemiological studies in endemic communities in northeast Thailand are underway to evaluate its usefulness under field condition.



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Session Details:	8/27/2013 The Joe Boray Session - What's new and wonderful in Parasitology 1140 - 1240 Meeting Room 5
Poster with 2 minute Oral Presentation Details:	Identification of <i>Anisakis</i> species (Nematoda: Anisakidae) in marine fish hosts from Papua New Guinea
Authors:	Melanie Koinari ^{1*} , Stephan Karl ² , Eileen Elliot ¹ , Una Ryan ¹ and Alan, .J. Lymbery ¹ ¹ Murdoch University, Perth, AUSTRALIA, ² The University of Western Australia, Perth, AUSTRALIA.
Poster Number:	203

In the last thirty years, there has been a marked increase in the prevalence of anisakiasis throughout the world, due in part to growing consumptions of raw or lightly cooked seafood. The present study investigated the prevalence of potentially zoonotic anisakid larvae in fish collected on the coastal shelves off Madang and Rabaul in Papua New Guinea (PNG) where fish represents a major component of the diet. A total of 276 fresh marine fish were obtained from the local fishermen. All fish were dissected and viewed under white light for the presence of nematodes which were found mostly on the visceral organs of their hosts. Anisakid larvae were found in seven fish species including *Decapterus macarellus*, *Gerres oblongus*, *Pinjalo lewisi*, *Pinjalo pinjalo*, *Selar crumenophthalmus*, *Scomberomorus maculatus* and *Thunnus albacares*. They were identified by both light and scanning electron microscopy as *Anisakis* Type I larvae. Sequencing and phylogenetic analysis of the ribosomal internal transcribed spacer (ITS) and the mitochondrial cytochrome C oxidase subunit II (*cox2*) gene identified all nematodes as *Anisakis typica*. This study represents the first in-depth characterisation of *Anisakis* larvae from seven new fish hosts in PNG. The overall prevalence of larvae was low (7.6%, 21/276) and no recognised zoonotic *Anisakis* species were identified, suggesting a very low threat of anisakiasis in PNG.

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Session Details:	8/27/2013 The Joe Boray Session - What's new and wonderful in Parasitology 1140 - 1240 Meeting Room 5
Poster with 2 minute Oral Presentation Details:	The findings of Serratospiculum in Great Tit (<i>Parus major</i>) in Slovakia
Authors:	Alžbeta Königová ^{1*} , Ladislav Molnár ² , Gabriela Hřčková ¹ , Marián Várady ¹ ¹ Institute of Parasitology SAS, Hlinkova 3, 040 01 Košice, Slovak Republic ² Clinic for Birds and Exotic Animals, The University of Veterinary Medicine and Pharmacy, Komenského 73, 041 81 Košice, Slovak Republic
Poster Number:	72

Serratospiculiasis is a parasitic disease caused by filariid nematodes of the genus *Serratospiculum*, the subfamily *Dicheilonematinae*. *Serratospiculum* spp., found in the air sacs, has often been reported in various species of Falcons, Bald Eagles and Cooper’s Hawk from many areas of the world. In the present study, serratospiculiasis was confirmed for the first time in Great Tit in Slovakia. Nematode infestation was identified post mortem. Lesions in the respiratory system (airsacculitis, pneumonia) were associated with presence of this nematode. Smears of necrotic lesions in the crop and oesophagus contained large numbers of embryonated ova. Faecal samples were examined by flotation method and *Serratospiculum* eggs were found. Adult parasites were cleared in lactophenol and used for the morphologic characterisation. Scattered inflammatory cells were seen in the mucosal and submucosal layers of infected oesophagus, stomach and inflammatory focci were found mainly in the stroma in air sacs.

PCR analyses of 18 S ribosomal DNA gene sequences indicated the *Serratospiculum* spp.

The presence of this filariid nematode in the vector species Great Tit, common in Slovakia, indicates the importance of monitoring of serratospiculiasis in the migrating birds. The parasite can cause serious health problems, even sudden death of their hosts, therefore suitable effective measures for their elimination should be implemented.

Acknowledgements:

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Session Details:	8/27/2013 The Joe Boray Session - What's new and wonderful in Parasitology 1140 - 1240 Meeting Room 5
Poster with 2 minute Oral Presentation Details:	First molecular genotyping of insensitive acetylcholinesterase in filariasis vector, <i>Culex quinquefasciatus</i> Say (Diptera: Culicidae) populations in Malaysia
Authors:	Van Lun Low ^{1*} , Chee Dhang Chen ¹ , Phaik Eem Lim ^{1,2} , Han Lim Lee ³ , Yvonne Ai Lian Lim ⁴ , Tiong Kai Tan ⁴ & Mohd Sofian-Azirun ¹ ¹ Institute of Biological Sciences, Faculty of Science, University of Malaya, 50603 Kuala Lumpur, MALAYSIA ² Institute of Ocean and Earth Sciences, University of Malaya, 50603 Kuala Lumpur, MALAYSIA ³ Medical Entomology Unit, WHO Collaborating Centre for Vectors, Institute for Medical Research, Jalan Pahang, 50588 Kuala Lumpur, MALAYSIA ⁴ Department of Parasitology, Faculty of Medicine, University of Malaya, 50603 Kuala Lumpur, MALAYSIA
Poster Number:	251

In Malaysia, susceptibility of mosquitoes against various insecticides has been studied extensively and described by various approaches such as WHO larval and adult bioassays, enzyme microassays and protein electrophoresis. However, so far nothing has been reported pertaining to insecticide resistance gene detection at the molecular level. There is a dearth of evidence of insecticide resistance in Malaysian mosquitoes on a molecular basis. Given that there is limited available information on the insensitive acetylcholinesterase in insect species in Malaysia, the present study aims to detect the presence of G119S mutation in the acetylcholinesterase gene of *Cx. quinquefasciatus* from 14 residential areas across 13 states and a federal territory in Malaysia. The *ace-1* sequence and PCR-RFLP test revealed the presence of glycine-serine *ace-1* mutation in the wild populations of *Cx. quinquefasciatus*. Both direct sequencing and PCR-RFLP methods demonstrated similar results and revealed the presence of a heterozygous genotype at a very low frequency (18 out of 140 individuals), while a homozygous resistant genotype was not detected across any study site in Malaysia. In addition, statistical analysis also revealed that malathion resistance is associated with the frequency of *ace-1^R* in *Cx. quinquefasciatus* populations. This study has demonstrated the first field-evolved instance of G119S mutation in Malaysian populations. Molecular identification of insensitive acetylcholinesterase provides significant insights into the evolution and adaptation of the Malaysian *Cx. quinquefasciatus* populations.

Acknowledgements:

This study was supported by a University of Malaya research grant (RG164/12SUS).

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Session Details:	8/27/2013 The Joe Boray Session - What's new and wonderful in Parasitology 1140 - 1240 Meeting Room 5
Poster with 2 minute Oral Presentation Details:	Dirofilaria immitis in dogs of beaches and fishing villages from Navolato, Sinaloa, México
Authors:	Rubio Robles Mario César, Gaxiola Camacho Soila Maribel, Castro del Campo Nohemí., Idalia Enríquez Verdugo, Borbolla Ibarra Jaime Eleazar, Gaxiola Montoya Joel, Castro Angulo Antemio, Pérez Corrales Ascención, Quintero Osuna Isabel, Barraza Tizoc Claudia, Vega Mendoza Gonzalo. Facultad de Medicina Veterinaria y Zootecnia, Universidad Autonoma de Sinaloa, Culiacan, Mexico
Poster Number:	252

Dirofilaria immitis, is a nematode also known as “heart worm” because it is located in the heart of dogs causing cardiopulmonary disease; the life cycle begins when a female mosquito of the genera *Culex*, *Anopheles* and *Aedes*, bites an infected dog that has been in his blood to the smaller and younger forms of the parasite called microfilaria, they enter the mosquito and go through the maturation phase through larval stages (of larva 1-3), once the parasite completes its larval stage becomes infectious, this indicates that may be able to infect other animals, the microfilaria are staying in the heart and pulmonary arteries where they produce and release microfilariae the blood to give a new cycle of transmission.the objective was determine the prevalence of *Dirofilaria immitis* microfilariae in dogs from beaches in the municipality of Navolato, Sinaloa, took 350 samples of blood from the cephalic vein of the forelimb of dogs over three months, the sample size was determined according to the following: $n = [t * SD / L]^2$, where n = sample size, t = value of normal distribution (t test) for a confidence level of 95% (t = 1.96), L = the acceptable error or precision (5%), SD = expected prevalence of the disease (%). The samples were kept in vacutainer tubes with EDTA stored at 4 ° C and transported to the Laboratory of Parasitology of the FMVZ-UAS, and processed and stained according to the technique of hemocolorante quick and observed at microscope with the objectives of 10x and 40x. Resulting in 104 (29.71%) heartworm positive samples, concluding that this is an important parasitic to the dog and a potential risk to health human being, because the area presents optimal characteristics for this disease, as has the presence of the intermediate host in large numbers.



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Poster with 2 minute Oral Presentation Details:	Evaluation of the Efficacy of 10 % Imidacloprid/ 2.5 % Moxidectin (Advocate®, Advantage Multi® Bayer) for the Prevention of <i>Dirofilaria repens</i> Infection in Dogs
Authors:	Gabriele Petry ² , Claudio Genchi ¹ , Marco Genchi ¹ , Eva Maria Kruedewagen ² , Roland Schaper ^{2*} ¹ University of Milan, Milan, Italy ² Bayer Animal Health GmbH, 51368 Leverkusen, Germany
Poster Number:	228

Dirofilaria repens (*D. repens*) is prevalent in several regions in the world, including Southern Europe, Africa and Southeast Asia. It is the main causative agent of cutaneous dirofilariosis in dogs. Humans can be infected as “dead end” hosts with increasing numbers of infections in Southern, Central and Eastern Europe. As dogs are the main reservoir, one important measure to protect humans from the risk of infection is to control cutaneous dirofilariosis in dogs.

The efficacy of Advocate® against experimental *D. repens* infection in dogs was evaluated in a blinded, negative controlled randomised laboratory efficacy study. On study day (SD) 0, eight dogs received a spot-on treatment at a dose of 10 mg imidacloprid and 2.5 mg moxidectin per kg body weight. Another 8 dogs were treated with placebo. On SD 28 each dog was infected with approximately 75 infective *D. repens* L3 larvae. Blood samples were collected monthly after treatment. A modified Knott test was conducted to detect mf (microfilaria). PCR analysis was performed with mf-positive blood samples. On SDs 245 and 246, dogs were euthanized for detection of *D. repens* worms. Blood samples of all treated dogs were negative for mf at all sampling days. Blood samples of control dogs were positive for mf in 5 out of 8 dogs with individual mf counts from 7 to 2800 mf/ml. In mf-positive blood samples, only *D. repens* was identified by PCR analysis. During necropsy *D. repens* worms could be detected in all 8 untreated control dogs (range: 3–21 worms per dog). No worm could be detected in any of the treated dogs. These results indicate 100 % preventive efficacy of a single treatment of Advocate® in dogs against experimental infection with *D. repens*. Advocate® was well tolerated in all dogs, no treatment related adverse reactions were observed.



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Session Details:	8/27/2013 The Joe Boray Session - What's new and wonderful in Parasitology 1140 - 1240 Meeting Room 5
Poster with 2 minute Oral Presentation Details:	Clinical, laboratory and pathological findings in cats experimentally infected with <i>Aelurostrongylus abstrusus</i>
Authors:	Manuela Schnyder ^{1*} , Angela Di Cesare ² , Walter Basso ¹ , Franco Guscelli ³ , Barbara Riond ⁴ , Tony Glaus ⁵ , Paolo Crisi ² , Peter Deplazes ¹ ¹ Institute of Parasitology, Vetsuisse Faculty, University of Zurich, Winterthurerstrasse 266a, CH-8057 Zürich, Switzerland ² Department of Comparative Biomedical Sciences, Faculty of Veterinary Medicine, Piazza Aldo Moro 45, 64100 Teramo, Italy ³ Institute of Veterinary Pathology, Vetsuisse Faculty, University of Zurich, Winterthurerstr. 268, CH-8057 Zurich, Switzerland ⁴ Clinical Labor, Vetsuisse Faculty, University of Zurich, Winterthurerstrasse 260, CH- 8057 Zürich, Switzerland ⁵ Clinic for Small Internal Medicine, University of Zurich, Winterthurerstrasse 260, CH- 8057 Zürich
Poster Number:	52

Aelurostrongylus abstrusus is a heteroxenous nematode parasite of the respiratory system which can seriously affect breathing and the general condition of cats. Six cats were intragastrically inoculated with 100 or 800 third stage larvae (L3) obtained from the terrestrial snail *Helix aspersa*. First stage larvae (L1) could be isolated from faecal samples after 35-41 days post inoculation (dpi) in five of the cats. Two cats excreted larvae until the end of the study at day 84 dpi. Abnormal respiratory sounds and coughing were first observed at 28-41 dpi, followed by severe signs such as dyspnoea and panting from 52 dpi. All cats had enlarged lymph nodes, and 4 cats showed intermittently reduced general condition with apathy and anorexia. From 56 dpi, all cats had a lower body weight. Cats developed eosinophilia and leucocytosis with partially massive lymphocytosis, and occasionally basophilia and monocytosis were also observed. Mild anaemia was present in five cats, while coagulation parameter values (PT, aPTT, TT and fibrinogen) were irregularly out of reference ranges. Upon necropsy, adult *A. abstrusus* specimens were isolated from the five cats with patent infections. Macroscopic changes, which were present in all lung lobes of the affected cats, were confirmed by histological examination and also, as previously reported, by diagnostic imaging (Dennler et al., 2013). Differences in the severity of lesions between cats inoculated with 100 or 800 L3 were not obvious. Given that sophisticated diagnostic imaging is becoming more and more routine in the diagnosis of pulmonary disease in pets, parasitic diseases should especially be considered in the differential diagnoses of lung affections because massive lung changes without the presence of clinical signs and larval excretion can be induced by *A. abstrusus* upon infections with as few as 100 L3.

Acknowledgements:

The authors kindly thank A. Ruedemann, E. Merz, L. Kohler and R. Fiechter for their great participation and support throughout the study.

References:

Dennler et al., 2013: Thoracic CT findings in cats experimentally infected with *Aelurostrongylus abstrusus*, Veterinary Radiology & Ultrasound, in press.



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Session Details:	8/27/2013 The Joe Boray Session - What's new and wonderful in Parasitology 1140 - 1240 Meeting Room 5
Poster with 2 minute Oral Presentation Details:	Brain larval distribution and neuropathological changes in the paratenic mouse host model after <i>Toxocara</i> spp. infection
Authors:	Elisabeth Janecek ¹ , Andreas Beineke ² , Thomas Schnieder ^{1†} , Christina Strube ^{1*} ¹ Institute for Parasitology, University of Veterinary Medicine Hannover, GERMANY ² Institute for Pathology, University of Veterinary Medicine Hannover, GERMANY
Poster Number:	263

The worldwide distributed roundworm *Toxocara canis* causes zoonotic infections due to persistence of infectious larvae in paratenic hosts' tissue. Former studies show an increased neural affinity of *T. canis* whereas only little is known about the distribution of *T. cati* in the paratenic host. Therefore, larval distribution in the mouse as model for paratenic hosts was evaluated for both, *T. canis* and *T. cati*, by artificially digesting organs and determining number of larvae microscopically at eight time points post infection (2000 embryonated eggs each), mainly focusing on the brain. Results showed a higher neural affinity of *T. canis* whereat larval counts ranged from 0.3 to 32.2 larvae on average. *T. cati* larvae in the brain ranged from 0.3 to 9 in C57Bl/6J mice and 0.2 to 21.7 in Balb/c mice. Starting day 42 p.i., larval counts in *T. cati* infected mice started to considerably rise whereas *T. canis* infected mice larval counts slightly dropped. Analysis of the eyes and spinal cord of both infection groups did not reveal any differences and only 0.0 to 1.6 larvae could be counted on average in the eyes and 0.0 to 1.5 larvae in the spinal cord. Interestingly, *T. cati* larvae were mostly located in the cerebellum (14%-100%) whereat most *T. canis* larvae where located in the cerebrum (50%-80%). Histopathological examinations to determine effects on brain structure are currently in progress.

Overall, brain infection pattern of *T. canis* and *T. cati* revealed differences and need to be further characterized. Larval counts in the remaining organs, histopathology as well as molecular approaches will provide further data concerning differences between both roundworm species in the paratenic host leading to an inevitable foundation for further research on (neuro) toxocarosis.



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Poster with 2 minute Oral Presentation Details:	Tolerance to low temperatures of <i>Toxocara cati</i> larvae in chicken muscle tissue
Authors:	Kensuke Taira* Azabu University, Kanagawa, JAPAN
Poster Number:	262

The infectivity of *Toxocara cati* larvae in muscle tissue of chickens following storage at 4°C and -25°C was assessed using a bioassay in mice, to provide information on the risk of meat-borne toxocarosis. Muscle tissue samples of chickens infected with 30-day-old *T. cati* larvae were stored at 4°C for 14 and 28 days, and at -25°C for 12, 24 and 48 hours, then larvae were released by digestion and inoculated into mice. For each experimental group, the released larvae were inoculated in six mice. After 15 days, mice were euthanized and larval burden was assessed by digestion. In the control group (no storage of the infected chicken meat), a mean of 47.9 % of the inoculated larvae established in mice, whereas storage of meat at 4°C for 14 days or 28 days reduced the recovery percentages to means of 24.1 % or 3.3 %, respectively. Muscle larvae exposed to -25°C for 12, 24 or 48 hours did not establish in the mice. The present study demonstrated that *T. cati* larvae in chicken muscle tissue were highly infective even after 14 days refrigeration at 4°C, but also that deep freezing appear to be an effective inactivation measure. The results indicate that *T. cati* in poultry may pose a food safety risk if infected chicken is consumed raw or undercooked without prior deep freezing, and thus support the assumption that *T. cati* in poultry may be an agent of human toxocarosis.



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Session Details:	8/27/2013 The Joe Boray Session - What's new and wonderful in Parasitology 1140 - 1240 Meeting Room 5
Poster with 2 minute Oral Presentation Details:	Geographical distribution of <i>Angiostrongylus spp.</i> in Eastern Australia.
Authors:	Mahdis Aghazadeh ^{1,2} , Rebecca Traub ^{1,2} , Simon Reid ³ , James McCarthy ² and Malcolm Jones ^{1,2} ¹ School of Veterinary Science, University of Queensland, Gatton QLD 4343, Australia ² Queensland Institute of Medical Research, Herston, QLD4006, Australia ³ School of Population health, University of Queensland, Herston, QLD 4006, Australia
Poster Number:	158

The rat lungworm *Angiostrongylus cantonensis* is transmitted to humans and other accidental hosts through a variety of mollusc species acting as an intermediate host for the parasite. Although rats are definitive host for this nematode, the effect of infection is quite minor in rats, helping the parasite to spread in the environment for a long period of time. *Angiostrongylus cantonensis* has been reported from both feral and native rat species of Australia. However, the epidemiology of the parasite in not well studied in this country (Prociv et al., 2000). Understanding the epidemiology of *Angiostrongylus spp.* in Australia is complicated by the presence of the nearly identical species, *Angiostrongylus mackerrasae*, in *Rattus fuscipes*, the bush rats. The prevalence of *A. cantonensis* and *A. mackerrasae* in the definite and intermediate hosts has not been investigated in Australia at the molecular level and neither is it understood which species of molluscs are the most important intermediate hosts. Feral and native rats from Brisbane and surrounds were trapped, euthanazed and examined for the presence of *Angiostrongylus spp.* in the lung. Mollusc species collected from eastern Australia were digested and examined for the presence of *Angiostrongylus spp.* larvae. PCR of numerous ribosomal and mitochondrial sequences is being performed to determine genetic diversity of *Angiostrongylus* populations in SE Queensland and to determine whether multiple species of the genus exist in Eastern Australia. Spatial mapping of the parasites in the study area is being performed to determine possible hotspots of transmission.

Acknowledgements:

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Poster with 2 minute Oral Presentation Details:	Emerging from the shadows: Resurrection and redescription of <i>Varestrongylus alces</i> , a pathogenic lungworm of the Eurasian elk (<i>Alces alces</i>)
Authors:	Guilherme G. Verocai ^{1*} , Eric P. Hoberg ² , Turid Vikoren ³ , Rebecca K. Davidson ³ , Andrew M. Rezansoff ¹ , Bjørnar Ytrehus ³ , Kjell Handeland ³ , Susan J. Kutz ^{1,4} ¹ University of Calgary, Calgary, CANADA ² United States Department of Agriculture, US National Parasite Collection, Beltsville, USA ³ Norwegian Veterinary Institute, Oslo, NORWAY ⁴ Canadian Cooperative Wildlife Health Centre, Calgary, CANADA
Poster Number:	73

Definitions of diversity are the first step in understanding factors influencing host and geographic distributions of parasites and patterns of disease. Protostrongylid nematodes are pathogenic parasites of ungulates globally¹. Our recent discoveries within this group, including a new species of *Varestrongylus* in North America, and the intricate taxonomic history for the genus, indicate that its diversity has been underestimated^{1,2}. We now propose the resurrection of *Varestrongylus alces*³, a lungworm of Eurasian elk from Europe, and provide morphological and molecular grounds for its separation from *V. capreoli* in European roe deer.

We examined male (n=8) and female (n=12) nematodes, and larvae (n=15) from the terminal bronchioles of four Eurasian elks from Norway. DNA was extracted, and PCR performed targeting the ITS-2 region of the nuclear ribosomal DNA

Morphologically, specimens attributable to *V. alces* are distinguished from *V. capreoli* by constant structural differences among males (gubernaculum, denticulate crura, spicules, dorsal ray); females cannot be easily differentiated. Genetically, sequences of the ITS-2 region support species validity, and distinguish *V. alces* from 4 of 9 congeners for which there is molecular data available; including the other two species with short spicules in North America and Eurasia.

Histological examination of pulmonary lesions showed acute to sub-acute focal verminous pneumonia, restricted to the parenchyma. Numerous larvae were present in the lumen of surrounding large bronchioles, and cross-sections of adults were found in the alveoli. Parasites were surrounded by multinucleated giant cells, macrophages, eosinophils and lymphocytes.

Varestrongylus alces is valid and distinct from congeners, particularly from *V. capreoli* with which it had been synonymized. Further, we can recognize a complex of minuscule and poorly differentiated species of *Varestrongylus* that collectively have distributions extending from Eurasia into the Nearctic, consistent with the historical biogeographic patterns that influenced the diversity of the Holarctic fauna.

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Acknowledgements:

This research was funded by Alberta Innovates Health Solutions, NSERC, the Faculty of Veterinary Medicine of the University of Calgary, and the Norwegian Veterinary Institute (NVI). We also thank technicians at the NVI that assisted in collection and processing samples.

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Session Details:	8/27/2013 Resistance is futile! 1140 - 1240 <i>Meeting Room 6</i>
Poster with 2 minute Oral Presentation Details:	Body condition score used as a selection tool for Targeted Selective Treatment nematode control strategies
Authors:	Meghan Cornelius ^{1,2*} , Caroline Jacobson ² , Brown Besier ^{1,3} ¹ Cooperative Research Centre for Sheep Industry Innovation, AUSTRALIA ² School of Veterinary and Life Sciences, Murdoch University, Murdoch, WESTERN AUSTRALIA ³ Department of Agriculture and Food, Albany, WESTERN AUSTRALIA
Poster Number:	10

The concept that body condition may indicate resilience to worms in sheep stems from the assumption that sheep in poor body condition suffer more production losses from worms than sheep in higher body condition with similar worm burdens. An experiment was conducted to test the theory that high body condition can indicate a sheep’s ability to better cope with worms. Two flocks on two private farms located in south west Western Australia were measured for body condition score, body weight and worm egg counts between May and December, where half of the ewes in each flock received an anthelmintic treatment and half remained untreated. Response to treatment was analysed in terms of body condition score change and percentage live weight change. A response to treatment was observed in low body condition score ewes where nutrition was sub-optimal and worm burdens were high. Sheep in low body condition pre-lambing were also more likely to fall into a critically low body condition score (<2) if left untreated. Recommendations can be made to leave a proportion of the higher body condition sheep untreated in a targeted selective treatment program to provide a source of non-resistant worms to delay development of resistance.

Acknowledgements:

This work was funded by the Sheep Cooperative Research Centre



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Session Details:	8/27/2013 Resistance is futile! 1140 - 1240 Meeting Room 6
Poster with 2 minute Oral Presentation Details:	Anthelmintic resistance status in three Estonian sheep flocks
Authors:	Anja Joachim*, Ann Mari Anupõld, Barbara Hinney Institute of Parasitology, Department of Pathobiology, University of Veterinary Medicine Vienna, Veterinärplatz 1, 1210 Vienna, Austria
Poster Number:	122

Currently, little is known about the extent of anthelmintic resistance in ovine gastrointestinal strongyles in the reconvening Estonian sheep farming. We therefore conducted a pilot study to examine the efficacy of two commonly used anthelmintics in three Estonian sheep flocks. From September to November 2012, faecal egg count reduction tests (FECRT) were carried out in three farms, two from the south-east and one from the west of Estonia, testing the efficacy of albendazole (ABZ) and ivermectin (IVM). On each farm 3 trial groups with 18-20 animals each were formed except for farm 3 with n=3 for the IVM group. One group received ABZ, one group received IVM and one control group was left untreated. Individual faecal samples were taken at the day of treatment and 10 to 14 days later. The anthelmintic treatment was carried out with IVM (Bimectin® 10 mg/ml, Bimeda Chemicals Export) subcutaneously in the dose of 0.2 mg/kg BW or ABZ (Endospec® 10%, Bimeda Chemicals Export) orally in the dose of 5 mg/kg BW. Each individual faecal sample was analysed using a modified McMaster-method. The FECRT was carried out according to the WAAVP Guidelines. On farm 1 the FECRT showed a moderately reduced efficacy for ABZ and IVM with 66% and 65% FECR accordingly. With 26% FECR the results of farm 2 show a pronounced ABZ resistance. Farm 3 shows nearly 100% efficacy of ABZ and IVM, but past problems with high endoparasite burden and mortality indicate that there is probably a developing ABZ resistance that could not yet be detected with the FECRT. The results of this study indicate that in Estonia resistance against benzimidazoles and macrocyclic lactones occurs. To investigate this, further studies, including a larger number of farms, will have to be carried out.



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Session Details:	8/27/2013 Resistance is futile! 1140 - 1240 Meeting Room 6
Poster with 2 minute Oral Presentation Details:	Evaluation of anthelmintic resistance in internal parasites of dairy cattle in Maffra, Victoria
Authors:	Jane Kelley ^{1*} , Timothy Elliott ¹ , Terry Spithill ¹ ¹ Department of Agricultural Sciences and Centre for AgriBioscience, La Trobe University, Bundoora, AUSTRALIA
Poster Number:	120

Anthelmintics are the most common method of control for internal parasites in cattle in Australia but this method has limited longevity as internal parasite resistance in cattle is increasing. Anthelmintic resistance is a major threat to animal health and the productivity of livestock. Resistance to various anthelmintics in Australia has been identified in *Fasciola hepatica* (liver fluke) and gastrointestinal worms (GIW) such as *Ostertagia ostertagi*, *Cooperia* spp. and *Trichostrongylus* spp. However the extent and prevalence of resistance in these parasite species in Victorian dairy cattle is unknown. Using a questionnaire, we will assess the current and historical drench practices to provide insight into regional fluke and GIW management in dairy farms in Maffra. In conjunction, we will conduct a drench trial on one local dairy farm to assess the efficacy of several commercially available drenches, used individually and in combination, against GIW and liver fluke. Anthelmintic efficacy will be assessed by faecal egg count reduction tests (FECRT) for GIW and liver fluke. In addition, a coproantigen reduction test (CRT) will be implemented using the liver fluke Bio X ELISA kit. Faecal samples will be collected directly from the animal prior to the commencement of the trial and then 14 days post drenching to assess both liver fluke and GIW infection levels. Faecal samples will then be collected every 21 days until 77 days post drenching to assess the efficacy of the liver fluke treatments against the immature and early immature liver flukes. At the end of the trial an estimation of current levels of resistance and prevalence for *F. hepatica* and GIW within the region will be determined from the diagnostics tests and the questionnaires. If the outcomes suggest resistance is a problem, an integrated parasite management program (IPM) specific for the dairy farm will be designed and implemented.



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Session Details:	8/27/2013 Resistance is futile! 1140 - 1240 Meeting Room 6
Poster with 2 minute Oral Presentation Details:	Benzimidazole resistance in goats raised in semiarid areas from Brazil.
Authors:	Sabrina Mota Lambert* ¹ , Sandra Mayumi Nishi ¹ , Livia Ribeiro Mendonça ¹ , Maria Angela Ornelas de Almeida ¹ . ¹ Escola de Medicina Veterinária e Zootecnia, Universidade Federal da Bahia, Salvador, Brazil.
Poster Number:	121

Goat production is considered one of the main economical activities in semiarid areas in Brazil, characterized by small farming systems and familiar sustenance. The continuous use of anthelmintics, particularly of benzimidazoles against gastrointestinal nematode infection (GIN) has lead to the development of resistance and turned up an important constraint affecting goat production. This resistance is strongly linked to a point mutation in position 200 of isotype 1 b-tubulin gene, which replaces a phenylalanine for a tyrosine, causing loss of affinity to receptors. In this study, LNA probes for Real-Time PCR were used for F200Y polymorphism detection and compared to in vivo and in vitro tests. Faecal samples from twelve goat herds in Bahia state, Brazil, were collected for Faecal egg count reduction test (FECRT), Egg Hatch Assay (EHA) and b-tubulin F200Y allelic discrimination analysis. All herds analyzed showed resistance to benzimidazole both in vivo test (percentage reductions ranging from 0-92%), and in vitro test (EC50 above 0.1 µg / mL). The frequency of SS genotype varied from 5-43%, SR from 27-64% and RR from 3-50%; whereas the frequency of the S and R alleles in the populations was 52 and 48%, respectively. Molecular results agree with EHA and to a lesser extent to FECRT, but it is worth noting the possible subdosage of AH medications due to the use of recommended dose for sheep. Many factors contribute for AH development, mainly associated to sanitary management as most of the herds were raised under extensive farming system, with several herds sharing the same pasture area, lack of technical assistance and incorrect use of medication.

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Session Details:	8/27/2013 Resistance is futile! 1140 - 1240 Meeting Room 6
Poster with 2 minute Oral Presentation Details:	Moxidectin remains efficacious against ivermectin-resistant <i>Haemonchus contortus</i> : Comparative pharmacological assessment of single and double dose-responses
Authors:	Lifschitz A. ¹ , Lloberas M. ² , Alvarez L. ¹ , Entrocasso C. ² , Ballent M. ¹ , Virkel G. ¹ , Luque S., Lanusse C. ¹ * 1. Laboratorio de Farmacología, Centro de Investigación Veterinaria de Tandil (CIVETAN), CONICET, Facultad de Ciencias Veterinarias, UNCPBA. Tandil, Argentina 2. Laboratorio de Parasitología, EEA INTA Balcarce, Argentina.
Poster Number:	230

Although the macrocyclic lactones ivermectin (IVM) and moxidectin (MXD) share some pharmacological properties, a differential pattern of efficacy against resistant nematodes has been described (Vickers et al., 2001). Enhanced drug concentration within the worm and improved efficacy against resistant *Haemonchus contortus* have been recently reported after the intraruminal administration of IVM compared to the subcutaneous treatment (Lloberas et al., 2012). This work aimed to assess the relationship between anthelmintic activity and host tissue/parasite exposure for IVM and MXD in lambs naturally-infected with resistant *H. contortus*. The influence of a 2-fold dosage on the drug concentrations achieved at the host (bloodstream, gastrointestinal content/tissues) and within *H. contortus* were simultaneously evaluated with the clinical efficacy. Forty eight (48) naturally parasitised lambs were assigned into four (4) experimental groups and intraruminally treated with either IVM or MXD at 0.2 and 0.4 mg/kg. Blood samples were collected over 14 days post-treatment. Parasitological post-mortem examination was done at day 15 post-treatment. The recovered worms were identified by species and counted. Additionally, mucosal and fluid content samples and adult specimens of *H. contortus* were recovered at day 1 post-treatment. IVM and MXD were measured by HPLC. Both IVM and MXD concentration profiles measured within *H. contortus* reflected those observed in the abomasal contents. In spite of the high concentrations recovered from the abomasal content and within the worm, IVM completely failed to control *H. contortus* (0% efficacy) at both dose rates. Oppositely, MXD efficacy against this IVM-resistant *H. contortus* strain was 94.2 (therapeutic dosage) and 99.1% (double dose). The improved drug exposure (target worm) achieved after the oral/intraruminal treatment compared to the subcutaneous injection (Lloberas et al., 2012), as well, as the advantageous MXD efficacy performance observed at twice the dose should be seriously considered to optimise nematode control before a complete therapeutic failure is observed.

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Session Details:	8/27/2013 Resistance is futile! 1140 - 1240 Meeting Room 6
Poster with 2 minute Oral Presentation Details:	Prevalence of anthelmintic resistance in cattle nematodes and risk factors: A systematic review-meta-analysis approach
Authors:	Mederos, A. ^{1*} , Carracelas, B. ¹ , Minho, A. ² , Fernández, S. ³ , Sánchez, J. ⁴ 1. Instituto Nacional de Investigación Agropecuaria, Ruta 5 km 386, Tacuarembó 45000, Uruguay, email: amederos@inia.org.uy ; 2. Empresa Brasileira de Pesquisa Agropecuária, Bagé, RS, Brazil; 3. BioNem Research Centre, Guelph, ON, Canada; 4. University of Prince Edward Island, Charlottetown, PEI, Canada
Poster Number:	124

The main goal of this study was to identify the potential risk factors (RF) associated with the prevalence of anthelmintic resistance (AR) of bovine gastrointestinal nematodes. A systematic review (SR) and meta-analysis (MA) was conducted to collate, assess and summarize the scientific literature. This methodology has been used in order to minimize biases, obtain more precise estimates and identify sources of variability that could explain the differences in the prevalence of anthelmintic resistance. A systematic review protocol was designed a priori, validated and tested. A search algorithm was applied to four electronic databases and one level of relevance screening was conducted by two reviewers. Quality assessment and data extraction were performed in one single step. A random effects MA was performed to summarize the evidence of AR prevalence for each drug evaluated and RF were assessed qualitatively.

Twenty three studies (5 cross-sectional, 9 prevalence surveys and 9 field trials) from 15 countries were included in this review. The overall percentage of farms with AR in at least one drug was 82.1% (95% CI=70.5 to 93.7), and the between study heterogeneity was high ($I^2=94.8\%$). The sub-group analysis showed the following prevalence by drug class: ivermectin 77.0%; moxidectin 74.2%; benzimidazole 44.3% and levamisole 35.0%. The main nematode genera involved in the AR cases were *Cooperia* spp., *Ostertagia* spp., *Haemonchus* sp., *Trichostrongylus* spp. and *Oesophagostomum* spp.

RF were assessed from 5 studies. One reported significant association for treatment frequency ($p<0.05$), one was significant for avermectins use in the past ($p<0.005$), while grazing management ($n=2$) and refugia ($n=1$) were reported no significant.

The results suggest that macrocyclic lactones are the drug class with higher prevalence of AR in cattle nematodes. Scientific evidence on RF is still scarce. Additional results will be presented and discussed at the conference.

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Poster with 2 minute Oral Presentation Details:	Identification and quantification of polymorphisms responsible for the resistance to benzimidazoles in <i>Haemonchus contortus</i> isolated in the state of Ceara, Northeastern of Brazil
Authors:	Jessica Maria Leite dos Santos ¹ , Jomar Patrício Monteiro ^{2*} , Wesley Lyeverton Correia Ribeiro ¹ , Iara Tersia Freitas Macedo ¹ , Janice Araújo Fontenele ² ; Edilson Freitas ² ; Juliana de Carvalho Ribeiro ¹ ; Rafaele Almeida Sampaio ¹ ; Vilemar Araújo Filho ¹ ; Ana Lourdes Fernandes Camurça-Vasconcelos ¹ ; Luiz da Silva Vieira ² ; Claudia Maria Leal Bevilaqua ¹ ¹ Postgraduate Program in Veterinary Science - State University of Ceara, Fortaleza, BRAZIL ² Brazilian Agricultural Research Corporation - Goats and Sheep, Sobral, BRAZIL
Poster Number:	125

Haemonchus contortus is the most prevalent nematode in the Northeast region of Brazil. Control based on benzimidazole utilization is widespread and its inadequate use quickly selects the parasite population for resistance. Phenotypic methods such as faecal egg count reduction test (FECRT) and egg hatch assay (EHA) are widely used to characterize anthelmintic resistance (AR). PCR based methods are also used to diagnose resistance to benzimidazoles in *H. contortus*. These methods detect SNPs (F167Y, E198A and F200Y) in the beta tubulin isotype 1 gene. The objective of this study was to select populations of *H. contortus* for benzimidazole resistance and characterize it using Real-time PCR for each known SNP. Real-time PCR was done using DNA from a pool of 10 adult male *H. contortus* from a single animal per farm. FECRT and EHT were used to determine the original resistance. Tested samples were obtained from 6 farms located in 5 counties in the Ceará State: Tauá (TA1, TA2), Boa Viagem (BV), Quixadá (QX), Santa Quitéria (SQ) and Solanópole (SO). Dr. J. Cabaret (INRA, France) kindly provided the Inbred-susceptible-Edinburgh (ISE) isolate, previously reported as benzimidazole susceptible, as reference for comparison purposes. Benzimidazole resistance was detected by FECRT and EHT in all farms. Real time PCR results showed high frequencies of the resistant SNPs F200Y and F167Y. The most frequent resistant allele in the studied populations was in SNP F167Y and resistance in SNP E198A was not detected. Resistant allele frequencies for the ISE isolate were 1.7%, 0% and 0% for SNPs F200Y, F167Y and E198A respectively. Our results suggest that the SNPs F167Y and F200Y are both important for benzimidazole resistance in the studied populations. We plan to keep using the developed real time PCR test in future studies to assess benzimidazole resistance in natural *H. contortus* populations in Brazilian farms.

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Poster with 2 minute Oral Presentation Details:	Differential Molecular Characterization of <i>Fasciola Hepatica</i> in Several Hosts of Cajamarca, Perú. It's Implication In The Development of Anthelmintic Resistance
Authors:	Silvana Scarcella ¹ . Cesar Fiel ² , Heber Silva Díaz ³ , Pedro Ortiz Oblitas ^{3*} , Hugo Solana ¹ ¹ Laboratorio de Biología Celular y Molecular. Centro de Investigación Veterinaria de Tandil (CIVETAN), CONICET, Facultad de Ciencias Veterinarias, UNCPBA, Tandil, Argentina ² Laboratorio de Parasitología, Centro de Investigación Veterinaria de Tandil (CIVETAN), CONICET, Facultad de Ciencias Veterinarias, UNCPBA, Tandil, Argentina ³ Facultad de Ciencias Veterinarias. Universidad Nacional de Cajamarca, Cajamarca, Perú. E-mail: silvanas@vet.unicen.edu.ar
Poster Number:	188

Fasciolosis caused by the trematode *Fasciola hepatica* is a parasitic disease prevalent in ruminants raised in temperate regions of the world. This parasitism is maintained in the field for their ability to infect different species such as cattle, sheep or pig among others. It is economically important with losses due to infection estimated as US\$ 2000–3000 million yearly. The infection affects up to the 75% of dairy cattle raised in the northern region of Cajamarca, Peru. Furthermore, fasciolosis is an emergent zoonotic disease in many countries, including this region of Peru, where has been reported a prevalence of 24.4% in school children. Given the epidemiological and economic importance of this disease, it is necessary to have information relating to genetic variants in this trematode. Using the RAPD-PCR technique, in this paper we evaluate the molecular characteristics of adult flukes from three different hosts, sheep, cattle and pigs. We compared the genetic profiles of *F. hepatica* from different hosts detected a differential expression of polymorphic fragments (RAPD) between the species under study. The results obtained confirm a high level of polymorphism in the genome of *F. hepatica* showing a manifest genetic variability between flukes from different hosts. It is valid postulate that this polymorphism enhanced the adaptability in the host and at the environment. For any selection pressure, whether natural or artificial (bad use of fasciolicides and / or control and management measures), the existence of different genetically distinct populations within the species, allow one or more populations of *F. hepatica* can survive and create resistance or adaptability to this selective pressure.

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Authors:	Christina Rock, William Pomroy, Erica Gee E, Ian Scott Institute of Veterinary, Animal and Biomedical Sciences, Massey University, Private Bag 11-222, Palmerston North, New Zealand
Poster Number:	123

Macrocytic lactone resistant *Oxyuris equi* in New Zealand. There have been anecdotal reports of resistance to *Oxyuris equi* over the last few years throughout New Zealand. Many report the almost continuous (re) appearance of these large parasites (presumably females that have completed egg-laying) despite regular treatment with macrocytic lactone (ML) anthelmintics. This parasite is of limited pathological significance except that as the female lays eggs around the perineum it can induce pruritis with the horse subsequently displaying tail rubbing which is often pronounced. *Oxyuris* eggs do not get shed into faeces so conducting a typical egg count reduction test is inappropriate. For two horses from different locations, a critical study was conducted where each horse was treated with an appropriate dose of an ML anthelmintic and all faeces were then collected for two days and frozen. After 7 days the horses were treated with an appropriate dose of benzimidazole anthelmintic and faeces were again collected for two days. Later the faeces were thawed and sieved through a 100µm sieve with the retentate examined for parasites. Horse 1 had been treated with an ML approx 2 weeks prior to commencing this study. Despite this treatment, *Oxyuris* eggs were recovered from the perineum/faeces. The horse was treated with ivermectin+praziquantel on Day 0 and over the next two days faeces were examined and no parasites were seen. On Day 8 the horse was treated with oxfendazole and five adult *Oxyuris* were seen over the next two days of collection. Horse 2 was treated on Day 0 with abamectin and 9 *Oxyuris* were recovered over the next 2 days. On Day 7 it was treated with oxfendazole and 11 *Oxyuris* were collected over the following two days. The studies on these two horses provide some evidence to support the anecdotal reports of ML resistance in *Oxyuris equi* in New Zealand.



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Session Details:	8/27/2013 Resistance is futile! 1140 - 1240 Meeting Room 6
Poster with 2 minute Oral Presentation Details:	Gene expression in mesenteric lymph nodes of pigs with two different genotypes associated with resistance or susceptibility to <i>Ascaris suum</i>
Authors:	Per Skallerup ^{1,2,*} , Peter Nejsum ^{1,2} , Claus B. Jørgensen ² , Susanna Cirera ² , Kerstin Skovgaard ³ , Christian B. Pipper ⁴ , Merete Fredholm ² , Stig M. Thamsborg ¹ ¹ Department of Veterinary Disease Biology, University of Copenhagen, DENMARK ² Department of Veterinary Clinical and Animal Sciences, University of Copenhagen, DENMARK ³ National Veterinary Institute, Technical University of Denmark, DENMARK ⁴ Department of Public Health, University of Copenhagen, DENMARK
Poster Number:	170

In pigs, two single nucleotide polymorphisms (SNP TXNIP and SNP ARNT), both on chromosome 4, have been reported to be associated with roundworm (*Ascaris suum*) burden. In the present study, we selected pigs with two TXNIP genotypes (AA; n=24 and AB; n=24. Pigs were trickle-infected with *A. suum* from eight weeks of age until week eight post first infection (PI) when the pigs were slaughtered. An uninfected control group (AA; n=5 and AB; n=5) was also included. At necropsy, we collected lymph nodes for expression studies and recorded worm burdens (macroscopic worm burden and total worm burden) and faecal egg counts. Data indicated that pigs of the AA genotype were resistant to infection and AB pigs were susceptible. Gene expression in mesenteric lymph nodes was evaluated by qPCR using a microfluidic-based platform. We included markers of different T cell responses (e.g., T_H1-type response, T_H2-type response, regulatory T cells) as well as different candidate genes in linkage disequilibrium with the SNP TXNIP marker. Twenty-seven genes passed quality testing and were included in the analysis. Preliminary data analysis using a mixed model with genotype and infection status as fixed effects showed that CCL17 (P<0.05), IL4 (P<0.05) and TGFB1 (P=0.055) were more abundantly expressed in *A. suum*-infected pigs than in the control group. Interestingly, the expression of IL13 was higher in pigs of the susceptible AB genotype than in pigs of the AA genotype (P=0.064). A mixed model with genotype and total worm burden as fixed effects showed a significant correlation between relative expression level and total worm burden for CCL2 (P<0.05), IL13RA2 (P<0.01), NOS2 (P<0.01) and STAT6 (P<0.01). Further analyses of qPCR data will reveal some of the key genes involved in the pig's response to *A. suum* infection.



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Session Details:	8/27/2013 Ticked Off! 1140 - 1240 Meeting Room 7
Poster with 2 minute Oral Presentation Details:	The effects of a flumethrin and fluazuron combination pour-on formulation used on cattle exposed to a boosted <i>Rhipicephalus decoloratus</i> and <i>R. microplus</i> population in the Eastern Cape region of South Africa.
Authors:	Clinton M Austin ^{1,4*} , Chandra Bhushan ² , Josephus J Fourie ³ , Julian E Liebenberg ³ , Roaland Jooste ¹ , Pumzile Qwalela ¹ ¹ Bayer HealthCare, Johannesburg, South Africa ² Bayer GmbH, Monheim, Germany ³ Clinivet International (Pty) Ltd, Bloemfontein, South Africa ⁴ University of Pretoria, Faculty of Veterinary Science, Onderstepoort, South Africa
Poster Number:	253

The study was conducted to investigate the effect of introducing animals treated with a Flumethrin 1% and Fluazuron 2.5% (Drastic Deadline eXtreme®- Bayer) combination product on tick population on the pasture. Twenty-six cattle (n=26) were used in a study on a pasture with boosted tick numbers. The climate and tick population data for the pasture from the previous year was available. A group of 6 cattle was introduced onto the pasture and treated with Drastic Deadline eXtreme on Day 0, +63, +126 and +189. The animals were left to graze naturally on the pasture for the duration of the study (259 days). On 10 occasions (every 28 days), 2 untreated, tracer calves were introduced onto the pasture and left to graze naturally for 7 days, before being removed from pasture and tick burdens determined. Monthly tick drags on the pasture were also conducted and compared to the previous year, along with climatological data. The tracer animals showed a 75% (Day +63) to 100% (Day +146) reduction in the mean number of *R. decoloratus* ticks collected (95% CI 57.10 - 100), and a 97.5% (Day +35) to 100% (Day +146) reduction in *R. microplus* ticks collected (95% CI 98.78 - 100). When compared to the previous year in similar climatological conditions, the mean reduction in ticks numbers as determined by monthly drags ranged from 40.7% on Day +28 to 100% on Day +140 (95% CI 72.59 - 100). Tick numbers on the treated animals showed an initial sharp decline and were maintained at a consistently low level for the rest of the study. This study demonstrates that cattle treated with this acaricide combination are able to reduce the tick burdens on pasture.

Acknowledgements:

Bayer Animal Health
Dohne Research Station



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Session Details:	8/27/2013 Ticked Off! 1140 - 1240 Meeting Room 7
Poster with 2 minute Oral Presentation Details:	Life, hosts and control strategies for the Australian paralysis tick <i>Ixodes holocyclus</i>
Authors:	Greta Busch ^{1*} , Manuel Rodriguez Valle ¹ , Ala Lew-Tabor ¹ ¹ Queensland Alliance for Agriculture and Food Innovation, University of Queensland, Brisbane, AUSTRALIA
Poster Number:	53

The Australian paralysis tick *Ixodes holocyclus* is distributed along the eastern coast of Australia from northern Queensland to south-eastern Victoria however there are reports of an expanding range. It is primarily found on bandicoots but may also attach to different hosts including, other native animals, dogs, cats, cattle, horses and occasionally humans. Low numbers of adult ticks are present year-round but peak in spring and early summer, the time of year known as the ‘tick season’. At least one low molecular weight toxin in the tick’s saliva causes an ascending flaccid paralysis most notably in domestic dogs and cattle. Left untreated, this paralysis is usually fatal. Prevention methods are limited to frequent treatment of domestic animals with topical acaricides such as Frontline Plus® and Advantix®, which may not be 100% effective and whose long term treatment regimes can become expensive. Treatment of paralysed animals relies on a tick paralysis anti-serum obtained from hyperimmunized dogs. This is only effective in the early stages of the disease and is expensive, particularly in cattle, where treatment costs frequently outweigh the actual and emotional value of the individual animals. Further characterization of the effects and action/s of natural and recombinant putative toxins will provide the basis for new prevention and treatment strategies.

Acknowledgements:
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Session Details:	8/27/2013 Ticked Off! 1140 - 1240 Meeting Room 7
Poster with 2 minute Oral Presentation Details:	Epidemiology of tick and tick-borne diseases in poultry birds of Pothwar region, Pakistan
Authors:	Farhana Riaz Chaudhary ^{1*} , Ashraf Anjum ² , Khurum Qazi ³ , Muhammad Atif ² , Naveed Iftikhar ⁴ ¹ Department of Zoology, Pir Mehr Ali Shah-Arid Agriculture University, Rawalpindi. ² Poultry Research Institute, Rawalpindi. ³ Poultry Research Institute, Dina-Jhelum ² Poultry Research Institute, Attock
Poster Number:	11

Poultry ticks are common nocturnal and temporary ectoparasite owing to direct damage on their hosts and, especially, because they are vectors of large variety of pathogens. Such pathogens are diverse and include viruses, bacteria, protozoa and spirochaetosis cause important economic losses to poultry industry, globally. So, one year study was designed with the aim to monitor seasonal trend of poultry ticks on commercial layers and cross breeds in government farms as compared to environmental control sheds, in selected three districts viz; Rawalpindi, Jhelum and Attock. Furthermore, to be observed the pathogenic effects in terms of hematological parameters, tick-borne diseases and estimation of total economic losses in selected farms. Data revealed that ticks (*Argas persicus*) were found to be present throughout the year but highest prevalence was observed in summer 50% (n= 21177) and lowest in monsoon 21% in Rawalpindi sheds followed by Attock (n=4560) {47% monsoon; 23% winter} and in Jhelum (n=15009) {45% monsoon; 16% winter}, respectively. Additionally, ticks being hematophagus parasites so, hematological parameters viz; RBCs counts, Hb, PCV, MCH and MCHC levels were found to be decreased with increase tick infestation burden. No association was found between ectoparasitism and sex, breed and fur colour (P >0.05), however a strong positive association was observed with presence of cracks and holes in sheds, existence of vegetation around sheds and repeatedly utilization of same sheds (P <0.05). Further detailed study with particular reference to tickborne pathogen demonstrated that Spirochaetosis significantly effects (P <0.05) in post monsoon with 18% mortality, 25% egg reduction and total economic losses in \$1010 followed by Mycoplamosis, Fowl cholera, Salmonellosis, Staphlococus and bursal diseases, respectively. Such information will provide sufficient basis for the effective tick control programs of poultry ticks in order to enhance the well being and productivity of poultry to save farmers from economic losses.

Acknowledgements:

We would like to thank the Department of Zoology, Pir Mehr Ali Shah Arid Agriculture University Rawalpindi for funding this research.



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Session Details:	8/27/2013 Ticked Off! 1140 - 1240 Meeting Room 7
Poster with 2 minute Oral Presentation Details:	Acaricidal activity of essential oils from five endemic conifers of New Caledonia on the cattle tick <i>Rhipicephalus (Boophilus) microplus</i>
Authors:	Nicolas Lebouvier ¹ , Thomas Hue ^{2*} , Edouard Hnawia ¹ , Leila Lesaffre ¹ , Chantal Menut ³ , Mohammed Nour ¹ ¹ Université de la Nouvelle-Calédonie, New Caledonia, FRANCE ² Institut Agronomique néo-Calédonien, New Caledonia, FRANCE ³ Institut des Biomolécules Max Mousseron, Faculté de Pharmacie de Montpellier, France
Poster Number:	231

Despite decades using chemical acaricides, ticks are still a major burden for cattle in tropical areas in terms of cost of control, tick-born disease and loss of production. Acaricidal activity of essential oils extracted from resin and heartwood of five endemic conifers of New Caledonia (*Araucaria columnaris*, *Agathis moorei*, *Agathis ovata*, *Callitris sulcata* and *Neocallitropsis pancheri*) was evaluated on 14-21-days-old *Rhipicephalus microplus* tick larvae using the LPT bioassay. A first screening with a 5% dilution was carried out and the oils with 100% of mortality at this rate (*C. sulcata*, *N. pancheri* and *A. columnaris*) were diluted until no activity was shown. The three most active oils were obtained from *N. pancheri*, *C. sulcata* and *A. columnaris* with LC₅₀ values of 0.55%, 0.65% and 1.62% respectively. The chemical composition of the essential oil from resin of *A. columnaris* was characterised by GC-MS. The most abundant components were aromadendrene (23.1%) and bicyclogermacrene (16.0%). The “essential oil efficiency EOE” which can be measured as the ratio between the yield of extraction and LC₅₀ value shows that *A. columnaris* and *N. pancheri* might provide valuable and effective natural acaricide for control of the cattle tick *Rhipicephalus microplus*.

References:

Lebouvier N., H   T., Hnawia E., Lesaffre L., Menut C., Nour M. Acaricidal activity of essential oils from five endemic conifers of New Caledonia on the cattle tick *Rhipicephalus (Boophilus) microplus*. Parasitol Res (2013) 112:1379–1384



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Session Details:	8/27/2013 Ticked Off! 1140 - 1240 Meeting Room 7
Poster with 2 minute Oral Presentation Details:	Efficacy of neem oil against engorged <i>Rhipicephalus (Boophilus) microplus</i> ticks on <i>in vitro</i> tests
Authors:	Andréia Buzatti ¹ , Lew Kan Sprenger ¹ , Thais Kucharsky ¹ , Evandro Richter ² , Marcelo Beltrão Molento ^{1*} ¹ Federal University of Parana, Curitiba, PR, BRAZIL ² Agroecology Reference Center of Parana, Pinhais, BRAZIL
Poster Number:	232

Rhipicephalus (Boophilus) microplus stands out as one of the ectoparasites that most affect the productive performance of cattle. The use of chemical acaricides is the main instrument of control of this tick. Although currently this control is characterized by the presence of parasite resistance (Veiga et al., 2012) we are still seeing an increase of the frequency of applications of chemical products. There is an urgent need for research on alternative and sustainable methods of tick control and the use of plant compounds with acaricide activity may represent an opportunity for reducing the problem. The aim of this study was to evaluate the *in vitro* acaricide action using a tick-immersion test with neem oil (*Azadiractha indica*) against the engorged females of *R. (B.) microplus*. Engorged ticks were collected from cattle at the Agroecology Reference Center of Parana-CPRA, Pinhais, Brazil. The study design was completely randomized with eight treatments and three replicates each consisting of seven concentrations of neem oil: 0.16, 0.32, 0.64, 1.28, 2.56, 5.12 and 10.24% and a control group, composed of distilled water. Results from larval hatchability were similar to each other (P>0.05). Reproductive efficiency and efficacy of the treatments was statistically significant (P<0,05). The efficacy ranged from 14.77±3.55 to 40.09±2.14%, corresponding to the concentrations 0.16% and 10.24%, respectively. The efficacy of 10.24% of neem oil was statistically higher than the others (P<0.05). Neem oil did not affect the percentage of larval hatchability, but have demonstrated a significant effect on the reproductive efficiency of *R. (B.) microplus* at the concentrations used. The results showed that neem seed oil may be considered as a potential acaricide, where the percentage of efficacy of each treatment is directly related to their concentration.

Acknowledgements: The authors wish to thank the technical support of CPRA, Brazil.

References: Veiga LP, Souza AP, Bellato V, Sartor AA, Nunes AP, Cardoso HM. 2012. Resistance to cypermethrin and amitraz in *Rhipicephalus (Boophilus) microplus* on the Santa Catarina Plateau, Brazil. Rev Bras Parasitol Vet. 21:133-6.



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Session Details:	8/27/2013 Ticked Off! 1140 - 1240 Meeting Room 7
Poster with 2 minute Oral Presentation Details:	Cattle tick: Genome sequencing for gene discovery through to control
Authors:	Matthew Bellgard ^{1*} , Paula Moolhuijzen ^{1*} , John McCooke ¹ , Roberto Barrero ¹ , Gabriel Keeble, ¹ Felix D. Guerrero ² ¹ Centre for Comparative Genomics, Murdoch University, Perth, Australia ² USDA-ARS Knippling-Bushland US Livestock Insects Research Laboratory, Kerrville, USA
Poster Number:	14

The global cattle population is estimated at approximately 1 billion head. Of this population, 80% live in areas considered suitable habitat for ticks and tick-borne diseases. The tropical/southern cattle tick, Rhipicephalus (Boophilus) microplus, is considered the most significant cattle parasite in the world, having established populations in most of the world's tropical and subtropical countries. The cattle tick genome is large and complex in structure, with a genome size estimated to be 7.1 Gbp, over twice the size of the human genome, and consisting of over 70% repetitive DNA. In order to adequately assemble this difficult genome as well as identify key biological features, we adopted a strategy to integrate sequence generated from a variety of next- and third-generation sequencing technologies [1]. Illumina, 454, Sanger, and PacBio approaches have been conducted on total genomic and Cot-filtered DNA, transcriptomic samples and BAC clones. Over 80 Gigabases (> 10x coverage) of sequence have been obtained from the cattle tick genomic DNA, including >52 Gigabases from gene-enriched regions in Cot-filtered genomic DNA. Over 3000 BACs have sequenced with an Illumina approach and merged with > 24 Gigabases of PacBio-derived sequence from 178 PacBio SMRT cells to create scaffolds. A number of tissue specific/development stage transcriptomes have also been sequenced.

References:

1. Bellgard, M.I., et al., *CattleTickBase: an integrated Internet-based bioinformatics resource for Rhipicephalus (Boophilus) microplus*. Int J Parasitol. **42**(2): p. 161-9.

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Session Details:	8/27/2013 Ticked Off! 1140 - 1240 Meeting Room 7
Poster with 2 minute Oral Presentation Details:	Acaricide resistance-associated mutation screening and evaluation of selection pressure in <i>Rhipicephalus microplus</i> and <i>Rhipicephalus decoloratus</i> ticks in South Africa.
Authors:	Samantha Reinecke ^{1*} , Albe van der Merwe ¹ , Christine Maritz Olivier ¹ (presenting author asterisked) ¹ University of Pretoria, Pretoria, SOUTH AFRICA, Department of Genetics
Poster Number:	126

R. microplus constitutes a main vector for asiatic babesiosis and anaplasmosis which are known to plague cattle. The lack of sufficient tick control strategies and management programs manifests into a severe economic burden threatening the sustainability of the livestock industry in South Africa, as well as globally. The principal method for tick control is the use of chemical acaricides. This form of tick control is however, becoming less adequate due to an increase in the frequency of mutant alleles being selected in the population allowing ticks to develop resistance [1]. In this study, a country-wide survey is conducted to determine the presence and frequency of mutant alleles of ticks resistant to the different chemical acaricide classes. Approximately 160 farms across South Africa have been sampled and *R. microplus* and *R. decoloratus* ticks were screened for all published single nucleotide polymorphisms (SNPs) [2].

The presence of these SNPs will be evaluated geographically to determine whether climatic conditions and geographical locations influence the frequency of these SNPs. The intensity of selection pressure acting on the target gene will be determined and coalescent studies done to determine the rate at which ticks are becoming resistant. Gametic disequilibrium studies will be done and the level of inbreeding and migration among populations will be determined. By defining the level of resistance across South Africa a tailored tick control program can be developed for improved use of acaricides and development of vaccines.

Acknowledgements:
Pfizer for funding this research
Pfizer representatives for tick collections across South Africa

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1. Foil, L.D., et al., *Factors that influence the prevalence of acaricide resistance and tick-borne diseases*. Vet Parasitol, 2004. 151: p. 163–181.
2. Guerrero, F.D., L. Lovis, and J.R. Martins, *Acaricide resistance mechanisms in Rhipicephalus (Boophilus) microplus*. Rev Bras Parasitol Vet, 2012. 21(1): p. 1-6.

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Poster with 2 minute Oral Presentation Details:	Efficiency of spray techniques of applying acaricide against <i>Rhipicephalus (Boophilus) microplus</i> (Canestrini, 1887).
Authors:	Daniel Sobreira Rodrigues ^{1*} , Carolina Maria Viana de Freitas ² , Ricardo Araújo Nascimento ² , Eduardo Bastianetto ² , Luciano Bastos Lopes ³ , Rebeca Passos Bispos Wanderley Muller ² , Paulo de Oliveira ¹ , Romário Cerqueira Leite ² . ¹ Empresa de Pesquisa Agropecuária de Minas Gerais - EPAMIG, Minas Gerais, BRASIL ² Universidade Federal de Minas Gerais – UFMG, Minas Gerais, BRASIL ³ Empresa Brasileira de Pesquisa Agropecuária – EMBRAPA, Mato Grosso, BRASIL
Poster Number:	12

The aim of this study was to assess the efficiency of spray techniques of applying acaricide in dairy cattle. For this purpose were used 12 cows for each of the five evaluated groups. The animals were kept at the same pasture 35 days before the treatment and 22 days after that. The control group was sprayed with water and the treated ones with an association between cypermethrin high-cis 6% and chlorpyrifos 50% with one of the following techniques: Power Spray, Hand Pumped Backpack Sprayer, Spray Race and a modified hand pumped backpack sprayer used with no contained cattle commonly practiced by the local farmers defined as Usual technique. Counts of ticks 4.5 to 8 mm in length were conducted on the right side of each animal individually contained within squeeze chute on days 01, 06, 08, 13, 15, 20 and 22 after treatment. The counting data were multiplied by two and evaluated by the nonparametric Kruskal-Wallis test. The efficiency of each technique was calculated according to the following formula: [(CT) / C] x 100, where C = total number of ticks observed in the control group and T = total number of ticks observed in the treated group. The mean and standard deviation for the respective groups were: 791 ± 844; 331 ± 461, 344 ± 386, 407 ± 411, 433 ± 475. The Power Spray treatment killed 58% of the ticks and was more efficient in reducing tick burden (p<0.001) than Usual and Spray Race that killed 45% and 48%, respectively. There was no significantly difference between the Backpack Sprayer and the others. The poor efficiency observed could be related with the historical of resistance of tick population that showed an efficiency of 87.5%at immersion of engorged females test. Among the techniques evaluated the power spray should be prioritized.

Acknowledgements:
FAPEMIG , CNPq, MAPA and INCT em Informação Genético Sanitária.



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Session Details:	8/27/2013 Ticked Off! 1140 - 1240 Meeting Room 7
Poster with 2 minute Oral Presentation Details:	Differences in acaricide susceptibility of the parasitic stages of <i>Rhipicephalus (Boophilus) microplus</i> (Canestrini, 1887).
Authors:	Daniel Sobreira Rodrigues ^{1*} , Carolina Maria Viana de Freitas ² , Ricardo Araújo Nascimento ² , Eduardo Bastianetto ² , Luciano Bastos Lopes ³ , Rebeca Passos Bispos Wanderley Muller ² , Paulo de Oliveira ¹ , Romário Cerqueira Leite ² . ¹ Empresa de Pesquisa Agropecuária de Minas Gerais - EPAMIG, Minas Gerais, BRASIL ² Universidade Federal de Minas Gerais – UFMG, Minas Gerais, BRASIL ³ Empresa Brasileira de Pesquisa Agropecuária – EMBRAPA, Mato Grosso, BRASIL
Poster Number:	13

The aim of this study was to demonstrate the difference in parasitic stages susceptibility of *R. (B.) microplus* to a high-cis cypermethrin 6% and chlorpyrifos 50% association under field conditions. Wide differences in tick mortality were observed among the dates of assessment, with a similar pattern for all treated groups in a previous field trial about efficiency of spray treatments. The values obtained from 12 dairy cows for each of the four treated groups on days 01, 06, 08, 13, 15, 20 and 22 after treatment were plotted and evaluated by Adherence Chi-Square test. Also, the plotted values were transformed to log 10 basis (x+1) and compared by analysis of variance (ANOVA). The mortality curves produced for all groups were not different (p<0.01). The mean and standard deviation for each date were, respectively: 18 ± 0.13%, 61 ± 0.08%, 23 ± 0.08%, 47 ± 0.07%, 58 ± 0, 12%, 74% and 69 ± 0.11 ± 0.15%. On days 01 and 08, that corresponds to the moment which prevailed respectively engorged females and metanymphs, the lower mortality was observed (p<0.001). On days 13 and 20, which respectively corresponds to the predominance of the early stages of nymphs and larvae, the larvae mortality rates were higher than for nymphs, but the values did not differ from the dates 06, 15 and 22, corresponding to unfed females, metalarvae and unfed larvae (p<0.001). These observations demonstrate a tendency to increase the tick susceptibility to some acaricides as the engorgement state and the development stage of the parasite evolves. The results are in agreement with the observations obtained by Souza and Gonzáles (1980). In specific situations, as in low efficacy of the active and severe tick burden, it is suggested a five day rest acaricide treatments intending to strike unfed adults that survived as metanymphs.

Acknowledgements:
FAPEMIG , CNPq, MAPA and INCT em Informação Genético Sanitária.

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Session Details:	8/27/2013 Ticked Off! 1140 - 1240 Meeting Room 7
Poster with 2 minute Oral Presentation Details:	Transcriptome analysis of different stages of <i>Ixodes holocyclus</i> using next generation sequencing Illumina and 454 technologies
Authors:	Manuel Rodriguez-Valle ^{1*} , Paula Moolhuijzen ² , Diane Vankan ³ , Matthew Bellgard ² , and Ala Lew- Tabor ^{1,2} ¹ The University of Queensland, Queensland Alliance for Agriculture & Food Innovation, St. Lucia, Brisbane, Qld, Australia. ² Murdoch University, Centre for Comparative Genomics, Perth, Western Australia, Australia. ³ The University of Queensland, School of Veterinary Science, Gatton, Qld, Australia.
Poster Number:	189

I. holocyclus occurs along the eastern coast of Australia from far north Queensland to southern Victoria and is the most virulent tick species in terms of paralysis. Each year *I. holocyclus* affects ~100 000 domestic animals, with up to 10,000 companion animals. Also, humans are affected by tick bites provoking hypersensitivity reactions. Toxin is produced as the adult female tick engorges and paralysis is frequently induced just prior to detachment. Here we describe a transcriptome survey from salivary glands and viscera samples obtained from full-engorged *I. holocyclus* tick. Ticks were collected from cats and dogs with paralysis symptoms at Brisbane veterinary clinics, in southeast Queensland. cDNA from salivary glands and viscera were sequenced using Illumina technologies producing 141 million paired reads with a total of 94 944 assembled transcripts. A total of 24 isocontigs related with four holotoxins were identified in cat and dog salivary glands and five cytotoxin transcripts were related in the tick viscera. Different transcripts related with holotoxins were obtained in cats and dogs compared with transcripts obtained from *I. holocyclus* fed on bandicoots. Data showed that holotoxins are conformed for multivariable protein family with a highly conserved structure. Finally, a comprehensive analysis in the Ixode specie will be conducted comparing transcripts from *Ixode holocyclus* and *scapularis* ticks.

Acknowledgments

This research was supported by Elanco Animal Health, Australia. The authors wish to give special thanks to Anthea Bruyeres (Qld Department of Agriculture, Fisheries & Forestry) for her technical support and the Veterinary staff from The Manly Rd Veterinary Hospital, Brisbane, Qld in supporting the collection of ticks from companion animal cases.



Session Details:	8/27/2013 Ticked Off! 1140 - 1240 Meeting Room 7
Poster with 2 minute Oral Presentation Details:	Acaricidal activity of extracts from <i>Annona reticulata</i> (Annonaceae), <i>Solanum melongena</i> (Solanaceae), <i>Rosmarinus officinalis</i> (Lamiaceae) against the cattle tick, <i>Rhipicephalus microplus</i> resistant to acaricides
Authors:	1*José Alberto Rosado-Aguilar, 2Ronnie Arieta-Román, 1Roger Iván Rodríguez-Vivas, 1José Rodrigo Carrillo-Peraza1, 3Álvaro Peniche-Cardena 1Facultad de Medicina Veterinaria y Zootecnia. Universidad Autónoma de Yucatán. Km. 15.5 carretera Mérida-Xmatkuil. CP. 97000. Mérida, Yucatán, México; alberto.rosadoaguilar@gmail.com 2Facultad de Ingeniería en Sistemas de Producción Agropecuaria. Universidad Veracruzana. Campus Acayucan, Veracruz, México. 3Facultad de Medicina Veterinaria y Zootecnia. Universidad Veracruzana. Veracruz, Ver., México.
Poster Number:	127

The aim of this study was to evaluate the acaricidal activity of crude extracts from leaves of *Annona reticulata* (Annonaceae), *Solanum melongena* (Solanaceae), and *Rosmarinus officinalis* (Lamiaceae) on larvae and adults of *R. microplus* (resistant to organophosphates, pyrethroids and amitraz) using the larval immersion test (LIT) and adult immersion test (AIT). In the LIT crude extracts of *A. reticulata* evaluated at 10% (100 mg/ml) and 20% (200 mg/ml) concentration against larvae of *R. microplus* showed acaricidal activity of 96.2±5.3% and 100% respectivelyThe activity for *S. melongena* was 41.7± 8.4% and 94.5± 6.4%, for 10% and 20% concentrations respectively, meanwhile leaf extracts of *R. officinalis* showed acaricidal activity of 2.4±2.0% and 16.3±3.2%, respectively. Based on these results, leaf extracts of *A. reticulata* were selected to be evaluated against adults of *R. microplus*. In the AIT the crude extracts from *A. reticulata* at 10% and 20% concentrations evaluated against *R. microplus* engorged females showed mortality of 0.0% and 22.2±9.6%, respectively. The 10% and 20% of these crude extracts showed 25.8±9.3% and 51.7±17.6% of egg laying inhibition, respectively. Furthermore, these crude extracts showed a larval hatching inhibition of 75.0±10.4% and 91.33±9.02%, respectively. Our results showed that crude extracts of *A. reticulate* and *S. melongena* are promising candidates to control larvae of *R. microplus* multi-acaricide resistant. In addition *A. reticulata* reduced the ability of engorged females to lay eggs and substantially affected the larval hatchability of *R. microplus*. Further studies are required to identify the active fractions and compound of these crude extracts.

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Session Details:	8/27/2013 Ticked Off! 1140 - 1240 Meeting Room 7
Poster with 2 minute Oral Presentation Details:	Questing ticks of two important recreational areas of Croatia
Authors:	Michal Stanko ^{1,2*} , Martin Bona ¹ , Bronislava Víchová ¹ , Ladislav Mošanský ¹ , Branislav Petko ¹ ¹ Institute of Parasitology, Slovak Academy of Sciences, Košice, Slovakia ² Institute of Zoology, Slovak Academy of Sciences, Košice, Slovakia
Poster Number:	256

The authors present results of mapping of ticks during expedition in May 2011. The aim of the expedition was mapping of the occurrence, species composition and relative density of ticks in Croatia with emphasis on tick communities in two recreational areas - around the National Park Plitvice lakes and the Adriatic coast between Split and Dubrovnik towns. Ticks were collected at 18 locations, on the route Varaždin – Novi Marof – Draganič – Grabovac – Bunič – Gospič – Makarska. Together were registered 1702 ticks belonging to five species: *Ixodes ricinus*, *Dermacentor reticulatus*, *D. marginatus*, *Haemaphysalis punctata*, *Rhipicephalus sanguineus*. The predominant species was *Ixodes ricinus* (376 males, 357 females, 630 nymphs), occurs mainly in the northern part of Croatia as well as in surroundings of Plitvice Lakes area. Next two ticks, *D. reticulatus* (69 males, 100 females) were registered at 5 locations and *D. marginatus* (18 males, 30 females) at 6 locations. In the northern part of Croatia we recorded 490 ticks belonging to three species - *I. ricinus* (69.6 %, *D. reticulatus* (27.1 %), *D. marginatus* (3.3 %) and relative density was 80 ticks per 1 hour flagging. In the areas around Plitvice lakes 4 tick species were registered - *I. ricinus* (91.5 %), *D. marginatus*, *D. reticulatus*, *H. punctata*. For the xerothermic coastal regions were characteristic *R. sanguineus* tick (99 % of tick material) with low average relative density 7.3 tick/hour of sampling. We assume that the ticks are little threat to tourists on Dalmatia during the summer. The tick fauna of Croatia in the spring aspect reflected the predominant of habitat type.

Acknowledgements:

The work was supported by grants APVV 0267-10 of the Slovak Research and Development Agency, and Environmental Protection Against Parasitozoonoses under the Influence of Global Climate and Social Changes (code ITMS: 26220220116), supported by the Research & Development Operational Programme funded by the ERDF (rate 0.3).

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Session Details:	8/27/2013 Ticked Off! 1140 - 1240 Meeting Room 7
Poster with 2 minute Oral Presentation Details:	Expression profiles of autophagy-related genes in the hard tick, <i>Haemaphysalis longicornis</i>
Authors:	Rika Umemiya-Shirafuji ^{1,2*} , Suguru Kawano ^{1,2} , Remil Linggatong Galay ² , Hiroki Maeda ² , Aiko Kume ^{1,2} , Tetsuya Tanaka ² , Hiroshi Suzuki ¹ , Kozo Fujisaki ^{2,3} ¹ Obihiro University of Agriculture and Veterinary Medicine, Hokkaido, JAPAN ² Kagoshima University, Kagoshima, JAPAN ³ National Agricultural and Food Research Organization, Ibaraki, JAPAN
Poster Number:	254

Ticks are gorging-fasting organisms with unique life cycles that are characterized by a long period of starvation. They can survive without meal during the host-seeking period for several months to years. To understand the molecular mechanisms underlying their starvation tolerance, we focused on autophagy, a proteolysis system via the lysosomes for various cellular processes that is induced during starvation in eukaryotes. We hypothesized that ticks utilize a scheme of autophagy to overcome the starved condition. To date, homologues of five autophagy-related (ATG) genes, *ATG3*, *ATG4*, *ATG6*, *ATG8*, and *ATG12* have been identified from the three-host tick *Haemaphysalis longicornis*. Real-time PCR results revealed that mRNA levels of each *H. longicornis* ATG (*HIATG*) gene were highest in the egg compared to other developmental stages. *HIATG* genes were found to be expressed at the highest level in developing eggs at 0-3 days after oviposition. In the other stages from nymph to adult, the expression level of each *HIATG* gene was down-regulated during blood feeding but was up-regulated after engorgement. The expression of *HIATGs* in salivary glands, midgut, ovary and fat body of unfed and fed adult ticks was also analyzed by real-time PCR. The starved condition appeared to be associated with the increased expression of *HIATG* genes in the midgut, a nutrient storage organ, of unfed tick; however, mRNA expression patterns of *HIATG* genes varied in other organs. These results suggest that the increased expression of *HIATG* genes is not always induced by starvation in all organs of the tick. Taken together, these data indicate the probability at the transcriptional level that *HIATG* genes are involved in starvation, embryonic development, and metamorphosis.

Acknowledgements: This work was supported by the Bio-oriented Technology Research Advancement Institution (BRAIN), a Grant-in-Aid for Scientific Research (A), and a Grant-in-Aid for Research Activity Start-up of the Japan Society for the Promotion of Science (JSPS). R. Umemiya-Shirafuji was supported by a Grant-in-Aid for JSPS Fellows.



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Session Details:	8/27/2013 Ticked Off! 1140 - 1240 Meeting Room 7
Poster with 2 minute Oral Presentation Details:	Spreading of ticks (Ixodida) and tick-borne pathogens in urban areas of Košice city, eastern Slovakia
Authors:	Bronislava Víchová ¹ *, Lucia Pangráčová ¹ , Božena Haklová ¹ , Michal Stanko ^{1,2} , Martin Bona ¹ , Ladislav Mošanský ¹ , Branislav Peťko ¹ ¹ Institute of Parasitology, Slovak Academy of Sciences, Košice, Slovakia ² Institute of Zoology, Slovak Academy of Sciences, Košice, Slovakia
Poster Number:	255

In the past decades, a new phenomenon has been observed, ticks spreading into urban areas. Along with this fact, also the risk of infection caused by tick-borne pathogens has risen in central and pericentral parts of the cities. The aim of this study was to monitor tick distribution and the spectrum of tick species and pathogens that occur in the agglomeration of Košice city in eastern Slovakia. During 2011–2012, over 1500 questing ticks were collected in 12 study areas within Košice. The vast majority of the collected ticks were *Ixodes ricinus*, epidemiologically the most important tick species in central Europe. By using molecular, PCR-based methods, we confirmed the presence of bacterial and protozoan pathogens as well. The prevalence of spirochaetes of the *Borrelia burgdorferi* sensu lato complex ranged from 4.6 - 44.73%, with *B. garinii* (14.28 - 44.44%) and *B. afzelii* (9.99 – 25.0%) as the predominant genospecies at all studied areas. Moreover, the presence of co-infections with two genospecies was confirmed (*B. garinii* + *B. valaisiana* or *B. afzelii* + *B. valaisiana*). *Anaplasma phagocytophilum* was detected with an average prevalence of 2.97%. Ticks were tested also for the presence of *Babesia* spp. using *B. microti*-specific PCR primers. The prevalence of infection was 2.68%. To date, several samples were analyzed by sequencing. Preliminary results show the circulation of *Babesia venatorum* (previously „EU1 strain“) and *B. microti* “Jena“ strain with strong zoonotic potential (Beck et al., 2011). The presence of infected *I. ricinus* ticks was confirmed at all sampling sites within Košice city (in central parks, on the residual forest vegetation between central and peripheral parts of the city, along the access roads in gardening settlements, between the gardens, and even in the gardens).

Acknowledgements:

This study has been realized thanks to the financial support of the Research & Development Operational Programme funded by the ERDF: Environmental protection against parasitozoonoses under the influence of global climate and social changes (code ITMS: 26220220116)

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Session Details:	8/27/2013 Ticked Off! 1140 - 1240 Meeting Room 7
Poster with 2 minute Oral Presentation Details:	Molecular and transcriptional analysis of <i>Rhipicephalus microplus</i> serpins
Authors:	Tao Xu ^{1*} , Manuel Rodriguez-Valle ¹ , Ala Lew-Tabor ^{1, 2} ¹ The University of Queensland, St. Lucia, Qld, Australia ² Murdoch University, Centre for Comparative Genomics, Perth, Western Australia, Australia
Poster Number:	243

Serine protease inhibitor (Serpins) is the largest protease inhibitor family (I4) with the diversely functions to modulate some essential proteolytic cascades. Fourteen serpin sequences were identified from the current available *Rhipicephalus microplus* sequence databases using a homology strategy. They are named from RMS-1 to RMS-14 (an acronym for *Rhipicephalus Microplus Serpins*). Rapid Amplification of cDNA Ends (RACE) was used to attain the full-length cDNA of RMS-4. The molecular analysis showed these RMSs shares a 30% similarity on the deduced amino acids sequences with 75 highly conserved amino acids. Seven of them have completed coding sequences. The expression pattern of the seven full-length RMSs was determined by PCR using different tissues/samples. These seven selected RMSs were ubiquitously expressed in eggs, nymphs, female salivary glands, ovaries and female guts. The Inhibitory activity of RMSs was predicted on the basis of the inhibitory amino acid motif located at the hinge region of their reactive centre loops (RCLs). All RMSs are putative inhibitory serpins, except for RMS-1 and RMS-5. Eight different residues on the P1 site of RCLs indicate the diverse targets of proteases. Additionally, RMS-3, RMS-4 and RMS-8 were predicted as potentially secreted serpins, which are most likely to be involved during the tick-host interaction. This study provides an initial step to understand the physiology roles of *R. microplus* serpins.

Acknowledgements

This research has been supported by the Beef CRC and Meat & Livestock Australia.



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Session Details:	8/27/2013 Who and How Many? 1140 - 1240 Meeting Room 8
Poster with 2 minute Oral Presentation Details:	Gastrointestinal and hepatic parasites affecting Alpacas (<i>Lama pacos</i>) and vicuñas (<i>Vicugna vicugna</i>) in Cajamarca, Perú
Authors:	María Cabrera ^{1*} ; Andrea Llanos ² ; Alonso Manrique ¹ , Pedro Ortiz ¹ ¹ Laboratorio de Inmunología e Investigaciones Veterinarias, Facultad de Ciencias Veterinarias, Universidad Nacional de Cajamarca, PERÚ ² Servicio Nacional de Sanidad Agraria, SENASA Cajamarca, PERÚ
Poster Number:	34

South American Camelids (SAC) are an important livestock resource to the rural population of Peru. Gastrointestinal parasites and liver fluke are among the most prevalent parasites affecting the productivity of these species. The present study describes the occurrence of gastrointestinal helminthes, coccidian and *Fasciola hepatica* in Peruvian domestic alpacas and wild vicuñas from the northern region of Cajamarca, Peru. Sample feces from two hundred and forty alpacas and one hundred and fifty vicuñas were examined by standard coprological techniques. The mean prevalence for *F. hepatica* was 38% in vicuñas and 30.66% in alpacas. The prevalence rates of gastrointestinal parasites in vicuñas were a total of 88%, the species of nematodes and cestodes identified by genera were: *Trichostrongylus spp* 68% (*Trichostrongylus axei*, *Ostertagia ostertagi*, *Bunostomum trigonocephalum* , *Cooperia oncophora*, *Cooperia sp*); *Lamanema chavez* 8%; *Nematodirus sp* 14% (*Nematodirus lamae*, *Nematodirus spathiger*); *Moniezia expansa* 8%, *Trichuris sp* 30%; *Capillaria sp* 12% and *Strongyloides papillosus* 4%. The prevalence rates of gastrointestinal nematodes in alpacas were a total of 88.66% infected animals: *Trichostrongylus spp* 88.66% (*Trichostrongylus axei*, *Haemonchus contortus*, *Ostertagia ostertagi*, *Ostertagia sp*, *Spiculopteragia peruvianus*, *Bunostomum trigonocephalum*, *Oesophagostomum sp*, *Cooperia oncophora*, *Chavertia ovina*), *Lamanema chavez* 8% *Nematodirus sp* 17.33% (*Nematodirus lamae*, *Nematodirus spathiger*), *Moniezia expansa* 12.6%, *Trichuris ovis* 10.6%; *Capillaria sp* 6%. The survey showed a higher mean excretion of *Trichostrongyle* eggs in vicuñas than in alpacas (840 EPG vs. 360 EPG, (p<0.001). Third stage larvae of *Trichostrongylus*, *Nematodirus*, *Cooperia* and *Bunostomum* were the most prevalent in the coprocultures from vicuñas, whereas larvae of *Trichostrongylus*, *Haemonchus*, *Oesophagostomum*, *Chavertia* and *Nematodirus* type dominated in alpacas. *Eimeria* oocytes were present in 38.66% of alpacas (120 EPG) and in 15% of vicuñas. Both species were negative to Paramphistomids. We conclude that both alpacas and vicuñas in Cajamarca have a high prevalence of gastrointestinal and liver parasites.

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Session Details:	8/27/2013 Who and How Many? 1140 - 1240 Meeting Room 8
Poster with 2 minute Oral Presentation Details:	The parasitic phase of <i>Ostertagia ostertagi</i> : quantification of the main life history traits using systematic review and meta-analysis.
Authors:	Sien Verschave ¹ , Jozef Vercruysse ¹ , Edwin Claerebout ¹ , Eric Morgan ² , Jan van Dijk ³ , Johannes Charlier ¹ . ¹ Ghent University, Merelbeke, BELGIUM ² University of Bristol, Bristol, UNITED KINGDOM ³ University of Liverpool, Liverpool, UNITED KINGDOM
Poster Number:	159

Model predictions of parasite life cycles can contribute to more targeted control and to a better understanding of the influences of climate and management changes on parasite epidemiology. The aim of this study was therefore to quantify the main life history traits of *Ostertagia ostertagi* and to assess factors affecting them. The three main parameters that determine parasite density during the parasitic phase of *O. ostertagi* are the larval establishment rate, adult worm fecundity and adult mortality rate. Since former mathematical models used estimates based on single experiments, models will benefit from more accurate estimates of these traits and their variation. Therefore, a systematic review was performed covering studies from 1962 to 2010, in which helminth-naïve calves were artificially infected with *O. ostertagi*. This obtained dataset was extended with unpublished results. Using random effect models, overall inverse variance weighted estimates were computed for each of the traits. A total of 27 studies (47 experiments) were used to compute the overall establishment rate (mean±SE), which was 25.7 ± 2.2%. A significant effect (*P* <0.005) of infection dose and host age on the establishment rate was found. This is in contrast with former studies that assumed establishment was independent of intensity of infection. The overall fecundity was calculated based on 9 studies (10 experiments) and was 2.3 ± 0.5 eggs/100 gram feces per female. Taking the fecal production into account, this corresponds to 345 eggs per day/female. This latter value is comparable to the previously described average daily fecundity of 316 eggs/female. Preliminary analysis resulted in a daily mortality rate of 0.3%. To our knowledge, this is the first study to summarize the available data for the main life history traits of *O. ostertagi* through systematic review and meta-analysis. It provides novel insights for the parameterization of life cycle based transmission models.

Acknowledgements:

This study received funding from FP7 GLOWORM project – Grant agreement N° 288975CP-TP-KBBE.2011.1.3-04.



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Session Details:	8/27/2013 Who and How Many? 1140 - 1240 Meeting Room 8
Poster with 2 minute Oral Presentation Details:	Nematode parasites from the abomasa of adult dairy cows in France: an abattoir survey
Authors:	Christophe Chartier ^{1*} , Alexandre Le Corre ¹ , Nadine Ravinet ^{1,2} , Alain Chauvin ¹ ¹ LUNAM Université, Oniris, Nantes-Atlantic College of Veterinary Medicine and Food sciences and Engineering, UMR BioEpAR, Nantes, France ² IDELE, French Livestock Institute, Nantes, France
Poster Number:	15

During the last decades, the impact of gastrointestinal nematodes in adult dairy cows has been scrutinized through the study of the individual or herd milk response following an anthelmintic treatment. Additional data from abattoir surveys were available for some northern Europe countries but are still missing for France. The objective of our study was thus to examine abomasa from culled adult dairy cows at slaughterhouse to determine prevalences and worm burdens for gastric nematodes and to evaluate indicators as faecal egg count (FEC expressed as egg per gram-epg-), pepsinogen concentration and serum *Ostertagia* ELISA ODR according to routine laboratory methods. Between December 2011 and January 2012, 93 abomasa, as well as faecal and blood samples, were randomly collected in a slaughterhouse located in western France. *Ostertagia ostertagi* and *Trichostrongylus axei* were the two species identified. The prevalences were 84±3.8% for abomasal nematode infection, 77.4±4.4% for *O. ostertagi*, 51.6±5.2% for *T. axei* and 45.2±5.2% for mixed infections. Worm count arithmetic means were 2813±10837 for total (range: 20-100837), 1680±4184 for immatures, 1047±2797 for *O. ostertagi* and 3000±14527 for *T. axei*. Seven (7.5%) or two (2.1%) cows had worm burdens respectively >5000 or >10000. FEC was ≥0.2 epg and >1 epg for 38% and 8.7% of cows respectively. FEC was significantly correlated with worm counts (r=0.36, p<0.01) and worm counts were significantly different when comparing animals with FEC<0.2 or >0.2 epg (769±1684 vs 2135±4855, p<0.01). Average pepsinogen concentration and *Ostertagia* ELISA ODR were 1708±554 mUTYR and 0.73±0.31 respectively. Neither pepsinogen nor ELISA ODR were correlated to worm counts but they were correlated to each other (r=0.30, p<0.01). These results indicated an over dispersed distribution of worms, a rather low worm burden and a possible interest of FEC for detecting highest infected cows and are updated data for gastric nematodes in adult dairy cows in western France.

Acknowledgements:

The authors thank Charal SAS (Cholet, France) for allowing us to work at the abattoir, Françoise Leray, Emmanuelle Blandin, Marie-Astrid Malard and Nadine Brisseau (ONIRIS) for technical assistance and the CASDAR project N°1127 (Ministère de l'Agriculture, de l'Agroalimentaire et de la Forêt) for financial support. This study was performed in the UMT "Cattle Herd Health Management" framework.



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Session Details:	8/27/2013 Who and How Many? 1140 - 1240 Meeting Room 8
Poster with 2 minute Oral Presentation Details:	Confidence Intervals for a Mean Faecal Worm Egg Count
Authors:	Andrew van Burgel ^{1*} ¹ Department of Agriculture and Food, 444 Albany Highway, Albany, WA, 6330, AUSTRALIA
Poster Number:	46

A simple formula is proposed for estimating confidence intervals for the mean faecal worm egg count based on individual faecal worm egg counts from a subsample of a mob of sheep.

Worms are a major cost to sheep producers world wide and faecal worm egg counts are thus an important tool for producers and researchers. The distribution of worm eggs in a mob is typically heavily skewed and faecal worm egg counts are often modelled with the negative binomial distribution. In practice the mean faecal worm egg count of a mob of sheep is obtained by laboratory analysis of samples from as few as ten sheep.

The proposed formula is easy to calculate as it is based on the sample mean and standard deviation and there is no need for lookup tables or transformations. It also does not produce illogical negative values. Simulations based on a range of large datasets of faecal worm egg counts was done to evaluate the proposed formula. The results indicate the formula performs reasonably well, for example 90% confidence intervals cover the true mean about 90% of the time. The formula proposed is implemented in a user friendly spreadsheet and also adapted to give confidence intervals for faecal worm egg counts calculated on a bulk sample.

This approach has potential for broader application wherever data displays a similar overdispersed distribution.



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Session Details:	8/27/2013 Who and How Many? 1140 - 1240 Meeting Room 8
Poster with 2 minute Oral Presentation Details:	Control measurements against parasitic infections in horses
Authors:	Inger Sofie Hamnes ^{1,*} , Cecilie Mejdell ¹ , Ann Margaret Grønndal ¹ , Carl Fredrik Ihler ² ¹ Norwegian Veterinary Institute, P.O. Box 750 Sentrum, N-0106 Oslo, Norway ² Norwegian School of Veterinary Science, Department of Companion Animal Sciences, P.O. Box 8146 Dep, N-0033 Oslo, Norway
Poster Number:	

A total of 191 large horse establishments (6-97 horses) and 65 small horse establishments (1-3 horses) were enrolled in a study aiming to investigate control measurements against parasitic infections in horses I Norway. A variety of establishments participated.

Main body of participating stables were from Eastern Norway, but the rest of the country was also represented. No of horses varied from 1-97.

Among large establishments 87, 5% use summer pastures compared to 98% off the small establishments. One quarter of the establishments graze horses with other livestock species (cattle, sheep and goats).

All large establishments used anthelmintic treatments whereas 15 % of small establishments did not use anthelmintic treatments on their horses.

All establishments considered parasitic treatment as important but the use of faecal egg counts (FEC) were low, less than 25 % had ever performed FEC on samples from their horses.

Large establishments treated their hoses more frequently than the small establishments did. More than 85% of large establishments treated 3 or more times a year whilst 31 % of the small establishments did the same. There were a marked difference in who was the most important source of information about control measurements between large and small establishments; 74, 1 % of large establishment considered the veterinarian as their most important source of information compared only 3, 1% of the small establishments.

Results show that is a substantial need for information many aspects of control strategies against parasitic infection in horses; use of non-medical measurements, pasture management and pasture rotation as well as the use for the right medical compound at the right time as anthelmintic resistance against both fenbendazole and pyrantel had been demonstrated in horses in Norway.

Acknowledgements:

The project has been founded by the Norwegian Research Council with funding from Norsk Rikstoto, Jordbruksavtalen and Stiftelsen Svensk Hästforskning.



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Session Details:	8/27/2013 Who and How Many? 1140 - 1240 Meeting Room 8
Poster with 2 minute Oral Presentation Details:	The diagnostic characteristics of a qPCR test for <i>Haemonchus</i> , <i>Trichostrongylus</i> and <i>Teladorsagia</i> .
Authors:	Jody McNally ¹ , Brendon O'Rourke ² , Naomi Porter ² , Peter Hunt ^{1*} ¹ Commonwealth (of Australia) Scientific and Industrial Research Organisation (CSIRO) Armidale, NSW, AUSTRALIA. ² New South Wales Department of Primary Industries, Menangle, NSW, AUSTRALIA.
Poster Number:	89

There has recently been considerable effort directed towards the development of DNA-based methodologies to increase the flexibility and precision of parasite management in livestock agriculture (Hunt, 2011). We have developed a qPCR assay to detect three genera of nematodes which infect sheep, using samples of faeces directly, rather than purified eggs (e.g. Bott et al., 2009). Our procedure uses DNA extracted from whole faeces, and ethanol is used as a preservative to prevent the embryonic development of nematode eggs post-sampling. In preparation for the widespread use of our tests, we have been establishing their diagnostic characteristics. Our poster will include data showing the specificity and sensitivity of the tests used either separately to detect eggs from each genus, or together to provide an estimate of the faecal worm egg count (FWEC). The quantitative relationship between FWEC derived from microscopy and that derived from qPCR is high (R-square values >0.95) when using standard faecal samples. We also show the relationship between FWEC derived from microscopy and that derived from qPCR using field samples. In addition, we will report on the relationship between species composition determined by faecal culture followed by larval differentiation compared to that determined by qPCR. Data demonstrating the repeatability and reproducibility of the qPCR tests will be discussed. Some experiments aimed at determining if the qPCR tests can detect non-egg nematode DNA will also be presented. These tests are now ready for diagnostic service providers to try, and we will provide methodological details to assist them on request.

Acknowledgements:

Meat and Livestock Australia have co-funded this work. We are grateful for valuable advice from many, including Peter Kirkland, Nathan Bott, David Callan, Una Ryan, Robin Gasser, Felice Driver and Johann Schroder.

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Session Details:	8/27/2013 Who and How Many? 1140 - 1240 Meeting Room 8
Poster with 2 minute Oral Presentation Details:	Serum antibody responses in pigs trickle infected with <i>Ascaris</i> and <i>Trichuris</i> : Heritabilities and associations with parasitological findings
Authors:	*Helene Kringel ^a , Peter Nejsum ^{a,b} , Heidi Huus Pedersen ^a , Harald Göring ^c , Tim Anderson ^c , Allan Roepstorff ^a , Stig Milan Thamsborg ^a a) Parasitology and Fish Diseases, Department of Veterinary Disease Biology, University of Copenhagen, Thorvaldsensvej 57, bldg. 1-34, DK-1871 Frederiksberg, Denmark b) Genetics and Bioinformatics, Department of Basic Animal and Veterinary Sciences, University of Copenhagen, Grønnegårdsvej 3, DK-1870 Frederiksberg, Denmark c) Texas Biomedical Research Institute, 7620 N. W. Loop 410, San Antonio, TX, USA
Poster Number:	224

The extent to which genetic factors regulate acquired immunity to helminth infections in pigs is not known. On this background we set out to estimate the heritability component of variation in measurable immune parameters in 195 pigs trickle infected with *Trichuris suis* and *Ascaris suum*. Most pigs remained positive for *A. suum* throughout the experiment while most pigs expelled *T. suis* between 7 and 14 weeks post start of infection (p.i.). Parasite specific serum antibodies of 3 different isotypes (IgG1, IgG2 and IgA) were measured in serum samples collected at 0, 7 and 14 weeks p.i.. Parasite specific IgG1 and IgA increased at 7 and 14 weeks p.i. whereas parasite specific IgG2 levels only changed slightly at 14 weeks p.i.. Only weak association between specific antibody isotype levels and worm load was found. The relative heritabilities of the different parasite specific isotypes were assessed and significant heritability estimates for parasite specific IgG1 and IgA at 7 and 14 weeks p.i. were found. The highest heritabilities were found for *A. suum* specific IgG1 (0.41 and 0.46). Thus, to some extend genetic factors regulate the IgG1 and IgA antibody isotype responses specific to two of the most common gastro intestinal nematode parasites of swine.



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Session Details:	8/27/2013 Who and How Many? 1140 - 1240 <i>Meeting Room 8</i>
Poster with 2 minute Oral Presentation Details:	Gastrointestinal parasites in pigs and humans of two technified farms from Cundinamarca-Colombia
Authors:	Adriana Pulido-Villamarín ^{1*} , Ma Fernanda Mendoza-Gómez ¹ , Angélica Barbosa-Buitrago ² ¹ Unidad de Investigaciones Agropecuarias (UNIDIA), Departament of Microbiology, Faculty of Sciences, Pontificia Universidad Javeriana, Bogotá, COLOMBIA ² Group Enfermedades crónicas y zoonóticas adquiridas ECZA – UniColmayor and Faculty of Agricultural Sciences and Natural Resources, Universidad de los Llanos, Villavicencio, COLOMBIA
Poster Number:	222

In Colombia, the technified swine production is distributed in 22 of the 32 departments of Colombia, one of them is Cundinamarca where the 2.6% of national production is located (22371 pigs). Worldwide, the gastrointestinal parasites affect both pigs and public health, by diminishing the husbandry levels of production and by the parasite transmission to the humans. The aim of this work was to determine the presence of gastrointestinal parasites in the swine and human population of two technified farms (> 200 sows) from Cundinamarca. A cross-sectional cohort study was undergone, with three serial samples of 15 days of intervals and a total of 92 samples coming from different groups were analyzed so: Sows (19), replacement sows (2), boars (2), piglets (20), pre-fattening (24) and fattening (25). The humans attended informed-consent about the study, 18 samples were collected (12 men, 4 women, 2 children). Stool samples grouped per pen and individual were evaluated by direct analysis, qualitative flotation technique, qualitative sedimentation technique and staining with modified Ziehl-Neelsen. The results obtained in the total population swine were averaged: *Balantidium coli* cysts (35,8%), *Ascaris suum* eggs (13,0%), *Endolimax nana* cysts (13,0%), *Iodamoeba bütschlii* cysts (7,6%), larvae of *Strongyloides* spp (3,26%) and *Trichuris suis* eggs (2,17%). In humans was detected, *Entamoeba coli* cysts (33,0%), *Endolimax nana* cyst (16,6%) and *Balantidium coli* cysts (5,5%). The presence of parasites as *Balantidium coli* and *Endolimax nana* in pigs and humans suggests possible rotation of parasite populations between pigs and humans, increasing the transmission of parasites with zoonotic potential between the two species.

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Session Details:	8/27/2013 Who and How Many? 1140 - 1240 Meeting Room 8
Poster with 2 minute Oral Presentation Details:	Development of a Loop-mediated Isothermal Amplification (LAMP) assay for the sensitive detection of <i>Haemonchus contortus</i> eggs in ovine faecal samples
Authors:	Lynsey Melville ^{1*} , Fiona Kenyon ¹ , Iain McElarney ² , Janina Demeler ³ & Philip Skuce ¹ ¹ Moredun Research Institute, UNITED KINGDOM ² Mast Group, Merseyside, UNITED KINGDOM ³ Freie Universität, Berlin, GERMANY
Poster Number:	88

A major constraint on the effective control and management of helminth parasites in livestock is the lack of rapid and reliable diagnostic tests to identify the parasite species responsible for disease and allow informed treatment decisions to be made. In the present study, we have developed a novel DNA-based assay for the detection of *Haemonchus contortus* using loop-mediated isothermal amplification (LAMP). LAMP allows for rapid detection of *H. contortus* in sheep faeces under isothermal incubation conditions. The robust nature of this assay negates the need for extensive DNA extraction, allowing amplification from crude samples of disrupted nematode eggs in solution. The LAMP assay uses an intercalating fluorescent detection dye which allows easy visualisation of results within one hour, without electrophoresis of amplification products, thus producing faster results with fewer steps than conventional PCR methods. Preliminary results suggest that LAMP can detect lower level infections compared to other PCR methods; less than five eggs per gram compared to 20 eggs per gram for PCR. Furthermore, LAMP showed no cross-reactivity with other helminth parasites which commonly co-infect sheep; this high sensitivity is due to the inclusion of six primers in the reaction mix. By including a fluorochrome dye, LAMP can be transferred to a real-time platform, allowing for semi-quantification of results. Early results indicate that in samples containing a high egg count, amplification was detectable after as little as 15 minutes. Semi-quantitative results obtained from 'real-time' LAMP allow rapid testing upon which informed treatment decisions could be made.

Acknowledgements:

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Session Details:	8/27/2013 Who and How Many? 1140 - 1240 Meeting Room 8
Poster with 2 minute Oral Presentation Details:	WORMTRAX – analysis of the Zoetis cattle worm egg count database from 2002-2012
Authors:	Lee Taylor^{1*}, Andrew Hodge² ¹Zoetis, 38-42 Wharf Rd, West Ryde, NSW 2114, AUSTRALIA ²Zoetis VMRD, 45 Poplar Road, Parkville VIC 3052, AUSTRALIA
Poster Number:	160

Zoetis has coordinated worm egg count testing of cattle from across Australia for 11 years. Results from samples submitted over this period have been analysed to provide contemporary data on worm egg count and worm species distribution in Australian cattle.

Ten faecal samples were collected from groups of cattle and worm egg counts and larval cultures were conducted using standard procedures.¹ Date of sampling, property address, age, average weight and production type of cattle sampled as well as last drench used were recorded. Regional analysis was done by postcode region and postcode regions were grouped into bioclimatic regions described in the MLA produced Cattle Parasite Atlas.²

A total of 5069 submissions were received to the end of 2012 representing over 50,000 individual dung samples. Eighty percent of cattle sampled were no more than 2 years of age with the remaining 20% representing a range of age groups . Samples were collected from all the cattle rearing regions of Australia. Worm species varied throughout Australia with *Cooperia* spp being most prevalent in all regions followed by *Haemonchus* spp and then *Oesophagostomum* spp in summer rainfall dominant regions and *Ostertagia* spp and *Trichostrongylus* spp in winter rainfall regions. Percent *Cooperia* spp cultured decreased as cattle aged but was still the main worm species cultured in cattle aged 4 years and older. Where previous drench use was reported, 89% were macrocyclic lactones alone or in combination with a flukicide or fluazuron.

There was a tendency for higher geometric mean worm egg counts in cattle in northern regions of Australia and in high rainfall areas along the east coast of Australia. Geometric mean worm egg counts for bioclimatic regions varied seasonally in line with rainfall patterns.

Acknowledgements:

The staff of Veterinary Health Research, Armidale, NSW are acknowledged for conducting WEC testing and collating necessary data from submission forms.

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Session Details:	8/27/2013 Who and How Many? 1140 - 1240 Meeting Room 8
Poster with 2 minute Oral Presentation Details:	Egg shedding of cyathostomins in horse farms from Italy
Authors:	Donato Traversa ^{*1} , Sarah Sconza ^{1,2} , Angela Di Cesare ¹ , Roberto Bartolini ¹ , Vincenzo Varasano ² , Raffaella Iorio ¹ , Barbara Paoletti ¹ ¹ University of Teramo, Department of Comparative Biomedical Sciences, Italy ² University of Teramo, Department of Veterinary Clinical Sciences, Italy
Poster Number:	129

Cyathostomins are the most important equine helminths, for their worldwide distribution, the spread of anthelmintic-resistant populations and the pathogenic impact they have at both adult and larval stages (Matthews, 2011). This study evaluated the extent of egg shedding in horse farms from Italy. Ten sites were selected based on a previous history of cyathostomiasis (Traversa et al., 2010). Individual faecal samples (n. 237) were collected (range of 8-43 sampled horses for each farm) and subjected to quali-quantitative copromicroscopy. All farms and 109 animals (46%) were positive for cyathostomins. Five sites were also positive for roundworms, in single and mixed infections with cyathostomins. Eighty-five horses (78%) scored positive for cyathostomin faecal egg count (FEC) with a range of EPG values of 50-2050, while 24 (22%) were positive for up to 50 EPG. Of the animals with a FEC >50 EPG, 50 (45.9%) and 35 (32.1%) showed EPG values of 50-200 and >200, respectively. The results indicate that the horses investigated are not homogeneously divided in different FEC categories. Although cyathostomins are present in the study area and pastures and properties are indeed contaminated, horses with a FEC >200 EPG were not the majority of the study populations. Specifically, these results differ from those obtained in a previous study carried out in Italy (Traversa et al., 2010), given that the percentage of “high egg shedders” horses was lower than that of the “low egg shedders” and that of the negative animals. This knowledge is a crucial point for planning intervention programs to maintain horse health while preserving the efficacy of parasiticides, as the FEC values are considered a reliable indication for the need of treatments via the so-called “selective treatments” which, however, should be thoroughly evaluated on a case by case basis, especially with regard to horse age classes (von Samson-Himmelstjerna, 2012).

Acknowledgements:

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Session Details:	8/27/2013 Who and How Many? 1140 - 1240 <i>Meeting Room 8</i>
Poster with 2 minute Oral Presentation Details:	Effect of <i>Haemonchus contortus</i> ES products on immunomodulation in a human monocyte-derived dendritic cells (mdDC) model
Authors:	Zia-ur-Rehman ^{1*} , J.M. Roberts ² , J.S. Knight ² , H.V. Simpson ¹ and A. Pernthaner ² ¹ Institute of Veterinary, Animal and Biomedical Sciences, Massey University, Private Bag 11-222, Palmerston North, New Zealand ² Hopkirk Research Institute, AgResearch Ltd., Private Bag11-008, Palmerston North, New Zealand
Poster Number:	190

Helminths are powerful immunoregulators able to skew host immune responses to achieve long term survival in a hostile environment. Many immunomodulators, including some which act directly on host antigen presenting cells, are found in excretory secretory (ES) products of different life cycle stages of helminths. Unveiling the interaction between antigen presenting cells and helminth immunomodulators could result in developing alternative parasite control strategies.

This experiment was designed to investigate whether the functions of human monocyte-derived dendritic cells (mdDCs) can be modulated by ES products from adult *Haemonchus contortus*, a highly pathogenic gastrointestinal nematode of small ruminants worldwide. Functional properties of human mdDCs stimulated with *H. contortus* adult ES products were assessed by multi colour flow cytometry. Changes in the expressions of CD14, CD11c, CD305, CD32, galectin, CD80, CD86, MHCII and CD40 were monitored. Secretion of a panel of cytokines and chemokines was also assessed. Three independent sets of experiments, each using cells from four healthy donors, revealed the ability of ES products to upregulate CD32 (Fcγ receptor II) and, to a lesser extent, CD86 and CD40 expressions. Interestingly, ES products were not able to induce classical maturation of mdDCs and the expressions of MHCII, CD80 and galectin essentially remained unchanged. Although the roles of the CD32 isoforms are not clearly understood, these results suggest that *H. contortus* adult ES products are potentially capable of inducing immune tolerance.

Acknowledgements:

Meat & Wool NZ and AgResearch Ltd are thanked for financially support. We are grateful to Mrs L. Shaw for collection of blood.



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Session Details:	8/27/2013 Who and How Many? 1140 - 1240 Meeting Room 8
Poster with 2 minute Oral Presentation Details:	Gastrointestinal helminths and protozoa in migratory camels in Multan, Pakistan
Authors:	Abdul Basit ¹ , Muhammad Mazhar Ayaz ¹ , Asif Raza ² , Hafiz Muhammad Arshad ¹ , Naveeda Chaudhary ³ , Ashar Raza ¹ and Zia-ur-Rehman ^{4*} ¹ Faculty of Veterinary Sciences, Bahauddin Zakariya University, Multan, Pakistan. ² Animal Husbandry in Tropics and Subtropics, University of Kassel, Germany. ³ Department of Physiology and Pharmacology, University of Agriculture, Faisalabad, Pakistan. ⁴ Institute of Veterinary, Animal and Biomedical sciences, Massey University, Palmerston North, New Zealand.
Poster Number:	244

Current experiment was designed to explore gastrointestinal helminth and protozoa population in migratory camels (*Camelus dromedarius*). A total number of 50 samples (20 males and 30 females) were collected from camels migrated from Tehsil Jalapur Pir Wala to Multan, during early summer (April and May) from various places in and around Multan. The revealed parasites were mixed helminthic and protozoal infection. Identified parasites include *strongylidae* spp, *trichostrongyle* spp, *coccidian/ eimeria* spp and *isospora* spp.

Keywords: Migratory camels, *strongylidae*, *trichostrongyle*, *coccidian/eimeria* and *isospora*.



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Session Details:	8/29/2013 All about Crypto 1130 - 1240 Riverside Theatre
Poster with 2 minute Oral Presentation Details:	Detection of <i>Cryptosporidium</i> oocysts in fresh calf faeces: characteristics of two simple tests and evaluation for a semi-quantitative approach
Authors:	Christophe Chartier ^{1*} , Anaïs Rieux ² , Arnaud Delafosse ³ , Anne Lehebel ¹ , Carine Paraud ² ¹ LUNAM Université, Oniris, Nantes-Atlantic College of Veterinary Medicine and Food sciences and Engineering, UMR BioEpAR, Nantes, France ² French Agency for Food, Environmental and Occupational Health and Safety, Niort laboratory, France ³ Groupement de Défense Sanitaire de l'Orne, Alençon, France
Poster Number:	90

The objective of the present study was to evaluate the characteristics of two rapid tests, a faecal smear staining (Heine technique) and an commercially available immunochromatographic (IC) assay (BIO K 155©, BioX Diagnostics, Rochefort, Belgium), against a direct immunofluorescent antibody test (IFAT) for the diagnosis of *Cryptosporidium* infections in 917 faecal samples of < 3 weeks calves. These rapid tests were performed on non concentrated faeces in a semi-quantitative approach using a 6 scores scale (0 to 5) for Heine staining according to the number of oocysts per microscopic field, and a 4 scores scale (0 to 3) for IC assay according to the intensity of the positive line compared to the control line. Direct IFAT (Merifluor® *Cryptosporidium/Giardia*, Meridian Bioscience Europe, Nice, France) was performed following a diethyl ether concentration and results were expressed as oocyst per gram of faeces (opg). Heine staining showed a sensitivity of 76.7% and a specificity of 90.7%. For faecal samples exhibiting ≥10,000 opg, sensitivity increased to 90.0%. The sensitivity of IC assay was lower, 61.8%, and the specificity was 100%. For faeces ≥100,000 opg, the sensitivity of IC reached 81%. Additional scoring (1 to 5) of Heine staining did correlate with corresponding direct IFAT results, particularly for oocyst ranges of 1,000 to >1,000,000 opg. As for Heine staining, additional scoring from 1 to 3 according to the thickness of the sample line for the IC test, correlated with increasing levels of *Cryptosporidium* opg measured by IFAT in the range of 10,000 to >1,000,000 opg. Both Heine staining and IC test showed acceptable levels of sensitivity for clinical cryptosporidiosis diagnosis and can be reliably used through a simple semi-quantitative scale for grossly quantifying oocyst output in calf faecal samples.

Acknowledgements:

The authors acknowledge Isabelle Pors, Françoise Leray and Emmanuelle Blandin for technical assistance. The authors also thank Bio-X Diagnostics SRPL Company (Rochefort, Belgique) for providing Immunochromatographic kits (BIO K 155). Anaïs Rieux was a grateful recipient of a grant from Anses/Région Poitou-Charentes. This study was performed in the UMT “Cattle Herd Health Management” framework.



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Session Details:	8/29/2013 All about Crypto 1130 - 1240 Riverside Theatre
Poster with 2 minute Oral Presentation Details:	Molecular characterization of <i>Cryptosporidium</i> isolates from <1 month-old beef calves during three successive years in one herd in Western France
Authors:	Anaïs Rieux ¹ , Christophe Chartier ^{2*} , Isabelle Pors ¹ , Carine Paraud ¹ ¹ French Agency for Food, Environmental and Occupational Health and Safety, Niort laboratory, France ² LUNAM Université, Oniris, Nantes-Atlantic College of Veterinary Medicine and Food sciences and Engineering, UMR BioEpAR, Nantes, France
Poster Number:	161

Cryptosporidium parasites are considered as a major cause of neonatal diarrhea in calves. *Cryptosporidium parvum* has been frequently recorded as the dominant species in diarrheic calves but several studies realized in dairy calves, have shown a sequence of *Cryptosporidium* species according to the age of calves. In the present study, cohorts of calves have been studied for *Cryptosporidium* oocyst output during 3 successive years in one beef cattle herd in Western France. Each year, 20 to 30 calves were weekly sampled, from 1 to 4 weeks of age in order to characterize oocyst output, parasite species and clinical features associated with infection. Fecal samples were screened for the presence of oocysts after concentration using immunofluorescence analysis. DNA was extracted and PCR-RFLP was performed on the SSU rRNA gene of *Cryptosporidium*. Finally, for the genotyping of *C. parvum*, a gp60 PCR was realized. 92 to 100% of animals excreted oocysts, at least once. The highest prevalence was observed at different dates: 4th week of age, 3rd week of age and between the 1st and 2nd week of age, respectively for year 1, 2 and 3. In contrast, the peak of excretion was observed almost at the same time between the end of the 1st week and the 2nd week of age with excretion levels ranging between 100 to 1.7x10⁷ oocysts /g of feces. Significant differences concerning the clinical signs were observed depending on the years. Finally, different species profiles were observed with a predominance of *C. bovis* in year 1, a *C. bovis/C. parvum* balance in year 2 and a predominance of *C. parvum* in year 3. Moreover according to the year, two different zoonotic subtypes of *C. parvum* were observed with the subtype IIaA15G2R1 and IIaA18G2R1. This study shows that according to the year, in a given farm, *Cryptosporidium* species as well as prevalence and level of excretion may give different patterns.

Acknowledgements:

Anaïs Rieux was a grateful recipient of a grant from Anses/Région Poitou-Charentes (France).



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Session Details:	8/29/2013 All about Crypto 1130 - 1240 Riverside Theatre
Poster with 2 minute Oral Presentation Details:	Detection of <i>Cryptosporidium serpentis</i> in snakes fecal samples using real-time PCR and melting curve analysis
Authors:	Deuvânia Carvalho da Silva ^{1*} , Philipp Ricardo Scaciotte de Oliveira ² , Camila Guariz Homem ¹ , Alex Akira Nakamura ² , Milena Sato de Souza ¹ , Valéria Chamas Miúria*, Marcelo Vasconcelos Meireles ¹ ¹ Faculdade de Medicina Veterinária, Univ Estadual Paulista, UNESP, Campus de Araçatuba ² Faculdade de Medicina Veterinária e Zootecnia, Universidade de São Paulo, USP.
Poster Number:	91

Infection by *Cryptosporidium serpentis* is common in reptiles, particularly in snakes, and is characterized by chronic infection with severe hypertrophic gastritis, which can be lethal. This research aimed to screen snakes fecal samples for *C. serpentis* DNA using real-time polymerase chain reaction (PCR) and melting curve analysis, targeting the heat shock protein (HSP-70) gene, and nested PCR targeting the 18SrRNA gene¹, following sequencing of amplified fragments. A total of 503 samples from 23 snakes species were purified by ether extraction following the extraction of genomic DNA using the QIAamp DNA Stool Mini Kit. Nested PCR resulted in amplification of *Cryptosporidium* spp. DNA fragments in 60 samples (11.98%). Real-time PCR was positive for *C. serpentis* in 17 samples (3.37%). Sequencing of 18SrRNA amplicons from 38 samples allowed the identification of *Cryptosporidium tyzzeri* in *Bothrops jararaca* (5), *Crotalus durissus terrificus* (1) and *Crotalus durissus collilineatus* (1); *Cryptosporidium muris* in *B. jararaca* (4); *Cryptosporidium varanii* in *Bothrops matogrossensis* (1), *Eunectes notaeus* (1) and *Pantherophis guttata* (12), and *C. serpentis* in *Pantherophis guttata* (13), *Epicrates cenchria cenchria* (1) and *Boa constrictor constrictor* (1). The epidemiological sensitivity and specificity of real-time PCR were, respectively, 93.3% and 99.4%. Although three samples were positive for *C. serpentis* only by real-time PCR and were considered as false-positives in the estimate of epidemiological specificity and sensibility, melting curve analysis showed that these samples presented the same melting temperature as *C. serpentis* samples. Thus, we can conclude that the real-time PCR targeting the HSP70 gene is a sensitive and specific method for detecting *C. serpentis* in snakes fecal samples.

Acknowledgements: Fundação de Amparo à Pesquisa do Estado de São Paulo (FAPESP) for the following grant: financial support (2010/03945-8)

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Poster with 2 minute Oral Presentation Details:	The development of highly sensitive real time immuno- PCR assay for detection of Waterborne <i>Cryptosporidium parvum</i> oocysts
Authors:	MingJun Deng ^{1*} , XiZhi Xiao ¹ , Xincheng Ji ² , Tao sun ¹ , Zhengxin Wu ¹ , Laihu Zhu ¹ ¹ Shandong Entry-Exit Inspection and Quarantine Bureau, Qingdao,CHINA ² Xinjiang Entry-Exit Inspection and Quarantine Bureau, Urumqi, CHINA
Poster Number:	16

With an aim at detecting the low concentration of *Cryptosporidium parvum* oocysts in environmental water samples , A highly sensitive hybrid assay, based on Immunology and polymerase chain reaction(IPCR) which combining enzyme immunoassay with DNA amplification, was developed. The TopYield microtiter plates were coated with *Cryptosporidium parvum* monoclonal antibody, and *Cryptosporidium parvum* oocysts were diluted in distilled water to 1 x 10³, 5 x 10² , 2 x 10², 1 x 10²,5 x 10¹ , 2 x 10¹, 1 x 10¹, 5 x 10⁰ oocysts per 200 µl,which was recognized by *Cryptosporidium parvum* polyclonal antibody that was directly linked with reporter DNA using a heterobifunctional cross-linker(SMCC). After extensive washing, the reporter DNA including a *Bam*H I- restriction site was released by a specific enzymatic restriction , then transferred to PCR tubes, amplified, and used as the signal for detection of *Cryptosporidium parvum* oocysts. In order to increase sensitivity and reduce background noise or nonspecific signals,the number of washing was optimized. Under the optimized condition ,real time immuno-PCR(real-time IPCR) method could detect 5 *Cryptosporidium parvum* oocysts per 200 µl of water samples.To further evaluate the specificity of this immuno-PCR (IPCR) assay for *Cryptosporidium parvum*, the *Entamoeba histolytica* eggs and *Giardia lamblia* cysts were collected and detected by IPCR. In order to demonstrate the detection sensitivity of IPCR for *Cryptosporidium parvum*,we also compared the sensitivity of IPCR with that of real time PCR performed by other researchers.Our data demonstrated that this monoclonal antibody-based immuno-PCR method is very sensitive and specific for the diagnostic analysis of environmental water samples, and provides us a platform capable of rapid screening of water samples from drinking water, wells, rivers, lakes, and recreational swimming pools for trace levels of *Cryptosporidium parvum* oocysts.

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This study received financial support from public welfare project of china (grant NO. 201110039).We thank colleagues in animal diease laboratoried of Shandong entry-exit inspection and quarantine bureau for the dilution and Enumeration of the *Cryptosporidium parvum* oocysts, *Giardia lamblia* cysts and the collection, purification and dilution of the *Entamoeba histolytica* eggs.



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Session Details:	8/29/2013 All about Crypto 1130 - 1240 Riverside Theatre
Poster with 2 minute Oral Presentation Details:	Cryptosporidium in organic pig farms: seasonal and age related variation in oocyst excretion and species/genotypes
Authors:	Heidi H Petersen ¹ , Jianmin Wang ² , Kiran K Katakam ¹ , Helena Mejer ¹ , Marie Ståhl ³ , Anders Dalsgaard ¹ , Annette Olsen ¹ , Stig M Thamsborg ¹ , Heidi L Enemark ^{3*} ¹ Faculty of Health and Medical Sciences, University of Copenhagen, Frederiksberg, DENMARK ² Shenyang Agricultural University, Shen Yang, PEOPLE'S REPUBLIC OF CHINA ³ National Veterinary Institute, Technical University of Denmark, Frederiksberg, DENMARK
Poster Number:	223

Although pigs are commonly infected with *Cryptosporidium* spp., and potential sources of environmental contamination with zoonotic species, longitudinal studies of these infections in pig farms are non-existing. Thus, to characterize seasonal and age related molecular variation in oocyst excretion as well as prevalence and intensity of infections at the farm level, oocyst shedding was monitored at quarterly intervals during September 2011 to June 2012 in each of three organic, Danish pig farms. Faecal samples for examination of *Cryptosporidium* spp. were collected from 856 pigs, distributed on the three farms and four sampling times, and allocated into four age groups; piglets (N=152), weaners (N=234), finishers (N=230) and sows (N=240). Oocysts were quantified by immunofluorescence microscopy; and representative *Cryptosporidium* positive subsamples were characterized by amplification and sequencing of the SSU rRNA, the HSP70 and the GP60 genes. The overall prevalence of *Cryptosporidium* spp. was found to be 41%. The overall prevalence varied significantly (p<0.0001) between age groups with 45±6.4% piglets, 66±4.5% weaners, 37±5.9% finishers and 3±0.9% sows testing positive. No significant difference in the overall prevalence was found between farms or seasons. Intensity of infection was significantly (p>0.0001) age dependent with highest intensities in piglets and weaners. No significant differences in the intensity of infections were seen between the four sampling times. The preliminary molecular results revealed *C. scrofarum* and *C. suis* in 72.5% and 27.5% of the analysed samples respectively. Although both of these species have been linked to human cryptosporidiosis they are not among the most commonly detected *Cryptosporidium* species in humans. Our results showed that *Cryptosporidium* infections were highly prevalent throughout the year in the organic study farms. However, based on the preliminary data we conclude that environmental oocyst contamination from these farms does not constitute a high zoonotic risk.

Acknowledgement:

This research was funded by Green Development and Demonstration Programme (GDDP) and Technical University of Denmark. The laboratory technicians Lise-Lotte Christiansen and Boi-Tien Thi Pham are thanked for the many hours spent on this project.



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Session Details:	8/29/2013 All about Crypto 1130 - 1240 <i>Riverside Theatre</i>
Poster with 2 minute Oral Presentation Details:	Occurrence of <i>Cryptosporidium</i> spp. in fecal samples from dogs and cats in the state of São Paulo, Brazil
Authors:	Camila Guariz Homem ^{1*} , Milena Sato Souza ¹ , Alex Akira Nakamura ¹ , Deuvânia Carvalho da Silva ¹ , Marcelo Vasconcelos Meireles ¹ ¹ Univ Estadual Paulista, UNESP, Araçatuba, BRAZIL
Poster Number:	54

Infection with some *Cryptosporidium* species and genotypes represents a significant risk to public health, primarily because of morbidity and mortality in children from zero to five years old and in immunocompromised patients. Although there are reports of *Cryptosporidium* infection in dogs and cats, the role of these animals in the epidemiology of human cryptosporidiosis is uncertain, and the literature related to this topic is still quite limited. *Cryptosporidium canis* and *Cryptosporidium felis* infect humans beyond their natural hosts, dogs and cats respectively. The aim of this study was to determine the occurrence of *Cryptosporidium* spp. in dogs and cats fecal samples from the state of São Paulo, Brazil, by nested polymerase chain reaction. In the period of January-October 2012, 300 cat faecal samples and 366 dog faecal samples were collected at shelters, homes, and pet shops from the cities of Araçatuba and Jaboticabal, located in the state of São Paulo, Brazil. The samples were purified by the centrifugal sedimentation in water/ether technique, followed by the extraction of genomic DNA from the oocysts. Nested-PCR was performed to amplify fragments from the small subunit (18S) ribosomal RNA gene. It was observed that 11.33% (34/300) of cats samples were positive for *Cryptosporidium*, whereas the positivity in dogs was observed in 10.38% (38/366) of the samples. Sequencing analysis of selected positive samples allowed the identification of *Cryptosporidium canis* in six faecal samples from dogs and *Cryptosporidium felis* in three cat fecal samples.

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Session Details:	8/29/2013 All about Crypto 1130 - 1240 Riverside Theatre
Poster with 2 minute Oral Presentation Details:	Molecular characterization of <i>Cryptosporidium</i> spp. in exotic animals raised as pets in Brazil
Authors:	Milena Sato de Souza ¹ , Camila Guariz Homem ^{1*} , Bruno Ribas Vieira ¹ , Henrique Guimarães Riva ¹ , Deuvânia Carvalho da Silva ¹ , Marcelo Vasconcelos Meireles ¹ ¹ Univ Estadual Paulista, UNESP, Araçatuba, BRAZIL
Poster Number:	55

The infection with some species or genotypes of *Cryptosporidium* represents a significant risk to public health, mainly because of morbidity and mortality in children aged zero to five years old and in immunosuppressed patients. Although there are some reports of *Cryptosporidium* infection in exotic animals, the role of animals in the epidemiology of human cryptosporidiosis remains uncertain, and the literature on this topic is still rather scarce. The aim of this study was to determine the prevalence of *Cryptosporidium* spp. in fecal samples from exotic animals raised as pets in Brazil. A total of 200 samples from 4 exotic animal species was collected and stored in 5% potassium dichromate solution at 4°C. Oocysts were purified by ether extraction following extraction of genomic DNA. Molecular analyses were performed using nested-PCR and real time PCR for amplification of fragments of the 18S subunit of rRNA gene. Amplification of *Cryptosporidium* DNA fragments was obtained in 9.5% (19/200) samples. Sequencing of amplified fragments and phylogenetic analyses allowed the identification of *Cryptosporidium tyzzeri* (*Cryptosporidium* mouse genotype I) in mice (*Mus musculus*); *Cryptosporidium muris* in mouse, hamster (*Mesocricetus auratus* and *Phodopus* spp.), and chinchilla (*Chinchilla lanigera*); *Cryptosporidium parvum* in chinchilla (*Chinchilla lanigera*) and *Cryptosporidium* sp. in guinea pig (*Cavia porcellus*). All 22 samples of ferrets (*Mustela putorius*) were negative by nested PCR.

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Session Details:	8/29/2013 All about Crypto 1130 - 1240 Riverside Theatre
Poster with 2 minute Oral Presentation Details:	Molecular detection and characterization of <i>Cryptosporidium</i> species in private-household dogs and pet shop puppies in Japan
Authors:	Naoyuki Itoh ¹ *, Yoshino Oohashi ¹ , Madoka Ichikawa-Seki ² , Tadashi Itagaki ² , Yoichi Ito ¹ , Kazutaka Kanai ¹ , Seishiro Chikazawa ¹ , Yasutomo Hori ¹ , Fumio Hoshi ¹ , Seiichi Higuchi ¹ ¹ Kitasato University, Towada, JAPAN ² Iwate University, Morioka, JAPAN
Poster Number:	264

Members of *Cryptosporidium* species, which are protozoan parasites, are prevalent worldwide and can cause diarrhoea in both humans and animals, including dogs. In addition, *Cryptosporidium* species harboured in dogs have the potential for zoonotic transmission. The purpose of the present study was to determine the prevalence of *Cryptosporidium* species infection and perform the molecular characterization of isolates in private-household dogs and pet shop puppies in Japan. Fresh faecal samples were collected from 529 private-household dogs (from 9 veterinary clinics located in 6 different regions) and 471 pet shop puppies (≤ 3 months old, from 4 pet shops located in 2 different regions) on a single occasion. A nested polymerase chain reaction (PCR) assay targeting the 18S rRNA gene was employed for detection of *Cryptosporidium* species, and the random 61 samples of PCR amplicons (about 500 bp) were sequenced for the molecular characterization of isolates. The prevalences of *Cryptosporidium* species in private-household dogs and pet shop puppies were 7.2% and 31.6%, respectively. In private-household dogs, no significant correlation was observed between the prevalence of *Cryptosporidium* species and the age (≤ 6 months vs. >6 months), living conditions (indoor vs. outdoor), faecal conditions (formed vs. unformed), and location of residence. In pet shop puppies, the prevalence of *Cryptosporidium* species did not differ with faecal conditions, however, the prevalence significantly differed among the pet shops. All of the 61 sequencing samples (6 from private-household dogs and 55 from pet shop puppies) were identified as *C. canis*. The present study demonstrates a high prevalence of *Cryptosporidium* species infections in pet shop puppies in Japan. However, since *C. hominis* and *C. parvum* are the most common causes of human infections, it is likely that the risk of zoonotic transmission of *Cryptosporidium* species from dogs to humans is low.



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Session Details:	8/29/2013 All about Crypto 1130 - 1240 Riverside Theatre
Poster with 2 minute Oral Presentation Details:	Evaluation of putative anti-cryptosporidial drugs in an <i>in vitro</i> culture system
Authors:	Maja Schupfner ¹ , Gisela Greif ² , Matthias Lendner ³ , Arwid Dauschies ³ , Christoph Lippuner ⁴ , Georg von Samson-Himmelstjerna ¹ , Jürgen Krücken ¹ ¹ Freie Universität Berlin, Berlin, Germany ² Bayer Animal Health GmbH, Leverkusen, Germany ³ University Leipzig, Leipzig, Germany ⁴ University of Zürich, Zürich, Switzerland
Poster Number:	130

Cryptosporidium species are major pathogens severely affecting the health of neonate animals, in particular calves, but also cause life-threatening infection of immunocompromised humans. Currently, only halofuginone is approved for prophylactic and metaphylactic treatment of calves but this drug suffers from its limited safety margins. For treatment of immunodeficient human patients, only nitazoxanide and paromomycin are used but data regarding their efficacy are controversial. Aim of the present study was to test a substituted benzimidazole (BCS-AF76184) and a heterocyclic substituted 1,2,4-triazin (BCS-AB24992), both drugs with known anti-protozoal activity, for their potential ability to interfere with *Cryptosporidium parvum* development *in vitro*. Development of *C. parvum* in HCT-8 cells treated with these compounds was compared to negative controls and parasites treated with paromomycin or halofuginone using real-time PCR targeting the 18S rDNAs of parasites and host cells as template. Potential cytotoxic and anti-proliferative effects of drugs were analysed using a lactate dehydrogenase and a WST-1 assay, respectively. BCS-AF76184 and paromomycin dose-dependently inhibited development of *C. parvum* with EC₅₀ values of 2.37 µM and 69.5 µM, respectively. Although high concentrations of halofuginone and BCS-AB24992 also significantly inhibited parasite development, effects of lower concentrations were very heterogeneous preventing calculation of EC₅₀ values. Halofuginone and BCS-AF76184 dose-dependently interfered with host cell proliferation (EC₅₀ values of 0.35 µM and 9.07 µM, respectively) and the latter also had direct cytotoxic effects (EC₅₀=48.78 µM). However, drug concentrations required for cytopathic effects were higher than those for effects against *C. parvum*. Therefore, both BCS-AB24992 and BCS-AF76184 should be considered for further evaluation, e.g. using *in vivo* models.



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Session Details:	8/29/2013 All about Crypto 1130 - 1240 Riverside Theatre
Poster with 2 minute Oral Presentation Details:	Super Expression of <i>Cryptosporidium hominis</i> glycoprotein GP60 in <i>E. coli</i>
Authors:	Valéria Miura ^{1,2*} , Sergio Aoki ² , Marcelo Meireles ¹ ¹ Univ Estadual Paulista, Araçatuba, BRAZIL ² Dnapta Biotechnology, São José do Rio Preto, BRAZIL
Poster Number:	171

Cryptosporidium spp. are intracellular parasites that infect the epithelial cells of digestive and respiratory tracts of a wide variety of animal hosts¹. *Cryptosporidium hominis* is the dominant anthroponotic *Cryptosporidium* species infecting humans². The development of diagnosis and control strategies for cryptosporidiosis in humans has become the main challenge of epidemiological studies³. The 60-kDa glycoprotein gene (gp60) is the most frequently genetic marker used and, therefore, the study of GP60 glycoprotein is extremely important as a potential useful target for diagnostics of cryptosporidiosis infection in humans⁴. In this study, an efficient method of protein expression in *Escherichia coli* has been made for the GP60 glycoprotein subtype Ib, which has been shown previously to be the most prevalent and widely subtype distributed in human populations⁴. The full-length nucleotide sequence of *C. hominis* GP60 gene was amplified by PCR with the addition of restriction sites for the enzymes XbaI and XhoI. The gene sequence was inserted into plasmid pET28-a by digestion reaction for both restriction enzymes, ligated and transformed in JM107 *E. coli* cells. Subcloning of successful colonies was performed in several different strains of BL21 *E. coli* and the best results were obtained with BL21 Xjb strain. Temperature, time and inducer concentration assays were also performed and analyzed by SDS-PAGE gel. The optimal conditions for total protein expression were observed at temperature of 37°C, overnight incubation and 1mM concentration of the inducer IPTG. The protein purification will be performed by affinity chromatography using Hi-Trap HP column for ÄKTA Purifier system. The recombinant GP60 glycoprotein can be useful for developing diagnostic assays to monitor cryptosporidiosis outbreaks in human population.

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Poster with 2 minute Oral Presentation Details:	Human cryptosporidiosis in Western Australia – a case of mixed <i>Cryptosporidium</i> infection
Authors:	Josephine S. Y. Ng-Hublin ^a *, Barry Combs ^b , Brian MacKenzie ^c , Una Ryan ^a ^a School of Veterinary and Life Sciences, Murdoch University, South Street, Murdoch, WA, 6150, Australia ^b OzFoodNet Communicable Disease Control Directorate, Perth, Western Australia, Australia ^c PathWest Laboratory Medicine, Locked Bag 2009, Nedlands, WA 6909, Australia
Poster Number:	213

Cryptosporidiosis is a gastroenteric disease which usually present as watery diarrhea and abdominal cramps in those that are immunocompetent, but infection can be chronic and morbid in those that are immunologically compromised. Caused by the protozoan *Cryptosporidium*, most infections in humans are caused by *C. hominis* and *C. parvum*, and to a lesser extent *C. meleagridis*, *C. felis* and *C. canis* with recent reports of *C. cuniculus* as an emerging human pathogen. In this study, a unique case of human cryptosporidiosis will be presented, where an immunocompetent individual suffered from diarrhea and a spectrum of other symptoms. Findings from molecular diagnostics revealed that the patient was infected with three different species of *Cryptosporidium*: *C. meleagridis*, *Cryptosporidium* mink genotype and an unknown *Cryptosporidium* species. This is the first time *Cryptosporidium* mink genotype is identified in a human as previously, this species has only been identified in minks. Although the pathogenecity of the *Cryptosporidium* mink genotype and the unknown species is not known, the patient’s clinical symptoms and potential source of infection will be discussed.



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Session Details:	8/29/2013 All about Crypto 1130 - 1240 Riverside Theatre
Poster with 2 minute Oral Presentation Details:	Detection of <i>Cryptosporidium</i> spp. and <i>Giardia</i> spp. in water samples from the border areas of Thailand
Authors:	Chantira Sutthikornchai*, Amorn Lekkla, Hirotake Mori Aongart Mahittikorn, Yaowalark Sukthana Department of Protozoology, Faculty of Tropical Medicine, Mahidol University, Bangkok, Thailand
Poster Number:	265

Cryptosporidium and *Giardia* are both common waterborne pathogenic intestinal protozoa found in humans and animals. In rural areas in Thailand, river water, rain water, underground water, and water reserved in tanks is commonly used for drinking purposes without any treatment such as filtration or chlorination. We investigated water contamination due to pathogenic intestinal protozoa for the purposes of evaluating health risks to villagers. A total of 24 samples were collected from river, rain and underground water sources in northern, western, and southern Thailand. More than 20 ml of water for each sample was collected and then analysed. Turbidity and pH were examined, and molecular techniques were employed after concentration for diagnosis of intestinal protozoa. Real-time PCR was used for the identification of *Cryptosporidium* and nested PCR was used for *Giardia*. The results showed 33.3% (8/24) and 4.1% (1/24) were positive for *Cryptosporidium* and *Giardia*, respectively. Intestinal protozoa were most frequently identified in sources of rain water held in tanks (16.7%).

Collection and analyses of water samples is currently underway. Domestic animals such as cattle were frequently observed in water collection areas; zoonotic transmission is suspected. In addition, the influence of turbidity and pH of the water samples on the detection of parasites is being analysed. The potential contamination of water sources and effective interventions in each area will be discussed in the presentation.



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Session Details:	8/29/2013 All about Crypto 1130 - 1240 Riverside Theatre
Poster with 2 minute Oral Presentation Details:	Multiplication of <i>Cryptosporidium parvum</i> in artificial <i>Pseudomonas aeruginosa</i> biofilm systems
Authors:	Wan Hon Koh ⁽¹⁾ , Peta Clode ⁽²⁾ , Paul Monis ⁽³⁾ , and Andrew Thompson ⁽¹⁾ ⁽¹⁾ World Health Organisation Collaborating Centre for the Molecular Epidemiology of Parasitic Infections, School of Veterinary and Biomedical Sciences, Murdoch University, Murdoch, Western Australia 6150, Australia, ⁽²⁾ Centre for Microscopy, Characterisation and Analysis, University of Western Australia, 35 Stirling HWY, Crawley, WA 6009, Australia, and ⁽³⁾ South Australian Water Corporation, Salisbury, SA, Australia.
Poster Number:	277

Cryptosporidium parvum is a common, opportunistic, diarrhoeal-causing, apicomplexan pathogen in humans, of which water is an important transmission vehicle. Recently, aquatic biofilms have been recognised as environmental reservoirs for the infective stage (oocysts) of *Cryptosporidium*, yet their fate after being trapped within biofilms is unknown. This study aimed to identify whether biofilms can support the multiplication of *Cryptosporidium* by measuring the change in *Cryptosporidium* DNA using quantitative polymerase chain reaction (qPCR) and microscopy. *Pseudomonas aeruginosa* biofilm flow cell systems were established and *C. parvum* oocysts were constantly supplied over 6 days, with results showing that the increase in *C. parvum* DNA to be highly significant (p<0.001, two-way ANOVA test). In addition, our correlative study using both scanning electron and confocal microscopy detected various *Cryptosporidium* developmental stages (sporozoites, trophozoites, meronts, and merozoites) within the biofilm system. This further confirmed that the increase in *Cryptosporidium* DNA in biofilm system was due to the development of *Cryptosporidium*, rather than degenerate/accumulated oocysts or yeast contamination. This study has successfully shown that biofilms can support the multiplication of *Cryptosporidium* in aquatic environments and offers new insights into the role of aquatic biofilms in the shaping of the *Cryptosporidium* life cycle.



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Session Details:	8/29/2013 All about Flukes 1130 - 1240 Meeting Room 1
Poster with 2 minute Oral Presentation Details:	Host response to Fasciola hepatica infection at a transcriptomic level
Authors:	Cristian Alvarez* ¹ , Aaron Jex ² , Robin Gasser ² and Jean-Pierre Scheerlinck ¹ ¹ Centre for Animal Biotechnology, The University of Melbourne, Australia ² Faculty of Veterinary Science, The University of Melbourne, Australia
Poster Number:	194

The interaction between the parasite and the host immune system is one the key aspects of the host-interplay, underpinning infection, often playing a central role in the pathogenesis of disease, and, if harnessed effectively, providing a major avenue for pathogen control through vaccination. The interaction between helminths and their hosts has been heavily researched involves, usually, a heavy bias towards a Th2/cellular response, often mediated by parasite derived secreted proteins. However, in many cases, parasites develop in their hosts by way of a defined set of stages and often migrate in and through tissues during the infection process. As parasites migrate through tissues they encounter different challenges as they are faced with diverse local tissue environments and components of the host's immune system. As a result, the host and the parasite influence each other mutually in each tissue. Hence, it becomes essential to study local immune responses in the tissues through which parasites migrate and/or where they reside at different stages of development. Yet, most studies of host/parasite interactions to date have focused on systemic immune responses and have largely ignored differences that may occur in different tissues. Here, we use RNA-seq technology to begin to explore tissue-specific and temporal changes in the host immune response to parasites, using the giant liver fluke, *Fasciola hepatica*, and sheep as a model system. This research sheds new light on the host-parasite interaction for a socioeconomically important helminth, and provides significant insight into the role of differential transcription and alternative splicing in the host immune response to initial infection, tissue migration and prolonged exposure to the parasite.



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Session Details:	8/29/2013 All about Flukes 1130 - 1240 Meeting Room 1
Poster with 2 minute Oral Presentation Details:	Characterisation of novel tegument proteins of the common liver fluke (<i>Fasciola hepatica</i>)
Authors:	Timothy Cameron ^{1*} , Hayley Toet ¹ , Robin Beat Gasser ² , Neil David Young ² , Terry Spithill ¹ ¹ Department of Agricultural Sciences and Centre for AgriBio Science, La Trobe University, Bundoora, Victoria, AUSTRALIA ² Department of Veterinary Science, The University of Melbourne, Parkville, Victoria, AUSTRALIA
Poster Number:	247

The parasite *Fasciola hepatica* has a significant impact on the global agricultural economy, costing at least \$3.2 billion per annum (Spithill *et al.* 1999). Due to the increasing resistance of *F. hepatica* to anthelmintics, such as triclabendazole, alternative methods of control are needed. Recently research has focussed on developing an efficacious vaccine, but none to date are commercially viable. A prospective vaccine antigen candidate against liver fluke would be located on the tegument (as it is the interface of host-parasite interactions), up-regulated in juvenile/immature fluke (due to an observed acquired immune response against these life stages) and would be *Fasciola* specific to avoid cross-reactivity with host proteins (Meeusen & Piedrafita 2003). The adult *F. hepatica* tegument proteome has recently been described, suggesting several possible vaccine antigen candidates (Wilson *et al.* 2011). These include proteins specific to *Fasciola*, which are of unknown function. Three of these proteins, annotated as FhTEG2, FhTEG3 and FhTEG5, were chosen for bioinformatic analysis. Expression of these proteins is up-regulated in the transcriptome of immature fluke compared to the adult fluke transcriptome using RNAseq analysis. FhTEG3 and FhTEG5 were found to be cysteine rich, with a cysteine content of at least 10%, and were hypothesised to be cystine knot proteins. FhTEG2 is a 362 amino acid protein, containing a signal peptide, indicating that this protein is secreted. To date, recombinant FhTEG2 has been expressed using the *Pichia pastoris* expression system, setting the basis for future work to determine antigenicity of this recombinant protein and for its potential as a vaccine candidate to be assessed. Antigenicity of FhTEG2 will be assessed by conducting ELISAs using sera from infected cattle and sheep against the recombinant protein.

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Wilson RA, Wright JM, de Castro-Borges W, Parker-Manuel SJ, Dowle AA, Ashton PD, Young ND, Gasser RB, Spithill TW (2011) Exploring the *Fasciola hepatica* tegument proteome. *International Journal of Parasitology* **41**, 1347-1359.



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Session Details:	8/29/2013 All about Flukes 1130 - 1240 Meeting Room 1
Poster with 2 minute Oral Presentation Details:	Optimisation of a new <i>in vitro</i> method for the investigation of gut tissue invasion by newly excysted juvenile <i>Fasciola hepatica</i>
Authors:	Andrés García Campos ^{1*} , Andreas Lazaros Chrysafidis ¹ , Silvia Teresa Talavera Arce ¹ , Yan Fu ¹ , Laura Garza Cuartero ¹ , Mary Sekiya ¹ , Alan Baird ¹ , Grace Mulcahy ¹ ¹ School of Veterinary Medicine, University College Dublin, IRELAND
Poster Number:	193

The immune response of cattle to *Fasciola hepatica* has been studied extensively, both to enhance basic understanding and in pursuit of a vaccine. However, relatively few studies have concentrated on the invasion of the gut epithelium by newly excysted juvenile liver flukes (NEJs) and the host response triggered by this event. Furthermore, such studies have relied on an *ex vivo* model. The aim of this work is to develop a robust *in vitro* model that reduces the requirement for live animals and that may be valuable in understanding the mechanism which NEJs employ to penetrate the gut epithelium.

F. hepatica metacercariae were excysted *in vitro* and placed into horizontal diffusion chambers containing rat distal jejunum. Two different methods were compared: in the first method, chambers containing 0.25 NEJ/mm² were immersed in a 5% CO₂ gassed Krebs-Henseleit solution at 37°C at 4 time points (1, 2, 3 and 4 hours). In the second one, chambers that housed between 1.5-2 NEJ/mm² were immersed in RPMI 1640 at 38°C at 5 time points (30, 60, 90, 120 and 150 min). Subsequently, the NEJ numbers in the apical, basolateral regions and in different gut layers were determined to identify the method that facilitated maximum invasion. Whereas no NEJs were found in the basolateral region in method 1, a significant number of NEJs was observed in this region in method 2, with the highest proportion found at 120 min (20.68%). Histological examination showed that migration progressed with increasing time of incubation, with the proportion of NEJs in the serosa increasing and that in the mucosa increasing. This *in vitro* methodology is being refined with a view to providing a method to study how gut penetration by the parasite is altered in immune animals and in the presence of vaccine-induced antibodies and other factors.

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Session Details:	8/29/2013 All about Flukes 1130 - 1240 <i>Meeting Room 1</i>
Poster with 2 minute Oral Presentation Details:	Farm specific risk assessment for <i>Fasciola hepatica</i>: Putting the pieces together
Authors:	Karen Soenen ¹ , Jozef Vercruysse ¹ , Els De Roeck ¹ , Frieke Van Coillie ¹ , Robert De Wulf ¹ , Wouter Hantson ² , Els Ducheyne ² , Guy Hendrickx ² , Johannes Charlier* ¹ ¹ Ghent University, Ghent, BELGIUM ² Avia-GIS, Zoersel, BELGIUM
Poster Number:	257

Fasciolosis, caused by the trematode parasite *Fasciola hepatica*, causes serious production losses in dairy cattle worldwide. This vector-borne disease is spread by the snail *Galba truncatula* which thrives in small water bodies (SWB). Developing up-to-date, small-scale risk maps requires more insights in environmental factors affecting the snail dynamics.

In this study (i) SWB suitable for *G. truncatula* were characterised by monthly field visits in four dairy farms in two geographically distinct areas in Belgium in 2012. These areas had either a predominant clay or sandy soil type; (ii) The population dynamics of *G. truncatula* were studied by performing snail counts and measuring the shell length; (iii) Rain and temperature variables were monitored during the study period to link these variables with the abundance of the snail; (iv) The transmission of *F. hepatica* to the cattle was determined by examining blood samples of different age classes before and after the grazing season.

Five suitable SWB were distinguished: pond, ditch, trench, furrow and moist area. In total 53 SWB were visited monthly and 953 *G. truncatula* snails were retrieved. Ponds and trenches contained the highest numbers of snails and in both regions highest snail densities were observed in July. A new generation of snails peaked in October/November in the clay area, which matched the peak of rainfall in that area. Moreover, anti-*F. hepatica* antibody levels in serum increased during the study in the clay area, while the prevalence of the herds in the sandy area remained stable. These results suggest different snail dynamics leading to different *F. hepatica* risk in the 2 study areas.

Further research includes combining the parameters discussed above into one prediction model. Extending this work on a larger number of farms could be the base for farm-specific risk maps leading to enhanced control measures.

Acknowledgements:

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Johannes Charlier is supported by the FP7 GLOWORM project, Grant agreement n° 288975CP-TP-KBBE.2011.1.3-04



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Session Details:	8/29/2013 All about Flukes 1130 - 1240 Meeting Room 1
Poster with 2 minute Oral Presentation Details:	Characterising Host Gene Expression during the Recovery of Hepatic Schistosomiasis
Authors:	Candy Chuah ^{1, 2, 3*} , Melissa L. Burke ⁴ , Helen Owen ² , Malcolm K. Jones ^{1, 2} and Geoffrey N. Gobert ^{2, 5} ¹ Parasite Cell Biology Laboratory, Queensland Institute of Medical Research, Herston, QLD, Australia ² School of Veterinary Science, The University of Queensland, QLD, Australia ³ School of Medical Sciences, Universiti Sains Malaysia, Kelantan, Malaysia ⁴ Division of Mycobacterial Research, National Institute for Medical Research, London, United Kingdom ⁵ Molecular Parasitology Laboratory, Queensland Institute of Medical Research, Herston, QLD, Australia
Poster Number:	191

Schistosomiasis is a chronic helminth disease of humans, infecting approximately 207 million people worldwide. In schistosomiasis japonica, the egg-induced granulomatous response and the development of extensive hepatic fibrosis is the main pathology. Numerous studies have been undertaken to investigate the molecular features that accompany the process of hepatic granuloma formation, however, information on the mechanisms associated with granuloma regression and the subsequent recovery events in the host liver following parasite elimination are still limited. In this study, a murine model of schistosomiasis japonica was used to examine the multicellular pathways occur during liver recovery. *Schistosoma japonicum*-infected C57BL/6 mice were administered with the drug, praziquantel (PZQ) after 7 weeks post infection, on a daily basis for five consecutive days to eliminate the adult parasites. The pathological changes in terms of hepatic egg burden and granuloma density after 3, 6 and 7 weeks post treatment were examined, along with assessment of cellular infiltration to the liver. Whole genome microarray analysis will be employed to compare the gene expression profiling between the non-treated, PZQ-treated and the control groups during the course of recovery. Differentially expressed genes involved in granuloma resolving process will be further identified and immunohistochemistry analysis will be performed to confirm these findings. The work proposed here will provide a better understanding of the gene signaling pathways associated with the regression of hepatic schistosomiasis, with important implications for the alleviation of this and other fibrotic diseases.



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Session Details:	8/29/2013 All about Flukes 1130 - 1240 Meeting Room 1
Poster with 2 minute Oral Presentation Details:	Assessment of <i>Fasciola hepatica</i> Egg Viability
Authors:	Yan Fu ^{1*} , Silvia T. Talavera-Arce ¹ , Andrés García-Campos ¹ , Andreas L. Chrysafidis ¹ , John P. Dalton ² , Grace Mulcahy ¹ ¹ School of Veterinary Medicine, University College Dublin – Belfield, IRELAND ² Institute of Parasitology, McGill University, CANADA
Poster Number:	248

Reduction in *Fasciola hepatica* egg viability is a parameter of interest when assessing efficacy of experimental treatments, such as a new vaccine. In this study, a protocol for evaluation of egg viability was standardised, based on modifications of previously published protocols (Dalton, et al., 1996, Hanna, et al., 2006, Alcala-Canto et al., 2007). To verify the best conditions for artificial incubation of *F. hepatica* eggs, adult liver flukes were collected from naturally-infected animals from a commercial slaughterhouse and divided in three groups of approximately 10 flukes kept in saline for 3 hours, 24 hours and 48 hours, respectively. For each group, eggs released by the flukes were collected, counted and subgroups of 1000 eggs were incubated in darkness at different temperatures and lengths of time. Then eggs were exposed to full daylight for 24 hours and examined using a stereoscope. From each subgroup, at least 300 eggs were assessed and categorised as ‘undeveloped’, ‘developing’ and ‘hatched’. Hatching percentage was optimal after 15 days of incubation at 25-27°C. This optimized protocol was repeated with *F. hepatica* eggs recovered from flukes and bile collected from animals in a vaccination trial. Recombinant mutant *F. hepatica* CL1 (rmFhCL1) in Montanide ISA 70 VG® was used as the vaccine, and animals were kept in commercial field conditions, exposed to natural infection. Four vaccinated young bulls and four respective controls were slaughtered and flukes and bile were collected. Significant differences in the percentage of hatched eggs comparing samples collected from vaccinated (flukes=23.4%; bile=86.3%) and control (flukes=46.1%; bile=93.8%) animals, with $p<0.01$ in Chi-Square analysis and Odds Ratio 0.4 in both cases, showing a degree of protection conferred by vaccine regarding to egg viability.

Acknowledgements:

We would like to thank to Dr. Egan, in School of Biology and Environmental Science, UCD who kindly provided the cool incubator. This work is funded by European Comission Framework 7 – Paravac.

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Session Details:	8/29/2013 All about Flukes 1130 - 1240 Meeting Room 1
Poster with 2 minute Oral Presentation Details:	Organisation of cathepsin cysteine proteases within the <i>Fasciola hepatica</i> genome
Authors:	Krystyna Cwiklinski ^{1*} , Steve Paterson ² , John Dalton ³ , Diana J. Williams ¹ , Jane E. Hodgkinson ¹ ¹ Institute of Infection and Global Health, University of Liverpool, Liverpool, UNITED KINGDOM ² Centre for Genomic Research, University of Liverpool, Liverpool, UNITED KINGDOM ³ Department?, Queen's University, Belfast, UNITED KINGDOM
Poster Number:	17

The liver fluke, *Fasciola hepatica* is an economically important pathogen of sheep and cattle that is also a major welfare concern. It has been recently described as a re-emerging zoonosis and is a major focus of anthelmintic resistance and vaccine development research. Acute fasciolosis is associated with the newly excysted juveniles (NEJ) migrating through the liver to the bile ducts whilst chronic disease is associated with the presence of mature adult flukes in the bile ducts. Excretory-secretory (ES) proteins, in particular cathepsin cysteine proteases act at the host-parasite interface and have been of significant interest. Historically, proteomic studies have identified several clades/subtypes of cathepsin L and B cysteine proteases, that are thought to suppress the host immune system at the different stages of migration. Recently we have generated an 897 Mb *F. hepatica* draft genome from a single adult fluke (Shrewsbury isolate, Ridgeway Research) by a combination of Roche 454 and Illumina sequencing. The data was assembled into contigs and scaffolds and annotation is underway, using automated pipelines to generate gene models based on *F. hepatica* transcriptome and Schistosoma protein sequence. This study reports mining of the *F. hepatica* genome to determine the genomic organisation of the cathepsin L and B genes. Comparative transcriptomics was performed for available lifecycle-stage to determine the relative transcription of the cathepsin protease family. . Cathepsin L clade proteases are transcribed by both the NEJ and the juvenile flukes, whereas the cathepsin B proteases are primarily transcribed by the NEJ. Continued proteases will further our understanding of the genomic organisation and expression of this important group of proteases.



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Session Details:	8/29/2013 All about Flukes 1130 - 1240 Meeting Room 1
Poster with 2 minute Oral Presentation Details:	Utilising the natural host, <i>Bos bubalis</i> , to engineer local antibody probes to identify vaccines and therapeutic targets in the blood fluke, <i>Schistosoma japonicum</i> .
Authors:	Christopher Hosking ^{1*} , Hamish McWilliam ¹ , Leodevico Ilag ² , Els Meeusen ¹ and Michael de Veer ¹ ¹ Biotechnology Research Laboratories, Monash University, Clayton, Victoria, Australia ² Bio21 Molecular Sciences and Biotechnology Institute, University of Melbourne, Parkville, Victoria, Australia
Poster Number:	207

Schistosomiasis is one of the most significant parasitic diseases and despite decades of significant effort still remains a serious threat to public health, causing high levels of morbidity in affected regions of China and the Philippines (McGarvey *et al*, 1999; Bergquist *et al*, 2002). Caused by a group of parasitic trematodes called schistosomes, these successful parasites have evolved a complex life cycle. Chemical therapeutic (Praziquantel) control of infection is currently the only effective mechanism to combat the disease, however this treatment regime has limitations, in particular, mass treatment does not prevent re-infection and sporadic resistance against this drug has been developed. Thus, it seems that the only effective way to truly control this parasitic infection lies with the ability to generate an efficacious vaccine in combination with alternative therapeutics (McManus and Loukas, 2008).

This present study will utilise methods of antibody engineering to develop fully species specific monoclonal antibodies for vaccine target identification and antibody therapies for schistosomiasis within the definitive host. To achieve this we will use a unique technique of isolating antibodies and RNA generated from plasma cells present within the local draining lymph nodes of an infected animal. Using phage display to amplify the variable regions of B-cells from infected animals we will prepare antibody repertoires specific to the juvenile stages of the schistosome parasite. These antibodies will offer a snapshot of the animal's immune response at the time of tissue collection and will be used to discover new vaccine, diagnostic and therapeutic lead candidates against the juvenile stage of the blood fluke, *Schistosoma japonicum*.

Acknowledgments:

Prof Don McManus and Dr Yuesheng Li

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Session Details:	8/29/2013 All about Flukes 1130 - 1240 Meeting Room 1
Poster with 2 minute Oral Presentation Details:	Bioinformatic analysis of FhCUB6 and FhCUB7 proteins in the liver fluke, <i>Fasciola hepatica</i>
Authors:	Siew May Loh ^{1*} , Hayley M. Toet ¹ , Terry W. Spithill ¹ ¹ Department of Agricultural Sciences and Centre for AgriBioscience, La Trobe University, Bundoora, Australia
Poster Number:	246

Fasciolosis is a disease caused by the liver fluke, *Fasciola hepatica*, affecting both livestock and humans. The disease has a major impact on the agricultural sector, causing losses of US\$3 billion each year. In addition, the occurrence of triclabendazole resistance in flukes has provided another issue in the control of the disease. The development of vaccines against fasciolosis will help to prevent further economic losses and improve animal health. The tegument of *F. hepatica* plays an important role in parasite survival and the establishment of disease in a host. The proteins present on the surface tegument are associated with nutrient uptake, fluke migration through host's tissue and host immune evasion. Recently, proteomic analysis was carried out on the *F. hepatica* tegument and analysed using bioinformatics (Wilson *et al.* 2011) and RNA sequence analysis. Five proteins containing CUB domains, annotated as FhCUB1-5, were found to be associated with the parasite tegument. In this study, another two CUB domain proteins were identified using bioinformatic analysis of the adult transcriptome, annotated as FhCUB6 and FhCUB7. We aim to clone FhCUB6 and, FhCUB7; the recombinant proteins will be expressed and tested for antigenicity in cattle and sheep using ELISA and Western blotting analysis. In addition, this study also aims to determine whether the FhCUB6 and FhCUB7 proteins are also expressed in juvenile and immature flukes.

References:

Wilson RA, Wright JM, de Castro-Borges W, Parker-Manuel SJ, Dowle AA, Ashton PD, Young ND, Gasser RB, Spithill TW (2011) Exploring the *Fasciola hepatica* tegument proteome. *International Journal for Parasitology* **41**, 1347-1359.



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Session Details:	8/29/2013 All about Flukes 1130 - 1240 Meeting Room 1
Poster with 2 minute Oral Presentation Details:	Fasciola spp: The <i>in vitro</i> anthelmintic effects of the plant derived compound, plumbagin, on newly excysted juvenile (NEJ) parasites
Authors:	Natcha Lorsuwannarat ^{1,2*} , David Piedrafita ² , Prasert Sobhon ¹ ¹ Mahidol University, Bangkok, THAILAND ² Monash University, VIC, AUSTRALIA
Poster Number:	131

Fasciolosis caused by *Fasciola* spp. are presently recognized as a major global health problem that affects both animals and humans. Presently, triclabendazole (TCZ) is the main drug used to control this infection. However, resistance to this drug has emerged and may pose a serious problem. Plumbagin (5-hydroxy-2-methyl-1,4-naphthoquinone, PB) is a compound derived from the roots of many plants, especially from *Plumbaginaceae* family, which is used as a traditional medicine for the treatments of several ailments. The objective of this study was to investigate the *in vitro* activities of PB against NEJ parasites of *Fasciola gigantica* and *hepatica* against TCZ toxicity based on the relative motility value (RM), survival index (SI) and tegumental alterations as observed by scanning electron microscopy (SEM). It was found that the RM and SI values of PB-treated NEJ flukes decreased significantly from 3 to 24 h at more rapid rates than TCZ-treated group. When observed by SEM, the tegument of flukes treated with both drugs revealed similar sequences of pathological changes, comprising swelling, blebbing, erosion, and finally the sloughing of the tegument. These data indicate that PB is an effective anthelmintic *in vitro*, whose mechanisms of action on the target organs, including the tegument, need to be studied further.



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Session Details:	8/29/2013 All about Flukes 1130 - 1240 Meeting Room 1
Poster with 2 minute Oral Presentation Details:	Bioinformatic Analysis of <i>Fasciola</i> - Specific Tegumental Proteins
Authors:	Timothy Merritt ^{1*} , Hayley Toet ¹ and Terry W Spithill ¹ 1 Department of Agricultural Sciences and Centre for AgriBioscience, La Trobe University, AUSTRALIA
Poster Number:	172

Resistance of *Fasciola hepatica* to various anthelmintic drugs such as triclabendazole is becoming an increasing problem worldwide and Fasciolosis is thought to be causing economic losses of up to 3.2 billion dollars per annum (Spithill *et al.* 1999). It is vital that alternate methods of preventing *F. hepatica* infection are developed and one such method would be the formulation of a commercially viable vaccine. Development of experimental vaccines against *F. hepatica* has been proven possible but a commercially viable vaccine is still to be produced. Antibody Dependent Cell-mediated Cytotoxicity (ADCC) in Indonesian Thin-Tailed Sheep has been shown to kill *Fasciola gigantica* after 2-4 weeks of infection, just after they have entered the liver parenchyma and reached the immature life stage (Piedrafita *et al.* 2007). It is for this reason that tegumental proteins up-regulated in the juvenile/immature form of the fluke may be potential vaccine candidates. The recently described adult *F. hepatica* tegument proteome has listed several proteins which may possibly be used as vaccine candidates (Wilson *et al.* 2011). Five *Fasciola*- specific proteins from this proteome (annotated as FhB01108, FhB00207, FhB03485, Fhc16922 and FhA01044) were chosen to undergo bioinformatic analysis in this study. These sequences will undergo transcript profiling using RNA seq data to determine whether any are up-regulated in either immature or adult flukes. In addition analysis of conserved domains will be performed in an attempt to identify possible protein function. Further analysis of these proteins will be conducted to determine if their expression varies during the transition from newly excysted juveniles (NEJ) to immature flukes. This study will help to determine the possible function of these sequences.

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Wilson RA, Wright JM, de Castro-Borges W, Parker-Manuel SJ, Dowle AA, Ashton PD, Young ND, Gasser RB, Spithill TW (2011) Exploring the *Fasciola hepatica* tegument proteome. *International Journal of Parasitology* **41**, 1347-1359.



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Session Details:	8/29/2013 All about Flukes 1130 - 1240 Meeting Room 1
Poster with 2 minute Oral Presentation Details:	Characterisation and localisation of <i>Schistosoma japonicum</i> acetylcholinesterase and its potential as a vaccine target.
Authors:	Gabor Pali ^{1,2*} , Hong You ¹ , Geoffrey Gobert ¹ , Donald McManus ¹ ¹ Queensland Institute of Medical Research, Brisbane, AUSTRALIA ² Griffith University, Brisbane, AUSTRALIA
Poster Number:	192

The risk of infection by *Schistosoma japonicum* is significant throughout endemic regions of the Philippines, Indonesia, and southern China¹. The enzyme acetylcholinesterase (AChE), in conjunction with nicotinic acetylcholine receptors, is strongly believed to influence the biology of schistosomes within the mammalian host. The presence of parasite AChE has been linked to glucose uptake, raising it by up to 60%, while the membrane impermeable AChE inhibitor BW284C51 has been shown to block any enhancement in glucose uptake². The biological relevance of AChE comes from its ability to prevent the desensitisation of tegumental nicotinic acetylcholine receptors, which occurs after prolonged activation by acetylcholine². The initial aim of this project is the complete sequencing of the AChE cDNA in *S. japonicum* from which a select segment will be cloned into *E. coli* and its product used for antibody production. These antibodies will then be used for immuno-localisation of the enzyme in male and female adult worms and schistosomula. Real-time PCR will be used to quantify the transcription levels of AChE mRNA across the parasites life stages. In addition the enzymatic activity of AChE will also be assessed across a variety of life stages using immuno-fluorescence assays. Together these allow the comparison of adult male and female worms, schistosomula, and cercariae. With the potential reduction in effectiveness of the anti-schistosomal drug praziquantel³, and a lack of alternative treatments, the identification of vaccine targets is ever more important. A major vaccine consideration has already been reported with no cross-reactivity between anti-*S. mansoni*-AChE antibodies and human AChE⁴. The potential effectiveness of these antibodies has also been reported *in vitro*, with *S. mansoni* showing polyclonal M-type antibodies caused complement dependent cytotoxic killing of the parasite⁵. The next logical step is an animal vaccination/challenge trial using recombinant *S. japonicum* AChE as a vaccine.

Acknowledgements:

I wish to acknowledge the helpful discussions with Associate Professor Alejandro Lopez (Griffith University).

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Session Details:	8/29/2013 All about Flukes 1130 - 1240 Meeting Room 1
Poster with 2 minute Oral Presentation Details:	Diagnostic sensitivity and specificity of a <i>F. hepatica</i> copro-antigen ELISA# and its use for maintaining freedom of liver fluke infection in Western Australia
Authors:	Dieter Gerd Palmer, Jill Lyon, Mike Palmer, David Forshaw Department of Agriculture and Food, WESTERN AUSTRALIA
Poster Number:	92

The objective of this investigation was to determine the specificity and sensitivity of a commercial copro-antigen ELISA for the detection of *Fasciola hepatica* infection in cattle and sheep and to assess the suitability of the test for use in horses.

Testing was done on over 100 negative faecal samples from each of sheep, cattle and horses and on at least 40 positive faecal samples from each species. Positive samples were selected based on a positive sedimentation test for liver fluke eggs. Negative samples were selected from animals in Western Australia, the state being free of liver fluke infection. Specificity and sensitivity were assessed for each species using the recommended kit cut-off and also species specific custom cut-offs based on the mean + 3SD of the negative samples for each species.

Using the kit recommended cut-off, the specificity was 100% for all species and the sensitivity 88%, 80% and 9% for sheep, cattle and horses, respectively. Using the lower custom cut-offs for each species improved the sensitivity to 100% for sheep, 87% for cattle and 28% for horses, while maintaining the specificity above 99% for all species.

The sensitivity of the commercial copro antigen ELISA is lower than claimed by the kit manufacturer. However, the sensitivity of the test can be improved by the use of custom cut-offs for each species and could be used as an alternative test to the currently used sedimentation test for sheep and cattle entering the liver fluke free state of Western Australia. The test is not suitable for use in horses.

Acknowledgements:

The authors would like to thank Jenny Cotter for providing fluke free cattle faecal samples and all diagnostic parasitology laboratories in other states who provided us with fluke positive samples for this study. Special thanks for the staff in the Albany Animal Health Laboratories, Department of Agriculture and Food WA for assistance with the processing of the samples.

References:

F. hepatica copro-antigen ELISA (Bio K 201, Bio-X Diagnostics, B-5580 Jemelle, Belgium)



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Session Details:	8/29/2013 All about Flukes 1130 - 1240 Meeting Room 1
Poster with 2 minute Oral Presentation Details:	Utilising transposons to understand the function of insulin receptors in Schistosoma mansoni
Authors:	Najju Ranjit ^{1*} , Don Mcmanus ¹ ¹ Queensland Institute of Medical Research, Brisbane, Australia
Poster Number:	173

In order to advance our ability to develop novel interventions for schistosomiasis, there is likely to be a valuable role for stable heritable transgenic lines of schistosomes. Unlike some protozoan parasites for which techniques for genetic manipulation are well-advanced schistosomes and other helminths lag substantially in terms of tools for genetic manipulation. Establishment of lines of transgenic schistosomes requires integration of transgenes into the chromosomes of the schistosome germ line. The transgenes not only have to integrate into the genome, they have to specifically integrate into the germ cells. The fundamental nature of the schistosome makes this challenging. Ideally, target stages for the introduction of transgenes into the genome of *S. mansoni* would be either the immature/newly laid egg or the early larval stages.

Insulin signalling is a very ancient and well-conserved pathway in metazoan cells, dependent on insulin receptors (IR), which are transmembrane proteins with tyrosine kinase activity. It has been demonstrated that this pathway is vital for the development and survival of numerous helminths. Adult schistosomes reside in the mesenteric veins where they use huge quantities of glucose, taken up via two glucose transporters localized asymmetrically on basal and apical membranes of the external body surface or tegument. Two distinct IR homologs know as SmIR-1 and SmIR-2 have been identified in the *S. mansoni* genome.

Using the piggybac transposon mediated transgenesis, the *S.mansoni* insulin receptors SmIR-1 and SmIR-2 have been targeted in order to understand the role of the distinct receptors and identify which region of the kinase domains is crucial for the function of the insulin signaling pathway.



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Session Details:	8/29/2013 All about sheep 1130 - 1240 Meeting Room 2
Poster with 2 minute Oral Presentation Details:	The prevalence of anthelmintic resistance on Australian sheep farms (2009 - 2012)
Presentation Time:	-
Authors:	Justin Bailey ^{1*} , Matt Playford ² , Stephen Love ³ , Brown Besier ⁴ , Alison Smith ² , Pat Kluver ¹ ¹ Novartis Animal Health Australasia Pty Ltd, North Ryde NSW 2113, Australia ² Dawbuts Pty Ltd, Camden NSW 2570, Australia ³ NSW Department of Primary Industries, Armidale, NSW 2351, Australia ⁴ Department of Agriculture and Food Western Australia, Albany WA 6330, Australia
Poster Number:	135

Aim: This study was conducted in response to the need for up-to-date information on anthelmintic resistance in the Australian sheep industry to help inform management decisions, advisory practices and future research.

Methods: Providers, including government and private parasitology laboratories, pharmaceutical companies and veterinarians who were known to have conducted Worm Egg Count Reduction Tests (WECRT's) between 2009 and 2012, were asked to submit all test results that conformed to standards set by the World Association for the Advancement of Veterinary Parasitology. Of those submitted, 390 tests met these criteria.

Results: The percentage of farms on which <95% efficacy was found in any of *Haemonchus*, *Teladorsagia* or *Trichostrongylus* spp. (and the number of farms tested) for the four broad-spectrum drench groups was:

- benzimidazoles 96% (80);
- levamisole 96% (111);
- macrocyclic lactones (represented by ivermectin) 84% (92) and
- aminoacetoneitrile derivatives (monepantel) 0% (4).

Against the same criteria, and compared with the findings above, the results for moxidectin 57% (136) and three-way combinations - containing abamectin, levamisole and a benzimidazole 28% (50) - clearly show that drench effectiveness needs to be assessed at an individual farm level. We will also present the range of efficacies found by active.

Conclusion: These findings contrast sharply with the results of a national drench resistance survey conducted in 1994 which found no evidence of ML resistance¹. The current study highlights the urgent need to better manage existing anthelmintic resources and to promote adoption of appropriate non-chemical control measures on individual farms as part of an Integrated Parasite Management (IPM) approach.



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Acknowledgements:
Greg Croft, Lewis Kahn, Paul Nilon, David Hucker, Matt Playford, Nicole Swan, Brown Besier, Elizabeth Patrick and Novartis Animal Health

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Session Details:	8/29/2013 All about sheep 1130 - 1240 Meeting Room 2
Poster with 2 minute Oral Presentation Details:	Protection of grazing periparturient ewes and lambs against haemonchosis after immunization with antigens from the intestinal membranes from <i>Haemonchus contortus</i>
Authors:	C. C. Bassetto ^{1*} , M. É. Picharillo ¹ , G. F. J. Newlands ² , W. D. Smith ² , S. Fernandes ¹ , E. R. Siqueira ¹ , A. F. T. Amarante ¹ ¹ UNESP - Universidade Estadual Paulista, Botucatu, SP, BRAZIL ² Moredun Research Institute, Edinburgh, UK Corresponding author: cesarbassetto@gmail.com
Poster Number:	31

A vaccine containing integral membrane glycoproteins from the intestine of *Haemonchus contortus* was evaluated in 3 groups of grazing sheep each consisting of 13 ewes and their 16 lambs. Vaccinates received either 5 or 50 µg of antigen in 1mg saponin, while the controls got adjuvant alone. Ewes received five shots and lambs six shots 21 days apart. Mean antibody titres (±SE) in the ewes vaccinated with 5 or 50 µg antigen peaked a week after the last shot at 7,058 (±4,111) and 7,071 (±3,788), respectively. However, these titres did not confer significant protection since egg counts remained high in all groups (P>0.05), with means one week after the last shot of 4,008 (±877), 2,438 (±974) and 2,523 (±639) in the 5 µg, 50 µg and control groups, respectively. In addition 5 of the 5 µg, 8 of the 50 µg and 5 controls required salvage treatment at some point during the trial. In contrast, mean lamb titres were much higher, peaking at 79,073 (±15,033) and 108,152 (±27,437) in the 5 µg and 50 µg groups and resulted in significantly (P<0.01) reduced egg counts with means of 325 (±63), 688 (±240) and 5,738 (±5,332) in the 5 µg, 50 µg and control groups, respectively. Similarly, at the end of the trial, mean lamb *H. contortus* burdens were 995 (±327), 1,769 (±537) and 3,113 (±760), respectively. It was concluded, that the vaccine protected lambs but not their mothers against natural exposure to *H. contortus* and that 5 µg of antigen was as effective as 50 µg.

Acknowledgements:

European Commission, PARAVAC Project (Grant Number 265862)
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Session Details:	8/29/2013 All about sheep 1130 - 1240 Meeting Room 2
Poster with 2 minute Oral Presentation Details:	Isolation and purification of <i>Trichostrongylus vitrinus</i> from mixed naturally-acquired Trichostrongylid infections in sheep
Authors:	Paul Blackburn ^{1, 2*} , Ian Carmichael ¹ , Sarah Greenslade ¹ , Stephen Walkden-Brown ² ¹ South Australian Research and Development Institute, Adelaide, AUSTRALIA ² University of New England, Armidale, AUSTRALIA
Poster Number:	48

Extensive enquiries in 2011 confirmed that a pure strain of the sheep small intestinal parasite *Trichostrongylus vitrinus* (*T. vitrinus*) was no longer held in Australian laboratories. To provide for planned research, a pure strain of *T. vitrinus* was isolated in the laboratory from mixed infections of sheep at Bransholme (South-west Victoria) and Kalangadoo (South-east South Australia). Parasite species confirmed on the properties included *Teladorsagia circumcincta* (*Tel. circumcincta*), *T. vitrinus*, *T. colubriformis*, *T. axei* and *T. rugatus* (one property). Faecal samples were collected *per rectum* at each site in spring 2011. Faeces from each site were mixed in culture pots, covered and incubated at 4°C for 54-68 days, to prevent development of *T. colubriformis* and *T. rugatus* (Beveridge *et al.*,1989). Harvested third stage larvae (L₃) comprised *Trichostrongylus* spp. (undifferentiated), small numbers of *T. axei*, and *Tel. circumcincta*. L₃ from each site were then passaged through housed worm-free Merino lambs to separate *Tel. circumcincta* and *T. axei* (abomasum parasites) from *T. vitrinus*. Following patency lambs were euthanased and the contents of the proximal 5 metres of small intestine were washed and collected on a sieve (413µm), and examined microscopically. At least 100 male worms were examined for spicule morphology to confirm purity of *T. vitrinus* infection, and all adult females recovered. Females from each site were mashed with a glass pestle in a small tube containing water to release eggs. The suspension containing eggs was mixed through “worm free” faeces, incubated at 25°C for 10 days and L₃ recovered. Recovered larvae were combined and amplified with further passage through housed “worm free” Merino lambs. An additional lamb was used to verify strain purity; no worms were recovered from the abomasum and all male worms from the small intestine were *T. vitrinus*. This strain has been cryopreserved and is available for future research.

Acknowledgements:

This project was fully funded by Meat and Livestock Australia.
PhD stipend of primary author provided through an Australian Post Graduate Award from the University of New England, and the Sheep Cooperative Research Centre.
All research was conducted with approval from Primary Industry and Resources South Australia (18/11) and University of New England (AEC12-008) Animal Ethics Committees.

References:

Beveridge, I., Pullman, A.L., Martin, R.R., Barelds, A., 1989. Effects of temperature and relative humidity on development and survival of the free-living stages of *Trichostrongylus colubriformis*, *T. rugatus* and *T. vitrinus*. *Veterinary Parasitology* 33, 143-153.



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Session Details:	8/29/2013 All about sheep 1130 - 1240 Meeting Room 2
Poster with 2 minute Oral Presentation Details:	Impact of grazing management on sheep parasites, weight gains and development of anthelmintic resistance
Authors:	Michaela Dolinská*, Alžbeta Königová, Elena Školníková, Marián Várady Institute of Parasitology, Slovak Academy of Sciences, Košice, SLOVAK REPUBLIC
Poster Number:	132

The experiment was conducted during two consecutive seasons from May to November of 2011 and 2012. The presented data showed a part of the study carried out during grazing seasons of 2011-2014. The main objective of the whole project will be to verify that 'sustainable' farming and grazing methods that allow optimum animal stocking rate on the pastures are directly associated with a low intensity of infection which may reduce the emergence and development of resistant parasites in grazing animals. The paddocks were divided into 9 areas with the same size of 0,43 ha. All the time nine groups of lambs (sheep breed Improved Valachian) were kept in electrically fenced off areas to protect mixing of animals. We tested 3 concentration of animals – low (3 sheep), medium (6 sheep) and high (9 sheep). At the beginning of pasture season all animals were infected with 2000 L3 larvae of susceptible strain of Haemonchus contortus (MHco3). Three groups of animals were used as a control group, other three groups were treated once per pasture season and last three groups were treated three times per pasture season. Sheep were treated with recommended dose of albendazole. Our results demonstrate relationship between stocking rate and intensity of infection in grazing animals. The number of eggs per gram (EPG) increased with higher stocking rate. With increasing stocking rate smaller weight gains in animals were measured. The treatment has a positive effect on the weight gains of lambs. During the pasture season of 2012 phenomenon of “self-cure” has been seen. The influence of grazing management on the development of anthelmintic resistance will be evaluated after 4 years of our experimental study.

Acknowledgements: The study was supported by Slovak Research and Development Agency Project No. APVV – 0539 -10



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Session Details:	8/29/2013 All about sheep 1130 - 1240 Meeting Room 2
Poster with 2 minute Oral Presentation Details:	The Effect of Neem Oil (1% Azadirachtin) on Larvae of <i>Lucilia sericata</i> , the Sheep Blowfly.
Authors:	Peter Bates ¹ , Sarah Harrison ^{2*} , Rachel Whitehouse ² , Nick Dean ² , Abby Lusty ² , Maggie Fisher ² , Bryan Shand ³ ¹ Veterinary Medical Entomology Consultancy (VMEC), 68 Eastworth Road, Chertsey, Surrey, KT16 8DR ² Ridgeway Research Ltd., Park Farm Buildings, Park Lane, St. Briavels, Lydney, GL156QX ³ Agropharm Ltd, Buckingham Place, Church Road, Penn, Buckinghamshire, HP10 8LN
Poster Number:	136

Blowfly strike, caused by larvae of the sheep blowfly (*Lucilia sericata*) can compromise the welfare of affected sheep and can be the cause of significant mortality. In the UK strike is currently prevented or cured using synthetic pyrethroid (SP) or insect growth regulator (IGR) based pour-on's or plunge dipping in wash made up with the organophosphate (OP) diazinon. In this study an *in vitro* bioassay method was used to assess the effect of Neem Oil (1% azadirachtin) solution on the development of *L.sericata* larvae. Under the conditions of this assay 1% azadirachtin caused significant mortality at all dilutions tested after 24 hours exposure, culminating in 93.8% to 100.0% mortality after 72 hrs, compared to only 20% mortality in the untreated control group at the same time point. In addition to mortality any surviving larvae exposed to Neem Oil were significantly stunted in their growth, possibly due to an anti-feeding effect possessed by azadirachtin. Although this activity was only apparent between 24 and 48 hours exposure, it could have a profound effect on the subsequent development of both the infesting larvae and the development of blowfly strike lesion plus the potential to attract further adult flies (causing secondary and tertiary strikes). Exposed larvae never grew larger than that recorded for first stage (L₁) larvae (1.7 to 3.5mm) and would therefore be unlikely to cause significant damage.

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Session Details:	8/29/2013 All about sheep 1130 - 1240 <i>Meeting Room 2</i>
Poster with 2 minute Oral Presentation Details:	Selection of sheep for resistance to nematode parasites: from experimental design to natural infections.
Authors:	Jacquet P. ^{1, 2} , Lienard E. ^{1, 2} , Grisez C. ^{1, 2} , Prévot F. ^{1, 2} , Bergeaud J.P. ^{1, 2} , François D. ³ , Chile K. ⁴ , Pantel C. ⁴ 1: INRA-IE, UMT Maîtrise de la Santé des Troupeaux de Petits Ruminants, Ecole Nationale Vétérinaire de Toulouse, 23 Chemin des Capelles, F-31076 Toulouse cedex 3, France 2: Université de Toulouse, INP-ENVIT, UMR 1225, Ecole Nationale Vétérinaire de Toulouse, 23 Chemin des Capelles, F-31076 Toulouse cedex 3, France 3: INRA, UR631, Station d'Amélioration Génétique des Animaux, CS 52627, 31 326, Castanet-Tolosan, France 4: FEDATEST, La Roue, 43300 Mazeyrat d'Allier, France.
Poster Number:	233

Gastro-intestinal nematodes are one of the main health issues in grazing sheep. Due to the development of anthelmintic resistance, selection for animals that resist nematode infection may provide a feasible long-term control strategy. This experiment was conducted to assess the efficiency of a selection on the basis of fecal egg excretion during two artificial challenges in subsequent natural infections. Among 104 five months-old ewe lambs experimentally infected with *Haemonchus contortus*, the 28 highest (susceptible) and lowest (resistant) excreting individuals were selected, treated with an efficient anthelmintic and went to pasture together on the same paddocks. Artificial inseminations were done on these individuals at the beginning of each pasture season. Then, quantifications of egg excretions and parasites' identifications after fecal cultures were compared between susceptible and resistant ewes at four time-points during two successive pasture seasons. In addition, production traits as growth rates, fertility and prolificacy of females and average weight gains and mortality of their lambs (birth to weaning) were compared between the two groups. In the first grazing season, resistant ewes shed 23 to 50% less eggs than susceptible ones according to the time of sampling ($P < 0.025$). In the second grazing period, egg excretions of resistant ewes were 8 to 30% less than those of susceptible ones; however, this difference was not significant. Similar mixed infections with predominance of *H. contortus*, *Teladorsagia circumcincta* and *Trichostrongylus* spp. were recorded in the two groups. No significant difference in production traits was noticed between resistant and susceptible animals along the study. In conclusion, a phenotypic selection of resistant and susceptible animals in experimental conditions allowed a significant reduction of egg excretion in the former animals during the first grazing season. No adverse effect on production traits were shown in resistant animals compared to susceptible ones.



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Session Details:	8/29/2013 All about sheep 1130 - 1240 Meeting Room 2
Poster with 2 minute Oral Presentation Details:	Prevalence of anthelmintic resistance in <i>Haemonchus contortus</i> of sheep in Southern Queensland
Authors:	Maxine Lyndal-Murphy ¹ , Wayne Ehrlich ¹ , Judy Gemmell ¹ , David Mayer ¹ ¹ Departament of Agriculture, Forestry and Fisheries, Brisbane, AUSTRALIA
Poster Number:	133

The Faecal Egg Count Reduction Test was conducted on sheep farms (n=19) across southern Queensland and northern New South Wales where *Haemonchus contortus* is the predominant pathogenic gastrointestinal nematode. Ten farms were in region 1 (650 to 750 mm) and 9 in region 2 (500 to 650 mm rainfall zone).

Five anthelmintic treatments selected from the following, levamisole (LEV), naphthalophos (NAP), combinations of BZ (benzimidazole)+LEV, BZ+LEV+ABA (abamectin) or BZ+LEV+ABA+CLOS (closantel), CLOS+ABA or moxidectin (MOX) LA injection, were tested at the manufacturer's recommended dose rates on groups of sheep (n=15). Pre- and post-drench Faecal Egg Counts (FEC) and larval differentiations of control and treatment groups were used in the calculation of percent reduction. Resistance was inferred when there was <95% reduction in FEC 10–14 days after treatment with the lower confidence limit (CL_L < 90%).

There was no significant effect of region (P = 0.13), with the overall prevalence of resistance being 58.8% (±6.4%) for region 1 and 44.4% (±6.8%) for region 2. There was no region by treatment interaction (P = 0.81), indicating that treatments were equally effective in both regions. No resistance was detected to the 4-active combination product, although the number of farms tested was small (n=4) and the confidence interval wide. A high prevalence of resistance (≥50%) was detected for all other drugs except NAP which was effective on 87% of farms. The following table lists the results for all treatments.

Drench active	Properties with resistance	Total properties tested	Prevalence	95% confidence interval
LEV	13	19	68%	41% - 87%
NAP	2	15	13%	2% - 48%
BZ+LEV	4	9	44%	14% - 80%
BZ+LEV+ABA	7	13	54%	24% - 81%
BZ+LEV+ABA+CLOS	0	4	0%	0% - 51%
CLOS+ABA	12	16	75%	43% - 92%
MOX LA injection	9	15	60%	30% - 84%

Acknowledgement: Meat and Livestock Australia and Australian Wool Innovation funded this work.



Session Details:	8/29/2013 All about sheep 1130 - 1240 Meeting Room 2
Poster with 2 minute Oral Presentation Details:	Selecting superior production animals through microbiome characterisation: Interactions between <i>Haemonchus contortus</i> and the gut microbiome of sheep
Authors:	Md. Abdullah Al Mamun*, David Piedrafita, Mark Sandeman, Andrew R. Greenhill School of Applied Sciences and Engineering, Monash University Gippsland campus, Churchill, Victoria 3842 Australia
Poster Number:	18

Parasite infections are a major impediment to livestock productivity and human health globally. *Haemonchous contortus* is the most important parasite in small ruminant production animals worldwide, with severe infection leading to animal death and subclinical infections reducing output. It is well established that good nutrition confers immune resistance to infection but the link between good nutrition, species specific gut microbiota and resistance to infection are poorly understood. Recent advances in molecular biology have led to studies investigating the full microbiological composition (the microbiome) of the gut. To date little work has been conducted on the relationship of gut microbiome and predisposition to enteric pathogens. We will conduct a challenge experiment using 30 sheep with a known genetic spectrum of production traits for wool growth, meat and fat deposition and immunity to enteric parasites. Initial microbial community analysis will be conducted using automated ribosomal intergenic spacer analysis (ARISA) and for more sensitive determination of community composition selected samples will be further analysed using next generation sequencing (NGS). We will analyse the gut microbiome pre- and post-infection to gain a better understanding of the role of, and response to, the gut microbiome to enteric parasite infection. This may lead to selection for better production animals and potentially novel ways of preventing enteric parasite infection.

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Session Details:	8/29/2013 All about sheep 1130 - 1240 Meeting Room 2
Poster with 2 minute Oral Presentation Details:	Immune traits associated with sheep resistance to gastrointestinal nematode (GIN) parasites
Authors:	Amanda Peers-Adams*, Dr Michael De Veer, Associate Professor David Piedrafita Monash University, Victoria, Australia
Poster Number:	177

GINs persist as one of the most prevalent parasitic diseases concerning small ruminants globally and are a major constraint on animal health and production, causing serious economic losses. Anthelmintic drenches are the corner stone of GIN control, however heavy usage has resulted in the emergence of multi drug-resistant parasite strains. Utilization of the host immune response through vaccination has been an object of considerable research activity and exemplifies an alternative, non-chemical and sustainable approach to parasite control. Between and within breeds of sheep, a number of manifestations of the immune response contribute to cases of resistance to infection; however these mechanisms remain unclear. Comparing immune responses of animals to a range of stimuli enables determination of immunocompetence to further build immune profiles predicting the likely resistance or susceptibility to a range of pathogens and ameliorate the success of vaccination programs; a concept currently being investigated in the bovine and porcine industries. We will conduct similar studies and measure a range of immune traits in sheep with known Australian standard breeding values for worm resistance, where the relationship between traits measured and worm resistance will then be identified. A preliminary trial involved the intradermal injection of a range of immune stimuli into sheep. Delayed and intermediate hypersensitivity reaction at the site was measured by assessment of wheal size and temperature at 4 and 24 hour post injection, respectively. Biopsies were taken at 24 hours to measure recruitment of immune cell populations and gene expression changes. Early results indicate some correlations between immune reactivity to nematode parasite and allergen stimuli injections with FEC data.



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Session Details:	8/29/2013 All about sheep 1130 - 1240 Meeting Room 2
Poster with 2 minute Oral Presentation Details:	Over-wintering of free-living gastrointestinal nematode larvae of sheep in Ontario, Canada
Authors:	Laura C. Falzon ¹ , Paula I. Menzies ¹ , John VanLeeuwen ² , Krishna P. Shakya ³ , Andria Jones-Bitton ¹ , Jacob Avula ³ , Jocelyn T. Jansen ⁴ , Andrew S. Peregrine ^{3*} ¹ Department of Population Medicine, Ontario Veterinary College, University of Guelph, Guelph, Ontario, Canada; ² Department of Health Management, Atlantic Veterinary College, University of Prince Edward Island, Charlottetown, Prince Edward Island, Canada; ³ Department of Pathobiology, Ontario Veterinary College, University of Guelph, Guelph, Ontario, Canada; ⁴ Ontario Ministry of Agriculture, Food and Rural Affairs, Elora, Ontario, Canada
Poster Number:	162

This study was carried out to describe pasture-level environmental conditions that may be associated with overwintering survival and infectivity of free-living gastro-intestinal nematode (GIN) stages on pasture. A one acre section of pasture grazed during the previous season by GIN-infected sheep was assessed on three farms in Ontario, Canada, starting in December 2009 after animal removal, until the following spring (May 2010) before animal turn-out. Environmental data were collected using electronic data-loggers. The presence and type of GIN larvae on the pasture sections were assessed by collecting monthly herbage and soil samples over the winter months. Infectivity of over-wintered larvae in the spring was assessed by grazing 16 naïve lambs for 28 days, after which the lambs were slaughtered and the contents of their gastro-intestinal tracts analysed for the presence of GINs. The lowest daily air and soil temperatures, and the lowest air relative humidity, were recorded in January, while the lowest daily soil water content was recorded in March. Free-living stages of *Trichostrongylus* spp. and *Nematodirus* spp. were isolated from herbage samples collected in March on one farm; no larvae were isolated from the other herbage and soil samples collected. GINs were recovered from all tracer lambs on all three farms. Overall, *Teladorsagia* sp. was the predominant species recovered, followed by *Nematodirus* spp. and *Trichostrongylus* spp. *Haemonchus contortus* was recovered from one animal on one of the farms, but at a very low level (50 parasites). Since the three farms were all selected on the basis of a reported history of clinical haemonchosis, the results suggest that *Haemonchus* larvae do not survive well on pasture during a central Canadian winter. In contrast, *Teladorsagia* sp., *Trichostrongylus* spp. and *Nematodirus* spp. are able to overwinter on pasture, even with limited snow cover, and are still infective for sheep in the spring.

Acknowledgements: This research was supported by the Ontario Ministry of Agriculture, Food and Rural Affairs – New Directions Research Program, with additional financial assistance from the Ontario Sheep Marketing Agency, the Nova Scotia Agricultural College – Organic Science Cluster, and the University of Guelph.



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Session Details:	8/29/2013 All about sheep 1130 - 1240 Meeting Room 2
Poster with 2 minute Oral Presentation Details:	Efficacy of monepantel against native US gastrointestinal parasites in sheep
Authors:	James Carmichael ¹ , Peter Rolfe ^{2*} , Krissy Utter ¹ , Linda Roycroft ¹ , Elizabeth Roberts ¹ , Richard Ehrhardt ³ , Tom Yazwinski ⁴ , Gil Myers ⁵ , Ray Kaplan ⁶ ¹ Novartis Animal Health US, Inc. Greensboro, NC USA; ² Novartis Animal Health Australasia Limited, NSW, Australia; ³ Michigan State University, East Lansing, MI USA; ⁴ University of Arkansas, Fayetteville, AR USA; ⁵ Myers Parasitology Services, Magnolia, KY USA; ⁶ University of Georgia, Athens, GA USA
Poster Number:	134

Monepantel is the first commercialized anthelmintic from the novel class of amino-acetonitrile derivatives (AAD) and is licensed in numerous countries. Currently in the United States (US), monepantel is registered under an Investigational New Animal Drug Application intended for use in sheep but is not approved for sale. The following studies were conducted to demonstrate effectiveness of monepantel against sheep nematodes acquired under natural grazing conditions in the US.

A dose confirmation study was conducted in lambs grazed on pastures in Kentucky and Indiana to assess the efficacy of monepantel (dose rate of 2.5 mg/kg body weight). Efficacy was determined by the reduction in worm burdens at necropsy in treated versus untreated animals (n=12 in each group). The second study was a multisite field study with locations in Arkansas, Georgia and Michigan. This later study was conducted with sheep of differing breeds, ages and physiological status (lambs, wethers, rams, non-lactating and lactating ewes). Efficacy was determined by fecal egg count (FEC) reduction between monepantel-treated (n=154) and negative control animals. Safety observations were also conducted.

In the dose confirmation study, monepantel was well-tolerated and effective against the adult stages of *Haemonchus contortus*, *Trichostrongylus axei*, *T. colubriformis*, *Teladorsagia circumcincta*, *Oesophagostomum venulosum*, and *Nematodirus spathiger*. The calculated percent efficacies based on geometric means were 99.8, 99.7, 97.0, 99.2, 98.4 and 95.9 respectively. Lambs treated with monepantel gained significantly more body weight compared to the control group (p<0.01). In the multisite field study, monepantel was safe and >99% effective in reducing both geometric and arithmetic mean FECs.

Monepantel was safe and highly effective in sheep at the minimum targeted dose of 2.5 mg/kg body weight against naturally acquired infections of gastrointestinal nematodes.

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Poster with 2 minute Oral Presentation Details:	Seasonal and environmental moderators of <i>Lucilia cuprina</i> populations in a Mediterranean climate
Authors:	Anthony Schlink*, Johan Greeff, John Karlsson Department of Agriculture and Food Western Australia, Mount Barker, Western Australia
Poster Number:	198

Lucilia cuprina (Weidemann) has long been recognized as the primary myiasis fly of sheep in Australia and costs the Australian sheep industry \$280 million/year (Horton and Hogan 2010). FlyBoss has been developed to predict the occurrence of fly strike and contains estimations of *Lucilia cuprina* populations throughout the year (Horton and Hogan 2010). This model was developed from weather records, fly populations and flystrike reports collected in eastern Australia.

Breech strike flock funded by AWI was used to determine whether breech strike was a heritable trait in un-mulesed Merino sheep in a Mediterranean climate zone at Mount Barker, Western Australia. The flock was not treated with chemicals or crutching to specifically prevent fly strike. All cases of fly strike were treated immediately by clipping the infected area and the area treated with a short-acting chemical. Fly trapping was undertaken to determine the onset of fly strike each year. Since 2010, fly traps were opened for 24 hours once a week during the peak fly season and less frequent for the remainder of the year. Weather records from the Mount Barker weather station were used.

Over 3 years, *Lucilia* populations peaked in November (week 47) with an average of 31.1 flies/trap. *Lucilia* was trapped in all months except August. Trap location significantly affected the number of *Lucilia* trapped. Traps located near trees averaged 6.25, 5.7 in the open areas and 3.4 flies/trap near water sources. When sheep were present in the paddock there were 7.1 flies/trap compared to 3.6 when sheep were not present. Fly population in the previous week, and weather data predicted fly trapping rates (r^2 adj.=0.538). If fly population in the previous week was excluded from the prediction model, then r^2 adjusted dropped to 0.485. Another set of traps has been established to evaluation the prediction models.

Acknowledgements:
Australian Wool Innovations Ltd for funding.

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Session Details:	8/29/2013 All about sheep 1130 - 1240 Meeting Room 2
Poster with 2 minute Oral Presentation Details:	Immunization of Sheep With Integral Gut Membrane Glycoprotein of <i>Haemonchus Contortus</i> in Northeastern Brazil
Authors:	Marcel Teixeira ¹ , David Smith ^{2*} , Jomar P. Monteiro ¹ , Fernando M. A. Albuquerque ¹ ¹ Brazilian Agricultural Research Corporation, Sobral, BRAZIL ² Moredun Research Institute, Midlothian, UNITED KINGDOM
Poster Number:	234

It is common knowledge that the parasite with the most negative impact on economic sheep farming in Brazil is *Haemonchus contortus*. In some of the traditional sheep farming areas of Brazil this parasite has developed multiple drug resistance, rendering sheep farming non-viable. A vaccine against *H. contortus* would be of massive benefit to the sheep industry. The aim of this work is to present data from experiment designed to study the use of low dose, native antigen sub-unit vaccine in a sheep farm in the semi-arid climate in Brazil. The vaccine was used strategically to prevent *Haemonchus* producing eggs during the period of highest incidence of worms on local conditions. About 90 ewes (> 12 months) grazing native pasture (Caatinga) were separated in two groups (n=45) vaccinated or not. The vaccine was administered subcutaneously to sheep according to the following schedule: three priming doses before the rainy season on days 0, 21 and 42 post vaccination; booster dose every six weeks for all ewes and a extra dose for peri parturient ewes. Clinical (Famacha score), parasitological (fecal egg counts) and haematological parameters (packet cell volume and eosinophil) were accessed each 15days and performance (weight gains and score corporation) monthly. The vaccination of sheep was able to reduce fecal egg counts significantly after 21days. Subsequent EPG counts reduced in the vaccinated group but not significantly, probably because *Haemonchus* challenge was mild. A slightly eosinophilia was observed in vaccinated sheep after third dose of vaccine but no differences was observed in the packet cell volume counts. Performance parameters (score corporation and weight gains) were not significantly affected by the vaccination. However, Famacha scores were slightly reduced in vaccinated sheep and during the first four months of experiment no sheep needed a salvage treatment. These are preliminary data from a long-term experiment.

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Session Details:	8/29/2013 All about sheep 1130 - 1240 Meeting Room 2
Poster with 2 minute Oral Presentation Details:	Comparison of three praziquantel (Cestocur®) treatment schedules for tapeworm (<i>Moniezia spp.</i>) infections and their impact on body weight gains in a German sheep flock
Authors:	Heinz Strobel ¹ , Martina de Ponte ² , Chandra Bhushan ³ ¹ Am Hopfenberg 8, 89352 Stoffenried, Germany, ² Martina de Ponte, Bayer Vital GmbH, 51368 Leverkusen, Germany, ³ Chandra Bhushan, Bayer Animal Health GmbH, 51368 Leverkusen, Germany,
Poster Number:	47

Three different treatment schedules with praziquantel (Cestocur®) were assessed in a Merino sheep flock from Southern Germany with history of severe recurrent *Moniezia spp.* infections. Three hundred Merino lambs between eight and 14 weeks of age were weighed and randomly allocated (by a handling unit for sheep) to three different groups after turn out on the pasture heavily contaminated with orbatid mites. They were treated with praziquantel (Cestocur®) at a dose of 3.75 mg/kg BW using the following schedules: Group 1 was treated four times at a monthly interval (Days 1, 31, 59 and 91). Group 2 was treated three times at six weeks intervals (Days 16, 59 and 105), and Group 3 was treated twice at an eight weeks interval (Day 31 and 91). Based on fecal examinations all lambs were negative for *Moniezia spp.* on Day 1.

On each observation day, body weights were recorded and fecal samples were examined for the presence of *Moniezia spp.* juveniles and proglottids. A flotation technique with saturated sodium chloride solution was used to detect *Moniezia spp.* eggs. All the animals were treated twice with moxidectin (on Days 16 and 105) in order to control concurrent gastrointestinal nematode infections.

On Day 126, Group 1 had a higher average body weight (49.9 ± 5.8 kg) than Group 2 (48.7 ± 5.5 kg) and Group 3 (47.5 ± 5.4 kg). Overall weight gains were significantly higher in Group 1 (22.5 ± 1.8 kg) when compared to Group 2 (20.8 ± 1.4 kg, p<0.0001) and Group 3 (19.3 ± 2.2 kg, p<0.0001).

Moniezia spp. proglottids were seen in the feces over time and in all three groups, however considerably lower in Group 1 when compared to Groups 2 and 3.



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Session Details:	08/29/2013 All about sheep 1130 – 1240 Meeting Room 2
Poster with 2 minute Oral Presentation Details:	Drench Use Practices: results of a questionnaire survey of beef cattle producers in Southern WA
Authors:	Jenny Cotter*, Brown Besier, Andrew van Burgel Department of Agriculture and Food Albany Western Australia, Australia
Poster Number:	128

A survey questionnaire regarding worm control and anthelmintic use practices was mailed to a random selection of about 100 beef cattle farmers in southern Western Australia (WA) in 2009. Subsequent phone conversations helped obtain 84 completed responses. This survey aimed to provide preliminary information for a following survey of anthelmintic resistance in cattle worms in WA.

Responses indicated that anthelmintics were used on 82% of beef farms, suggesting that the remaining 18% did not believe that worm infections were of significance in their herds. On properties where drenches were used, about 40% treated only when they believed parasites were ‘causing a problem’, while the remainder drenched at set times regardless of evidence of parasitism and not always at recommended seasonally strategic times. This indicates that drenching practices extended from too little use (and potentially poor worm control) to overuse (potentially leading to anthelmintic resistance). Of the anthelmintics used, 94% of treatments were with macrocyclic lactones (ML), with over 80% solely using pour on formulations. Scales to weigh cattle were used on only 22% of beef farms, suggesting the potential for under-estimating weights. When asked whether drenching resolved a parasite problem on the farm, 90% believed that drenches were working effectively, and were unaware that anthelmintic resistance was a potential risk.

The survey suggests that inefficient anthelmintic use may be widespread in WA, especially as a failure to follow recommended strategic programs, and potentially due to inaccurate dose administration. The heavy reliance on the ML group as a pour on formulation may have contributed to macrocyclic lactone resistance development (later detected by a faecal egg count reduction test survey). However, the likely causal factors for fenbendazole and levamisole resistance, also detected, are not clear from the questionnaire results.



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Session Details:	8/29/2013 Cause and Effect 1130 - 1240 Meeting Room 3
Poster with 2 minute Oral Presentation Details:	An overview of tissue inhibitors of metalloproteases of parasitic helminths – what we know and what we don't
Authors:	Cinzia Cantacessi ^{1*} , Andreas Hofmann ² , Alex Loukas ¹ ¹ James Cook University, Cairns, AUSTRALIA ² Griffith University, Brisbane, AUSTRALIA
Poster Number:	195

Tissue inhibitors of metalloproteases (TIMPs) are a multifunctional family of proteins that orchestrate extracellular matrix turnover, tissue remodelling and other cellular processes. In parasitic helminths, such as hookworms, TIMPs have been proposed to play key roles in the host-parasite interplay, including invasion of and establishment in the vertebrate animal host. Currently, knowledge of helminth TIMPs is limited to a small number of studies on canine hookworms, whereas no information is available on the occurrence of TIMPs in other parasitic helminths causing neglected diseases. In the present study, we conduct a large-scale investigation of TIMP proteins of a range of neglected human parasites (including the hookworm *Necator americanus*, the roundworm *Ascaris suum*, the liver flukes *Clonorchis sinensis* and *Opisthorchis viverrini*, as well as the schistosome blood flukes). This entails mining available transcriptomic and/or genomic sequence datasets for the presence of homologues of known TIMPs, predicting secondary structures of defined protein sequences, systematic phylogenetic analyses and assessment of differential expression of genes encoding putative TIMPs in the developmental stages of *A. suum*, *N. americanus* and *S. haematobium* which infect the mammalian host. Supported by the availability of gene manipulation technologies such as RNA interference and/or transgenesis, this work provides a basis for future functional explorations of helminth TIMPs and, in particular, of their role/s in fundamental biological pathways linked to long-term establishment in the vertebrate host, with a view towards the development of novel approaches for the control of neglected helminthiases.

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Session Details:	8/29/2013 Cause and Effect 1130 - 1240 Meeting Room 3
Poster with 2 minute Oral Presentation Details:	Impact of <i>Haemonchus contortus</i> within small ruminants in terms of host-parasite interaction
Authors:	Farhana Riaz Chaudhary ^{1*} , Muhammad Mushtaq ² , Muhammad. Fatah Ullah. Khan ³ , Mazhar Qayyum ¹ ¹ Department of Zoology, Pir Mehr Ali Shah-Arid Agriculture University, Rawalpindi. ² Livestock Khairmurat Production Unit, Fateh Jang, Attock ³ Small Ruminant Research Program, Animal Sciences Institute, National Agricultural Research Centre, Park Road, Islamabad
Poster Number:	56

Haemonchus contortus is a blood sucking endoparasite responsible for acute and chronic outbreaks of haemonchosis that may be associated with mortalities mainly in young ruminants. Said situation is mostly distressing in developing countries like Pakistan where, gastrointestinal worm burden pose a direct threat to both agricultural income and animal welfare. Thus proposed study was designed with specific aim to observe the trend of adaptation within *H. contortus* worms inside the host body in response to exposure of different climatic conditions. Such aspects were demonstrated in terms of parasitological and haematological changes within host body. A field trial of 12 months was conducted at selected farm (semi-arid: Livestock Kharimurat Production Unit), Potohar region, Pakistan. A total of 48 native tracer animals (24 kids; 24 lambs) were allocated randomly to assess the monthly fluctuations in the population structure of *H. contortus*. For one year, every month a batch of worm-free animals (n=4) were allowed to graze with their adults for 4 week before to be necropsied. Based on autopsy results higher significant level (P<0.05) of hypobiosis was observed in lambs than kids attaining a peak of hypobiotic larval frequency (L: 77%; K: 46%) in June. Parasitological results relying on the intensity of worm burden, faecal egg counts and larval cultures confirmed that sheep were significantly (P<0.05) more susceptible to worm infection than goats. Moreover, significant (P<0.05) correlation was exhibited between higher Wb and FECs with PCV and Hb levels. Moreover, FAMACHA® scoring has proved to be a good tool to depict varying degrees of anaemia and found to be significantly (P<0.05) more valid in lambs than kids. Result based findings had made it possible to explore the choice of effective strategic anthelmintic programmes for the prophylaxis and control of *H. contortus* in small ruminants that would help in reducing haemonchosis incidence in young animals.

Acknowledgements:

We would like to thank the Department of Zoology, Pir Mehr Ali Shah Arid Agriculture University Rawalpindi for funding this research.



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Session Details:	8/29/2013 Cause and Effect 1130 - 1240 Meeting Room 3
Poster with 2 minute Oral Presentation Details:	Glucan stimulation of Th1 host immune response is effective in defense against <i>Ascaris suum</i> larval migration
Authors:	Emília Dvorožňáková ^{1*} , Lýdia Hermanovská ¹ , Viera Revajová ² ¹ Institute of Parasitology, Slovak Academy of Sciences, Kosice, Slovak Republic ² University of Veterinary Medicine and Pharmacy in Kosice, Kosice, Slovak Republic
Poster Number:	235

The *Ascaris suum* infection induces elevated immunoglobulins IgE, eosinophilia and mastocytosis in the host due to the development of Th2 immune responses, particularly in the intestinal phase. The Th1 response present during the larval development of the parasite is inhibited by products of the Th2 cells. The study examined the effect of glucan immunomodulator (Th1 activator) in mice with experimental ascariasis. Glucans are β -(1,3)-D polymers of glucose present as a basic component of cellular wall of bacteria, fungi or yeasts.

In comparison with infected mice without glucan treatment, the parasite burden was reduced in mice treated with glucan. The numbers of *A.suum* larvae in the liver were significantly decreased (about 36 %) on day 4 post infection (p.i.) and also pulmonary larval migration was reduced on days 7 and 14 p.i. (about 38% and 17.6%, respectively).

Glucan increased the proliferative activity of splenic T cells within 2 weeks of the treatment and subsequent *A.suum* infection stimulated it even more for next 2 weeks. *A.suum* infection prolonged the stimulation of CD4+ T cells induced by glucan for next 2 weeks. Cytokine response of mice with glucan treatment was directed into Th1 type, production of IFN-gama was increased and subsequent *A.suum* infection did not reduced the cytokine synthesis. Th2 cytokine generation (IL-5, IL-10, IL-4) in infected mice was significantly decreased after glucan immunomodulation. Production of superoxide anion (O_2^-) in peritoneal and pulmonary macrophages was stimulated with maximum in glucan immunomodulated mice after *A.suum* infection on weeks 1 and 2 post infection.

The results suggest the glucan immunomodulation positively influenced the prime effectors of cell-mediated immunity, it stimulated synthesis of IFN-gama and metabolic activity of macrophages, that could contribute to a significant reduction of the parasitic infection in host.

Acknowledgements:

The work was supported by the Project “Competence centre for biomodulators and nutritional supplements - Probiotech (ITMS-26220220152)” on the basis of support from Operational Programme Research and Development, funded by the European Regional Development Fund.



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Session Details:	8/29/2013 Cause and Effect 1130 - 1240 Meeting Room 3
Poster with 2 minute Oral Presentation Details:	Persistent Canine Demodicosis in a Local Bred Mongrel Bitch following Prolonged treatment with Ivermectin and Oxytetracycline LA with Topical application of Cypermethrin
Authors:	George B.D.J. Ahmadu Bello University, Zaria, NIGERIA
Poster Number:	196

An eight year old mongrel bitch locally bred in Zaria, Nigeria has persistently suffered from a generalized, squamous demodicosis in the last one year despite regimented parenteral and topical treatment with ivermectin (Promectine LA, 10mg/ml, Invesa), Oxytetracycline dihydrate (oxy-200 LA,20%, VETINDIA Pharmaceuticals Ltd) and Cypermethrin (Cypermil pour-on, 5mg/ml, Ouro Fino). Treatments were carried out initially at monthly intervals but later changed to two-week intervals. The bitch littered seven puppies during this time which have remained apparently uninfected three months later. Low immunological competence due to age and stress of pregnancy may be immediately responsible for treatment failure but the efficacy and authenticity of the drugs/chemicals used may not be guaranteed considering the existing proliferation of adulterated/fake medication imported/manufactured in and outside Nigeria. Alternatively, more recent and efficient therapeutic combinations needs be tried.

Acknowledgements:

I wish to thank the authorities and staff of the Department of Veterinary Parasitology and Entomology Ahmadu Bello University, Zaria, Nigeria for the provision of facilities that enabled me to carry out this work.

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Session Details:	8/29/2013 Cause and Effect 1130 - 1240 Meeting Room 3
Poster with 2 minute Oral Presentation Details:	Molecular identification of Paramphistomes from cattle in Cajamarca, Peru
Authors:	Alonso Manrique ^{1*} , Rodrigo Sanabria ² , María Cabrera ¹ , Pedro Ortiz ¹ ¹ Laboratorio de Inmunología e Investigaciones Veterinarias, Facultad de Ciencias Veterinarias, Universidad Nacional de Cajamarca, PERÚ ² Centro de Diagnóstico e Investigaciones Veterinarias (CEDIVE), Facultad de Ciencias Veterinarias, Universidad Nacional de la Plata, Chascomús, ARGENTINA
Poster Number:	19

Paramphistomosis is a disease of domestic ruminants caused by digenetic trematodes, which mainly belong to the family paramphistomidae. The disease is an emerging problem in dairy cattle in the Cajamarca region of Peru during the last decade with a recent estimated prevalence of 59%. Morphological identification of paramphistomes species is difficult and the present study has adopted a molecular approach to identify the species affecting dairy cattle in this area. Thirty samples of *Paramphistomum* spp. collected individually from the rumen and reticula of cattle slaughtered at the Cajamarca's abattoir were analyzed by PCR-RFLP using the ITS2+ molecular marker from ribosomal DNA (rDNA), DNA from previously characterized *Paramphistomum leydeni* samples served as controls. All parasites amplified a band of ~500 bp. These amplicons were then restricted by the endonucleases *Hinf*I and *Tru*1I, and the latter produced identical fragments to *Calicophoron microbothrioides*. This finding supported a previous morphological classification. To confirm these results, two amplicons were selected, sequenced and compared with those reported in GenBank. A consensus sequence of 427 bp was 99% identical to *C. microbothrioides*. This is the first report of molecular characterization of the paramphistomes affecting dairy cattle in this region of Peru.

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Session Details:	8/29/2013 Cause and Effect 1130 - 1240 Meeting Room 3
Poster with 2 minute Oral Presentation Details:	RNA interference in adult <i>Ascaris suum</i> : A platform for drug target validation
Authors:	Ciaran J. McCoy ^{1*} , Neil D. Warnock ¹ , Erwan Atcheson ¹ , Louise E. Atkinson ¹ , Nikki J. Marks ¹ , Aaron G. Maule ¹ & Angela Mousley ¹ ¹ Queen's University Belfast, Belfast, UNITED KINGDOM
Poster Number:	174

Nematode parasites have a major socioeconomic impact worldwide. *Ascaris suum* is a gastrointestinal nematode parasite of swine which imposes a significant economic impact on pig farming profitability (see Roepstorff *et al.*, 2011), and has recently been recognised as an important zoonotic pathogen (Nejsum *et al.*, 2012). The large size of *A. suum* has facilitated its development as a tractable model species for nematode parasite biochemistry, neurobiology and physiology research, driving comparative studies with the free-living model *Caenorhabditis elegans*. In addition, the recent characterization of the *A. suum* genome and transcriptome (Jex *et al.*, 2011) has facilitated genome-guided drug discovery biology and prompted the development of functional genomics tools in this species. RNA interference (RNAi) is a reverse genetic technique which can be utilized to investigate gene function, and validate novel antiparasite-drug targets. Whilst RNAi has been reported in the L3 larval stage of *A. suum* (Islam *et al.*, 2005; Xu *et al.*, 2010; Chen *et al.*, 2011), it has not been demonstrated in adults, limiting the utility of this gene silencing tool. Here we report the development of an RNAi platform for adult *A. suum*. Double stranded (ds)RNAs were injected into the pseudocoelomic cavity of adult female worms and successful induction of RNAi was determined through quantitative PCR transcript analysis, and by monitoring encoded protein expression and worm phenotype. In this study RNAi responses are reported for a range of gene targets, expressed in a variety of tissue types. The data presented demonstrates that adult *A. suum* possess a functional RNAi pathway that can be triggered by the injection of dsRNA (200 ng/µl) into the pseudocoelomic cavity. In addition, we highlight the RNAi-susceptibility of target genes with disparate expression patterns and the ability to induce RNAi in tissues distant from the site of dsRNA injection.

Acknowledgements:

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Session Details:	8/29/2013 Cause and Effect 1130 - 1240 Meeting Room 3
Poster with 2 minute Oral Presentation Details:	Lectins and cytokines expression in abomasums of naturally helminth infected ovine.
Authors:	Lívia Ribeiro Mendonça* ¹ , Sandra Mayumi Nishi ¹ , Cristiane Carina Yuki ¹ , Bárbara Maria Paraná Silva Souza ¹ , Sabrina Mota Lambert ¹ , Maria Angela Ornelas de Almeida ¹ ¹ Escola de Medicina Veterinária e Zootecnia, Universidade Federal da Bahia, Salvador, Bahia, Brazil.
Poster Number:	20

Lectins are carbohydrate binding proteins involved in both innate and adaptive immune response against helminthes inducing a Th2 response and promoting specific activity of eosinophils, basophils and mast cells. The aim of the study was to detect collectins, galectins and cytokines gene expression in ovine abomasum during natural helminth infection evaluating different age groups. Three groups of six males were formed according to age: (I) up to one month, (II) four to six months and (III) more than 18 months. They were necropsied, parasite burden determined and fragments of the abomasums were properly secured to molecular techniques. After RNA extration using Trizol, samples were DNase treated and gene expression quantification was performed by using real time RT-PCR for surfactant protein A, conglutinin, galectin 14 and 15, interleukine 4 and interferon-gamma. *Haemonchus contortus* was the major parasite observed in the abomasal content with average of 173, 1306 and 956 in groups I, II and III, respectively. Surfactant protein A, conglutinin, galectin 14 and 15, interleukine 4 and interferon-gamma were detected in abomasal tissue in all groups, and statistically significant differences were observed at conglutinin-like and galectin 15 genes up-regulation in Group II (p < 0.05), whereas no difference was detected between Group I and III. There was no correlation between parasite burden and age with galectin-15 and conglutinin like expression.

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Session Details:	8/29/2013 Cause and Effect 1130 - 1240 Meeting Room 3
Poster with 2 minute Oral Presentation Details:	Effects of hydrolase inhibitors on proteomic profiles of <i>Oesophagostomum dentatum</i> larvae
Authors:	Martina Ondrovics ^{1*} , Katja Silbermayr ¹ , Robin B. Gasser ² , Makedonka Mitreva ^{3,4} , Neil D. Young ² , Ebrahim Razzazi-Fazeli ⁵ , Anja Joachim ¹ ¹ Institute of Parasitology, Department of Pathobiology, University of Veterinary Medicine Vienna, Veterinaerplatz, Vienna, AUSTRIA ² Faculty of Veterinary Science, The University of Melbourne, Parkville, Victoria, AUSTRALIA ³ Genome Institute, Washington University School of Medicine, MO, USA ⁴ Division of Infectious Diseases, Department of Internal Medicine, Washington University School of Medicine, MO, USA ⁵ VetCore, University of Veterinary Medicine Vienna, Veterinaerplatz, Vienna, AUSTRIA
Poster Number:	175

Parasitic nematodes of animals and humans are of major socioeconomic importance worldwide. Widespread anthelmintic drug resistance has stimulated fundamental research toward designing new interventions. Central to this effort could be the discovery of new drug targets through an improved understanding of developmental processes at the molecular level. Here, we combined *in vitro* drug testing with transcriptomic, proteomic and bioinformatic approaches to identify and characterize proteins involved in the larval development of *Oesophagostomum dentatum*, the porcine nodule worm. We assessed the effects of four different hydrolase inhibitors on the *in vitro* development of third-stage to fourth-stage larvae of *O. dentatum*. Adding 1.4 mM 1,2-epoxy-3-(4p-nitrophenoxy)propane, 125 µM iodoacetamide, 12.5 µM o-phenanthroline, or 5 mM sodium fluoride impeded normal larval development by 93.0 ± 5.6%, 93.9 ± 5.1%, 100%, and 90.8 ± 3.2%, respectively, inhibiting larval development in *O. dentatum*. We compared the proteomic profiles of development-inhibited larvae with those of uninhibited control larvae by two-dimensional gel electrophoresis and selected 28 differentially expressed protein spots and one reference spot for subsequent MALDI-TOF mass spectrometric analysis. We then annotated the 29 protein sequences using available expressed sequence tag (EST) data for *O. dentatum* and assigned 22 distinct proteins, and identified 12 and three proteins inferred to be involved in various larval developmental processes and moulting, respectively, to be down-regulated in development-inhibited larvae. This first proteomic analysis of *O. dentatum* provides foundation for investigating key biological and biochemical pathways in this parasite and assessing new drug targets.



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Session Details:	8/29/2013 Cause and Effect 1130 - 1240 <i>Meeting Room 3</i>
Poster with 2 minute Oral Presentation Details:	Monepantel – characteristics of MPTL-1 receptor in <i>Xenopus</i> oocytes
Authors:	Lucien Rufener, Erwin Sigel, Roland Bauer, Robin Beech, Ronald kaminsky
Poster Number:	137

Previous studies have shown that the MPTL-1 receptor is the primary target of monepantel (Zolvix). Phylogenetic studies have demonstrated that *mptl-1* belongs to the nematode specific DEG-3 subfamily which is genetically diverse from other receptor families like the levamisole and macrocyclic lactone sensitive receptors. It was possible to reconstitute a functional MPTL-1 channel in *Xenopus* oocytes. The channel is modulated by choline chloride preferentially, and to a lesser extent by nicotine and acetylcholine. Monepantel acts as a direct agonist on the receptor in the nanomolar range, and binds irreversibly to MPTL-1 resulting in a constant activation of the channel. The different mode of action of monepantel to the other anthelmintics explains the efficacy of monepantel against levamisole-, benzimidazole-, and macrocyclic lactone-resistant nematodes including multidrug resistant isolates.



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Session Details:	8/29/2013 Cause and Effect 1130 - 1240 Meeting Room 3
Poster with 2 minute Oral Presentation Details:	Identification and Modulation of cells and mediators up regulated in parasite resistant sheep
Authors:	MD. Shakif-UI-Azam ¹ , Mark Sandeman ¹ , David Piedrafita ¹ ¹ Monash University, Gippsland Campus, Churchill, VIC, Australia
Poster Number:	236

Nearly 700 million of the world’s poorest people rely on livestock for their survival. Farm animals, such as goats and sheep, represent a critical and often sole source of economic security for people in the developing world. Successful livestock management forms a key stepping stone in sustainable and economic growth (1) with global average losses due to animal disease estimated at 20% (2).

Gastrointestinal nematode (GIN) worm infections are a major disease problem in small ruminants such as sheep & goats. Of the GIN parasites, *Haemonchus contortus* is the most economically important disease of sheep and goats (3). And these gastrointestinal nematodes cost the Australian sheep industry \$370 million annually or around 8.7% of its total value (4). Widespread resistance to most current drug treatments will require the development of better control strategies and protective immune responses.

The aim of the current project is to use molecular assays to identify innate mediators involved in parasite rejection using sheep at the extremes of genetic resistance to worm infection in a commercial sheep flock. A range of techniques including histology, DTH reactions and real time RT-PCR will be used. Molecules that vary in response to parasite infection will be candidates for diagnostic tests or use as genetic markers of resistance/susceptibility. The use of metabolic inhibitors in the ex-vivo/in vitro assays may also allow the modulation of the protective larval rejection response and elucidate the major biological mediators of this rejection mechanism.

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Session Details:	8/29/2013 Drugs - do they REALLY work? 1130 - 1240 Meeting Room 5
Poster with 2 minute Oral Presentation Details:	Efficiency of different genotypes of <i>Lippia sidoides</i> on eggs and larvae of <i>Haemonchus contortus</i>
Authors:	Suzana Gomes Lopes ¹ , Giselle Cutrim de Oliveira ¹ , Lilyan Bruna Gomes Barros ¹ , Ítala Caroline Pereira Duarte Lobo ¹ , Elizangela Mércia de Oliveira Cruz ² , Arie Fitzgerald Blank ² , Livio Martins Costa-Júnior ^{1*} ¹ Laboratory of Veterinary Parasitology (LPA), Federal University of Maranhão, Maranhão, BRAZIL ² Department of Agronomy, Federal University of Sergipe, Sergipe, BRAZIL
Poster Number:	239

The nematodes are the major sanitary problem of goat farms in Brazil. The anthelmintic resistance is widespread. Plants can be used to helminth control, however phenotypic and genotypic features can change the phytochemical composition and this may influence the biological activities. The present study aimed to evaluate different genotypes of *Lippia sidoides* and their effect on eggs and larvae of *Haemonchus contortus*. Three genotypes of *L. sidoides* were maintained under the same conditions. The essential oils (EO) were extracted by hydrodestillation and their chemical analysis was performed using a CG-MS. Egg hatch and larval exsheathment tests were performed. The effects of EO of *L. sidoides* on *H. contortus* diverged among genotypes (p<0.001). The 103 and 104 genotypes were more efficient to inhibit the hatching of eggs showing the lowest values of IC₅₀, 661.9 and 469.7 µg.mL⁻¹ respectively. The ovicidal effect of 006 genotype was only observed at higher concentrations thus obtaining the IC₅₀ value of 7,906.0 µg.mL⁻¹. Comparing the efficiency of different genotypes, only the 103 e 104 produced a significant inhibitory effect on hatch eggs of *H. contortus* compared to the control group. The exsheathment larval was affected negatively only by 006 genotype differing significantly to the control and the other genotypes of *L. sidoides*. All EO of *L. sidoides* genotypes were efficient against eggs of *H. contortus*, however differences in this efficiency were observed according to the genotype. Studies about anthelmintic effect on other target-parasites and *in vivo* tests are essential to analyze how the *L. sidoides* genotype, and your phytochemical composition, is the best against gastrointestinal nematodes of goats.

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Session Details:	8/29/2013 Drugs - do they REALLY work? 1130 - 1240 Meeting Room 5
Poster with 2 minute Oral Presentation Details:	A decrease in the efficacy of worm suppressive treatments observed during lactation in ewes.
Authors:	Michelle Dever* ¹ , Lewis Kahn ¹ , and Sara Bowers ¹ ¹ Animal Science, School of Environmental and Rural Science, University of New England, Armidale NSW 2351 AUSTRALIA
Poster Number:	24

A common strategy for controlling parasitic nematodes in peri-parturient ewes in Australia is to administer Cydectin® Long Acting (moxidectin 20g/L, Virbac Animal Health) or an anthelmintic capsule pre-lambing. An experiment was conducted with two mobs of 120 Border Leicester x Merino ewes on each of three farms. Half the ewes (CAP) were serially treated (60-105 day intervals) with a combination of long (Cydectin® LA and albendazole 100-day Extender capsule, Merial) and short (Zolvix®, Novartis Animal Health Australia) acting anthelmintics to suppress infection. All ewes also received short-acting treatments at 2 weeks pre and 5 and 17 weeks post lambing. At commencement of experiment, efficacy (mean, lower - upper 95% confidence limits) of moxidectin oral (1g/L) against *Haemonchus contortus* for the three farms (A, B & C) was 93% (80-97), 90% (53-98) and 100% (98-100) and albendazole (19g/L) was 90% (78-96), 74% (0-94) and 99% (98-100).

Worm egg counts were conducted 2 weeks pre-lambing and 5, 17 (weaning) and 26 weeks post lambing (9 weeks after weaning). Mean efficacies against *H. contortus* on the farms were 100%, 99%, 100% pre-lambing (35-49 day treatment interval), 85%, 86%, 100% at 5 weeks, 0%, 0%, 99% at 17 weeks (80-105 day interval) and 96%, 88%, 99% at 26 weeks post lambing (60-68 day interval) respectively for each farm (A, B & C).

The decrease in effectiveness of the suppressive treatments observed in lactating ewes may be attributed to moxidectin due to its extreme lipophilic nature and excretion in milk, while benzimidazoles are not lipophilic. That efficacy against *H. contortus* declined on farms where moxidectin oral was already ineffective suggests that loss of moxidectin via milk may have been sufficient to have significant effects on the survival of “resistant” *H. contortus*. If confirmed, these observations may impact the timing of administering Cydectin® LA in ewes.

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Session Details:	8/29/2013 Drugs - do they REALLY work? 1130 - 1240 Meeting Room 5
Poster with 2 minute Oral Presentation Details:	The efficacy of 4 anthelmintic treatments against strongylids in horses in Spain
Authors:	Douglas Rugg ¹ , Thomas Geurden ¹ , Bruno Besognet ¹ , Alejandro Bohórquez ² , Elkin Florez ² , Nélide Fernández Pato ² , Francisco Rojo Vázquez ³ , Aránzazu Meana ² ¹ Zoetis ² Universidad Complutense de Madrid, Facultad de Veterinaria, Madrid, Spain. ³ Universidad de León, Avda. Facultad de Veterinaria,León, Spain
Poster Number:	166

The efficacy after an oral treatment with ivermectin (IVM), moxidecin (MOX), pyrantel (PYR) and fenbendazole (FEN) was evaluated on 11 study sites in Spain. In total, 207 horses were examined. All horses were naturally infected with gastro-intestinal nematodes. The animals were randomly allocated to one of the treatment groups based on the pre-treatment FEC. The FEC were performed before treatment and 14 days after treatment. All faecal samples were examined using a modified McMaster technique, with a sensitivity of 10 eggs per gram of faeces. Assessment of efficacy was based on the difference between the arithmetic mean FEC prior to treatment and 14 days post treatment, for each treatment group separately. The efficacy of MOX was high (99-100%) on all study sites, except one study site with an efficacy of 95% (95% confidence interval 79-100%), due to the observation of eggs in 2 out of the 5 animals after treatment. The efficacy of IVM was high (99-100%) on all farms. The efficacy of PYR was somewhat variable (94-100%), with the lower 95% CI dropping below 90% on 4 farms. The efficacy of FEN was not evaluated on 1 farm. On the remaining 9 farms the efficacy was high (99-100%). The high efficacy of MOX and IVM at D14 is in line with other reports in Europe. The high efficacy of PYR and FEN is in contrast to other studies, and might be due to the lower frequency of deworming of horses in Spain compared to other European horses.



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Session Details:	8/29/2013 Drugs - do they REALLY work? 1130 - 1240 Meeting Room 5
Poster with 2 minute Oral Presentation Details:	In vitro validation of the anthelmintic properties of Ethiopian medicinal plant extracts
Authors:	Spiridoula Athanasiadou ¹ , Etana Debela ² , Aduugna Tolerra ³ , Ketema Tolossa ⁴ , Sandra Terry ¹ and Jos GM Houdijk ^{1*} ¹ Scotland's Rural College (SRUC), Edinburgh, UNITED KINGDOM ² School of Veterinary Medicine, Hawassa University, Hawassa, ETHIOPIA ³ School of Animal and Range Science, Hawassa University, Hawassa, ETHIOPIA ⁴ Department of Chemistry, Hawassa University, Hawassa, ETHIOPIA
Poster Number:	208

Although medicinal plants play an important role for parasite control in developing countries, scientific evidence on plant efficacy and side effects is scarce, hampering the establishment of phytomedicine as a reliable parasite control strategy. Here, we present the validation on the anthelmintic properties of medicinal plant preparations originating from Ethiopia against *Teladorsagia circumcincta*. The selection of plants was based on an ethno-botanical survey (Tolossa et al., 2013), which consisted of a detailed review of existing, anecdotal information on medicinal plants use for endo-parasite control in Ethiopia. A larval motility assay was adapted from Smout et al. (2010) to quantify the anthelmintic activity of the plant extracts, where worm motility was recorded for 24 h prior and 24 h after the addition of the extract. In total 90 extracts were tested from 30 plants; dried plant matter was extracted by three solvents, methanol, 70% methanol and H₂O. From the 30 plants, 25 were routinely used by the traditional healers against endo-parasites. For 23 of these plants, this activity was validated in extracts originating from one, two or all three solvents. Efficacy of these extracts varied, with at least one of the extracts of each plant resulting in 100% inhibition of motility, a statistically significant outcome compared to motility of control larvae. Furthermore, 3 plants that have not previously been associated with endo-parasite control, showed anthelmintic activity *in vitro*. The study shows the importance of validating ethnoveterinary knowledge with controlled experiments. Although the possibility that procedures used here did not result in the extraction of the active compounds in the unvalidated plants can not be excluded at this stage, it is more likely that these are just not present. *In vitro* validations as presented here will be followed by *in vivo* testing of active and selected inactive extracts to confirm biological activity.

Acknowledgements:

The authors gratefully acknowledge funding from the DFID/BBSRC/SG CIDLID program (BB/H009299/1).

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Tolossa K, Debela E, Athanasiadou S, Tolera A, Houdijk JGM (2013) Assessment of ethno-medicinal plants used for treatment of livestock ailments by traditional healers in southern Ethiopia. Proceedings of the 24th International Conference of the World Association for the Advancement of Veterinary Parasitology (submitted)

Smout M.J., Kotze A.C., McCarthy J.S., Loukas, A. 2010. PLoS Neglected Tropical Diseases 4(11), e885.



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Session Details:	8/29/2013 Drugs - do they REALLY work? 1130 - 1240 Meeting Room 5
Poster with 2 minute Oral Presentation Details:	Efficacy and safety of an new oral praziquantel formulation against <i>Dicrocoelium dendriticum</i> in llamas
Authors:	Agnes M. Dadak ¹ , Claudia Wieser ¹ , Anja Joachim ^{2*} , Sonja Franz ³ ¹ Department of Biomedical Sciences, Institute of Pharmacology and Toxicology, University of Veterinary Medicine Vienna, 1210 Vienna, Austria ² Department of Pathobiology, Institute of Parasitology, University of Veterinary Medicine Vienna, 1210 Vienna, Austria ³ Department for Farm Animals and Veterinary Public Health, Clinic for Ruminants, University of Veterinary Medicine Vienna, 1210 Vienna, Austria
Poster Number:	35

In contrast to other ruminants, South American camelids (SAC) are highly susceptible to infections with *Dicrocoelium dendriticum* and may suffer from severe pathological changes of the liver and bile system due to infection. Therapeutic options for treatment are limited. The drug of choice is praziquantel but the dose recommended for effective treatment requires large volumes of the currently available commercial formulations which have to be applied by gavage. To address this problem, the efficacy of two different dose rates of praziquantel in a special, patented formulation was investigated in llamas suffering from natural *D. dendriticum* infections. 53 llamas of mixed sex and age were examined under field conditions. At the beginning of the study, the animals were examined (including faecal examination), weighed, randomly allocated to one of the treatment groups (n = 21 each) or the control group (n = 11) and dosed orally using a praziquantel-containing paste specifically produced for high-dose treatment (250 mg/ml) at a dose of either 25 mg (group 1) or 50 mg (group 2) per kg BW. Criteria for efficacy were faecal egg count reduction (FECR) and extensity effect. No animal showed signs of clinical dicrocoeliosis during the study. Animals from group 1 showed a FECR of 85%, those from group 2 a FECR of 91%. Almost twice the number of animals of group 1 (33%) still shed eggs two weeks after treatment compared with group 2 (19%). No side effects were recorded; dosing with the praziquantel paste was easy and convenient and did not require gavage. The results of this study indicate that 50 mg/kg oral praziquantel is required for efficacious dosing and that this dose rate in the paste formulation is safe in llamas and thus is recommended for the treatment of SAC naturally infected with *D. dendriticum*.



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Session Details:	8/29/2013 Drugs - do they REALLY work? 1130 - 1240 Meeting Room 5
Poster with 2 minute Oral Presentation Details:	Relative potency of macrocyclic lactones in <i>in vitro</i> assays with larvae of susceptible and drug-resistant Australian isolates of <i>Haemonchus contortus</i> and <i>H. placei</i>
Authors:	Angela Ruffell ¹ , Gareth Kelly ² , Malcolm Knox ³ , Andrew Kotze ^{1*} ¹ CSIRO Animal, Food and Health Sciences, Brisbane, Australia ² Virbac Animal Health, Australia ³ CSIRO Animal, Food and Health Sciences, Armidale, Australia
Poster Number:	139

The present study aimed to use larval development assays to determine the relative potency of various commercial macrocyclic lactone (ML) actives against drug-susceptible and drug-resistant Australian isolates of important parasites of sheep and cattle, *Haemonchus contortus* and *H. placei*, respectively. Abamectin was the most potent chemical (lowest IC₅₀ values) towards the drug-susceptible *H. contortus* Kirby 1981 isolate. The abamectin IC₅₀ values were approximately 2-fold lower than for ivermectin, moxidectin, eprinomectin and doramectin. Moxidectin and abamectin were the most potent chemicals towards the resistant *H. contortus* isolate (Wallangra 2003). This isolate showed resistance ratios up to 70-fold towards eprinomectin. The resistance ratio for this species was lowest with moxidectin (ratio of 4.0-fold). Abamectin was also the most potent chemical towards both drug-susceptible (Bremner 1973) and drug-resistant (Dayboro 2011) *H. placei* isolates. The larval development assay only showed low levels of resistance for the drug-resistant *H. placei*, with resistance ratios ranging from 1.7-2.0 fold for moxidectin and abamectin, up to 3.3-fold for eprinomectin. The distinctions between the relative resistance ratios for the various drugs towards *H. placei* were less clear than for *H. contortus*, in accordance with the lower resistance shown by this isolate *in vivo* compared to the highly resistant *H. contortus* isolate. This study has examined the readily-accessible larval life stages of these parasites in *in vitro* assays, and, hence, the relationship between our findings and relative drug efficacies *in vivo* remains to be determined. Despite this, the study accords with some evidence from the use of these commercial anthelmintics in the field in demonstrating the potency of moxidectin and abamectin against ML-resistant *H. contortus*. The study also highlights the usefulness of eprinomectin as a readily-available compound which is a more sensitive marker for ML resistance in *in vitro* assays than the other ML compounds examined.

Acknowledgements:

The authors wish to thank Virbac Australia for financial support.



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Session Details:	8/29/2013 Drugs - do they REALLY work? 1130 - 1240 Meeting Room 5
Poster with 2 minute Oral Presentation Details:	Evaluation of nematocidal activity of ethnomedicinal plant extracts using the model nematode <i>Caenorhabditis elegans</i>
Authors:	Kumarasingha, R. ^{1,2*} , Shaw, J. ¹ , Palombo, E.A. ¹ , Bhawe, M. ¹ , Yeo, T.C. ³ , Lim, D.S.L. ³ , Tu, C.L. ³ , Boag, P.R. ² ¹ Environment and Biotechnology Centre, Faculty of Life and Social Sciences, Swinburne University of Technology, Australia. ² Department of Biochemistry and Molecular Biology, Monash University, Australia. ³ Sarawak Biodiversity Centre, Kuching, Sarawak, Malaysia.
Poster Number:	138

A wide variety of plants have been used in traditional medicine for the prevention and treatment of gastrointestinal parasites. Among these plants and plant products, there may be some that are effective against worms that have already developed resistance to commercially available anthelmintic drugs. In this study, we selected plant extracts that indigenous community from Sarawak, Malaysia, used in their de-worming remedies and tested their anthelmintic activity using the model nematode, *C. elegans*. To further investigate their effect on *C. elegans*, we took advantage of the vast genetic resource of *C. elegans* to characterize the stress responses of the plant extracts. The plant extracts were applied to transgenic *C. elegans* worms that contained reporter genes for specific stress response pathways (mitochondrial, proteasomal etc.). Most of the plant extracts showed some anthelmintic activity and interestingly, the induced stress responses differed between the plant extracts and were different to those of current commercial available anthelmintics, Doramectin and Levamisole. This demonstrates that selecting plants on the basis of their traditional application may be an important approach to identify new anthelmintic compounds. Moreover, the use of *C. elegans* model system provides a tool for rapidly screening the potency and mechanism of action of plant extracts *in vitro*.



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Session Details:	8/29/2013 Drugs - do they REALLY work? 1130 - 1240 Meeting Room 5
Poster with 2 minute Oral Presentation Details:	Pharmacokinetics and efficacy of large ivermectin doses in lambs parasitized with resistant <i>Haemonchus contortus</i>
Authors:	Luis Alvarez ¹ , Gonzalo Suarez ² , Adrian Lifschitz ¹ , Candela Cantón ¹ , Laura Ceballos ¹ , Laura Moreno ¹ , Carlos Lanusse* ¹ ¹ Laboratorio de Farmacología, Centro de Investigación Veterinaria de Tandil (CIVETAN), CONICET, Facultad de Ciencias Veterinarias, UNCPBA. Tandil, ARGENTINA. ² Laboratorio de Farmacología, FCV, UDELAR, Montevideo, URUGUAY.
Poster Number:	237

The main goals of the current work were: a) to assess the ivermectin (IVM) plasma disposition kinetics after its administration at the recommended, x5 and x10 times dose rates to lambs and, b) to compare the clinical efficacy of the same IVM dosages in lambs infected with an IVM-resistant strain of *Haemonchus contortus*. There was two separated trials, where IVM was administered either subcutaneously (Experiment I) or intraruminally (Experiment II). Each experiment involved twenty-four (24) lambs artificially infected with a highly resistant *H. contortus* strain. Animals were allocated into 4 groups (n=6) and treated with IVM at either 0.2 (IVM_{x1}), 1 (IVM_{x5}) or 2 mg/kg (IVM_{x10}). Plasma samples were collected up-to 12 days post-treatment and analysed by HPLC. An untreated-control Group was included to assess the comparative anthelmintic efficacy of the different treatments. Parametric and non-parametric tests were used to compare the statistical significance of the results (P<0.05). After the subcutaneous treatment, the IVM plasma area under the concentration-time curve (AUC) increased from 41.9 (IVM_{x1}) up to 221 (IVM_{x5}) and 265 ng.day/mL (IVM_{x10}), indicating some type of non-proportionality in the dose-systemic exposure relationship. Consistently, the efficacies against resistant *H. contortus* after the subcutaneous treatment were 44% (IVM_{x1}), 75% (ABZ_{x5}) and 76% (ABZ_{x10}). However, the intraruminal IVM treatment reached clinical efficacies ranging from 48 (IVM_{x1}) up to 96 (IVM_{x5}), and 98% (IVM_{x10}). The large IVM concentrations achieved at the abomasal content after its intraruminal/oral administration compared to the subcutaneous injection (Lloberas et al, 2011), may have accounted for a greater amount of drug reaching the adult parasite. An enhanced abomasal drug exposure may explain the improved efficacy against this recalcitrant *H. contortus* strain observed only after the intraruminal administration at 5 and 10-fold the IVM therapeutic dosage.

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Session Details:	8/29/2013 Drugs - do they REALLY work? 1130 - 1240 Meeting Room 5
Poster with 2 minute Oral Presentation Details:	Pharmaco-therapeutic evaluation of the closantel-moxidectin combination in lambs
Authors:	Gonzalo Suarez ¹ , Luis Alvarez ² , Daniel Castells ³ , Cecilia Berretta ¹ , Silvia Bentancor ¹ , Pietro Fagiolino ⁴ , Carlos Lanusse ^{*2} ¹ Area Farmacología, Facultad Veterinaria, UDELAR, URUGUAY. ² Laboratorio de Farmacología, Centro de Investigación Veterinaria de Tandil (CIVETAN), CONICET, Facultad de Ciencias Veterinarias, UNCPBA. ARGENTINA. ³ Secretariado Uruguayo de la Lana, URUGUAY. ⁴ Departamento Ciencias Farmacéuticas, Facultad Química, UDELAR, URUGUAY.
Poster Number:	144

The serious widespread development of nematode resistance has motivated the use of combined anthelmintic formulations. However, the advantages/disadvantages of the combined use of anthelmintics require further scientific characterization. The goals of the current trial were: a) to characterize the pharmacokinetics (PK) of CLS and MXD administered orally and subcutaneously either separately or co-administered (CLS+MXD) to lambs; b) to compare the nematocidal activity of both molecules given separately or co-administered to lambs infected with resistant nematodes. Seventy (70) Corriedale lambs naturally infected with multiple resistant gastrointestinal nematodes were involved on the following trials: a) *PK trial*: The animals were allocated into six groups and treated with either CLS (10 mg/kg), MXD (0.2 mg/kg) or with the a CLS+MXD combined formulation by both the oral and subcutaneous routes. Blood samples were collected over 28 days post-treatment and drug plasma concentrations measured by HPLC. b) *Efficacy trial*: An untreated control group (n=10) was included. The efficacy at 13 days post-treatment was estimated by the faecal egg count reduction test (FECRT). A higher systemic exposure (~ 55 and 208% measured as plasma AUC) of both CLS and MXD were observed after the parenteral compared to the oral administration of both molecules in lambs. The combined administration of both anthelmintics did not markedly alter their disposition kinetics. The administration of both molecules as a single active principle reached efficacy levels (estimated as the FECRT) ranging from 80% (MXD oral), 84% (CLS oral) up to 85% (CLS sc) and 92% (MXD sc). However, the combined treatments given both orally and subcutaneously reached a 100% efficacy. While the co-administration CLS+MXD did not show any adverse pharmacokinetic interaction, their combined anthelmintic effect was sufficient to restore the maximum efficacy levels, which were not reached by the individual active ingredients. This work is a further contribution to the need of more pharmacological investigation before drug combinations are developed and introduced into the market.



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Session Details:	8/29/2013 Drugs - do they REALLY work? 1130 - 1240 Meeting Room 5
Poster with 2 minute Oral Presentation Details:	Field assessment of the effect of condensed tannins from Quebracho (<i>Schinopsis balansae</i>) against gastrointestinal nematodes of cattle under range conditions, in Uruguay
Authors:	America Mederos ^{1*} ; Georgget Banchero ¹ ; Jose Piaggio ² ; Beatriz Carracelas ¹ ; Rodney López ³ ; Martin do Carmo ¹ ; F. Montossi ¹ ¹ National Research Institute for Agriculture, URUGUAY; ² Veterinary Faculty, Montevideo, URUGUAY; ³ Private Veterinary Surgeon, Salto, URUGUAY
Poster Number:	238

Reports on the development of anthelmintic resistance in cattle gastrointestinal nematodes (GINs) are becoming more common. While several studies have been performed to investigate the use of alternative control methods in small ruminants, there is little in the literature on their use in cattle. The aim of this study was to evaluate the effect of condensed tannins extracted from Quebracho (QT) on GINs in cattle.

A complete randomized field trial was conducted at La Magnolia research station, Tacuarembó, Uruguay. Forty six Braford yearling heifers (mean weight=200kg) with mixed GIN infections were randomly assigned to two experimental groups: control or treatment. The control group received a concentrate containing 15% protein while the treatment group received the same supplement, plus 4% QT (Bioquina®) at 1% body weight. Each group was randomly allocated to a native grass paddock of 9.5Ha, and left to graze for a period of 63 days (July-September 2012). Production traits were recorded and fecal samples were collected from individual animals fortnightly. Infective GIN larvae were identified from coprocultures and pasture. Summary statistics were performed, and a mixed linear regression model using the log fecal egg counts (FECs), was fit using SAS 9.2.

The arithmetic mean FECs decreased from 372 to 102 and from 200 to 33 for the control and treatment group, respectively. The main GIN genus identified through coprocultures was *Cooperia* spp (88% and 83% in control and treatment groups, respectively). The statistical analysis indicated that the median FECs were 16.2 times higher in the control group, compared with the treatment group (p<0.0001).

These results suggest that the addition of 4% QT to a feed supplement effectively reduced the FEC burden of yearling heifers kept under range conditions. The production performance of the heifers was good and there was no statistical difference between treatments (results not presented).

Acknowledgements:

We acknowledge Dr. Andres Salvo for providing the quebracho extract Bioquina®

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Session Details:	8/29/2013 Drugs - do they REALLY work? 1130 - 1240 Meeting Room 5
Poster with 2 minute Oral Presentation Details:	First report of multiple anthelmintic resistance in gastrointestinal nematodes of sheep in Colombia
Authors:	Carlos Manuel Barragán García ¹ , Lew Kan Sprenger ² , Efraín Benavides Ortiz ¹ , Marcelo Beltrão Molento ^{2*} ¹ Universidad De La Salle, Bogota, COLOMBIA ² Federal University of Paraná, Curitiba, BRAZIL
Poster Number:	143

Sheep production may have considerable losses caused by gastrointestinal nematodes. This study aimed to report the presence of parasite resistance to anthelmintics in Colombia. Four farms were selected where the animals were not treated with anthelmintics for a minimum of four months prior to the study. Animals were selected based on the faecal egg count (above 150) and aged from 3 to 6 months. Lambs were allocated into 6 groups, each consisting of 6 animals. The drugs and dosages used were, ivermectin 1% (0,2 mg/kg); albendazole 25% (5 mg/kg); fenbendazole 10% (5 mg/kg); levamisole 10% (5 mg/kg); moxidectin 1% (0,2 mg/kg) and a control with no treatment. Anthelmintic efficacy was detected using the faecal egg count reduction test (FECRT) with EPG recorded at day 0 and 14 days post-treatment. Although the efficacy of albendazole and fenbendazole on farm 1 was above 95%, there was the indication of low efficacy, due to the marginal value (89%) of the lower confidence interval. In the other cases, ivermectin showed an efficacy of 93.1% on Farm 2, where all others were below 78% including moxidectin (49.2%). This study reports for the first time the existence of sheep gastrointestinal nematode populations with multidrug resistance in Colombia.



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Poster with 2 minute Oral Presentation Details:	Characterisation of a bioactive compound from the Australian plant <i>Alectryon oleifolius</i> with anthelmintic activity against cyathostomins <i>in vitro</i>
Authors:	Stephanie E. Payne ^{1*} , Gavin R. Flematti ¹ , Andrew C.Kotze ² , Zoey Durmic ¹ , Philip E. Vercoe ¹ ¹ University of Western Australia, Perth WA, AUSTRALIA ² CSIRO Animal, Food and Health Science Division, St Lucia QLD, AUSTRALIA
Poster Number:	221

Anthelmintic resistance in cyathostomin parasites of horses is increasing, and bioactive plants and their active compounds could play a role in new sustainable management practices. *Alectryon oleifolius* is a shrub native to Australia which has been traditionally used as fodder when pasture is scarce (Cunningham et al., 2011). *Alectryon oleifolius* has been shown to have antimicrobial properties (Kurekci et al., 2012), and we have previously found that crude water extracts of *A. oleifolius* had significant anthelmintic activity against cyathostomin larvae *in vitro* (Payne et al., 2013). However, no compounds responsible for the bioactivity of *A. oleifolius* have been identified. Using bioassay guided fractionation, the current study aimed to identify the compounds responsible for the anthelmintic action. The anthelmintic activities of extracts were assessed using larval development assays, measuring the ability of the extract to inhibit development of eggs to the third larval stage. Comparison of extracts obtained with several solvent systems showed that the greatest bioactivity was associated with a 4:1 methanol/water extract. Further fractionation of this extract using silica gel column chromatography and semi-preparative high performance liquid chromatography (HPLC) enabled the isolation of an active compound. Identification of the active compound has been achieved using nuclear magnetic resonance (NMR) spectroscopy and mass spectrometry. Details of the structure and physical properties of the bioactive compound will be presented, as well as concentrations within the plant material, and details on the levels of activity in *in vitro* larval development assays.

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Cunningham, G.M., Mulham, W.E., Milthorpe, P.L., Leigh, J.H., 2011. Plants of Western New South Wales. CSIRO Publishing, Australia, p. 474.

Payne, S.E., Kotze, A.C., Durmic, Z., Vercoe, P.E., 2013. Australian plants show anthelmintic activity toward equine cyathostomins *in vitro*. Veterinary Parasitology. <http://dx.doi.org/10.1016/j.vetpar.2013.01.012>

Kurekci, C., Bishop-Hurley, S.L., Vercoe, P.E., Durmic, Z., Al Jassim, R.A.M., McSweeney, C.S., 2012. Screening of Australian Plants for Antimicrobial Acitvty against *Campylobacter jejuni*. Phytotherapy Research 26, 186-190.



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Session Details:	8/29/2013 Drugs - do they REALLY work? 1130 - 1240 Meeting Room 5
Poster with 2 minute Oral Presentation Details:	Treatment and control of <i>Toxocara vitulorum</i> in a smallholder cattle and buffalo farming system in South East Asia
Authors:	Rast L ^{1*} , Khounsy S ² , Toribio J-ALML ¹ , Windsor PA ¹ ¹ Faculty of Veterinary Science, University of Sydney, Camden, NSW 2570, Australia ² Department of Livestock and Fisheries, Luang Prabang, Lao PDR
Poster Number:	218

T. vitulorum infection in large ruminants is endemic in many tropical countries and a single treatment of calves with pyrantel at 14-21 days of age effectively controls the parasite. Despite this treatment being readily available, *T. vitulorum* infection remains common and widespread, shown in a recent prevalence study in northern Lao where overall prevalence was 22.6 % in calves <3 months old and 76.8% of sampled villages had infected calves. We examined treatment practices and knowledge of smallholder farmers of this parasite, plus bovine production parameters to assess the impact of the disease. Interviews were conducted with 273 smallholder farmers who had calves tested for *T. vitulorum* 4-6 months earlier. Reproductive rates of 0.6 and 0.4 calves per annum in cattle and buffalo respectively, and annual calf (aged <12 months) morbidity and mortality of 42.6% (CI 0.38-0.47) and 37.3% (CI 0.37-0.42) respectively, were identified. Interviewed farmers had either none (80.6%) or only minimal (19.4%) knowledge about *T. vitulorum* and only 3.6% of the farmers treated their calves using the recommended regime. Financial analysis using partial budgeting showed a net benefit of USD 6.0, 11.9, 17.5 or 23.5 per calf when treating calves with pyrantel and attributing 25%, 50%, 75% or 100% of morbidity and mortality to *T.vitulorum*. Poor reproduction, high calf morbidity and mortality and endemic levels of *T. vitulorum*, combined with very limited knowledge of Toxocariasis control, contribute to suboptimal large ruminant production in mixed smallholder farming systems in upland Laos. Improved knowledge of the large net benefit per calf achievable by a single pyrantel treatment should drive implementation of this intervention by smallholder farmers, especially as demand for livestock products increases in this region. Capacity building that ensures knowledge transfer of this intervention to smallholder farmers and other livestock production stakeholders is required.



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Session Details:	8/29/2013 Drugs - do they REALLY work? 1130 - 1240 Meeting Room 5
Poster with 2 minute Oral Presentation Details:	Activity of Ivermectin Long-acting Injectable (IVOMEC® GOLD) in First-Season Grazing Cattle under Natural Challenge Conditions in Germany
Authors:	Steffen Rehbein ¹ , Martin Knaus ¹ , Martin Visser ¹ , Renate Winter ¹ , Stephen Yoon ² , Luiz Cramer ² ¹ Merial GmbH, Kathrinenhof Research Center, Rohrdorf, GERMANY ² Merial Limited, Duluth, GA, USA
Poster Number:	22

The persistent activity of ivermectin long-acting injection (IVM LAI; IVOMEC® GOLD, Merial; 3.15% ivermectin w/v) against nematode infections of cattle was evaluated under natural challenge conditions in a controlled study conducted in the south of Germany in 2006. Seventy nematode-free, 4 to 7 month old male Brown Swiss calves were blocked by pre-treatment bodyweight and allocated randomly to 7 groups of 10 animals each: saline (control) once on Day 0 or IVM LAI on either Days 0, 7, 14, 21, 28 or 35. Treatments were injected subcutaneously in front of the shoulder at 1 mL/50 kg bodyweight. Until Day 35, calves were housed to preclude nematode infections, and thereafter they grazed as one group on naturally contaminated pasture until Day 77. Following housing for four weeks after Day 77, calves were humanely euthanized and necropsied for parasite recovery and count.

Based on the comparison of parasite counts of calves administered either saline (control) or IVM LAI at weekly intervals prior to start of grazing, treatment with IVM LAI prevented the establishment (>90%, p<0.05) of *Dictyocaulus viviparus* (100%), *Bunostomum phlebotomum* (100%), *Haemonchus contortus* (98.6%), *Ostertagia ostertagi/lyrata* (94.9%) and *Oesophagostomum radiatum* (93.3%) for at least 77 days; *O. leptospicularis* (99.1%) for 63 days; *Cooperia punctata* (97.7%), *Trichostrongylus axei* (96.5%) and *Ostertagia* spp. inhibited larvae (93.3%) for 56 days; *Cooperia* spp. inhibited larvae (98.8%), *C. oncophora/turnabada* (96.9%) and *Trichuris discolor* (93.6%) for 42 days.

Calves of groups treated with IVM LAI had significantly (p<0.01) higher Day 77 bodyweights and mean daily gains than the controls (0.26-0.50 kg vs. 0.03 kg).

This study demonstrated a very high efficacy of IVOMEC GOLD against a wide range of bovine nematodes for up to 77 days after treatment and this was associated with increased productivity.

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Session Details:	8/29/2013 Drugs - do they REALLY work? 1130 - 1240 Meeting Room 5
Poster with 2 minute Oral Presentation Details:	Pharmacokinetics and Anthelmintic Efficacy of Topical Eprinomectin in Goats Prevented from Grooming
Authors:	Steffen Rehbein ¹ , Michael Kellermann ¹ , Teresa Wehner ² ¹ Merial GmbH, Kathrinenhof Research Center, Rohrdorf, GERMANY ² Merial Limited, North Brunswick, NJ, USA
Poster Number:	23

In cattle, there has been speculation that after topical treatment with macrocyclic lactones, oral exposure via grooming plays an important role with respect to the efficacy of those products. However, evidence from several previous publications and a recently reported study indicated that oral ingestion is not required to achieve adequate anthelmintic efficacy (Rehbein et al., 2012).

A study using 16 approximately 7 months old male castrated German White Noble goats harbouring induced infections of adults gastrointestinal nematodes was conducted in order to determine the pharmacokinetic profile of eprinomectin following topical application to goats that were prevented from self-grooming and having physical contact with others. Goats were blocked based on pre-treatment bodyweight (range, 22.4-36.4 kg) and then randomly allocated to an untreated control group or a group treated with topical eprinomectin (EPRINEX® Pour-On, Merial; 0.5% w/v eprinomectin) at 2 mL/10 kg bodyweight (equivalent to 1 mg eprinomectin/kg). Plasma samples collected prior to treatment and at intervals up to 14 days following treatment were analyzed to determine the concentrations of eprinomectin (B1a component). For parasite recovery, identification and count, animals were humanely euthanized 14 days after treatment.

Goats treated with topical eprinomectin had significantly (p<0.01) fewer (≥99% reduction) adult *Cooperia curticei*, *Haemonchus contortus*, *Nematodirus battus*, *Oesophagostomum venulosum*, *Ostertagia circumcincta*, and *Trichostrongylus colubriformis* than the untreated controls. Basic pharmacokinetic parameters of eprinomectin B1a were: AUC_{infinity}, 37.1 ± 15.2 day*ng/mL; T_½, 5.11 ± 2.83 days; and C_{max}, 5.93 ± 1.87 ng/mL; individual maximal concentrations were observed one or two days after treatment.

Results of this study indicate that percutaneous absorption occurs after treatment of goats with topical eprinomectin and that oral ingestion is not required to achieve adequate exposure for anthelmintic efficacy.

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Reference:

Rehbein et al., 2012. Parasitology Research 111, 1343-1347.



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Session Details:	8/29/2013 Drugs - do they REALLY work? 1130 - 1130 Meeting Room 5
Oral Presentation Details:	Efficacy of monepantel combined with abamectin against gastro-intestinal nematodes in sheep
Authors:	Heinz Sager ^{1*} , Béatrice Bapst ¹ , Peter Rolfe ² , Sarah George ² , Phil Stein ² , Nikki Potgieter ² and Ronald Kaminsky ¹ ¹ Novartis Animal Health Research Center, Chemin de la Petite Glâne, 1566 St-Aubin (FR), SWITZERLAND ² Novartis Animal Health Australasia Pty Ltd, Research Centre YARRANDOO, 245 Western Road, Kemps Creek, NSW 2178, AUSTRALIA

Monepantel (MPL; Zolvix®; 25 g/L) has been developed to treat and control infections with gastro-intestinal parasites in sheep and, due to its unique mode of action, to manage the widespread resistance that is present to currently available classes of anthelmintics. Mathematical modelling has shown the beneficial effect of combining active product ingredients in order to delay development of resistance (Dobson et al., 2011). It was therefore of interest to demonstrate the feasibility of a combination of MPL with another anthelmintic class. This presentation shows the feasibility of a combination of MPL with the macrocyclic lactone abamectin (ABA).

Eight dose confirmation studies with experimentally infected sheep were performed to demonstrate the efficacy of oral treatment with MPL at 2.5 mg/kg combined with ABA at 0.2 mg/kg against adult and larval stages of gastro-intestinal nematodes. The isolates were characterized and several of these showed resistance against benzimidazoles, and to some extent to levamisole and macrocyclic lactones and combinations of these. The combination of MPL and ABA resulted in >99.9% efficacy against most isolates and was always higher than 98.9%.

It can be concluded that the combination of MPL and ABA does not result in unwanted interactions. On the contrary, the efficacy has been similar if not better than the treatments with the individual compounds, and all treatments were well tolerated by the sheep.

References:

Dobson RJ, Hosking BC, Besier RB, Love S, Larsen JW, Rolfe PF, Bailey JN. 2011.
Minimising the development of anthelmintic resistance, and optimising the use of the novel anthelmintic monepantel, for the sustainable control of nematode parasites in Australian sheep grazing systems. Aust Vet J 89:160-166.



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Session Details:	8/29/2013 Drugs - do they REALLY work? 1130 - 1240 Meeting Room 5
Poster with 2 minute Oral Presentation Details:	Preliminary Phytochemical Studies And <i>in vitro</i> Anthelmintic Investigation On Aqueous Extracts Of <i>Mitragyna Speciosa</i> Korth, Red and White Vein Leaves Against Sheep Gastrointestinal Nematodes In Malaysia
Authors:	Shaharul Akmar Talib ^{1*} and Nor Aini Saidin ² ¹ Department Of Veterinary Services,Ministry of Agriculture & Agro-Based Industry Malaysia, Wisma Tani, Block Podium, Lot 4G1, Precint 4 ,Federal Government Administrative Center, 62624 Putrajaya, MALAYSIA ² Advanced Medical & Dental Institute, Universiti Sains Malaysia, No 1-8 (Lot 8), Persiaran Seksyen 4/1, Bandar Putra Bertam, 13200 Kepala Batas. Pulau Pinang, MALAYSIA
Poster Number:	141

Using plants as alternative sources medicine had been practice since thousands years ago. *Mitragyna speciosa* korth (MSK), MSK mainly grows in South East Asia and globally known as 'kratom'. In Malaysia, there are two well-known varieties which are easily distinguished by a different colour of the leaf vein either red or white. The MSK leaves widely used in human due to psychoactive effect that will act as stimulant for the labourer that works during the hot weather. Traditionally, MSK also been used as anthelmintic for human and animal especially small ruminants. These studies were carried out to determine the phytochemical constituent of these two types of MSK and to compare their anthelmintic efficacies with the commercially available anthelmintic by *in vitro* analysis on adult gastrointestinal nematodes. The phytochemical constituent screened qualitatively and gave the positive results on alkaloids, tannins and polyphenolics compounds. From the *in vitro* studied show that both of the plant extracts have inhibitory effects to the adult gastro intestinal nematodes with the dose and time dependent. The more potent effects were usually observed with the highest concentration and longer exposure to the extracts. The results of the study indicated that MSK do possess anthelmintic properties and validated the basis for the traditional used of these plant as a anthelmintic for controlling the gastrointestinal nematodes in ruminants. Further investigation should be continued by in vivo studies to confirm the effects of these plants on gastrointestinal nematodes in ruminants.

Acknowledgements:

This study was funded by a grant from the Advanced Medical & Dental Institute, Universiti Sains Malaysia. The staffs of Malaysian Animal Health Laboratories, Bukit Tengah, Penang especially Ms Jamaiah Mat Isa for the assistance.

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HOUNZANGBE-ADOTE, M. S., PAOLINI, V., FOURASTE, I., MOUTAIROU, K. & HOSTE, H. 2005. In vitro effects of four tropical plants on three life-cycle stages of the parasitic nematode, Haemonchus contortus. Research in Veterinary Science, 78, 155-160.



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JACKSON, F. & HOSTE, H. 2010. In Vitro Methods for the Primary Screening of Plant Products for Direct Activity against Ruminant Gastrointestinal Nematodes. In: VERCOE, P. E., MAKKAR, H. P. S. & SCH-LINK, A. C. (eds.) In vitro screening of plant resources for extra-nutritional attributes in ruminants: nuclear and related methodologies. Springer Netherlands.

SAIDIN, N. A., RANDALL, T., TAKAYAMA, H., HOLMES, E. & GOODERHAM, N. J. 2008. Malaysian Kratom, a phyto-pharmaceutical of abuse: Studies on the mechanism of its cytotoxicity. Toxicology, 253, 19-20.

VICKNASINGAM, B., NARAYANAN, S., BENG, G. T. & MANSOR, S. M. 2010. The informal use of ketum (*Mitragyna speciosa*) for opioid withdrawal in the northern states of peninsular Malaysia and implications for drug substitution therapy. International Journal of Drug Policy, 21, 283-288.



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Session Details:	8/29/2013 Drugs - do they REALLY work? 1130 - 1240 Meeting Room 5
Poster with 2 minute Oral Presentation Details:	Assessment of ethno-medicinal plants used for treatment of livestock ailments by traditional healers in southern Ethiopia
Authors:	Ketema Tolossa ^{1*} , Etana Debela ² , Spiridoula Athanasiadou ³ , Aduugna Tolera ⁴ , Jos GM Houdijk ³ ¹ Department of Chemistry, Hawassa University, Hawassa, ETHIOPIA ² School of Veterinary Medicine, Hawassa University, Hawassa, ETHIOPIA ³ Scotland's Rural College (SRUC), Edinburgh, UNITED KINGDOM ⁴ School of Animal and Range Science, Hawassa University, Hawassa, ETHIOPIA
Poster Number:	142

Plant preparations have traditionally been used for treatment of livestock ailments in Ethiopia, including endo- and ecto-parasitism. However, the knowledge has not been adequately documented, impeding scientific evaluation and widespread plant use. This study was conducted to document the indigenous knowledge and practices of traditional healers from four ethnic groups (Borana Oromo, Aari, Maale and Bena-Tsemay) in southern Ethiopia. A cross-sectional study was carried out using a semi-structured questionnaire. Sixty-two healers (50 male and 12 female) were included in the interview and data were analyzed using descriptive statistics. Healers reported 111 plant species with claimed medicinal properties against 34 livestock but also human or both livestock and human ailments, in almost equal proportions. Medicinal plants claimed were distributed across 77 genera and 43 families, of which *Lamiaceae*, *Solanaceae*, *Fabaceae*, *Asteraceae*, *Menispermaceae*, *Plumbaginaceae* and *Geraniaceae* accounted for 11.7%, 8.1%, 7.2%, 6.5%, 6.3%, 5.4% and 3.6%, respectively. Nine (8.1%) and 27 (24.3%) plant species were cited solely for treatment of livestock ecto- and endoparasites, respectively. Woody plants contributed 54.9% (shrubs 23.4% and trees 31.5%) of plants claimed for medicinal properties; herbs and climbers accounted for the remaining 35.1% and 10%, respectively. Roots (41.4%) and leaves (36.1%) were the major plant parts used. Healers mostly (70.3%) administer the remedies orally. Multiple medicinal plants but also mixing of different medicinal plants was cited against particular ailments. This study confirms that medicinal plants play a significant role in animal and human healthcare needs of the ethnic groups studied. Cultural acceptability and affordability of plant-based remedies, and limited access to conventional drugs, could be the main driving factors. Further studies are being undertaken to validate anti-parasitic efficacy of selected plant preparations (Athanasiadou et al., 2013a, b).

Acknowledgements:

The authors gratefully acknowledge funding from the DFID/BBSRC/SG CIDLID program (BB/H009299/1).

References:

Athanasiadou S, Debela E, Tolera A, Tolossa K, Terry S, Houdijk JGM (2013). *In vitro* validation of the anthelmintic properties of Ethiopian medicinal plant extracts. Proceedings of the 24th International Conference of the World Association for the Advancement of Veterinary Parasitology (submitted).



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Athanasiadou S, Debela E, Tolera A, Tolossa K, Burgess S, Connelley T, Terry S, Houdijk JGM (2013). *In vitro* validation of Ethiopian medicinal plants against ticks and mites. Proceedings of the 24th International Conference of the World Association for the Advancement of Veterinary Parasitology (submitted).



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Session Details:	8/29/2013 Parasites in my blood! 1130 - 1240 Meeting Room 6
Poster with 2 minute Oral Presentation Details:	Understanding the Function of Apicomplexan Histone Deacetylases Using <i>P. falciparum</i> Malaria Parasites as a Model
Authors:	Jess Engel ^{1,2*} and Kathy Andrews ^{1,2} ¹ Eskitis Institute for Cell and Molecular Therapies, Griffith University, Nathan, QLD ² Queensland Institute of Medical Research, QIMR, Herston, QLD
Poster Number:	145

Histone deacetylases (HDACs) are enzymes that act on histone and non-histone proteins. As a result, they contribute to alterations in gene transcription, DNA replication and repair, cell-cycle regulation and differentiation, and apoptosis. HDACs are validated drug targets for certain types of cancer and are showing promise as therapeutic targets for a range of other human diseases. Some parasites that cause disease in humans and animals are also susceptible to inhibitors of HDAC enzymes, indicating that parasitic HDACs, or proteins that are essential for their function, may also be “druggable” anti-parasitic targets. In an effort to better understand the biology of HDACs in Apicomplexan parasites, we are using *Plasmodium falciparum* malaria parasites as a model system. *P. falciparum* is easily cultured *in vitro* and amenable to forward and reverse genetic approaches. An improved understanding of the biology of *P. falciparum* HDACs, which have already been shown to be promising drug targets in this parasite species (reviewed in [1]), may also contribute to ongoing drug discovery efforts. In this project we are investigating the functional role of *P. falciparum* HDACs on non-histone proteins and trying to identify key members of the multi-protein complexes these enzymes form in order to function.

References:

1. Andrews, K.T., T.N. Tran, and D.P. Fairlie, *Towards histone deacetylase inhibitors as new antimalarial drugs*. Curr Pharm Des, 2012. **18**(24): p. 3467-79.



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Session Details:	8/29/2013 Parasites in my blood! 1130 - 1240 <i>Meeting Room 6</i>
Poster with 2 minute Oral Presentation Details:	High 5 to B₅ – Identification of pantothenate kinases in <i>Plasmodium falciparum</i>
Authors:	Vanessa Howieson* and Kevin J. Saliba Research School of Biology, The Australian National University, Canberra, ACT, Australia
Poster Number:	38

The emergence of artemisinin resistance in South East Asia has highlighted the need for new antimalarials. Nutrient pathways in *Plasmodium* have successfully been targeted in the past with the use of sulphonamides to target folate (vitamin B₉) synthesis. During its red blood cell stage, *P. falciparum* requires an extracellular supply of vitamin B₅ (pantothenate) in order to grow and multiply. Pantothenate is converted into coenzyme A (CoA), an essential cofactor in many cellular processes, including fatty acid synthesis. The transport of pantothenate into the parasite and its metabolism to CoA, therefore, represent promising drug targets. The first of five enzymes in the CoAbiosynthesis pathway is pantothenate kinase (PanK). There are two genes identified as putative PanKs in *P. falciparum*, referred to as *PfPanK1* and *PfPanK2*. Previous attempts at heterologous expression of a functional *PfPanK1* (in various systems) have failed. In light of the fact that *P. falciparum* proteins that have not previously been amenable to heterologous expression have been successfully overexpressed and characterised within the parasite, we decided to overexpress untagged versions of both *PfPanK1* and *PfPanK2* within *P. falciparum*. We will present results from our attempts to identify these genes, which will hopefully encourage further study into their structure and regulation as future drug targets.



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Session Details:	8/29/2013 Parasites in my blood! 1130 - 1240 Meeting Room 6
Poster with 2 minute Oral Presentation Details:	Identification and Characterisation of Pantetheinase-Resistant Pantothenamides
Authors:	Eleanor Kerdo ^{1*} , Emelia Awuah ² , Anaïs Saquet ¹ , Zhiyang Lin ¹ , Stephanie Tan ¹ , Karine Auclair ² , Kevin J Saliba ¹ ¹ Research School of Biology, The Australian National University, Canberra AUSTRALIA ² Department of Chemistry, McGill University, CANADA
Poster Number:	146

Drug resistance has been reported for all antimalarial drug treatments currently on the market. There is therefore a need for the continual development of novel antimalarial therapies. *P. falciparum* has an absolute requirement for an extracellular supply of pantothenate (vitamin B₅) during its intraerythrocytic stage. Pantothenate is the first metabolite in the coenzyme A (CoA) biosynthesis pathway. By preventing *P. falciparum* from utilising or synthesising CoA effectively, parasite growth can be inhibited. We are therefore investigating analogues of pantothenate as potential antimalarials. Pantothenamides, amide-containing pantothenate analogues, have recently been shown to possess potent (nM) antiplasmodial activity. Their activity, however, is destroyed due to their degradation by the serum enzyme pantetheinase. We therefore need to identify pantothenamides that are resistant to pantetheinase degradation while maintaining antiplasmodial activity. To this end, we are investigating a recently-described series of pantothenamides that contain various substituents in place of the geminal dimethyl groups of pantothenate. We will present data on the antiplasmodial activity of these compounds in the presence and absence of pantetheinase, their selectivity towards the parasite and specificity against CoA biosynthesis/utilisation.



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Session Details:	8/29/2013 Parasites in my blood! 1130 - 1240 <i>Meeting Room 6</i>
Poster with 2 minute Oral Presentation Details:	Babesiosis in dogs, the variability of clinical symptoms and laboratory findings
Authors:	Edina Sesztáková ¹ , Alžbeta Königová ^{2*} , Vladimír Vrabec ¹ , Mária Fialkovičová ¹ ¹ Clinic for Birds and Exotic Animals, The University of Veterinary Medicine and Pharmacy, Komenského 73, 041 81 Košice, Slovak Republic ² Parasitological Institute of SAS, Hlinkova 3, 040 01 Košice, Slovak Republic
Poster Number:	57

Canine babesiosis is clinically significant vector-borne disease caused by geographically widespread hemoprotozoan parasites of the genus *Babesia*. Herein we present the variability of clinical symptoms, laboratory findings, course and treatment of babesiosis in dogs. In the first patient (Cavalier King Charles Spaniel), the disease was accompanied by hyperthermia, marked apathy and anorexia. Laboratory findings were not significantly modified, haemoglobinuria and proteinuria was reported. The second dog (a crossbreed) showed signs of mild apathy, loss of appetite, marked jaundice of the skin and visible mucous membranes and haemoglobinuria and proteinuria. The biochemical parameters such as hyperbilirubinemia (> 213 mmol/l), alkaline phosphatase (1.6 µkat/l) and uraemia (14.2 mmol/l) were detected. The third dog (Labrador Retriever) showed signs of anaemia and visible signs of cerebellar ataxia. Laboratory tests showed anaemia (2.59 T/l), leucopenia (1.48 G/l), elevated creatinine (201.1 mmol/l), uraemia (20.1 mmol/l) and hyperbilirubinaemia (15.8 mmol/l). Haemoglobinuria and proteinuria in the urine was reported. *Babesia canis* was identified in all three patients by the polymerase chain reaction (PCR) method. Iminocarb dipropionate (Imizol a.u.v) was used, having positive therapeutic effects. Antiprotozoic treatment was supplemented with antibiotics, rehydration and supportive therapy.

The presence of canine babesiosis in Slovakia indicates the importance of monitoring of this hemoprotozoan disease in the domesticated dogs and wild canids. It is equally important that practitioners know how to diagnose diseases which are less common.



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Session Details:	8/29/2013 Parasites in my blood! 1130 - 1240 Meeting Room 6
Poster with 2 minute Oral Presentation Details:	Molecular detection of rickettsioses in animals and arthropod vectors in Malaysia.
Authors:	Kho Kai Ling ^{1*} , Tay Sun Tee ¹ Department of Medical Microbiology, Faculty of Medicine, University of Malaya, Malaysia.
Poster Number:	258

Flea-borne infection are emerging and re-emerging throughout the world. Rapid spreading of flea-borne pathogens such as *Rickettsia* to human populations is possible due to the frequent feeding behavior and mobility of fleas. Rickettsiae are short, Gram-negative intracellular organisms that are found in the animal ectoparasites such as ticks, fleas and mites. Transmission of rickettsiae to human can occur via the bites of infected fleas. This study was conducted to identify types of rickettsiae circulating in the cat fleas (*Ctenocephalides felis*) infesting pet animals in Malaysia. Genus specific polymerase chain reaction assays were used for the detection of rickettsiae in cat fleas collected from domestic cats and dogs in five villages located at different geographical regions of West Malaysia. A total of 140 pools of fleas were examined, of which 99 (70.7%) pools of fleas were positive for rickettsiae, demonstrating high occurrences of rickettsiae in cat fleas in all the villages. Sequence analysis demonstrated 99% sequence homologies of the amplified products with that of *Rickettsia* sp. RF2125, a genotype closely related to *Rickettsia felis* which had recently recognized as an emerging global health threat. Therefore, an active surveillance of flea as vector of rickettsial diseases is essential for prevention and control of flea-borne rickettsioses in this region. Further studies in isolating the responsible rickettsial organisms are necessary.

Acknowledgements:

This project was funded by University of Malaya Research Grant RP013-2012A; HIR-MOHE E000013-20001.



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Session Details:	8/29/2013 Parasites in my blood! 1130 - 1240 Meeting Room 6
Poster with 2 minute Oral Presentation Details:	Anaplasmosis In Local Cattle - A Prevalence Study In 13 States In Malaysia
Authors:	Zaini Che Mamat ^{1*} ,Premaalatha Bathmanaban ¹ , Samantha Pong Chia Yi ² , Chandrawathani Panchadcharam ¹ & Zary Shariman Yahya ² ¹ Veterinary Research Institute, Department of Veterinary Services, 31400 Ipoh, Perak, Malaysia ² School of Biological Sciences, University Sains Malaysia, 11800 USM, Penang, Malaysia
Poster Number:	245

A seroprevalence study on bovine anaplasmosis was conducted on sera samples of mix ages of cattle from different breeds from randomly chosen farms from thirteen different states in Malaysia .Samples examined for the presence of *Anaplasmosis marginale* antibodies by Competitive Enzyme-Linked Immonusorbant Assay (c-ELISA). Out off 418 sera samples, 328 (78.5%) tested positive for bovine anaplasmosis.

Acknowledgements:

The authors would like to thank the Director and Deputy Director of Veterinary Research Institute (VRI), Ipoh Malaysia for supporting the study. A special thanks to all staff from Parasitology and Haematology section, Master student and lecturers from USM for their full support and help that leads to the successfulness of this project.

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Session Details:	8/29/2013 Parasites in my blood! 1130 - 1240 Meeting Room 6
Poster with 2 minute Oral Presentation Details:	Identification of haematozoan parasites of Australian birds
Authors:	Peter O'Donoghue*, Odette Pletzer The University of Queensland, Brisbane, AUSTRALIA
Poster Number:	74

Previous studies have described a wide variety of haematozoa in birds throughout the world, but comparatively few studies have examined the unique avifauna of Australia, home to some 800 bird species (half endemic). An opportunistic survey was conducted on blood samples from wild and aviary birds presented to veterinarians in the course of wildlife management, fauna rescue and bird banding programmes. Parasite taxa were identified by morphometric characterization of intraerythrocytic developmental stages. Samples were examined from 480 birds belonging to 112 species, 35 families and 16 orders. Haematozoa were detected in 35 birds (prevalence of 7.3%) belonging to 14 species (12.5%), 11 families (31%) and nine orders (56%). A total of 15 parasite species were detected: eight species of *Haemoproteus* (*H. danilewskyi*, *H. pittae*, *H. noctuae*, *H. columbae*, *H. centropi*, *H. nettionis*, *H. handai* and a novel morphotype); four species of *Plasmodium* (*P. relictum*, *P. anasum*, *P. dissanaikai* and *P. circumflexum*); two species of *Leucocytozoon* (*L. artamidis* and *L. toddi*); and one species of *Babesia* (*B. peircei*). Collectively, these results include nine new host records of infection and extend the geographic range of another four parasite species to include Australia. The majority of infections were low in parasitaemia (< 0.1%) and most parasite stages had little observable effect on host erythrocyte numbers or morphology. Several birds exhibited systemic clinical signs, possibly associated with pre-erythrocytic developmental stages of *Haemoproteus* or *Leucocytozoon* spp. forming megalo-meronts in host tissues. Most parasite species were specific for closely-related bird species within individual families (stenoxenous), but were broadly distributed (recorded in birds from other continents).



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Session Details:	8/29/2013 Parasites in my blood! 1130 - 1240 Meeting Room 6
Poster with 2 minute Oral Presentation Details:	Taxonomic Reassessment of Terrestrial Tortoise Haemogregarine, <i>Haemogregarina Fitzsimonsi</i> Dias, 1953, With Identification of Its Vectors.
Authors:	Courtney A. Cook ^{1,2} , Angela J. Davies ^{1,3} , Scott P. Lawton ³ Nico J. Smit ^{1*} ¹ Water Research Group (Ecology), Unit for Environmental Sciences and Management, North West University, Potchefstroom, SOUTH AFRICA, ² Department of Zoology, University of Johannesburg, Johannesburg, SOUTH AFRICA, ³ School of Life Sciences, Kingston University, Surrey, London, UK.
Poster Number:	75

Two haemogregarine genera are known to infect chelonians, *Haemogregarina (sensu stricto)* and *Hemolivia*. *Haemogregarina* (s. s.) species, according to Siddall's (1995) taxonomic review, are solely transmitted by leech vectors. However, this appears improbable for terrestrial South African tortoises, from which leeches are absent. Ticks, however, such as *Hyalomma aegyptium*, known to transmit the apicomplexan *Hemolivia mauritanicum* between Palearctic tortoise species are more plausible vectors. It was therefore, hypothesized that *Haemogregarina fitzsimonsi* Dias, 1953, a common South African tortoise haemogregarine is transmitted by tick vectors and furthermore, may need to be taxonomically reassessed. Blood collected from 270 tortoises of 5 genera and 7 species was used to prepare thin, fixed and stained smears. Films were screened for parasites, identified as *H. fitzsimonsi*. Ticks from tortoises were fixed in 70% molecular grade ethanol, and possible *H. fitzsimonsi* sporocyst and sporozoite stages were identified on dissection of adult *Ambylomma sylvaticum* and *A. marmoreum* ticks from apparently infected and non-infected tortoises. Parasite DNA was extracted from both slides and ticks using a DNeasy Animal Tissue Kit and PCR was undertaken with three primer sets: HEMO1 and HEMO2, HepF300 and HepR900 and 4558F and 2773R. Results indicated that apicomplexan DNA extracted from blood films and both species of tick had been amplified by one or more primer sets. *Haemogregarina fitzsimonsi* 18s rRNA sequences aligned with those of species of *Hepatozoon* and this is the first report of an *Hepatozoon* from any terrestrial chelonian. Furthermore, *H. fitzsimonsi* appeared to be neither intermediate host nor vector specific, perhaps having the ability to infect novel tortoise and tick hosts. Since tortoises are popular in the pet trade, and are not necessarily kept free of ectoparasites in these circumstances, there may be reason for concern for naive tortoise species' welfare.



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Session Details:	8/29/2013 Parasites in my blood! 1130 - 1240 Meeting Room 6
Poster with 2 minute Oral Presentation Details:	Blood parasites of reef associated fishes of the eastern Caribbean
Authors:	Courtney A, Cook ¹ , Nico J. Smit ^{1*} , Angela J Davies ^{1,2} , Paul C. Sikkell ³ ¹ Water Research Group (Ecology), Unit for Environmental Sciences and Management, North West University, Potchefstroom, SOUTH AFRICA, ² School of Life Sciences, Kingston University, Surrey, London, UNITED KINGDOM ³ Department of Biology, Arkansas State University, State University, UNITED STATES OF AMERICA *presenting author
Poster Number:	204

Although hemogregarines (Apicomplexa) are common parasitic protozoans of the blood of many vertebrates, no systematic surveys of their occurrence in Caribbean fishes have been undertaken since the 1960's. The aim of this study was to determine the biodiversity of fish blood parasites from the Caribbean and to use these results to initiate further research on their potential effect on host fishes, and their mode of transmission. Fishes were collected by divers or obtained from local fishermen from St. John and St. Thomas (US Virgin Islands), Culebra, Puerto Rico and Guana Island, British Virgin Islands. Blood was taken from the caudal vein of anaesthetized fish by needle and syringe, smeared on clean, glass slides, fixed in absolute methanol, and Giemsa-stained. Smears were examined with a Nikon Eclipse 80i microscope. In total, blood from 927 fishes from 81 species in 26 families were studied and of these 54 (5.8%) individuals were infected with blood parasites. Species infected included the damselfishes *Stegastes diencaeus* (12/39), *S. fuscus* (16/32), *S. leucostictus* (8/18), and *S. planifrons* (4/4); princess parrotfish, *Scarus taeniopterus* (1/4); white mullet, *Mugil curema* (1/2); bigeye scad *Selar crumenophthalmus* (1/1), barred blenny, *Hypleurochilus bermudensis* (1/6); yellowtail snapper, *Ocyurus chrysurus* (6/7); emerald parrotfish, *Nicholsina usta* (3/4) and the gray angelfish *Pomocanthus arcuatus* (2/8). None of the blood parasites found conformed to the description of any of the parasites previously reported from the Caribbean or worldwide. Parasites found resembled in morphology typical *Haemogregarina*-like intraerythrocytic parasites as well as *Haemohormidium*-like parasites collected from fishes on the GBR, Australia. In total, seven distinct types of blood parasites were found and future work will include classifying these to species level through molecular analysis. Surprisingly, although tetraodontiform fishes have been found to harbour blood parasites in the Indo-Pacific, none of the 10 tetraodontiform species sampled in this study were infected.



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Session Details:	8/29/2013 Parasites in my blood! 1130 - 1240 Meeting Room 6
Poster with 2 minute Oral Presentation Details:	Epidemiological role of <i>Apodemus agrarius</i> (Rodentia) in Central Europe
Authors:	Michal Stanko ^{1,2*} , Markéta Derdáková ^{1,2} , Lydia Čisláková ³ , Jana Jareková ⁴ , ¹ Institute of Parasitology, Slovak Academy of Sciences, Košice, Slovakia ² Institute of Zoology, Slovak Academy of Sciences, Košice, Slovakia ³ Institute of Epidemiology, Faculty of Medicine, P.J. Šafarik University, Košice, Slovakia ⁴ Institute of Epidemiology, Faculty of Medicine, Comenius University Bratislava, Slovakia;
Poster Number:	260

Black-striped field mouse (*Apodemus agrarius* Pall.) discontinuously occurs in Central Europe. Long-term study in Slovakia confirmed that this species is the most abundant with frequent occurrence in broad habitat spectrum. Rodent species evident has been spread its area in Central Europe during last forty-fifty years.

About 1400 specimen of *A. agrarius* in lowland condition of Slovakia were sampled during several years (1996-2006) with aim of its epidemiological role evaluation. Authors present serological and microbiological analysis of blood serum and other tissues on presence of many pathogens (*Chlamydia* sp., *Leptospira* sp., *Borrelia* sp., *Toxocara* sp.). Antibodies against *Chlamydophila* (*Chlamydia*) *psittaci* were confirmed in 15.3 % of rodents. Smear slides from approximately four hundred animals were examined on presence of blood parasites. Blood parasites were detected in 18.9 % of *A. agrarius* – *Trypanosoma* sp. (frequency 12.7 %), *Bartonella* sp. (7.3%), *Babesia* sp. (0.8 %). More than 800 *A. agrarius* animals were examined microscopically and serologically for leptospiral cariership. Using the microscopic agglutination test in 151 animals (16.4 %), antibodies against *Leptospira* sp. were found for five serovars, for the most frequently was *pomona* (74.8 %), next *grippothyphosa* (11.9 %), *sejroe* and *australis* (both 4.0 %) and *bataviae* (0.7). Serological and molecular analysis of blood and other black-striped field mouse tissues confirmed role the rodents in circulation of hantaviruses, borreliae and *Anaplasma phagocytophilum* in natural foci of Slovakia.

During 2001 – 2008 more than 1.300 individuals of *A. agrarius* were serologically examined on the presence of antibodies against *Toxocara* sp., antibodies were confirmed in 11.3 % of *A. agrarius*. Long-term researches of rodents in Slovakia confirmed that *Apodemus agrarius* play the very important role as reservoir of many pathogens in natural foci of diseases.

Acknowledgements:

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Session Details:	8/29/2013 Parasites in my blood! 1130 - 1240 Meeting Room 6
Poster with 2 minute Oral Presentation Details:	Forward genetic studies in <i>Plasmodium falciparum</i> using ENU mutagenesis
Authors:	Erick T. Tjhin* and Kevin J. Saliba Research School of Biology, The Australian National University, Canberra, ACT, Australia
Poster Number:	176

N-ethyl-*N*-nitrosourea (ENU) is a chemical mutagen that has been used mainly in animal studies to generate point mutations in sperm-producing stem cells for forward (phenotype-based) genetic screens. To a more limited extent it has also been applied to mammalian cell cultures in order to induce mutations that are capable of generating drug resistance. It has also recently been applied in studies using *Toxoplasma gondii* to identify a conditional mutant with impaired host cell invasion and egress. To the best of our knowledge, ENU mutagenesis has not been applied to the human malaria parasite *Plasmodium falciparum* in order to identify interesting phenotypes and the genes responsible for these phenotypes. We will present results from our initial experiments aimed at: (i) identifying the maximum concentration of ENU that is tolerated by the intraerythrocytic stage of *P. falciparum* but which is still capable of introducing a desirable number of mutations, (ii) determining the duration of exposure required for insertion of mutations, (iii) estimating the type and rate of mutations in a selected group of genes, and (iv) isolating mutant parasites with clearly identifiable phenotypes. We hope that a library of ENU-mutated parasites can be generated that will allow researchers to investigate phenotypes of interest in the hope of identifying suitable proteins that can be targeted for the development of novel antimalarials.



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Session Details:	8/29/2013 Parasites in my blood! 1130 - 1240 Meeting Room 6
Poster with 2 minute Oral Presentation Details:	A Flow Cytometry-based, Field Applicable Method for Measuring Ex Vivo Drug Susceptibility in clinical <i>Plasmodium falciparum</i> and <i>P. vivax</i> isolates
Authors:	Grennady Wirjanata ^{1*} , Boni F Sebayang ² , Ferryanto Chalfein ³ , Pak Prayoga ³ , Irene Handayuni ¹ , Rintis Noviyanti ² , Enny Kenangalem ^{3,4} , Nicholas M Anstey ¹ , Ric N Price ^{1,5} , Jutta Marfurt ¹ 1. Global and Tropical Health Division, Menzies School of Health Research, Charles Darwin University, Darwin, Australia 2. Eijkman Institute for Molecular Biology, Jakarta, Indonesia 3. Papuan Health and Community Development Foundation (PHCDF), Timika, Papua, Indonesia 4. District Ministry of Health, Timika, Papua, Indonesia 5. Centre for Tropical Medicine, Nuffield Department of Clinical Medicine, University of Oxford, United Kingdom
Poster Number:	215

The emergence and spread of multidrug-resistant *P. falciparum* has increased the need for objective measures of *in vitro* drug susceptibility. For *P. falciparum*, assay systems are available using a variety of methods for quantifying parasite growth including: microscopy, incorporation of radio-labelled nucleotide precursors, enzyme-linked immunosorbent assays, DNA micro-fluorometric tests, and flow cytometry-based methods. Methods of quantifying growth in *P. vivax* remain mostly reliant on more subjective measures, although automated techniques are being developed. *P. vivax* preferential invasion of young red blood cells results in generally lower parasitaemias and more asynchronous cultures, and these factors reduce signal-to-noise ratios and confound analysis.

In this study, a robust and rapid approach for quantifying red blood cells infected with *Plasmodium* was developed using the nucleic acid stains hydroethidine for *P. falciparum* and SYBR Green I for *P. vivax* followed by flow cytometry-based signal calling. The flow-cytometry based assay was validated using the WHO microtest which quantifies schizont maturation by microscopy and is currently still the gold standard for assessing *ex vivo* drug efficacy in *P. vivax*. The assay was validated in 20 field isolates of *P. falciparum* and *P. vivax*, respectively, using the standard anti-malarial drugs chloroquine, amodiaquine, piperazine, and mefloquine. Regression analysis and Bland-Altman plots showed that IC₅₀ values for all the drugs tested agreed well between the two methods. Using a portable cytometer and a 96-well high-throughput sampler, this novel flow cytometry-based assay provides a fast and versatile platform for epidemiological monitoring of *ex vivo* drug susceptibility and screening novel blood schizonticidal drugs against *P. falciparum* and *P. vivax* field isolates.



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Session Details:	8/29/2013 Parasites in my blood! 1130 - 1240 Meeting Room 6
Poster with 2 minute Oral Presentation Details:	Molecular detection of <i>Ehrlichia</i> and <i>Anaplasma</i> species in domestic animals and tick vectors in Malaysia
Authors:	Koh Fui Xian ^{1*} , Ong Bee Lee ² , Panchacharam Chandrawathani ³ , Tay Sun Tee ¹ ¹ Department of Medical Microbiology, Faculty of Medicine, University of Malaya, 50603 Malaysia ² Department of Veterinary Clinical Studies, Faculty of Veterinary Medicine, University Putra Malaysia, 43400 UPM Serdang, Selangor, Malaysia ³ Veterinary Research Institute, Jalan Sultan Azlan Shah, Ipoh, Perak, Malaysia
Poster Number:	259

Anaplasmosis and ehrlichiosis are tickborne diseases that have been reported in humans and domestic animals in many parts of the world. However, little data is available on the prevalence of these diseases in Malaysia. Our current research aims to use molecular methods for detection of the presence of anaplasma and ehrlichiae from domestic animals and ticks. Of the 118 blood samples collected from different animals (majority were cattle) and 140 ticks collected from different animal hosts, 44.1% and 13.6% are positive for the presence of anaplasma and ehrlichiae, respectively. Sequence analysis of the amplified products shows the identification of *Ehrlichia canis*, *Anaplasma phagocytophilum*, *A. platys* and *A. marginale* in 1 (0.8%), 5 (4.2%), 7 (5.9%) and 39 (33.1%) of the animal blood samples, respectively. *E. canis*, *A. platys*, *A. phagocytophilum* and *A. marginale* were detected in 8 (42.1%), 2 (10.5%), 8 (42.1%) and 1(5.3%) ticks, respectively. The finding presented here provides preliminary data regarding the presence of Anaplasma and *Ehrlichia* species in animals and ticks in Malaysia.

Acknowledgements:

This project was funded by the research grant (RP013-2012A) provided by University of Malaya, Malaysia

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Inokuma, H., Ohno, K., Onishi, T., Raoult, D., Brouqui, P., 2001a. Detection of ehrlichial infection by PCR in dogs from Yamaguchi and Okinawa Prefectures, Japan. J. Vet. Med. Sci. 63, 815–817.



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Session Details:	8/29/2013 Pets, Pits and People 1130 - 1240 <i>Meeting Room 7</i>
Poster with 2 minute Oral Presentation Details:	Parasite prevalences in diagnostic faecal samples from horses, ruminants, pigs, dogs, cats, hedgehogs and rabbits
Authors:	Claudia Böhm*, Sonja Wolken, Petra Thomas, Thomas Schnieder†, Christina Strube Institute for Parasitology, University of Veterinary Medicine Hannover, GERMANY
Poster Number:	93

In a retrospective study the results of coproscopical examinations of faecal samples from horses, cattle, sheep, goats, pigs, dogs, cats, hedgehogs and rabbits were analysed. Samples were sent in as diagnostic material to our Diagnostic Unit between 2008 and 2012. During these 5 years, 1898 samples from horses were examined. 38.4% of the samples were positive for nematodes, 0.1% for cestodes and trematodes, and 0.2% for protozoans. The examination of 926 cattle samples resulted in 15.7% positive for nematodes, 0.9% for cestodes, 0.8% for trematodes, and 32.4% for protozoans. A number of 191 sheep samples were analysed and 66.5% were positive for nematodes, 5.2% for cestodes, 6.8% for trematodes, and 38.2% for protozoans. A percentage of 82.8% of the 64 samples of goats were positive for nematodes, 3.1% for cestodes and 28.1% for protozoans. Nematodes were found in 6.7% of the 450 samples of pigs and 5.3% of the samples were positive for protozoans. Of the 2087 samples of dogs, 6% were positive for nematodes, 0.5% for cestodes and 5.8% for protozoans. Overall 783 samples of cats were analysed and 4.1% were positive for nematodes, 0.5% for cestodes and 4% for protozoans. Examination of 138 hedgehog samples resulted in 41.3% positive for nematodes and 14.5% positive for protozoans. From rabbits, 276 samples were analysed and 4.3% were positive for nematodes and 21.7% for protozoans.



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Session Details:	8/29/2013 Pets, Pits and People 1130 - 1240 Meeting Room 7
Poster with 2 minute Oral Presentation Details:	The prevalence of intestinal nematodes in cats and dogs from Lancashire, north-west England.
Authors:	Chris Sherwin, Mohammed Nasr, Emma Gale, Metin Petek, Kathryn Stafford, Marilyn Turp, Gerald Coles* School of Veterinary Sciences, University of Bristol, Langford House, Bristol BS40 5DU, UK.
Poster Number:	59

Introduction: the importance of nematodes in the recent breeds of egg laying hens in the UK is not known.

Methods: 19 flocks were visited 3-4 times and details of housing, husbandry, health, welfare and range used were determined. Faecal samples were collected from 65 week old bird and counted using FLOTAC (1)accurate to 1 epg.

Results: All flocks had at least one nematode species with 17/19 infected with *Heterakis*, 16 with *Ascaridia* , 9 with *Trichostronglyus* and 6 with *Syngamus*. Four of the flocks had been treated with anthelmintic but egg counts were not significantly different from untreated flocks. There was no significant difference between organic (9) and non-organic (10) flocks and between static (n=8) and mobile flocks (n=11). None of the faecal egg counts for any of the species were correlated with egg production or cumulative mortality suggesting the infections were not severe. Faecal egg counts were correlated with a range of housing, husbandry and management practices which varied between nematode species and included depth of litter, percentage of hens using the range and the number of dead hens.

Discussion: How far the egg counts may represent birds at end of lay which have developed natural immunity is not known. However, the relationship between faecal egg counts, housing and husbandry variables suggests that these could be used to assist in future control of parasitic nematodes.

Acknowledgements: Funded by the RSPCA.

References: (1) Cringoli G, et al. Nature Protocols 2010;5:503.



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Session Details:	8/29/2013 Pets, Pits and People 1130 - 1240 <i>Meeting Room 7</i>
Poster with 2 minute Oral Presentation Details:	Soil contamination with <i>Toxocara</i> spp. eggs (Nematoda) in selected towns of Laguna, Philippines
Authors:	Hannah Mei R. Medina, Zuriele G. Arambulo, Vachel Gay V. Paller* Animal Biology Division, Institute of Biological Sciences, University of the Philippines Los Baños, Los Baños, Laguna 4031.
Poster Number:	266

This study aimed to determine the extent of soil contamination with soil transmitted helminthes (STH) eggs, particularly *Toxocara* spp., from soils in selected towns of Laguna, Philippines. Soil samples were collected from public schools, house yards and empty lots of Bay, Calauan, Los Baños, and Calamba, Laguna. Presence of STH eggs were examined using modified sucrose flotation technique. Results revealed that of the 1480 samples collected, 429 (31%) were found positive for *Toxocara* sp. eggs. Other STH recovered were *Ascaris* sp. (11%), hookworms (7%), and *Trichuris* sp. (5%). There were no significant differences in the prevalence and intensity of *Toxocara* sp. eggs among the various towns and sampling sites ($P>0.05$). Also, some soil physico-chemical parameters were determined and correlated with *Toxocara* eggs prevalence and intensity. Results revealed that *Toxocara* sp. eggs were most prevalent in less acidic, relatively high temperature and high moisture soil conditions. They were also prevalent in sandy, silty and loamy soil textures but less prevalent in clayey. No significant differences were found between depth 1 (0-5cm) and depth 2 (6-10cm). This study revealed that *Toxocara* sp. eggs are ubiquitous and the extent of contamination in soils from the selected towns of Laguna, Philippines is relatively high. Hence, the data generated in this study can be used in promoting public awareness, particularly for pet owners and local health officials, for effective prevention and control of this parasitosis.



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Session Details:	8/29/2013 Pets, Pits and People 1130 - 1240 <i>Meeting Room 7</i>
Poster with 2 minute Oral Presentation Details:	Parasite contamination of sand samples from sandpits in Slovak Republic
Authors:	Ingrid Papajová ^{1*} , Ján Papaj ² , Jana Pipiková ¹ , Peter Juriš ¹ , Branislav Pet'ko ¹ ¹ Institute of Parasitology, Slovak Academy of Sciences, Košice, Slovakia ² Technical University of Košice, Košice, Slovakia
Poster Number:	163

Due to the limited open green areas for a dog walking and a rising popularity of keeping dogs in urban agglomeration, their concentration increases in the public areas. Their excrements contaminate the environment and if these dogs are infected they are also a source of infection for other dogs, cats and animals. High prevalence of intestinal parasite eggs in dog populations pointed to the contamination of the environment, in which animals move. The aims of this study were as follows: to study parasitological contamination of sandpits in the selected towns in Slovakia and to evaluate the effect of anaerobic stabilisation (in the piles) of different organic wastes on the survival of model *Toxocara canis* embryonated. Totally 252 sand samples were collected from the children's sandpits of Košice, Prešov, Trenčín, Liptovský Mikuláš and Zvolen from areas with frequent movement of dogs and examined for the presence of the parasites. Eggs of *Toxocara* spp., *Toxascaris* spp., *Ascaris* spp. and eggs from the family Ancylostomatidae were detected in 12.3% of examined samples. The most prevalent were the eggs of *Toxocara* spp. which were found in 6.3% sandpits from Košice, 10.0% from Prešov, 16.7 % from Trenčín, 27.8% from Zvolen and 50.0% from Liptovský Mikuláš. Our results indicate the necessity of safe sanitation of municipal wastes from public area with some potential zoonotic agents. One possibility is the anaerobic stabilisation in the piles. Anaerobic stabilisation of organic waste from public areas with a temperature max. up to 35 °C has only decreased the viability of *T. canis* eggs (by 50 %). Environment contaminated with eggs of endoparasites might pose the potential risk for spread of parasitosis among animals, but also in human population.

Acknowledgements:

This study has been realized thanks to the financial support of the Research & Development Operational Programme funded by the ERDF: Environmental protection against parasitozoonoses under the influence of global climate and social changes (code ITMS: 26220220116) (1.0).



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Session Details:	8/29/2013 Pets, Pits and People 1130 - 1240 Meeting Room 7
Poster with 2 minute Oral Presentation Details:	Canine and Feline Strongyloidosis in France: Emerging and underestimated
Authors:	Laure Travers-Moussinet, René Chermette, Bruno Polack* Paris-Est, Ecole Nationale Vétérinaire d'Alfort , 7 avenue du général de Gaulle, 94704 Maisons-Alfort Cedex, France
Poster Number:	60

Canine and feline strongyloidosis is caused by the nematode *Strongyloides stercoralis* that infect also humans. This disease is well known in tropical country mainly on humans. In our veterinary school, *Strongyloides stercoralis* was not seen for more than 30 years (we practice more than 500 coproscopic examination per year on dogs and cats) before the cases described here.

Since 2006, we observed 15 clinical cases corresponding to 2 cats and 15 dogs (one case with three dogs from the same litter). The age at the first visit varied from 2.5 months to 6 years, most were one year old or less (14 animals). The onset of the disease was observed between 0.5 to 21 months before (mean 3.4 months). Main symptoms were diarrhea (in 13 dogs and in the 2 cats), generally severe chronic diarrhea persisting in spite of symptomatic treatment; Four dogs presented coughing in which 2 without digestive symptoms; Eleven dogs presented also a wasting syndrome characterized by an emaciation and in some dogs a very severe cachexia.

Diagnosis was generally carried out by Baermann technique or formol-ether sedimentation. In many cases, there were a tremendous number of larvae in the feces characteristic of hyper or disseminated infection with *S. stercoralis* in humans. Larvae were mainly L1 but L3 were also observed.

Animals were orally treated with fenbendazole 50 mg/kg SID for one month and in case of non efficacy (11 animals) and after MDR1 gene test for dogs with ivermectin 500 µg/kg for 7 days. Only two dogs died, the others fully recovered.

This is, to our knowledge, the first description of severe strongyloidosis in dogs in France. As coproscopic examination by flotation is not valuable for larvae, this disease is probably underestimated. Baermann technique should be promoted in case of severe chronic diarrhea in companion animals.



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Session Details:	8/29/2013 Pets, Pits and People 1130 - 1240 Meeting Room 7
Poster with 2 minute Oral Presentation Details:	Efficacy of emodepside 0,1 % plus toltrazuril 2 % suspension (Procox[®], Bayer) against <i>Trichuris vulpis</i> in naturally infected dogs.
Authors:	Gabriele Petry ¹ , Roland Schaper ^{1*} , Petro Swart ² , Dawie J Kok ² , Gertraut Altreuther ¹ ¹ Bayer Animal Health GmbH, 51368 Leverkusen, Germany ² ClinVet International (Pty) Ltd., Bloemfontein, Republic of South Africa
Poster Number:	240

The suspension of emodepside 0.1% + toltrazuril 2.0% (w/w)(Procox[®] Bayer) was developed against infection of dogs with *Toxocara canis*, *Ancylostoma caninum*, *Uncinaria stenocephala* and *Isospora* spp. To assess whether the product is also effective against whipworm infections a controlled, blinded GCP laboratory study was conducted. Twenty dogs naturally infected with *Trichuris vulpis* (*T. vulpis*) as demonstrated by two faecal egg counts ≥ 60 eggs per gram were included in the study and randomly allocated to two groups. On day 0 one group of dogs was treated with emodepside plus toltrazuril suspension at a dose of 0.45 mg emodepside plus 9 mg toltrazuril per kg body weight while the other group was left untreated as a control. Faeces were collected daily from day -3 until day 7 and examined for worms. On day 7 the dogs were euthanized and necropsied and the worms in the gastrointestinal tract were recovered, identified and counted. The response to treatment was evaluated by the comparison of *T. vulpis* worm counts in the treated dogs with those in the untreated control dogs.

All dogs in the control group were adequately infected with adult *T. vulpis* (range: 6-71 worms, geometric mean: 17.0) while no *T. vulpis* was obtained from the dogs that had been treated with emodepside plus toltrazuril suspension. The *T. vulpis* burdens of the treated and control groups differed significantly ($p < 0.0001$).

A treatment with emodepside plus toltrazuril suspension was 100% effective against a natural infection with *T. vulpis*. In the treated dogs all *T. vulpis* worms were expelled within 2 days after treatment. The suspension was well tolerated, no adverse events were observed that were regarded as treatment related.



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Session Details:	8/29/2013 Pets, Pits and People 1130 - 1240 <i>Meeting Room 7</i>
Poster with 2 minute Oral Presentation Details:	Age-Dependant Prevalence of Endoparasites in Young Dogs and Cats up to One Year of Age
Authors:	Dieter Barutzki ¹ , Roland Schaper ^{2*} ¹ Veterinary Laboratory Freiburg, P.O. Box 100120, 79120 Freiburg i. Br., Germany ² Bayer Animal Health GmbH, 51368 Leverkusen, Germany
Poster Number:	61

The results of parasitological examination of faecal samples from 1,206 cats and 2,319 dogs of known age up to one year were analysed. Eggs of *Toxocara canis* were detected in dogs for the first time at the beginning of the 3rd week, oocysts of *Isospora* spp. and cysts of *Giardia* spp. at the beginning of the 4th week p.p. High infection rates with *Giardia* spp. (52.5 %) were demonstrated in the 12th week, *I. canis* (30.0 %) in the 15th week, *I. ohioensis*-complex (44.0 %) in the 6th week, *Isospora* spp. (50.0 %) in the 7th week and *T. canis* (22.2 %) in the 4th week p.p. Co-infections with *Isospora* spp. + *Giardia* spp. (28.0 %), *T. canis* + *Isospora* spp. (16.0 %) and *T. canis* + *Giardia* spp. (12.0 %) were mainly seen in the 6th week p.p. In cats, oocysts of *Isospora* spp. and cysts of *Giardia* spp. were seen from the 3rd week and eggs of *Toxocara cati* from the 5th week p.p. High infection rates with *Giardia* spp. (66.7 %) were demonstrated in the 11th week, *Isospora* spp. (33.3 %) and *I. felis* (33.3 %) in the 15th week, *I. rivolta* (10.3 %) in the 10th week and *T. cati* (11.4 %) in the 8th week p.p. Co-infections with *T. cati* + *Isospora* spp. (9.1 %) were found in the 5th week, *Isospora* spp. + *Giardia* spp. (8.2 %) in the 12th week and *T. cati* + *Giardia* spp. (2.5 %) in the 22nd week p.p.



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Session Details:	8/29/2013 Pets, Pits and People 1130 - 1240 <i>Meeting Room 7</i>
Poster with 2 minute Oral Presentation Details:	Reptiles as paratenic hosts of feline parasites
Authors:	Rolf K. Schuster*, Saritha Sivakumar ¹ Central Veterinary Research Laboratory, Dubai, UAE
Poster Number:	58

A total of 292 stray cats were necropsied at the Central Veterinary Research laboratory between 2003 and 2012. The animals were trapped in the city centre and in the outskirts of Dubai as well as on camel and goat farms in the desert. The established parasite fauna in Dubai cats consisted of 18 species. Most of them occur in low prevalence and burdens. In the life cycles of 5 species (*Joyeuxiella pasqualei*, *J. fuhrmanni*, *Diplopylidium noelleri*, *Centrorhynchus aluconis* and *Macracanthorhynchus catulinus*) reptiles participate as paratenic hosts while the first intermediate host is unknown. A 71.6% prevalence of *Joyeuxiella pasqualei* in cats originating from the city center of Dubai was surprising and suggests that arthropods might be the true first intermediate host. Twenty-nine snakes of 3 species (*Echis carinatus*, *Cerastes gaspatti*, *Psammophis schokari*) and 79 lizards of 5 species (*Phrynocephalus arabicus*, *Acanthodactylus schmidtii*, *Chalcides ocellatus*, *Hemidactylus flaviviridis*, *H. turcicus*) were examined for parasites in the same time period. Larval stages of dipylidiid cestodes were found in 3 snake and 4 lizard species. Cystacanths of *C. aluconis* were present in all snake species and in *A. schmidtii* while the larval stage of *M. catulinus* was seen only in *C. gaspatti*. None of the examined *C. ocellatus* was infected either with cysticercoids or with cystacanths. Snakes showed the highest burden of these metazoan tissue parasites. Comparable worm burdens in snakes of different age suggest that infection has taken place in juvenile age when snakes feed on arthropods.



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Session Details:	8/29/2013 Pets, Pits and People 1130 - 1240 <i>Meeting Room 7</i>
Poster with 2 minute Oral Presentation Details:	One-year study on the prevalence of <i>Toxocara</i> eggs in sandpits in the city of Hanover, Germany
Authors:	Annika Kleine, Thomas Schnieder [†] , Christina Strube [*] Institute for Parasitology, University of Veterinary Medicine Hanover, GERMANY
Poster Number:	267

Toxocara spp. are worldwide distributed parasites of dogs and cats. As a zoonotic agent, they are a common threat to public health. Especially children are at risk of being infected with embryonated eggs due to geophagia and lacking hygiene awareness. To determine the contamination rate of playgrounds in the German city of Hanover, sand samples were collected monthly from January to December 2011 on 46 playgrounds distributed all over the city. To detect *Toxocara* eggs in the playground's sand, 250 g of each sample was prepared by a modified flotation technique (Horn al. 1990) and examined microscopically. Preliminary results show that between 0% (November) and 37% (17 sandpits, February) of the sandpits were positive for *Toxocara* eggs. Of these, between 0 % (January, May, September, October and November) and 24% (11 sandpits in February) were positive for infectious embryonated eggs. The average number of embryonated eggs per 250 g sand sample varied between 0 and 2.7 embryonated eggs. Obtained data suggest that the infection risk for children on playgrounds in Hanover seems to be moderate to low. Current work includes examination of further 250 g sand samples to increase the sample volume to a total of 500 gramm. Resulting data will be statistically analysed.

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Session Details:	8/29/2013 Pets, Pits and People 1130 - 1240 <i>Meeting Room 7</i>
Poster with 2 minute Oral Presentation Details:	The prevalence of intestinal parasites of domesticated bear in Korea
Authors:	Hee-Jeong Youn, Yong Suk Lim1, Kyong Hee Kim1, Min-Kyu Kim, Hwa-Young Youn, Nam-Shik Shin* Joon-Seok Chae College of Veterinary Medicine, Seoul National University, Seoul, 151-742, Korea, College of Veterinary Medicine, Chungnam National University, Daejeon, 305-764, Korea
Poster Number:	76

The bile juices of bears were used by traditional medicine until recently in Korea, but the Korean government try to prohibit to use it as medicine and control the domesticated bears because animal welfare and reservation of biological environment. In order to control the domesticated bears, we surveyed the biology and parasites of bears. We investigated the intestinal parasites of domesticated bears. The feces of one hundred of bears were collected from bear farms and intestinal parasites were investigated by sedimentation and floatation techniques. *Baylisascaris procyonis* were detected from nine of the 100 bear feces samples. The M±SD of egg size are 49.0± 2.4 in length and 38.1± 3.6 in width. Mites and their eggs were detected from five of the 100 bear feces samples. The M± SD of egg size were 148.7± 3.8 in length and 100.7± 3.3 in width. The M± SD of adult worms size were 145.9± 7.0 in length and 57.4± 3.6 in width. Unidentified nematodes were detected from three of the 100 bear feces samples.

The isolated ascarid eggs, nematode eggs, ticks and ticks' eggs will be identified by PCR and sequencing

Key-words : Bear, *Baylisascaris procyonis*, tick, intestinal parasite

Corresponding author : Nam-Shik Shin, College of Veterinary Medicine, Seoul National University, Seoul 151-742, Korea, +82-2-880-1260, nsshin@snu.ac.kr



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Session Details:	8/29/2013 Size really doesn't matter - enteric protozoa 1130 - 1240 Meeting Room 8
Poster with 2 minute Oral Presentation Details:	<i>Tritrichomonas foetus</i>: identifying critical proteins involved in the host-parasite interaction
Authors:	Leah Cronin ^{1, 3*} , Jens R. Coorssen ^{2, 3} , Jan Slapeta ⁴ , Colin Stack ^{1, 3} ¹ School of Science and Health, ² Molecular Physiology, School of Medicine, University of Western Sydney, AUSTRALIA ³ Molecular Medicine Research Group, University of Western Sydney, AUSTRALIA ⁴ Faculty of Veterinary Science, The University of Sydney, AUSTRALIA
Poster Number:	197

The protozoan parasite, *Tritrichomonas foetus* is a serious veterinary pathogen that causes bovine and feline trichomoniasis. In cows *T. foetus* infects the urogenital tract causing a sexually transmitted infection that may be asymptomatic or have symptoms including severe inflammation and infertility (Felleisen 1999). Treatment options are limited as culling is the only effective treatment for infected bulls. In cats, *T. foetus* infects the colon and ileum, causing chronic diarrhoea (Foster et al. 2004). The current treatment for feline trichomoniasis utilises the drug ronidazole. However, this drug has not been approved in many countries due to limited efficacy and narrow safety margin (Gookin et al. 2010; LeVine et al. 2011). The current burden these strains place on the veterinary field, call for the identification of novel biomarkers and targets for drug treatment. Interestingly, the epidemiology of *T. foetus* feline cannot be linked to *T. foetus* bovine. Recently a small genetic distinctness in a number of key virulence factors was identified between the strains (Slapeta et al. 2012), providing an indication that these pathogens are able to adapt to their particular environmental niches. We believe proteins unique to these strains or proteins expressed at different concentrations are key to their virulence; particularly membrane and secretory proteins, which are involved in adhesion, immune evasion, tissue destruction and nutrient acquisition. These molecules can be identified and characterised using a quantitative proteomic approach, whereby the proteome is resolved and characterised using coupled high resolution two-dimensional gel electrophoresis and mass spectrometry. The identification of proteins involved in the host-parasite interactions of both these strains will reveal novel targets for treatment and provide the basis for further analysis of *T. foetus*.

Acknowledgements:

The research was funded by the University of Western Sydney UWS Research Grant Scheme (Stack, Coorssen, Jones) and the University of Western Sydney School of Science and Health, Higher Degree Research Project funds.



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Session Details:	8/29/2013 Size really doesn't matter - enteric protozoa 1130 - 1240 Meeting Room 8
Poster with 2 minute Oral Presentation Details:	Risk factors and spatial distribution of <i>Giardia</i> spp and <i>Toxoplasma gondii</i> in domestic pets and 'urban adaptor' wildlife in the greater Perth region
Authors:	Alison Hillman* ¹ , Alan Lymbery ¹ , Ian Robertson ¹ , R.C. Andrew Thompson ¹ ¹ Murdoch University, Perth, AUSTRALIA
Poster Number:	209

Human encroachment into wildlife environments can result in the 'spill over' of human and domestic animal infections into wildlife species (1,2). Urban dwelling populations of 'urban adaptor' wildlife species (wildlife species that continue to survive- and in some cases, thrive- in urbanised areas) are considered particularly at risk of such 'spill over'. This is of concern from a 'One Health' triad of perspectives: 1) potential impact on wildlife population health, 2 & 3) creation of wildlife reservoirs of infection, from which infection can 'spill back' into domestic animals and/ or humans.

Preliminary studies have suggested that in Australia, the urban dwelling marsupials quenda (*Isodon obesulus fusciventer*) and common brushtail possums (*Trichosurus vulpecula*) may have a substantially increased risk of infection with the anthroponotic parasites *Giardia* spp and *Toxoplasma gondii*, respectively (3,4,5). We aim to investigate this hypothesis in the greater Perth region. Additionally, we aim to investigate the epidemiology of *Giardia* spp and *Toxoplasma gondii* in Perth's domestic cat and dog populations, as these populations may represent a substantial source of infection to wildlife, which could contribute to any observed infection risk associated with urbanisation.

This study is undertaking cross sectional sampling, and will utilise statistical modelling (multivariable logistic regression and spatial analysis). Models will investigate the demographic distribution of these parasites, putative risk factors for infection (including polyparasitism), and geographical clustering of infection risk associated with a gradient of urbanisation.

Acknowledgements:

Holsworth Wildlife Research Endowment; Australian Society for Parasitology

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(3) Eymann, J., Herbert, C., Cooper, D. & Dubey, J., 2006. Serological survey for *Toxoplasma gondii* and *Neospora caninum* in the common brushtail possum (*Trichosurus vulpecula*) from urban Sydney, Australia. *J. Parasitol*, 92(2), pp. 267-272.



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Session Details:	8/29/2013 Size really doesn't matter - enteric protozoa 1130 - 1240 Meeting Room 8
Poster with 2 minute Oral Presentation Details:	Development of nested PCR specific to bovine <i>Eimeria</i> species
Authors:	Takuya Kokuzawa, Madoka Ichikawa-Seki *, Tadashi Itagaki Iwate University, Morioka, JAPAN
Poster Number:	95

More than 13 *Eimeria* species have been known as causative agents of bovine coccidiosis and differ in pathogenicity to the host. Identification of *Eimeria* species is carried out by morphological characteristics of sporozoite-formed oocysts, however it is not easy to discriminate among the species showing similar morphology. We tried to develop nested PCR method for the species identification based on difference of nuclear ribosomal ITS2 sequences in *Eimeria* spp.

Oocysts of 10 *Eimeria* species, *E. alabamensis* (Eal), *E. auburnensis* (Eau), *E. bovis* (Ebo), *E. bukidnonensis* (Ebu), *E. canadensis* (Eca), *E. cylindrica* (Ecy), *E. ellipsoidalis* (Ee), *E. subspherica* (Es), *E. wyomingensis* (Ew), *E. zuernii* (Ez), were used in the study. Total DNA was extracted from single oocysts according to Kaya et al. (2007) and Honma et al. (2006). The sequences of 18S rDNA and ITS2 including partial 5.8S and 28S rDNA were determined by direct sequencing and cloning of nested PCR amplicons.

At least 10 oocysts of each *Eimeria* species originated in 1 to 7 isolates were analyzed. The ITS2 sequences obtained were grossly-different among *Eimeria* spp., and their base pairs were 390bp (Ebu) to 673bp (Ecy), base pair similarity was 25.8~82.6% among the species and 84.3~100% in intra-species and intra-individual. ITS2 primers (forward and /or reverse) specific to *Eimeria* species were designed based on the sequences and used for the second reaction of nested PCR. Nested PCR using primer set for each *Eimeria* species produced no amplicons in template DNA of the other *Eimeria* spp. suggesting species-specificity. Further, nested multiplex PCR using primer sets for 3 to 4 *Eimeria* species was also developed.



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Session Details:	8/29/2013 Size really doesn't matter - enteric protozoa 1130 - 1240 Meeting Room 8
Poster with 2 minute Oral Presentation Details:	Zoonotic <i>Blastocystis</i> in wildlife in western Thailand
Authors:	Aongart Mahittikorn ^{1*} , Hirotake Mori ¹ , Nathamon Kosoltanapiwat ² , Saengduen Moonsom ¹ , Supaluk Popruk ¹ , Marnoch Yindee ³ , Yaowalark Sukthana ¹ ¹ Department of Protozoology, ² Department of Microbiology and Immunology, Faculty of Tropical Medicine, Mahidol University, Bangkok, Thailand ³ Faculty of Veterinary Science, Mahidol University Salaya Campus, Nakhonpathom, Thailand
Poster Number:	269

Blastocystis is found worldwide and is one of the most commonly isolated protozoa in humans and animals. Recently, phylogenetic analysis targeting the small subunit ribosomal RNA gene enables subtyping and the evaluation of zoonotic potential and host specificity; to date, at least 13 subtypes (STs) have been identified. Our previous investigation among villagers in a rural community of western Thailand identified both zoonotic and anthroponotic subtypes; the zoonotic STs, ST1 and ST2, were detected. Pigs, cattle, birds, and monkeys are considered major animal hosts in ST1 or ST2. *Blastocystis* have not been fully investigated among wildlife, however. Therefore, we aimed to investigate forest wildlife near the community in Western Thailand that we investigated previously.

We collected feces of a variety of wildlife-bird (hornbill), wild boar, elephant, sambar deer (*Rusa unicolor*), pangolin, monkey, musk deer, and turtle. Stool samples were examined by microscopy after concentration technique, and nested PCR. PCR-positive samples were sequenced and analysed by phylogenetic tree. *Blastocystis* has been identified in elephants, gazelles, hyena, and turtles, with particularly high prevalence among elephants. Subtype analyses have so far identified animal-specific subtypes, not zoonotic strains.

Sample collection and stool-sample analysis are in process. After collecting wildlife samples, we plan to investigate domestic animals in the same area. In our presentation, we will discuss the results of investigations into wildlife and domestic animals in western Thailand. We will compare the subtype characteristics of animals and humans, and consider the potential risk and transmission routes of zoonotic *Blastocystis* in this area.



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Session Details:	8/29/2013 Size really doesn't matter - enteric protozoa 1130 - 1240 <i>Meeting Room 8</i>
Poster with 2 minute Oral Presentation Details:	Ultrastructure and physiological differences of the bovine and feline <i>Tritrichomonas foetus</i> strains
Authors:	Victoria Morin-Adeline ¹ , Neil Portman ¹ , Colin Stack ² and Jan Slapeta ¹ ¹ Faculty of Veterinary Science, The University of Sydney, NSW, Australia ² School of Biomedical and Health Science, University of Western Sydney, NSW, Australia
Poster Number:	39

In the past, *Tritrichomonas foetus* was exclusively recognised as an extracellular bovine urogenital tract parasite. In infected female cows, reproductive failure occurs through damage to the reproductive tract lining leading to abortion of calves. In an unpredictable twist, the past decade has seen *T. foetus* widely implicated in enteric disease of cats, causing profuse diarrhea. While the bovine *T. foetus* ultrastructural cellular landscape has been well described, there is currently no published data on the ultrastructural features of the feline *T. foetus* strain. The cellular complexity of the two strains will be characterized and compared using both electron microscopy and flow cytometry. Last but not least, a flow cytometric assay will be used for assessing the effects of pH on both *T. foetus* isolates. In mammalian systems, pH is known to set the balance between host and the parasite. Therefore, we want to investigate the pH tolerance of the feline/bovine *T. foetus* isolates to address the hypothesis that they reflect the niche from which they were isolated; i.e. the bovine genital tract (pH 7.4- 7.9) and the cat intestinal tract (pH5.3 - 6.4). The pH tolerance will be assayed in a platform that was validated using 5-nitromidazoles kill curves. In summary, this investigation will be the first to compare and contrast the ultrastructural and physiological features of the bovine and feline *T. foetus* strains.



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Session Details:	8/29/2013 Size really doesn't matter - enteric protozoa 1130 - 1240 Meeting Room 8
Poster with 2 minute Oral Presentation Details:	A trich(y) oxygen story
Authors:	Victoria Morin-Adeline ¹ , Neil Portman ¹ , Jan Slapeta ¹ ¹ Faculty of Veterinary Science, The University of Sydney, NSW, Australia
Poster Number:	40

Metabolic pathways for the production of energy in the form of ATP are regarded as a central dogma in cell biology. In aerobic eukaryotes, oxygen is instrumental in many of these fundamental biological reactions such as those that occur in the energy metabolism from carbohydrates within the mitochondria. Further to the natural roles of oxygen, its roles extend to applications in biotechnology for aiding research. Amidst the most celebrated of these is its pivotal role in the revolutionary advancement of protein localization through fluorescence microscopy that is green fluorescent protein (GFP). Upon expression, the GFP relies on oxygen for the maturation of the protein chromophore core that emits the fluorescence signal. So can GFP work in anaerobic parasites such as *Trichomonas vaginalis*, *Tritrichomonas foetus* and *Giardia duodenalis* within which a purely fermentative metabolism takes place without the need for oxygen? In this mini-review, we will mine the literature to compare the known metabolic pathways of these organisms and the impact of oxygen on their survival. Furthermore, their mechanisms for neutralizing oxygen will be outlined and potential biotechnological techniques that can be applied to overcome any problems when using GFP in these organisms will be investigated.



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Session Details:	8/29/2013 Size really doesn't matter - enteric protozoa 1130 - 1240 Meeting Room 8
Poster with 2 minute Oral Presentation Details:	Protein variation between the zoonotic and livestock specific assemblages of <i>Giardia duodenalis</i>
Authors:	Robert F. L. Steuart ^{1,2} , Ryan O'Handley ² , Richard Lipscombe ³ and R. C. Andrew Thompson ¹ ¹ School of Veterinary and Biological Sciences, Murdoch University, Perth, W.A. ² Curtin Health Innovation Research Institute, School of Biomedical Sciences, Curtin University, Perth, W.A. ³ School of Veterinary Sciences, University of Adelaide, S.A. ⁴ Proteomics International Pty Ltd, Perth, W.A.
Poster Number:	270

The genomes of the three assemblages of *Giardia duodenalis* currently able to be cultured (A, B, E) have recently been sequenced. The genomic information obtained is invaluable in the study of *G. duodenalis* however it does not give an indication as to which proteins are actively expressed in the parasite, or the level of this expression. The proteins produced at the trophozoite stage of the parasite *G. duodenalis* were compared using SDS-PAGE of the two zoonotic and the livestock specific assemblages to identify areas of variation between the assemblages. Overall twelve proteins were identified that showed difference in the migration pattern on SDS-PAGE gels. These included structural proteins (e.g. alpha tubulin and alpha 10 and 11 giardin), metabolic enzymes (e.g. NADP specific glutamate dehydrogenase) and cell cycle proteins (e.g. GLORF-C4 and 14-3-3). Some of the differences on the gel appear to be genome linked, however others are not and represent likely post-translational modifications and expression differences between the assemblages of *G. duodenalis*. We were unable to identify a single protein band which was specific for any of the assemblages, nor a protein which was specific only to the zoonotic assemblages. One protein, Dynamin, was identified from bands of the same molecular mass from the zoonotic assemblages and a smaller molecular mass from assemblage E. The biological relevance of this is as yet unknown. Understanding the protein variation between the assemblages of *G. duodenalis* may give an insight to the mechanisms responsible for host specificity.



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Poster with 2 minute Oral Presentation Details:	Does dietary starch have an impact on <i>Balantidium coli</i> infections in captive chimpanzees?
Authors:	Kateřina Schovancová ¹ , Kateřina Pomajbíková ^{2*} , Petr Procházka ³ , David Modrý ^{2,4,5} , Petra Bolechová ⁶ , Klára J. Petrželková ^{2,3,4,6} ¹ Institute of Botany and Zoology, Masaryk University, Brno, Czech Republic ² Department of Pathology and Parasitology, University of Veterinary and Pharmaceutical Sciences, Brno, Czech Republic ³ Institute of Vertebrate Biology, Academy of Sciences of the Czech Republic, Brno, Czech Republic ⁴ Biology Center of the Academy of Sciences of the Czech Republic, Institute of Parasitology, České Budějovice, Czech Republic ⁵ Central European Institute for Technology, Brno, Czech Republic ⁶ Liberec Zoo, Liberec, Czech Republic
Poster Number:	216

Although the infections by *Balantidium coli* in humans were recognized more than one and half century ago, many aspects of the epidemiology or mechanisms of pathogenicity remain unknown. Infections are asymptomatic in most hosts, but in humans and captive African great apes clinical infections manifested mainly by dysentery occasionally occur. Thus, *Balantidium* infections in captive African great apes offer an interesting model, which helps us to unravel the factors contributing to development of clinical balantidiasis in humans. Several almost forgotten experimental studies pointed to a possible effect of diet on *B. coli* infections in pigs and rats with the emphasis on the starch content. We studied the effect of dietary starch on the intensities of infection by *B. coli* in two groups of captive chimpanzees from the Hodonín Zoo and from the Brno Zoo, Czech Republic. We fed adult chimpanzees infected by *B. coli* with a high starch diet (HSD) (average 13.5% of starch), followed by a five-day transition period and subsequently with a period of low starch diet (LoSD) (average 0.1% of starch). We collected fecal samples during the last seven days of HSD and LoSD and stored them in 10% formalin. We quantified trophozoites of *B. coli* using the FLOTAC method. Generalized linear mixed-effects model showed significantly lower numbers of the *B. coli* trophozoites in the feces during the LoSD in comparison to the HSD. We conclude that a starch-rich diet can be responsible for high intensities of infection of *B. coli* in captive chimpanzees and might predispose them to clinically manifested balantidiasis. We discuss the potential nutritional modifications to diets that can be implemented in part to control *B. coli* infections in captive apes. Our finding opens also the question of the similar dietary effect on *B. coli* infection in humans.

Acknowledgements:

We would like to express our sincere thanks to the Hodonín and Brno Zoos for enabling us to conduct this study. We are particularly grateful to Jaroslav Hyjánek, Jiří Ingr, Petra Bílková, Lukáš Baránek (Zoo Hodonín) and Martin Hovorka, Jiří Vítek, Iva Slaninová, Marcela Němečková, Mariana Hubíková (Zoo Brno). The manuscript benefited from valuable comments and language revision by Dr. J. M. Rothman from the Department of Anthropology, Hunter College at the City University of New York (USA).



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- The Joe Boray Session
- Resistance is futile!
- Ticked Off!
- Who and How Many?
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- Cause and Effect
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25-29 August 2013
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Session Details:	8/29/2013 Size really doesn't matter - enteric protozoa 1130 - 1240 Meeting Room 8
Poster with 2 minute Oral Presentation Details:	Effect of sample composition and storage on detection of <i>Neoparamoeba perurans</i> using qPCR
Authors:	Kingsley Tam ^{1*} , Andrew Bridle ¹ , Philip Crosbie ¹ , Barbara Nowak ¹ ¹ National Centre for Marine Conservation and Resource Sustainability, Australian Maritime College, University of Tasmania, Tasmania, Australia
Poster Number:	29

The protozoan *Neoparamoeba perurans* is the aetiological agent of amoebic gill disease (AGD) in marine farmed Atlantic salmon in Tasmania and is emerging as a threat to global marine aquaculture. AGD is major concern to the industry due to the significant mortality this disease can potentially inflict. AGD is becoming a significant disease in all salmon farming countries except Canada. *N. perurans* is a free living amoeba which becomes parasitic when it colonises gills of Atlantic salmon. The relationship between the presence of *N. perurans* in water and AGD severity is not understood. The only study investigating this relationship was an experimental infection where known number of gill-isolated amoebae were added to water and the severity of AGD was shown to be directly related to the concentration of the amoebae in the water. While a qPCR-based method for *N. perurans* detection in fish and environmental samples has been developed, there is an interest in distinguishing between live and dead amoebae and the effects of sample composition and storage conditions. This study aimed to determine the dynamics of *N. perurans* in water during an experimental infection. The effects of sample compositions and sample storage conditions on the results were investigated. Finally, a detection method distinguishing between the presence of live and dead *N. perurans* by combining real-time polymerase chain reaction and propidium monoazide (PMA) has been explored.

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Session Details:	8/29/2013 Size really doesn't matter - enteric protozoa 1130 - 1240 Meeting Room 8
Poster with 2 minute Oral Presentation Details:	First Molecular Characterization of <i>Giardia duodenalis</i> from Goats in Malaysia
Authors:	Yvonne A.L. Lim ^{1,2} , Mohammed A.K. Mahdy ¹ , Tiong K. Tan ^{1*} , Xiang T. Goh ¹ , Aaron R. Jex ² , Matthew J. Nolan ² , Reuben S.K. Sharma ³ , Robin B. Gasser ² ¹ Department of Parasitology, Faculty of Medicine, University of Malaya, 50603 Kuala Lumpur, Malaysia ² Department of Veterinary Science, The University of Melbourne, Parkville, Victoria 3010, Australia ³ Department of Veterinary Pathology and Microbiology, Faculty of Veterinary Medicine, Universiti Putra Malaysia, 43400 UPM Serdang, Selangor Darul Ehsan, Malaysia
Poster Number:	36

Presently, there is considerable information on the epidemiology of *Giardia* in ruminants, particularly goats [1,2,3]. However, molecular studies have not been widely conducted on *Giardia* in animals in Malaysia. The present study genetically characterized, for the first time, *Giardia* from goats in this country to assess whether they harbour genotypes with the potential to infect humans. In the present study, 310 faecal samples from goats from eight different farms in Malaysia were tested for the presence of *Giardia* using a PCR-coupled approach. The nested PCR for SSU amplified products of the expected size (~200 bp) from 21 of 310 (6.8%) samples. Sixteen of these 21 products could be sequenced successfully and represented six distinct sequence types. Phylogenetic analysis of the SSU sequence data using Bayesian Inference (BI) identified *Giardia duodenalis* assemblages A, B and E. The identification of the 'zoonotic' assemblages A and B suggests that *Giardia*-infected goats represent a possible reservoir for human giardiasis in Malaysia. In conclusion, although *G. duodenalis* assemblage E is reported to be dominant in goats in the present study, and in ruminants in general [4,5], this assemblage has also been detected in humans living in close contact with livestock [6], suggesting a potential for zoonotic transmission in particular epidemiological circumstances (i.e., close human-animal contact). However, more studies are needed to test this proposal. Importantly, the identification of the 'zoonotic' assemblages A and B in the present study suggests that *Giardia*-infected goats represent a possible source for human infections in Malaysia. Large-scale epidemiological studies of domesticated and native animals as well as humans are needed to gain better insights into the prevalence, host affiliations and geographical distributions of the different assemblages of *G. duodenalis* in Malaysia.

Acknowledgements:

The authors thank the farmers for their collaborative efforts and Bakhtiar Affendi Bukari for his technical assistance. We acknowledge the funding support from the Ministry of Higher Education, Malaysia, University of Malaya [projects RG221-10HTM (YLAL and RBG) and PV024/2011B (YLAL and TKT)]. Funding support from the Australian Research Council (ARC) and Melbourne Water Corporation are gratefully acknowledged (RBG and ARJ).



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Session Details:	8/29/2013 Size really doesn't matter - enteric protozoa 1130 - 1240 Meeting Room 8
Poster with 2 minute Oral Presentation Details:	In vitro screening of antimicrobial compounds against Neoparamoeba perurans, the aetiological agent of amoebic gill disease.
Authors:	Ting YiHui*, Phil Crosbie, Mark Adams University of Tasmania, Newnham, Tasmania, Australia
Poster Number:	30

Amoebic gill disease (AGD) has affected cultured Atlantic salmon in Tasmania and many other countries such as USA, Chile, Ireland and Scotland. It affects the culture of Atlantic salmon during the marine 'grow-out' phase of production. The causative agent is *Neoparamoeba perurans* which causes rapid proliferation of gill tissues and high mortality in untreated stocks. AGD is currently the most significant disease facing the Tasmanian salmon industry. The current treatment bathing of affected stock in freshwater baths is time consuming and costly. Thus there is a need to explore other treatment options and this project aims to screen a variety of potential growth inhibitors against *N.perurans in vitro* to identify candidates for future *in vivo* assessment.

A range of antimicrobial compounds were tested for their amoebicidal efficacy in replicate wells of 24 well tissue plates using previously established protocols. *N. perurans* were isolated from AGD-affected salmon gills and exposed on a short term basis (up to 60 mins) to various compounds. Survival was assessed both immediately after initial exposure and 24 hour post treatment using an inclusion dye (neutral red) assay. The data obtained were analysed using ANOVA. Results and subsequent implications for future *in vivo* screening are discussed.



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Session Details:	8/26/2013 Poster Session 1 1800 - 1930
Poster Details:	Drug resistance in nematodes of herbivores host in Argentina
Authors:	Oscar S. Anziani ^{1*} ¹ EEA Rafaela, National Institute of Agriculture Technology, Argentina
Poster Number:	09

Anthelmintic resistance (AR) in nematodes parasiting domestic hervibores is an animal welfare and production problem in central and nortnen Argentina. Prevalence is particularly high in sheep nematodes of the northeast where *Haemonchus contortus* is the prevalent genera. In this area, more than 90 % of the farms are showing failure to control this parasite with closantel, avermectins, benzimidazoles or levamisole. Multiple resistance to two or three of these compounds are common and recently it was reported an isolation of *H. contortus* in sheep in central Argentina with resistance to all four drugs. *Trichostrongylus* spp has also showed resistance to avermectins, bencimidazole or levamisole. In goats, the situation of AR prevalence is similar to sheep with *Haemonchus* spp and *Trichostrongylus* spp showing widespread resistance (inclusive multiple AR) to the above anthelmintics. Ivermectin failure to control *Haemonchus* spp in an alpaca farm was also reported. In cattle nematodes, AR is present in more than 50 % of beef or dairy herds. *Cooperia* species and avermectins are implicated in most of the cases, but there are a few reports about *Ostertagia* spp resistant to benzimidazoles and *Haemonchus* spp with multiple resistance to avermectins and benzimidazoles. In dairy calves, resistance of intestinal nematodes *Trichostrongylus colubriformis* , *T. longispicularis* and *Nematodirus helvetianus* to macrociclic lactones has been recently published. At present, there are not reports about abomasal or intestinal cattle nematodes resistant to levamisole. In horses, populations of cyathostomins resistant to benzimidazoles are widespread in the central area of Argentina while macrocyclic lactones remain active against these parasites. However, ivermectin has showed inefficacy to control *Parascaris equorum* in a horse farm.





Session Details:	8/26/2013 Poster Session 1 1800 - 1930
Poster Details:	The efficacy of commonly used anthelmintics against gastro-intestinal nematodes in sheep and cattle in Spain
Authors:	Thomas Geurden ^{1*} , Francisco A. Rojo Vazquez ² , María Martínez-Valladares Vazquez ³ , Jose Manuel Martinez-Perez ³ , David Robles-Perez ³ , Maria Aránzazu Meana Manes ⁴ . David Bartram ¹ , ¹ Zoetis ² Universidad de León, Avda. Facultad de Veterinaria 25, 24071 León, Spain ³ Instituto de Ganadería de Montaña, Instituto de Ganadería de Montaña CSIC/University of León ⁴ Universidad Complutense de Madrid, Facultad de Veterinaria, Madrid, Spain
Poster Number:	115

This study aimed to evaluate the efficacy of commonly used anthelmintics against gastro-intestinal nematodes in sheep and cattle in Spain. For each animal species, ten study sites were selected based on a history of frequent use of anthelmintics. On the sheep farms, animals were allocated into 4 treatment groups of 10 animals each. Three groups were treated with either an injectable formulation of moxidectin or ivermectin, or oral formulations of fenbendazole or levamisole. One group remained untreated. A modified McMaster technique, with a sensitivity of 15 eggs per gram of faeces was used to monitor faecal egg counts (FEC). Assessment of efficacy was based on the arithmetic mean FEC of each treatment group versus the control group 14 days after treatment. The efficacy of MOX and IVM was evaluated on 8 farms only. MOX was effective on 6 farms (100% efficacy). On the other 2 farms reduced efficacy was detected (77% and 94%). IVM was effective on 2 farms (100%). On the other 6 farms, efficacy was reduced. After treatment, mainly *Teladorsagia* (90-100% of larvae) was identified. Reduced efficacy was observed for fenbendazole on 3 farms and for levamisole on 6 farms. For the cattle study, animals were allocated into 2 treatment groups based on the individual pre-treatment FEC. Assessment of efficacy was based on the difference between the arithmetic mean FEC prior to treatment and 14 days post treatment, for each treatment group separately. Verified results for the cattle study will be presented at the conference.



Session Details:	8/26/2013 Poster Session 1 1800 - 1930
Poster Details:	The comparison of FECPAK, McMaster and FLOTAC techniques for gastrointestinal strongyle faecal egg counts in cattle
Authors:	Laura Rinaldi ¹ , Maria Paola Maurelli ¹ , Antonio Bosco ¹ , Gerald Coles^{2*} , Giuseppe Cringoli ¹ ¹ Department of Veterinary Medicine and Animal Productions, University of Naples Federico II, CREMOPAR Regione Campania, Naples, Italy; ² School of Veterinary Sciences, University of Bristol, Langford House, Bristol BS40 5DU, UK
Poster Number:	77

Introduction: The sensitivity and accuracy of three faecal egg count techniques - FECPAK, McMaster and FLOTAC (1)- were compared for the diagnosis of gastrointestinal (GI) strongyles in cattle, naturally infected with high (>800 epg) and low (10epg) burdens of eggs.

Methods: Two composite samples were prepared, one composite having a low and one having a high GI strongyle eggs per gram (EPG). From each pooled sample, 12 replicates for each of the three methods were analysed using a saturated NaCl flotation solution.

Results: FLOTAC was the only technique that gave positive results for all replicates of the composite sample with low numbers of strongyles eggs, thus making it more sensitive than FECPAK (66.7%) and McMaster (41.7%). FLOTAC also produced mean EPG values higher and coefficient of variation values lower than the other two techniques, both for high and low numbers of eggs. The results also show that reliability of FECPAK and McMaster techniques for the estimation of the GI strongyles EPG is influenced by the choice of the reading area (volume) both for low and high egg counts. The most striking result was the finding of the highest EPG values (151% for McMaster) where the smallest area of the slides were counted.

Discussion: The higher egg counts in the McMaster slide and lower in the FECPAK indicates that both slides are mis-estimating egg counts and counting eggs under the grid will give incorrect vales.

Acknowledgements: The staff at CREMOPAR.

References: (1) Cringoli G, et al. Nature Protocols 2010;5:503.



Session Details:	8/26/2013 Poster Session 1 1800 - 1930
Poster Details:	Wild Roe deer (<i>Capreolus capreolus</i>) infected with benzimidazole resistant <i>Haemonchus contortus</i> .
Authors:	Cosmin Chintoan-Uta, Eric Morgan and Gerald Coles* School of Veterinary Sciences, University of Bristol, Langford House, Bristol BS40 5DU, UK.
Poster Number:	111

Introduction: Sheep, cattle and wild ruminants have previously been found to share a common field population of *Haemonchus contortus* (1). As benzimidazole (BZ) resistance is very common on sheep farms in the UK the possibility that wild deer might transmit resistant *H. contortus* was investigated.

Methods: 48 samples of intestine were collected from fallow (24), red (14) and roe deer (10) from farmed populations and from wild deer in areas of extensive and intensive cattle and sheep farming. Tests for BZ resistance were run using the egg hatch test (EHT), β -tubulin sequencing and treatment of artificially infected sheep and for macrocyclic lactones using the latter test.

Results: Roe deer grazing intensive areas of farming had abomasal worms largely different from fallow and red deer irrespective of where the other two species were grazing. Species in the abomasa were *H. contortus*, *Ostertagia ostertagi*, *Trichostrongylus axei*, *Trichostrongylus colubriformis*, *Spiculoptera spiculoptera* and *Ostertagia leptospicularis*. *H. contortus* from the roe deer had mutations at position 167 and 200 in β -tubulin. In an EHT 62% of eggs hatched in 0.1 μ g/ml thiabendazole (EC50 0.149 μ g/ml) and 5 mg/kg of fenbendazole removed 88.5% of worms from lambs.

Discussion: Roe deer were found naturally infected with BZ resistant *H. contortus* and can therefore spread the infection from farm to farm. In practice this infection is so common that spread of this resistance by roe deer may not be important but if the deer were infected with other resistant nematodes, for example with ML resistant *H. contortus* their role in the spread of resistance might be important and make the management of resistance even more difficult. On the other hand, wildlife might provide refugia for susceptible alleles. Further field studies are required to establish the importance of deer as vectors for anthelmintic resistant nematodes.

Acknowledgement: Supported by the Wellcome Trust.

Reference: (1) Cerutti, M.C., Citterio, C.V., Bazzocchi, C. et al. 2010. J.Helminthology; 84:194.



Session Details:	8/26/2013 Poster Session 1 1800 - 1930
Poster Details:	A SEM study of the micromorphology of the sucking louse <i>Linognathus angasi</i> from the Nyala <i>Tragelaphus angasi</i> from South Africa.
Authors:	E.D.Green Dept of Anatomy, University of Limpopo, Box 232, MEDUNSA, 0204, South Africa. Edward.Green@ul.ac.za
Poster Number:	63

A SEM study of the micromorphology of the sucking louse *Linognathus angasi* from the Nyala *Tragelaphus angasi* from South Africa.

Sucking lice collected from wild nyala in the Ndumu Game Reserve in Kwazulu-Natal, South Africa were identified by light microscopy as *Linognathus angasi* Weisser & Ledger 1977. As the four *Linognathus* species found on the related bushbuck, nyala and greater kudu are morphologically very similar and difficult to distinguish, it was decided to do a scanning electron microscope (SEM) study to investigate the micromorphological characteristics of *L. angasi*. The lice were ultrasonically cleaned and routinely prepared for SEM and viewed in a Zeiss SUPRA55VP FE-SEM.

Small scale-like setae covered the head, thorax and membranous abdomen. The post-antennal conical head bearing five pairs of setae, tapered to join the thorax while the short rounded pre-antennal part enclosed the flaps of the haustellum at the anterior tip. The antennal segments IV and V each bore a large pore organ with its sensory tufts, and two plate organs. The robust thorax bore a pair of large lateral spiracles and a pair of long setae on the mesothorax, and ventrally a linear sternal plate which is a distinguishing feature of *L. angasi*. Legs I each bore a slender claw while the claws of legs II and III were extremely robust closing against scaled distotibial pads for attachment. Abdominal segments II to VII bore large lateral spiracles while VI to VII were characterized by pairs of long marginal setae. The female gonopods VIII were curved medially each bearing a terminal fringe of setae while gonopods IX had a medial fringe of short setae. The abdomen of the male had a large genital plate that reached from segment VII posteriorly and terminated in a single bulbous process. The everted pseudopenis had a longitudinal keel-like ridge.

These micomorphological observations on *L. angasi* may contribute to the comparative taxonomy of the *Linognathus* species of the related *Tragelaphus* antelope.



Session Details:	8/26/2013 Poster Session 1 1800 - 1930
Poster Details:	Diagnostic of gastric cryptosporidiosis in birds using duplex real-time TaqMan PCR
Authors:	Alex Akira Nakamura ¹ , Camila Guariz Homem^{2*} , Marcelo Vasconcelos Meireles ² ¹ Faculdade de Medicina Veterinária e Zootecnia, Universidade de São Paulo - USP, São Paulo, BRAZIL ² Faculdade de Medicina Veterinária, Universidade Estadual Paulista – UNESP, Araçatuba, BRAZIL
Poster Number:	79

Three species and many *Cryptosporidium* genotypes are known to infect gastric or intestinal epithelium of birds. *Cryptosporidium galli* and *Cryptosporidium* avian genotype III are related to chronic infections in proventriculus similar to *Cryptosporidium serpentis* infection in snakes. Several methods are used for cryptosporidiosis diagnosis, but only those based on molecular biology are able to determine the *Cryptosporidium* species and genotypes. The aim of this research was the development of a duplex real-time PCR targeting 18S subunit of rRNA gene, by MBG TaqMan assay, to detect DNA of *C. galli* and *Cryptosporidium* avian genotype III in fecal samples, and to evaluate the diagnostic attributes of the duplex real-time PCR compared to nested PCR (XIAO et al., 2000), followed by sequencing of amplified fragments, using 1027 fecal samples from birds of the orders Passeriformes and Psittaciformes collected in an aviary from a wildlife conservation center. The duplex real time PCR showed positivity in 580/1027 (56.47%) for *C. galli*, whereas nested PCR was positive for *Cryptosporidium* spp. in 104/1027 (10.13%) samples. For *Cryptosporidium* avian genotype III, there was positivity in 21/1027 (2.04%) samples. The duplex real time PCR resulted in high analytical specificity when tested using DNA samples from other *Cryptosporidium* species and genotypes. The only exception was the amplification of DNA from *C. serpentis* with primers and probe for the detection of *Cryptosporidium* avian genotype III, although with lower efficiency. New avian hosts were identified for both gastric species, as well as it was possible to identify *C. baileyi* and, for the first time in Brazil, *Cryptosporidium* avian genotype V. It was concluded that the duplex real time PCR developed in this study is a fast and reliable tool for diagnosis of gastric cryptosporidiosis in birds.

Acknowledgements:

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Session Details:	8/26/2013 Poster Session 1 1800 - 1930
Poster Details:	Detection of vector-borne pathogens in <i>Echinophthirus horridus</i> originating from seals of the Wadden Sea
Authors:	Carlos Hermosilla ^{*1} , Guillermo Sanchez ² , Ana Rubio ² , Nynke Osinga ² , Jörg Hirzmann ¹ , Anja Taubert ¹ ¹ Justus Liebig University Giessen, Giessen, GERMANY ² Seal Rehabilitation and Research Centre, Pieterburen, THE NETHERLANDS
Poster Number:	199

The seal louse *Echinophthirus horridus* is one amongst few ectoparasites commonly found on seals of the Dutch Wadden Sea. To investigate whether *E. horridus* plays a role in vector-borne diseases, a total of 635 specimens were collected from 54 harbor seals (*Phoca vitulina*) and one grey seal (*Halichoerus grypus*) during their rehabilitation period at the Seal Rehabilitation and Research Center in Pieterburen, The Netherlands. Scanning electron microscopy analyses of *E. horridus*-adults and -eggs revealed unique morphological features which allow the adaption of this unique marine ectoparasite to its marine environment.

The 635 seal lice were grouped into 57 pools and DNA was extracted thereof for PCR analyses detecting *Acanthocheilonema spirocauda* and *Anaplasma* spp. DNA. PCR systems were established using *cox1*-gene and intergenic spacer (ITS)-1 and -2 region-genes as target sequences. In fact, in seal lice originating from the grey seal pool *Anaplasma*-DNA was detected. Sequence analysis revealed 100% homology to the zoonotic pathogen *A. phagocytophilum* concerning the ITS1/2- and *cox1*-genes. To our knowledge, this is the first report describing the detection of *A. phagocytophilum* in *E. horridus* seal lice. Additionally, seven seal lice pools proved positive for *A. spirocauda* DNA. As this heartworm nematode is well-known for its sometimes detrimental effects on seal health further investigations should be conducted to clarify the actual endemic situation of *A. spirocauda* infections in the Wadden Sea.



Session Details:	8/26/2013 Poster Session 1 1800 - 1930
Poster Details:	Simulium ornatum salivary gland components activate bovine endothelial cells
Authors:	Carlos Hermosilla*, Denis Wolf, Anja Taubert Justus Liebig University Giessen, GERMANY
Poster Number:	181

Black flies are blood feeders of domestic animals, humans and wildlife with *Simulium ornatum* representing one of the main causes of simuliotoxicosis in cattle in Western Europe. Although toxic effects of saliva components on endothelium have longtime been postulated, experimental data confirming these detrimental effects or analyzing underlying mechanisms are still lacking. In this study we present initial data on the effects of *S. ornatum* salivary gland components on primary bovine endothelial cells.

Salivary glands of *S. ornatum* females were isolated, homogenized and soluble proteins (sSGH) were subjected to one and two dimensional gel electrophoresis. For initial data, 16 protein spots were isolated from the 2-D gel and subjected to MALDI-TOF analyses.

Bovine umbilical vein endothelial cells (BUVEC) were stimulated with different concentrations of sSGH. Realtime RT-PCR was applied to determine the levels of gene transcription of several adhesion molecules (VCAM1, ICAM1, P- and E-selectin), chemokines (CXCL1, CXCL8, CXCL10, CCL2, CCL5), IL-6, iNOS, GM-CSF and COX-2 at different time points (3, 6, 24 h) after stimulation.

Silver staining of SDS gels showed reproducible patterns of protein bands in different sSGH isolates. 2-D analyses revealed a total of 392 protein spots in sSGH. Exemplary MALDI-TOF analyses of 16 proteins revealed no homologies with other molecules from *Simulium* spp. data bases. Stimulation of BUVEC with sSGH led to their activation as shown by differential up-regulation of adhesion molecules (P-selectin, ICAM-1, VCAM-1), chemokines (CXCL1, CXCL8), IL-6 und COX-2 gene transcripts, whilst the gene transcriptions of E-selectin, GM-CSF, iNOS, and CXCL10 were hardly affected. In general, most prominent reactions were detected 6 hours after stimulation.

These data clearly demonstrate the capacity of *S. ornatum* salivary gland components to activate bovine endothelial cells. Further studies will be conducted to identify the molecules responsible for these reactions and to analyze the endothelium-toxic potential of these molecules.

Session Details:	8/26/2013 Poster Session 1 1800 - 1930
Poster Details:	Health status of wildlife in New-Caledonia
Authors:	Patrick Barrière ¹ , Thomas Hüe ^{2*} , Céline Marchal ³ , Cyrille Goarant ⁴ ¹ Centre de Régulation des Gros Gibiers, New Caledonia, FRANCE ² Institut Agronomique néo-Calédonien, New Caledonia, FRANCE ³ Direction des Affaires Vétérinaires Agricoles et Rurales, New Caledonia, FRANCE ⁴ Institut Pasteur, New Caledonia, FRANCE
Poster Number:	49

Hunting is the main way of supplying meat in the outback of New-Caledonia. Wild pigs and deer are the main source but little was known about their sanitary status. This study was performed to improve knowledge of these populations and in particular of their potential to transmit disease to domestic animals or act as a source of zoonotic pathogens. Samples were collected from 66 hunted deer and 52 wild pigs. Analyses of parasitism were carried out by coproscopy and dissection, leptospirosis by PCR, toxoplasmosis and Hepatitis E by ELISA kits for deer and trichinosis and Aujesky disease with ELISA kits for pigs.

On deer, the main result is the high prevalence of toxoplasmosis (95%). Neither leptospirosis nor Hepatitis E virus was detected and only 3.3% had a positive coproscopy

In wild pigs, results were positive for 25% of animals for Hepatitis E virus, 95% for Toxoplasmosis but zero for Trichinosis or Aujesky. Leptospira were found in kidney in 4 animals (3 Pomona and 1 Icterohaemorrhagiae). Coproscopy was positive for 43% of animals and Kidney worm (*Stephanurus dentatus*) was observed in 59% of pigs.

This high prevalence of digestive parasites and Kidney worm in pigs can lead to a loss of productivity for animals caught for fattening before slaughter.

Most importantly, this study highlights the presence of two zoonosis in wildlife, with the high prevalence in both deer and pigs of toxoplasmosis and a moderate prevalence of Hepatitis E virus in pigs. These results need to be incorporated into recommendations concerning the use of these animals.

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Session Details:	8/26/2013 Poster Session 1 1800 - 1930
Poster Details:	Preliminary investigation on parasites in frogs and snakes from Nanning (Guangxi), Southern China
Authors:	Li Jian ^{1,2} , Zhou Qin-an ¹ , Quan Chen-yu ¹ , Shi Yun-liang ¹ , Shi Wei ¹ , Zeng Yun ¹ , Huang wei-yi ^{1,2*} ¹ College of Animal Science and Technology, Guangxi University, Nanning, Guangxi, CHINA ² Food Quanlity and Safety Center of Guangxi University, Nanning, Guangxi, CHINA
Poster Number:	03

Captive-bred frogs and snakes made great achievements in recent years, in Nanning, Guangxi, Southern China. Frogs and snakes eating are popular that presenting the possibility of zoonotic disease transmission. 641 frogs (included 617 *Rana limnocharis*, 8 *R. tigrina*, 13 *Rana* sp., 3 *Microhyla pulchra*) and 158 snakes (included 49 *Naja naja kaouthia*, 105 *Ptyas mucosus*, 2 *Elaphe carinata*, 1 *Amphiesma stolatum*, 1 *E. rufodorsata*) were collected from markets in Nanning from September 2011 to December 2012. Post-mortem examination showed that most samples are mixed parasitic infections, with an overall prevalence of 71.92% of frogs and 56.63% of snakes. The infected parasites and infection rates in frogs as follow: *Paracosmocerca mucronata* (23.01%), *Oswaldocruzaia heparia* (4.39%), *Rhabdias* sp. (1.40%), *Dipodiscus* sp. (*D. nigromaculati*, *D. tigrinus*, *D. mehrai*) (35.41%, 1.28), *Loxogenes sinense* (1.56%), *Halipengus ovocaudatus*.(0.47%), *Mesocoelium branchyenteron* (1.72%), *Rauschiella macrochium* (0.47%), unidentified of trematode (3.12%), Juvenile of unidentified trematode (2.49%), the plerocercoid of *Spirometra* sp.(10.76%), *Pseudacanthocephalus bufonis* (21.06%) and *Centrorhynchus* sp. (11.08%). And the snake infected parasites are *Kalicephalus* sp. (*K. bungari*, *K. indicus*, *K.branchycephalus*) (17.72%), *Rhabdias* sp. (10.76%), *Capillararia murinae* (5.06%), *Ophidascaris filaria* (0.63%), *Paradistomum megareceptaculum* (0.68%), *Encyclometra* sp. (*E. japonica*, *E. asymmetrica*) (5.76%), the plerocercoid of *Spirometra* sp. (22.15%), unidentified acanthocephalan (3.16%), *Raillietiella orientalis* (10.76%), *Kiricephalus pattoni* (2.53%), *Waddycephalus* sp. (*W. radiata*, unidentified *Waddycephalus* sp.) (1.27%) and *Porocephalus* sp. (0.63%). The results indicated that high infection rate and infection intensity of parasite diseases in captive-bred frogs and snakes in the south of China, especially the zoonosis of plerocercoid of *Spirometra* sp. Human could be infected by ingesting uncooked snake and flogs, for this reason, it is imperative to inspect and eliminate flogs and snake parasites before they are going to dinner table.

Li Jian, Zhou Qin-an contributed equally to the work. Li Jian, Zhou qin-an are co-first authors.



Session Details:	8/26/2013 Poster Session 1 1800 - 1930
Poster Details:	<i>In vitro</i> larval assays for anthelmintic resistance in cattle nematodes.
Authors:	Malcolm Knox^{1*} , Andrew Kotze ² , Grant Uphill ¹ , Troy Kalinowski ¹ ¹ CSIRO Animal, Food and Health Sciences, F.D. McMaster laboratory, Armidale, NSW 2350, AUSTRALIA ² CSIRO Animal, Food and Health Sciences, St Lucia, Queensland 4067, AUSTRALIA
Poster Number:	87

Recent research has suggested that resistance to macrocyclic lactone (ML) anthelmintics is increasing for nematode parasites of cattle. This project investigated whether *in vitro* methods for resistance detection could be used to estimate the presence of ML resistance in the major nematode parasite species of cattle. Through a process of isolation, infection and challenge with oral ivermectin, ML resistant isolates for three of the primary nematode parasites of cattle in sub-tropical and temperate Australia, *Cooperia oncophora*, *Cooperia punctata/pectinata* and *Haemonchus placei* were obtained. A similar process did not produce a ML resistant isolate of *Ostertagia ostertagi*. Resistant isolates of the 3 species were subjected to comparative tests with susceptible isolates of the same species to determine if the larval development assay (LDA) and larval migration assay (LMA) could be used for routine diagnostic purposes. For *C. punctata/pectinata* and *H. placei*, results for the LDA with ivermectin aglycone and the LMA with eprinomectin suggest that these tests could potentially be used as routine diagnostic tests to determine ML resistance status of field populations of these nematode species. For *C. oncophora*, results showed that only the LMA with eprinomectin was able to discriminate between susceptible and resistant isolates, however the level of discrimination was very low, suggesting that the *in vitro* methods could not be reliably used for diagnosis of ML resistance for this species. As no ML resistant *O. ostertagi* could be tested, the usefulness of the *in vitro* assays for resistance detection with this species remains unknown.

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Session Details:	8/26/2013 Poster Session 1 1800 - 1930
Poster Details:	What is the World Association for the Advancement of Veterinary Parasitology (WAAVP) African Foundation?
Authors:	Rosina C Krecek ^{1,2*} , Banie L Penzhorn ³ , D Theo de Waal ⁴ , Rose J Peter ⁵ , Roger Prichard ⁶ , Derek Sumption ⁷ , Annemarie Avenant-Oldewage ² , Mark D Soll ⁸ , Isaac K Phiri ⁹ , Yeonwoo Lebovitz ¹⁰ (presenting author asterisked) ¹ Ross University School of Veterinary Medicine, Basseterre, SAINT KITTS ² University of Johannesburg, Auckland Park, SOUTH AFRICA ³ University of Pretoria, Onderstepoort, SOUTH AFRICA ⁴ University College Dublin, Dublin, IRELAND ⁵ Nexvet, Johannesburg, SOUTH AFRICA ⁶ McGill University, Montreal, CANADA ⁷ Brantam Financial Services, Craighall, SOUTH AFRICA ⁸ Merial, Georgia, UNITED STATES ⁹ University of Zambia, Lusaka, ZAMBIA ¹⁰ Virginia, UNITED STATES
Poster Number:	167

Identifying and supporting the young parasitology researchers of tomorrow is a goal of the World Association for the Advancement of Veterinary Parasitology (WAAVP). Since 1997 the WAAVP African Foundation has supported African veterinary parasitologists to present their results at WAAVP Conferences. A surplus of US\$ 70 098 generated from the 16th WAAVP Conference in South Africa¹ was invested and a foundation established to manage the fund with the intention of using it to the mutual advantage of the WAAVP and African veterinary parasitologists. The initial investment has grown into a very successful endowment currently valued at US\$ 179 952. To date, 146 scholarship applications have been screened, and 63 full and partial scholarships awarded to young African veterinary parasitologists to attend subsequent biennial WAAVP Conferences. These scholarships have supported recipients to attend seven WAAVP Conferences (17th–24th) in 1999 (Denmark), 2001 (Italy)², 2003 (USA)³, 2005 (New Zealand)⁴, 2007 (Belgium)⁵, 2009 (Canada)⁶, 2011 (Argentina)⁷ and 2013 (Australia). Through the WAAVP African Foundation, recipients from 13 African countries presented current research results addressing problems in Africa to international audiences spanning six continents. The geographical diversity of applications continues to grow with multilingual outreach activities aimed at veterinary schools, research institutions, and other scientific networks in Africa. The countries from which applicants originated include: Algeria, Egypt, Ethiopia, The Gambia, Kenya, Mozambique, Nigeria, Sierra Leone, South Africa, Sudan, Tanzania, Uganda and Zambia. The upcoming 24th WAAVP Conference in Australia marks the sixteenth year since the inception of these scholarships which is managed by the African Foundation Committee (chaired by Dr Rosina C Krecek) and reports to the WAAVP Executive Committee.

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The authors thank the late Professor Anna Verster whose successful bid to the WAAVP Executive led to the 16th WAAVP Conference being held in South Africa; the members of the WAAVP African Foundation Committee who include, A Oldewage, I Phiri, M Soll, R Prichard, RC Krecek and BL Penzhorn; technical assistance from S Barth (USA), J Heller (USA), D John-King (USA), and J Moore (USA); N Strike (South

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Africa) for assistance with French translation and networking with Francophone institutions in Africa; and the fund’s accountant, A Cambanis (South Africa).

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Session Details:	8/26/2013 Poster Session 1 1800 - 1930
Poster Details:	Use of medicinal plants as an alternative for controlling <i>Haemonchus contortus</i> in sheep: <i>in vitro</i> and <i>in vivo</i> testes
Authors:	Oliveira, L. D. R. ¹ , Miranda, J. P. H. V. ² , Gomes, E. F. ³ , Katiki, L. M. ⁴ , Melo, F. R. ² , Louvandini, H ^{3*} . Universidade de Brasília, Faculdade de Agronomia e Medicina Veterinária, Brasília, Brazil ¹ União Pioneira de Integração Social, Brasília, Brazil ² Centro de Energia Nuclear na Agricultura, Universidade de São Paulo, São Paulo, Brazil ³ Instituto de Zootecnia, São Paulo, Brazil ⁴
Poster Number:	227

Anacardium humile, *Syzygium cumini*, *Genipa americana* and *Solanum lycocarpum* leaves were evaluated *in vitro* and *in vivo* as an alternative for the control of *Haemonchus contortus*. The *in vitro* test used was hatchability of eggs (EHT) using increasing concentrations (3,12 mg/mL, 6,25 mg/mL, 12,5 mg/mL, 25 mg/mL, 50 mg/mL and 100 mg/mL) of aqueous extract (AE). *A. humile* AE showed the lowest LC₅₀ value of 4,14 mg/mL, followed by *S. cumini* 12,35 mg/mL. In *S. lycocarpum* EHT, the highest concentration tested had an inhibition rate of 14,20% of hatchability, and in *G. americana*, there was an inhibition rate of 18,27%, thus it was not possible to determine the LC₅₀ of these plants. For *in vivo* tests, 30 lambs, Santa Ines (crossbred), naturally-infected were divided into: a negative control (no use of medicinal plant), and four others that received 30 g of the plants dried and milled. The experimental period covered 7 days of confinement adaptation, 14 days for the treatment and 7 days for the residual period. After 7 days of adaptation, at 0, 7, 14 and 21 days, body weights, eosinophil count and fecal egg counts per gram of feces (EPG) were taken. The following reductions in EPG were observed: 30,99% in the control, 59,27% in *S. lycocarpum* treatment, 68,25% in *A. humile* treatment, 76,53% in *S. cumini* treatment and 81,71% in *G. americana* treatment. During the treatment, an increased rate of weight gain from 4,9 to 16,04%, however the control showed statistically only with *G. americana* treatment. Statistical analysis of the eosinophil count showed no statistical difference between treatments. This study showed that *A. humile* had the highest *in vitro* activity; however, in the *in vivo* activity, there was a statistical difference in EPG between the control and the treatments with *G. Americana*, *A. humile* and *S. lycocarpum*.

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Session Details:	8/26/2013 Poster Session 1 1800 - 1930
Poster Details:	Phosphorus metabolism in hair sheep artificially infected with <i>Haemonchus contortus</i>
Authors:	Helder Louvandini ¹ *, Aline Campeche Lopes ¹ , Maria Regina Sodero Peçanha ¹ , Lécio Aparecido Castilho ¹ , Joaquim Everaldo Martins dos Santos ¹ , Concepta M. McManus ² , Adibe Luiz Abdalla ¹ ¹ Universidade de São Paulo, Centro de Energia Nuclear na Agricultura, NAPTSA, CP 96, CEP 13.400-970, Piracicaba, SP, Brazil. ² Departamento de Zootecnia, Universidade Federal do Rio Grande do Sul, Porto Alegre, 91540-000 Rio Grande do Sul, Brasil.
Poster Number:	01

Hair sheep were infected with *Haemonchus contortus* to evaluate phosphorus metabolism (P) using 18 entire male lambs (37.3 ± 4.17 kg LW) divided in two treatments, one infected with 4,000 L3 *H. contortus* and the other without infection (control). The all animals received the same diet consisting of hay (*Cynodon dactylon*), concentrate mixture (corn and soybean meals), mineral and vitamins. After 60 days infection the lambs were kept in metabolic cages and received 7.4 MBq ³²P through the jugular vein. During 7 days intake, faeces and urine excretion as well as endogenous loss phosphorus were monitored to evaluate the mineral metabolism. No differences were observed for intake, excretion, endogenous faeces, absorbed, retained and biological availability of P. In conclusion the intestine was an important key to maintain homeostasis of P metabolism in infected sheep with *H. contortus*.

All staff of LANA, INCT/Pecuária Informação Genético-Sanitária da Pecuária Brasileira/CNPq. NAPTSA/CENA/USP.

Session Details:	8/26/2013 Poster Session 1 1800 - 1930
Poster Details:	Endoparasite infection in hair sheep (Morada Nova and Santa Inês) reared in intensive grazing systems in southeastern Brazil
Authors:	Juliano Issakowicz ¹ , Ana Claudia Koki Sampaio ¹ , André Torres Geraldo ² , Luara Paula Lameirinha ² , Ricardo Lopes Dias da Costa ² , Mauro Sartori Bueno ² , Adibe Luiz Abdalla ¹ , Helder Louvandini¹* ¹ Universidade de São Paulo, Centro de Energia Nuclear na Agricultura, NAPTSA, CP 96, CEP 13.400-970, Piracicaba, SP, Brazil. ² Instituto de Zootecnia/APTA/SAA-SP, CP 60, CEP 13460000, Nova Odessa, SP, Brazil.
Poster Number:	219

In southeastern of Brazil, parasitosis is a big obstacle to sheep production, due to the high prevalence of gastrointestinal parasitic species such *Haemonchus contortus* causing reduction in the performance of the animals. This shows the continuing need for studies directed at the sector, mainly in search of breed better adapted and resistant. This study aimed to evaluate parameters that may indicate susceptibility to gastrointestinal parasites in ewes Santa Inês and Morada Nova reared in southeastern Brazil. Forty-nine adult ewes Santa Inês with 51.8 ± 7.07 Kg of initial body weight and forty-nine Morada Nova with 33.1 ± 4.98 were used. The animals were reared on intensive grazing systems with rotational grazing in pasture of grass Aruana (*Panicum maximum* cv.IZ-5). Faeces and blood samples were taken every 28 days for 56 days to monitor the fecal egg counting (FEC) and packed cell volume (PCV). Along the collections was evaluated the staining of the ocular conjunctiva by the method FAMACHA® and the body condition score (BCS). Statistical analysis was carried using GLM procedure of SAS®. The FEC did not differ with values of 89.2±23.9 and 104.2±23.9 for Morada Nova and Santa Inês group respectively. PCV was also similar between groups, with values of 29.8±0.4% for Morada Nova and 30.28±0.4% for Santa Inês. Likewise, the subjective evaluations of FAMACHA and BCS were similar in the groups studied with values for FAMACHA of 1.73±0.06 and 1.63±0.06 for Morada Nova and Santa Inês, and 3.04±0.15 and 3.09±0.15 for BCS between groups. Based on these values it is possible to say that both genetic groups showed good response in situation of intensive grazing systems with rotational grazing in southeastern Brazil.

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All staff of LANA and Instituto de Zootecnia.



Session Details:	8/26/2013 Poster Session 1 1800 - 1930
Poster Details:	Rumen volatile fatty acids in sheep artificially infected with <i>Haemonchus contortus</i> or <i>Trichostrongylus colubriformis</i>
Authors:	Juliano Issakowicz ¹ , Ana Claudia Koki Sampaio ¹ , Carina Nazato ¹ , Concepta M. McManus ² , Adibe Luiz Abdalla ¹ , Helder Louvandini ^{1*} ¹ Universidade de São Paulo, Centro de Energia Nuclear na Agricultura, NAPTSA, CP 96, CEP 13.400-970, Piracicaba, SP, Brazil. ² Departamento de Zootecnia, Universidade Federal do Rio Grande do Sul, Porto Alegre, 91540-000 Rio Grande do Sul, Brasil.
Poster Number:	21

Recently, changes in patterns of ruminal fermentation have been reported on animals with gastrointestinal infection. However, sheep are infected by a range of parasites that can promote different changes in the metabolism of the animal. For this, was evaluated the effects of gastrointestinal infection with *Haemonchus contortus* or *Trichostrongylus colubriformis* on rumen profile of volatile fatty acids (VFA) in sheep. Sixteen animals were used, of which six were experimentally infected with 10.000 L₃ of *T. colubriformis*, six with 5.000 L₃ of *H. contortus* and four were a non-infected (control). Fecal egg counts were carried out one day before the beginning of the experiment (30 days after infection), aiming to confirm infection (2916 and 366 eggs/g to *H. contortus* group and *T. colubriformis* group, respectively). The animals received only Tifton-85 hay (*Cynodon dactylon* sp.) in the diet. To determine the total concentrations of volatile fatty acids, ruminal fluid samples were collected 3 hours after feeding. Samples were determined in a Shimadzu 2014 gas chromatograph coupled to a Flame Ionization Detector, with a column GP 10% SP-1200/1 H3PO4 80/100 Chromosorb WAW. Total concentration (acetic + propionic + isobutyric + butyric + valeric + isovaleric) and ratio acetate:propionate VFA were measured. Statistical analysis were carried out using GLM procedure of SAS®. The mean comparisons were carried out using Tukey. The total concentration did not differ (P> 0.05) with a value of 74.189, 76.096 and 73.749 mmol/L between the Control, *Haemonchus* and *Trichostrongylus* group respectively, however, the ratio acetate:propionate was lower (P = 0.09) in animals infected with *Haemonchus* (4.55) compared to the control (5.10) with larger propionate displacement and similar to the *Trichostrongylus* group (4.59), suggesting increased production of acid precursors of energy to meet the higher demands of the infected animal.

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Session Details:	8/26/2013 Poster Session 1 1800 - 1930
Poster Details:	APPROACH TO MOLECULAR CHARACTERIZATION OF <i>FASCIOLA HEPATICA</i> ISOLATES SUSCEPTIBLE AND RESISTANT TO TRICLABENDAZOLE BY TECHNIQUE RAPDS-PCR
Authors:	Silvana Scarcella ¹ , Laura Ceballos ² , Rodrigo Sanabria ³ , Pedro Ortiz Oblitas^{4*} , Hugo Solana ¹ ¹ Laboratorio de Biología Celular y Molecular. Centro de Investigación Veterinaria de Tandil (CIVETAN), CONICET, Facultad de Ciencias Veterinarias, UNCPBA, Tandil, Argentina ² Laboratorio de Farmacología, Centro de Investigación Veterinaria de Tandil (CIVETAN), CONICET, Facultad de Ciencias Veterinarias, UNCPBA, Tandil, Argentina ³ Centro de Diagnóstico e Investigaciones Veterinarias (CEDIVE), Facultad de Ciencias Veterinarias, Universidad Nacional de la Plata, Chascomús, Argentina ⁴ Facultad de Ciencias Veterinarias. Universidad Nacional de Cajamarca, Cajamarca, Perú. E-mail: silvanas@vet.unicen.edu.ar
Poster Number:	99

Liver flukes *Fasciola hepatica* are among the causes of foodborne diseases of parasitic etiology. These parasites cause significant public health problems and substantial economic losses to the livestock industry. Its control is mainly based on the use of triclabendazole (TCBZ), a halogenated benzimidazole thiol derivative which shows excellent efficacy against both juvenile (immature) and adult stages. Anthelmintic resistance in parasitic of livestock is a chronic problem in the world. The intensive use of TCBZ has resulted in the development of resistant liver flukes. In nematodes the resistance to the benzimidazoles is caused by genetic changes in genes encoding β -tubulins. In the case of *F. hepatica* TCBZ resistant were not detected these genetic changes for which the resistance obtained is from other genetic or metabolic changes. The present study shows the comparative molecular characterization of *F. hepatica* susceptible and resistant to TCBZ using the Random Amplified Polymorphic ADN Fragments (RAPDs-PCR) technique. Were evaluated ten different primers and four isolates of *F. hepatica* Cullompton and CEDIVE (susceptibles) and Sligo and Cajamarca (resistant to TCBZ). The results provides evidence of genetic variations of *F. hepatica* between the different isolates, reinforcing previous studies where is proposed that the resistance is due to a combination of factors, which vary among different isolates.

Further work on this relevant area is required.

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TCBZ-susceptible isolate (Cullompton) and the TCBZ- resistant (Sligo) were kindly provided by Professor I. Fairweather, School of Biology and Biochemistry, The Queens University of Belfast, Northern Ireland, UK.



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Session Details:	8/26/2013 Poster Session 1 1800 - 1930
Poster Details:	Identification and characterization of Phase I detoxification enzymes in isolates of <i>Fasciola hepatica</i> susceptible and resistant to triclabendazole
Authors:	Pamela Lamenza ^{1,2} , Pedro Ortiz Oblitas ^{4*} , Carolina Ceriani ^{1,3} , Hugo Solana ^{1,2} ¹ Centro de Investigación Veterinaria de Tandil (CIVETAN) CONICET ² Laboratorio de Biología Celular y Molecular. FCV-UNCPBA, Tandil, Argentina ³ Laboratorio de Virología, FCV-UNCPBA, Tandil, Argentina ⁴ Facultad de Ciencias Veterinarias. Universidad Nacional de Cajamarca, Cajamarca, Perú.
Poster Number:	113

The helminthes possess biochemical mechanisms for detoxification. Overall, parasites may evade anthelmintic effects by: i) mutation of target receptors, ii) overexpression of efflux transport pumps, and/or iii) overexpression of metabolic enzymatic systems. The fasciolosis is a zoonotic disease caused by *Fasciola hepatica*. Its control is mainly based on the use of triclabendazole (TCBZ), a halogenated benzimidazole thiol derivative which shows efficacy against juvenile and adult stages. The intensive use of TCBZ resulted in the development of resistant liver flukes. In nematodes, the resistance to benzimidazoles is caused by mutation in the β -tubulin. In *F. hepatica* resistance to TCBZ has not been demonstrated by genetic changes.

In general, all organisms have xenobiotic metabolizing enzymes, which can deactivate toxic functions. Within this group the most important Phase I detoxification enzymes are Cytochrome P₄₅₀ (Cyt P₄₅₀) and Flavin-monooxygenases (FMOs). In *F. hepatica*, there is a lack of knowledge about the role of these enzymes in the development of resistance mechanisms against TCBZ. Therefore, the aim of this preliminary work was to assess, by RT-PCR, the characterization and expression of FMO and P₄₅₀ in *F. hepatica* susceptible and resistant to TCBZ. With this purpose, specific oligonucleotides were designed based on known sequences of related organisms. Both FMO and P₄₅₀ mRNAs were identified in *F. hepatica*.extracts.

The expression levels of both enzymes were compared using ImageJ® software. In the resistant strain, the FMO mRNA expression was significantly increased compared to the susceptible strain (1.5 times higher) meanwhile no significant differences were detected when comparing the expression levels of P₄₅₀ mRNA in both strains. These results confirmed that Phase I detoxification enzymes are not only involved in the detoxification mechanisms, but also participate actively in the development of resistance of *F. hepatica* to TCBZ.

Acknowledgements:

Fasciola hepatica TCBZ-susceptible (*Cullompton* strain) and TCBZ- resistant (*Sligo* strain) were kindly provided by Professor Ian Fairweather, School of Biology and Biochemistry, The Queens University of Belfast, Northern Ireland, UK.



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Session Details:	8/26/2013 Poster Session 1 1800 - 1930
Poster Details:	Acaricidal activity of extracts from <i>Ocimum basilicum</i> (Lamiaceae), <i>Persea americana</i> (Lauraceae) and <i>Andira galeottiana</i> (Fabaceae) against the cattle tick, <i>Rhipicephalus microplus</i> resistant to acaricides
Authors:	¹ * José Alberto Rosado-Aguilar , ² Ronnie Arieta-Román, ¹ Roger Iván Rodríguez-Vivas, ¹ José Rodrigo Carrillo-Peraza ¹ , ³ Álvaro Peniche-Cardena ¹ Facultad de Medicina Veterinaria y Zootecnia. Universidad Autónoma de Yucatán. Km. 15.5 carretera Mérida-Xmatkuil. CP. 97000. Mérida, Yucatán, México; alberto.rosadoaguilar@gmail.com ² Facultad de Ingeniería en Sistemas de Producción Agropecuaria. Universidad Veracruzana. Campus Acayucan, Veracruz, México. ³ Facultad de Medicina Veterinaria y Zootecnia. Universidad Veracruzana. Veracruz, Ver., México.
Poster Number:	117

Rhipicephalus microplus (Acari: ixodidae) is an endemic external parasite of cattle in tropical and subtropical regions of the world, causing major economic losses to cattle producers. Chemical acaricides have played a pivotal role in the control of *R. microplus*. However, as a consequence of extensive use of chemicals this tick specie has developed resistance to the major classes of acaricides in different countries. As a consequence new strategies for ticks control which are less hazardous and more environmentally friendly are searched for; such as the use of plant extracts, one of the most attractive methods for this aim. The objeotive of this study was to evaluate the acaricidal activity of methanolic extracts from leaves of *Ocimum basilicum* (Lamiaceae), *Persea americana* (Lauraceae) and *Andira galeottiana* (Fabaceae) on larvae of *R. microplus* (resistant to organophosphates, pyrethroids and amitraz) using the larval immersion test. The extracts of *O. bacilicum* evaluated at 10% (100 mg/ml) and 20% (200 mg/ml) concentrations against larvae of *R. microplus* showed acaricidal activity of 78.5±22.7% and 100%, respectively. The activity for *P. americana* was 74.9±12.3% and 87.8±10.2% for 10% and 20%, respectively, meanwhile the extracts of *A. galeottiana* showed acaricidal activity of 45.3±22.2% and 94.7±4.2%, respectively. In conclusion the methanolic extracts of *O. basilicum*, *P. americana* and *A. galeottiana* are a promising candidates to control larvae of *R. microplus* multiresistance to acaricides. Further studies are required to identify the active fractions and compound of these crude extracts.

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Session Details:	8/26/2013 Poster Session 1 1800 - 1930
Poster Details:	Treatment of naturally <i>Notoedres cati</i> infested cats with a combination of imidacloprid 10% / moxidectin 1% spot on (Advocate® / Advantage Multi® Bayer)
Authors:	Gabriele Petry ¹ Klaus Hellmann ² Dejan Cvejic ² Balazs Capari ³ Roland Schaper ^{1*} ¹ Bayer Animal Health GmbH, 51368 Leverkusen, Germany ² KLIFOVET AG, Geyerspergerstr. 27, 80689 München, Germany ³ Kapriol Bt., Vak Bottyan St. 1, 8330 Sümeg, Hungary
Poster Number:	225

Notoedric mange (feline scabies) is a rare, highly contagious disease of cats and kittens caused by *Notoedres cati* (*N. cati*), which can infest other animals and humans. The study objective was to determine the efficacy and safety of 10% imidacloprid / 1% moxidectin (Advocate®/Advantage Multi® spot on for cats) against natural *N. cati* infestation in cats. Sixteen cats were randomly assigned to treatment group or negative control group using pre-treatment mite counts. The treatment group received a single treatment of the investigational veterinary product (IVP) according to label instructions. The control group stayed untreated. Five cats from the negative control group were treated with the IVP at the end of the study and observed for further 28 days to increase the number of treated animals. Skin scrapings and mite counts were performed 28 days post treatment (p.t.). Notoedric skin lesion assessments with clinical scoring were performed regularly. Five animals had to be removed prematurely from the study population due to different reasons. The number of viable *N. cati* mites in all treated animals 28 days p.t. was zero compared with 2.8 ± 3.0 in the negative control group, being significantly lower for the treated cats (p = 0.0019, Wilcoxon test). The resulting efficacy was 100%. Clinical cure based on skin lesion assessment was achieved 28 days p.t. in 100% of all treated animals completing 28 study days.

Advocate showed a high therapeutic efficacy in curing *N. cati* infestations and clinical symptoms of feline scabies when applied at the minimal therapeutic dose of 10 mg imidacloprid / 1 mg moxidectin/kg body weight. The product was well tolerated and no adverse reactions were recorded.



Session Details:	8/26/2013 Poster Session 1 1800 - 1930
Poster Details:	Gastrointestinal helminths and protozoa in migratory camels in semi desert area in Multan, Pakistan
Authors:	Abdul Basit ¹ , Muhammad Mazhar Ayaz ¹ , Asif Raza ² , Hafiz Muhammad Arshad ¹ , Naveeda Chaudhary ³ , Ashar Raza ¹ , Jawaria Ali Khan ⁴ and Zia-ur-Rehman^{5*} ¹ Faculty of Veterinary Sciences, Bahauddin Zakariya University, Multan, Pakistan. ² Animal Husbandry in Tropics and Subtropics, University of Kassel, Germany. ³ Department of Physiology and Pharmacology, University of Agriculture, Faisalabad, Pakistan. ⁴ Department of Clinical Medicine and Surgery, University of Veterinary and Animal Sciences, Lahore, Pakistan. ⁵ Institute of Veterinary, Animal and Biomedical sciences, Massey University, Palmerston North, New Zealand.
Poster Number:	241

Current experiment was designed to explore gastrointestinal helminth and protozoa population in migratory camels (*Camelus dromedarius*). A total number of 50 samples (20 males and 30 females) were collected from camels migrated from semi desert/arid areas of Jalalpur Pir Wala to irrigated plains of Multan, during early summer (April and May) from various places in and around Multan. The revealed parasites were mixed helminthic and protozoal infection. Identified parasites include *strongylidae* spp, *trichostrongyle* spp, *coccidian/ eimeria* spp and *isospora* spp. This basic information will help to develop control strategies for parasites in irrigated areas of Multan.

Keywords: *Camelus dromedarius*, *strongylidae*, *trichostrongyle*, *coccidian/eimeria* and *isospora*.



Session Details:	8/27/2013 Poster Session 2 1730 - 1930
Poster Details:	Molecular characterization of <i>Stictodora tridactyla</i> (Digenea: Heterophyidae) using ITS1 and mtCO1 sequences in Kuwait
Authors:	Wafa Y. Al-Kandari ¹ , Suzanne A. Al-Bustan ¹ , Majed Alnaqeeb ¹ and Asha Isaac ¹ ¹ Department of Biological Sciences, Kuwait University, Kuwait
Poster Number:	154

Members of the family Heterophyidae are intestinal trematodes of birds and mammals including human. Human infections result in abdominal pain and diarrhoea (Kim *et al.*, 2006; Elsheikha and Elshazly, 2008). In addition to their effect on public health, heterophyids could interfere with aquaculture industry as fish pathogens (Thein *et al.*, 2007; Diaz *et al.*, 2008). Fish carry the metacercarial stage and serve as second intermediate host in the heterophyid's life cycle while snails serve as first intermediate hosts. The genus *Stictodora* (Digenea: Heterophyidae) have been reported in several studies as fish-born trematodes affecting human health (Kim *et al.*, 2006; Sohn *et al.*, 2009). In Kuwait, the adult stage of *S. tridactyla* was reported from a kitten and the larval stages were reported from the snail *Cerithidea cingulata* and the Arabian killifish. The identification of *S. tridactyla* in Kuwait was based on the morphological characteristics of the larval and adult stages using scanning electron microscope (Abdul-Salam *et al.*, 2000). Since specific determination of trematodes by morphological characters is often difficult and ambiguous, the use of molecular techniques allows accurate identification of these parasites. In the present study, sequences of ribosomal internal transcribed spacer region 1 (ITS1) and mitochondrial cytochrome oxidase subunit 1 (mtCO1) were used for accurate characterization of *S. tridactyla* in Kuwait. Similarity search for ITS1 and mtCO1 sequences in GenBank revealed 81% and 80% similarity respectively with corresponding sequences of *Cercaria batillariae*. Phylogenetic analysis using ITS1 and mtCO1 sequences grouped *S. tridactyla* with *Cercaria batillariae* in a single clade with bootstrap values ranging from 80-90. The lack of ITS1 and mtCO1 sequences in GenBank made it difficult to phylogenetically relate the *S. tridactyla* from Kuwait with other *Stictodora* species. This is the first molecular characterization of *S. tridactyla* in the literature.

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This work was supported by Kuwait University Research Grant No. [SL07/10]. Molecular analysis was performed with the support of the General Facility Project (GS 01/02) in the use of the ABI 3130XL Gene Analyzer at the Biotechnology Center, Faculty of Science, Kuwait University.

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Session Details:	8/27/2013 Poster Session 2 1730 - 1930
Poster Details:	Effects of Green Tea Extract and Cysteine Proteases Inhibitor on Symptomatic Genotypes of <i>Blastocystis hominis</i> in Vitro and in Vivo
Authors:	Hamdan I. Al-Mohammed ^{1*} and Eman M. Hussein ¹ ¹ Department of Microbiology and Medical Parasitology, College of Medicine, King Faisal University, KSA hamdan@kfu.edu.sa
Poster Number:	276

Blastocystis hominis is an anaerobic enteric protozoon that inhabits the human intestinal tract. Metronidazole (MTZ) is the drug of choice to treat although resistance is concern. The effects of green tea extract (GTE) and N-[N-(L-3-trans-carboxyoxirane-2-carbonyl)-L-leucyl]-agmatine (E-64), a broad spectrum cysteine protease inhibitor on growth, viability and ultra -structural of three *B. hominis* symptomatic genotype subtypes (I, III and IV) were assessed *in vitro*. *B. hominis* were twelve isolates (four/each genotype subtype) and one/ each genotype /subtype of them was resistance to MTZ. The role of GTE and E-64 against *B. hominis* was assessed *in vivo* by identifying parasitic output every three days and rates of infection eradication in relation to each genotype/ subtypes. *In vitro* study revealed that all of the *B. hominis* isolates were susceptible to both of GTE and E-64. The cytocidal effects of GTE ranged from 20-35 µg/ml and 15-30 µg/ml after 24 h and 72 hours, respectively. The cytocidal effects of E-64 ranged from 25-35 µg/ml and 20-30 µg/ml after 24 h and 72 hours, respectively. The highest concentrations of GTE and E-64 inducing the cytocidal effect and inhibition concentrations (ICs) were detected among all of the genotype/subtypes I. The ultra-structures of GTE and E-64 *in vitro* treated *B. hominis* by transmission electron microscopy (TEM) proved that increase in size, cytoplasmic membrane injury and disposition of vacuolated nonhomogenous particles in the cytoplasm, nucleus shifted periphery, expulsion of the cytoplasmic content then cell rupture were detected suggestive necrotic changes. *In vivo* study proved that in infected GTE and E-64 treated rats, cysts output numbers were less than the number of cysts output in infected non treated rats groups. Also, the duration of infection decreased in both of the majorities of treated rats at the first six days (91.7%). The differences were statistically non significant between both groups. So, GTE and E 64 proved useful in treatment and increase the host resistance to *B. hominis*.

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Session Details:	8/27/2013 Poster Session 2 1730 - 1930
Poster Details:	Prevalence of nematode infection and faecal egg counts in free range laying hens.
Authors:	Chris Sherwin, Mohammed Nasr, Emma Gale, Metin Petek, Kathryn Stafford, Marilyn Turp, Gerald Coles* School of Veterinary Sciences, University of Bristol, Langford House, Bristol BS40 5DU, UK.
Poster Number:	148

Introduction: the importance of nematodes in the recent breeds of egg laying hens in the UK is not known.

Methods: 19 flocks were visited 3-4 times and details of housing, husbandry, health, welfare and range used were determined. Faecal samples were collected from 65 week old bird and counted using FLOTAC (1)accurate to 1 egg.

Results: All flocks had at least one nematode species with 17/19 infected with *Heterakis*, 16 with *Ascaridia* , 9 with *Trichostronglyus* and 6 with *Syngamus*. Four of the flocks had been treated with anthelmintic but egg counts were not significantly different from untreated flocks. There was no significant difference between organic (9) and non-organic (10) flocks and between static (n=8) and mobile flocks (n=11). None of the faecal egg counts for any of the species were correlated with egg production or cumulative mortality suggesting the infections were not severe. Faecal egg counts were correlated with a range of housing, husbandry and management practices which varied between nematode species and included depth of litter, percentage of hens using the range and the number of dead hens.

Discussion: How far the egg counts may represent birds at end of lay which have developed natural immunity is not known. However, the relationship between faecal egg counts, housing and husbandry variables suggests that these could be used to assist in future control of parasitic nematodes.

Acknowledgements: Funded by the RSPCA.

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Session Details:	8/27/2013 Poster Session 2 1730 - 1930
Poster Details:	The Wonderful World of Parasitology Diagnostics: A Marriage of Microscopy, SEM and PCR
Authors:	Aileen Elliot ^{1*} , Louise Pallant ¹ , Andrew Thompson ¹ , Peta Clode ² ¹ Murdoch University University, Perth, Western Australia ² University of Western Australia, Perth, Western Australia
Poster Number:	80

Diagnosing parasitic infections in domestic and wild animals from ova, oocysts and cysts passed in the faeces can sometimes be extremely problematic due to low morphological detail and common morphological characteristics across species. As a consequence, traditional microscopical methods can be limited when used in isolation. Techniques such as PCR and Scanning Electron Microscopy (SEM) have become increasingly more accessible. These techniques when used in conjunction with more traditional microscopy mean that we can start to see the broader picture. Sometimes by combining all three methods we can arrive at an appropriate identification, and sometimes it serves to generate even more questions.

Here we present three case studies combining two or more of these methods to identify faecal parasites. And just like the sleuth in the best ‘who done it’ novel we are on the case and have been looking at all the clues! The journey has been a long and arduous one but we have found not only the answer we expected but also more questions and the unexpected!



Session Details:	8/27/2013 Poster Session 2 1730 - 1930
Poster Details:	Anthelmintic resistance in cattle: an emerging issue in England?
Authors:	Lindsay Heasman ^{1*} , Ian Nanjiani ¹ , Tim Potter ¹ , Dave Burden ² , Mike Taylor ³ ¹ Westpoint Veterinary Group, Dawes Barn, Warnham, West Sussex, RH12 3SH, UNITED KINGDOM ² Duilio, The Vicarage, Churcham, Gloucester, GL2 8AF, UNITED KINGDOM ³ VParST Ltd., Maple House, Market Weighton, East Yorkshire, YO43 3GE, UNITED KINGDOM
Poster Number:	272

Anthelmintic resistance (AR) in sheep nematode populations has been widely reported in the United Kingdom. Whilst there have been reports of AR in cattle nematodes, these have often involved anecdotal evidence of treatment failure, possibly resulting from underdosing or incorrect treatment. Preliminary results from a project evaluating methods for the detection of AR in cattle are presented.

During the 2012 grazing season, controlled field studies were conducted on 25 cattle farms across England. Youngstock were turned out to grass without any anthelmintic treatment, and faecal egg counts (FECs) were performed on bulked samples until a threshold of 150epg was reached. Wormer Tests (WT) were then performed on 10 farms, using an ivermectin-based pour-on, whilst Faecal Egg Count Reduction Tests (FECRT) were performed on 15 farms, to evaluate the efficacy of an injectable ivermectin product, compared with an untreated control group . Additionally, the efficacy of an oral drench containing fenbendazole was investigated by FECRT on six of the 15 farms. Individual animal weights were obtained, and treatments administered by competent personnel. Individual faecal samples were collected prior to treatment, and 14 days post-treatment, and FECs were performed using a modified McMaster technique sensitive to 15epg, and a sensitive centrifugal flotation technique sensitive to 1epg (MAFF 1986). Efficacy was calculated according to current WAAVP guidelines (Coles et al.1992, 2006)

Efficacy ranged from 100% to 69% following pour-on treatment, from 100% to 34% after administration of an injectable ivermectin, and from 100% to 74% following oral administration of fenbendazole. Whilst there appeared to be a lack of efficacy on some farms, this should be interpreted cautiously, as factors such as the sensitivity of the FEC technique, group sizes and statistical methodologies (Levecke et al. 2012), need to be considered when interpreting results and establishing the presence of resistant nematodes.

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Session Details:	8/27/2013 Poster Session 2 1730 - 1930
Poster Details:	<i>Oxyuris equi</i>: evidence for anthelmintic resistance against macrocyclic lactones?
Authors:	Carlos Hermosilla*, Denis Wolf, Anja Taubert Justus Liebig University Giessen, Giessen, GERMANY
Poster Number:	112

The equine pinworm *Oxyuris equi* is a common horse parasite with a worldwide geographical distribution. Whilst anthelmintic resistance of other nematodes, such as small strongyles, is well documented, anthelmintic failures against infections with *O. equi* have scarcely been published so far. Here we describe two clinical case report scenarios of equine oxyuriasis and the anthelmintic failure of moxidectin in properly killing *O. equi*. Persistent *O. equi*-infections with continuous egg shedding despite repeated treatment with macrocyclic lactones in two different horse herds in the Federal State of Hessa, Germany, were observed and subsequently reported to the Institute of Parasitology, Justus Liebig University Giessen. In herd A two geldings were kept: an 8 year old Welsh-Cob-Mix (“A1”) and a 7 year old Haflinger (“A2”). Herd B was composed of four animals: Two Connemara-mares (“B1” and “B2”), 31 and 19 years old, one 18 year old Connemara-gelding (“B3”) and a 27 year old Norwegian Fjord mare (“B4”). All animals had received various anthelmintic treatments with macrocyclic lactones in the last two years. Nonetheless, animals continued to shed *O. equi* nematodes and egg-masses sometimes within few days after respective anthelmintic medication. In this study, animals were treated anew with moxidectin by personnel of the Institute of Parasitology and were monitored on a continuous daily base by adhesive-film samples showing reappearance of *O. equi*-egg-excretion within 1 to 4 weeks after treatment. In contrast to ivermectin, a consecutive treatment of the animals with mebendazol proved effective and resulted in the clearance of *O. equi* infection.

This is the first report in Europe showing inefficacy of commercial ivermectin compounds and furthermore the first report at all documenting ineffectiveness of moxidectin compounds in the treatment of *O. equi*-infections in horses.



Session Details:	8/27/2013 Poster Session 2 1730 - 1930
Poster Details:	Intestinal helminthes parasites in feral dogs and cats from Nanning (China) and their risk to public health
Authors:	Fang fang ¹ , Li Jian ^{1,2} , Shi Yunliang ² , Wang dongying ^{1,2} , Huang tengfei ¹ , Huang weiyi ^{1,2*} ¹ College of Animal Science and Technology, Guangxi University, Nanning, Guangxi, CHINA ² Food Quanlity and Safety Center of Guangxi University, Nanning, Guangxi, CHINA
Poster Number:	268

In order to investigate parasite infection of feral dogs and cats, a total of 40 dogs and 39 cats from Nanning, China were post-mortem examined. The 40 dogs were collected in 2008 and the 39 cats were collected during the period of March to October in 2012. Viscera examination showed mixed helminthic infections in most dogs and cats, with an overall prevalence of 100% of dogs and 94.87% of cats. 11 and 13 species of helminthes parasite were found in dogs and cats, respectively. The species and infection rates are as follows: *Clonorchis sinensis* (dog-27.5%, cat-35.9%), *Echinochasmus perfoliatus*(dog-10.0%, cat-25.6%), *Echinochasmus liliputanus*(dog-10.0%), *Metagonimus yokogawai*(dog-5.0%, cat-12.8%), *Haplorchis taichui*(dog-12.5%, cat-2.6%), *Haplorchis pumilio*(cat-5.1%), *Pharyngostomum cordatum*(cat-20.5%), *Dipylidium caninum* (dog-72.5%, cat-38.5%), *Taenia taeniaeformis*(dog-5.0%, cat-15.4%), *Spirometra erinaceieuropaei*(dog-10.0%, cat-33.3%), *Ancylostoma ceylanicum*(dog-17.5%, cat-28.2%), *Ancylostoma caninum*(dog-10.0%), *Toxocara canis* (dog-30.0%), *Toxocara cati* (cat-5.1%) and *Toxascaris leonina* (cat-7.7%), except the *Pharyngostomum cordatum* all the detected parasites could be infected by human being. This study revealed that the feral dogs and cats infected and carried with different species of zoonotic parasites which pose a potential threat to the health of pets and local residents.



Session Details:	8/27/2013 Poster Session 2 1730 - 1930
Poster Details:	Apparent digestibility in sheep artificially infected with <i>Haemonchus contortus</i> or <i>Trichostrongylus columbriformis</i>
Authors:	Ana C. K. Sampaio ¹ , Juliano Issakowicz ¹ , Tais C. Martins ¹ , Tali P. L. Aspis ¹ , Maria R. S. R. Peçanha ¹ , Lécio A. Castilho ¹ , Joaquim E. M. Santos ¹ , Concepta M. McManus ² , Adibe L. Abdalla ¹ , Helder Louvandini^{1*} ¹ Universidade de São Paulo, Centro de Energia Nuclear na Agricultura, NAPTSA, CP 96, CEP 13.400-970, Piracicaba, SP, Brasil. ² Departamento de Zootecnia, Universidade Federal do Rio Grande do Sul, Porto Alegre, 91540-000 Rio Grande do Sul, Brasil.
Poster Number:	220

Effects on the digestion system when helminthic infections have been described, for example, the decrease of apparent digestion of organic matter. This study aims to evaluate the apparent digestibility of sheep artificially infected with *Haemonchus contortus* and *Trichostrongylus columbriformis*. Fifteen animals were used, of which six were experimentally infected with 10.000 L₃ of *T. colubriformis*, six with 5.000 L₃ of *H. contortus* and three were a non-infected (Control). Faecal egg counts were carried out one day before the beginning of the experiment (30 days after infection), aiming to confirm infection (2916 and 366 egg/g to *H. contortus* and *T. colubriformis*, respectively). The animals received only Tifton-85 hay (*Cynodon dactylon* sp.) in the diet. The adjustment period the diet was 30 days and 31 to day 35, the animals were kept in individual metabolism cages for the samplings of leftover food, feaces and urine. Were evaluated the digestibility of dry matter (DM), organic matter (OM), crude protein (CP), ether extract (EE), neutral detergent fiber (NDF), acid detergent fiber (ADF), cellulose (CEL), hemicellulose (HEM) and total carbohydrates (TC). Statistical analysis were carried out using GLM procedure of SAS®. Significant differences (p<0.05) were observed only in EE digestibility between Control and *H. contortus* (84.1 % and 80.7 % respectively) and CT, with averages of 52.1 % and 57.6 % for *H. contortus* and *T. columbriformis* (p<0.05), didn't differ (p>0.05) than Control (56.8 %). The parasitic infections with *H. contortus* interfere negatively in ether extract digestibility and total carbohydrates in sheep when compared *T. columbriformis*.

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Session Details:	8/27/2013 Poster Session 2 1730 - 1930
Poster Details:	<i>In vitro</i> anthelmintic action of <i>Acacia mearnsii</i> and <i>Caesalpinea bracteosa</i> against <i>Haemonchus contortus</i>
Authors:	Edgard Franco Gomes ¹ , Luciana Katiki ² , Egon Hion Ieda ¹ , Márcia Lucena ² , Luciana Dinato ³ , Fotini Manolaraki ⁴ , Adibe Luiz Abdalla ¹ , Hervé Hoste ⁴ , Helder Louvandini^{1*} ¹ Center for Nuclear Energy in Agriculture, NAPTISA, São Paulo, Brazil ² Instituto de Zootecnia, Nova Odessa, Brazil ³ Faculdade de Agronomia e Medicina Veterinária, University of Brasília, Distrito Federal, Brazil ⁴ UMR IHAP 1225 INRA/ENV, Ecole Nationale Vétérinaire de Toulouse, Toulouse, France
Poster Number:	226

Acacia mearnsii and *Caesalpinea bracteosa* are examples of plants found in Brazil and both are used in ethnomedicine. It is known that *A. mearnsii* and *C. bracteosa* have a high concentration of tannis, and *C. bracteosa* is vastly used in phytotherapy in communities from the Northeast region of Brazil. *C. bracteosa* has been used in the treatment from abdominal pain to some cases of cancer, also as a well acceptable forage for small ruminants. *A. Mearnsii* has been used for long to obtain leather and also in the nitrogen fixation in the soil. Some *in vitro* assays have been done by other authors using extracts from these plants confirming that they have gotten bactericidal, molluscicidal and larvicidal effect (Alonso-Díaz et al, 2011; Gomes et al, 2012; Santos et al, 2012). The present trial aimed at checking if these extracts have inhibitory effect on the eclosion of eggs of the parasite *Haemonchus contortus*. The extracts were obtained by the acetonic extraction of dry plant followed by washing with dichloromethane (Jackson et al, 1996). Thus, a 100 eggs solution was prepared and incubated for 24 hours with solutions of 50, 25, 12.5, 6.25, 3.12, 1.56, 0.78 and 0.39 mg/mL for *A. mearnsii* and 6.25, 3.12, 1.56, 0.78, 0.39 and 0.19 mg/mL for *C. bracteosa*. A dose-dependent effect was found for both plants, with a Lethal Dose LD50 of 7.14 mg/mL for *A. mearnsii* and 0.51 mg/mL for *C. bracteosa*. These results suggest that both plants can play a role also on ethnoveterinary.

Acknowledgements:

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Santos EA, Carvalho CM, Costa ALS, Conceição AS, Moura FBP, Santana AEG. Bioactivity evaluation of plant extracts used in indigenous medicine against the snail, *Biomphalaria glabrata*, and the larvae of *Aedes aegypti*. Evid Based Complement Alternat Med [periódico na Internet]. 2012 [accessed in 2013 Mar 21];2012[9 p.]. Available in: <http://www.ncbi.nlm.nih.gov/pubmed/22194773>



Session Details:	8/27/2013 Poster Session 2 1730 - 1930
Poster Details:	Viability of <i>Haemonchus contortus</i> and <i>Trichostrongylus colubriformis</i> larvae in a CO ₂ enriched environment
Authors:	Fernanda Cristina de Campos ¹ , Érika Breda Canova ¹ , Tali Pereira Lima Aspis ¹ , Concepta Margaret McManus Pimentel ² , Raquel Ghini ³ , Adibe Luiz Abdalla ¹ , Helder Louvandini^{1*} ¹ University of São Paulo, Center for Nuclear Energy in Agriculture, Piracicaba-SP, BRAZIL ² University of Brasília, Brasília-DF, BRAZIL ³ Embrapa Meio Ambiente, Jaguariúna-Sp, BRAZIL
Poster Number:	42

Haemonchus contortus (*Hc*) and *Trichostrongylus columbriformis* (*Tc*) are endoparasites of great veterinary interest and, on the other hand, climate change has been predicted in particular an increase in the concentration of atmospheric CO₂. Nevertheless, little is known on the biology of these larvae in enriched atmosphere with this gas. The objective of this study was to evaluate the viability of *Hc* and *Tc* larvae in the natural environment and that enriched with 200 µmol/ mol⁻¹CO₂. In twelve open cameras, six with natural and six enriched CO₂ atmosphere, approximately 5,000 L₃ *Hc* and *Tc* were placed in polyurethane bags for posterior recuperation of larvae. There were two replicates in each camera, totalling 48 bags. After 21 days all the bags were removed from the cameras and 100 larvae were counted in a light microscope in order to ascertain their viability. No significant differences were found for *Hc* and *Tc* into account different environments. The values of live larvae *Hc* (%) were 13.17 vs 19.15 (SE 3.63) for the cameras normal and enriched, respectively while for values of live larvae *Tc* (%) were 14.42 vs 22.67 (SE 6.45), respectively. CO₂ enriched atmosphere for 21 days did not influence *H. contortus* and *T. columbriformis* larval viability.

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Session Details:	8/27/2013 Poster Session 2 1730 - 1930
Poster Details:	Proteomic profiling of vitelline glands of <i>Schistosoma japonicum</i>
Authors:	D Malagón (1,2), J Mulvenna (1), GN, Gobert (1), Ponlapat Yonglitthipagon (1,4) , MK Jones (1,3). (1) Queensland Institute of Medical Research, Herston, Queensland 4029, Australia (2) Departamento de Parasitología, Universidad de Granada, 18071 Granada, Spain, and (3) School of Veterinary Sciences, The University of Queensland, Brisbane, Queensland 4072, Australia. (4) Department of Pathology, Khon Kaen University School of Medicine, Khon Kaen, Thailand.
Poster Number:	214

A hallmark feature of the Digeneans eggs is their shells, which are composed of highly cross-linked protein polymers. The shells are synthesised by secretions of specialised gland cells, the vitelline cells, which are thought to possess nearly all the components necessary for shell synthesis. Under secretory action of the Mehlis gland, the vitelline cells are induced during egg formation to release their secretory content to form the shell. We are interested in exploring the commitment of platyhelminths to reproduction and have sought to identify the suite of molecules produced by vitelline cells in egg formation. We combined the methods of Laser micro-dissection microscopy and enhanced proteomic analyses of low abundance proteins to profile the proteome of the vitellarium in *Schistosoma japonicum* (Philippine strain).



Session Details:	8/27/2013 Poster Session 2 1730 - 1930
Poster Details:	Canine Parasitology in South Australia – Trends Revealed Through Diagnostics
Authors:	Ryan O’Handley*, Adrian Hines ¹ Veterinary Diagnostic Laboratory, Parasitology Division, School of Animal and Veterinary Sciences, University of Adelaide, Roseworthy, South Australia University,
Poster Number:	94

Despite the development of “all in one” parasite control products, diagnostic parasitology remains an important tool in the practice of evidence based medicine. Parasitology diagnostic techniques are generally non-invasive, inexpensive, and can provide valuable information to the clinician for the education of the client and general public. Methods: Submissions for routine parasite diagnosis to the Veterinary Diagnostic Lab at the University of Adelaide were examined for trends regarding parasite prevalence in dogs and associations between parasite prevalence and breed. Zinc sulfate centrifugal flotation was the method used in the diagnosis of parasites from faecal samples. Results: Out of 74 submissions, *Cystoisospora* was identified in 11% of samples while *Giardia* and hookworm were identified in 10% of samples. *Toxocara* was identified in 6.8% of submissions with *Sarcocystis* and *Trichuris* being identified in 3% and 1% of submissions respectively. 60% of submissions were negative. Parasites were identified in 50% of greyhound samples compared to 30% of samples from other breed,s and this difference was found to be significant (P < 0.05). Conclusions: Although more data is required, it appears Greyhounds in South Australia are more likely to be parasitised than other breeds of dog. In addition, protozoal infections account for 60% of parasite positive samples with the potentially zoonotic parasite *Giardia* commonly identified in dogs. These results demonstrate some important trends in canine parasites in South Australia and can serve as the basis for future parasite control programs.



Session Details:	8/27/2013 Poster Session 2 1730 - 1930
Poster Details:	Identification and differential characterization of Glutathion S-Transferase in <i>Fasciola hepatica</i> susceptible and resistant at Triclabendazole
Authors:	Vanessa Fernández ¹ , Pamela Lamenza ¹ , Pedro Ortiz Oblitas^{2*} , Hugo Solana ¹ Laboratorio de Biología Celular y Molecular. Centro de Investigación Veterinaria de Tandil (CIVETAN), CONICET, FCV-UNCPBA, Tandil, Argentina ² Facultad de Ciencias Veterinarias. Universidad Nacional de Cajamarca, Cajamarca, Perú
Poster Number:	114

Fasciolosis, a zoonotic disease produced by *Fasciola hepatica*, is an economically important disease of livestock. This parasitic disease is controlled with Triclabendazole (TCBZ), a halogenated benzimidazole thiol derivative which shows efficacy against juvenile and adult stages. The bad use of this drug has resulted in the development of TCBZ-resistant (TCBZ-R) liver flukes. The helminthes parasites possess different biochemical mechanisms for detoxification. Overall, parasites may evade drug antiparasitic effects by: i) mutation of target receptors, ii) overexpression of efflux transport pumps, and/or iii) overexpression of metabolic enzymatic systems. In nematodes, the benzimidazole resistance is caused by genetic changes in β -tubulins (target receptor). In liver fluke TCBZ-R was not detected these genetic changes for which the resistance should be from other genetic or metabolic changes. In general, all organisms have xenobiotic metabolizing enzymes, which can deactivate toxic functions. Hence, is needed the extension of the knowledge of detoxification and resistance mechanisms in this trematode.

The Glutathion S-Transferases (GSTs) are ubiquitous multifunctional enzymes involved in the detoxification of endogenous and xenobiotic compounds using glutathione conjugation or glutathione peroxidase activity. Using specific oligonucleotides, the aim of this work was to identify and characterize by RT-PCR, the expression of the mRNA of Glutathion S-Transferase in strains of *F. hepatica* susceptible and resistant at TCBZ.

The mRNA of GST was identified in both strains of *F. hepatica* and using ImageJ® **software** were detected significant differences between both strains tested. The expression of the mRNA corresponding to GST of TCBZ-R was 3 times greater than the TCBZ-S flukes. This result confirms that GST enzyme participates actively in the development of resistance at TCBZ in *F. hepatica*. This resistance could be due by a multienzymatic action involving more than one metabolic pathway.

Acknowledgements:

Fasciola hepatica TCBZ-susceptible (*Cullompton* strain) and TCBZ- resistant (*Sligo* strain) were kindly provided by Professor Ian Fairweather, School of Biology and Biochemistry, The Queens University of Belfast, Northern Ireland, UK.



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Session Details:	8/27/2013 Poster Session 2 1730 - 1930
Poster Details:	A modified Larval Feeding Inhibition Assay (LFIA) to screen susceptible ovine trichostrongylids
Authors:	Benjamin U. Bauer ^{1,2} , William E. Pomroy ^{*1} , Ian Scott ¹ ¹ Massey University, Private Bag 11 – 222, Palmerston North, New Zealand ² Bavarian Sheep Health Service, Senator-Gerauer-Str. 23, 85586 Poing, Germany
Poster Number:	78

A variety of different assays have been used to assess anthelmintic resistance in trichostrongyloid nematodes. The aim of this study was to compare the dose responses of *Haemonchus contortus*, *Teladorsagia circumcincta* and *Trichostrongylus colubriformis* to ivermectin (IVM) in a modified Larval Feeding Inhibition Assay (LFIA). Eggs were recovered from lambs with single species infections and incubated in distilled water for 18 hours at 25°C until first stage larvae had hatched. IVM (in DMSO) was added to the fresh hatched unfed larvae at final concentrations of 0, 0.001, 0.01, 0.1, 1, 5, 50, 200 ng/ml. The larvae were then incubated for 2 hours at 25°C when fluorescent-labeled *E. coli* were added followed by a further 18 hours at 25°C. At this time the larvae were examined with a fluorescent microscope. The percentage of larvae fed was determined and the dose required to inhibit larval feeding by 50% (IC₅₀) and 90% (IC₉₀) was calculated. Reliable dose-response-curves could be achieved with all three nematode species (R²=0.90, 0.94, 0.97 respectively). *H. contortus* was the most sensitive trichostrongylid in this trial (IC₅₀ 0.005 ng/ml; IC₉₀ 0.024 ng/ml) then followed by *T. colubriformis* (IC₅₀ 0.339 ng/ml; IC₉₀ 6.061 ng/ml) and *T. circumcincta* (IC₅₀ 0.479 ng/ml; IC₉₀ 5.028 ng/ml). The pharyngeal pumping of *H. contortus* seems to be more sensitive to IVM. This variation in the IC₅₀ and IC₉₀ make it difficult to establish a uniform discrimination threshold for all three susceptible ovine trichostrongylids, especially as the assay utilises observations of first stage larvae that cannot be easily discriminated between genera. To be useful as a discriminatory phenotypic assay this needs to be combined with the use of some other markers such as PCR to determine the species involved. Further studies are also required to determine the threshold values for other strongyloid species in sheep.



Session Details:	8/27/2013 Poster Session 2 1730 - 1930
Poster Details:	Acaricidal activity of extracts from <i>Diospyros anisandra</i> (Ebenaceae) against the cattle tick, <i>Rhipicephalus microplus</i> resistant to acaricides
Authors:	¹José Alberto Rosado-Aguilar , ¹ Roger Iván Rodríguez-Vivas, ¹ Fernando Peraza-Quintal ¹ Arturo Caamal-Maldonado ¹ José Rodrigo Carrillo-Peraza ¹ , ² Martha Méndez-González, ² Rocío Borges-Argáez, ¹ Jorge C. Rodríguez-Buenfil, ¹ Iris Trinidad-Martínez, ¹ Manuel Bolio-González ¹ Facultad de Medicina Veterinaria y Zootecnia. Universidad Autónoma de Yucatán. Km. 15.5 carretera Mérida-Xmatkuil. CP. 97000. Mérida, Yucatán, México; alberto.rosadoaguilar@gmail.com ² Centro de Investigación Científica de Yucatán. Calle 43 No 130 Colonia Chuburná de Hidalgo. CP 97200. Mérida, Yucatán, México.
Poster Number:	116

Commercial acaricides are usually toxic to humans and leave residues in the environment. However, acaricide from plants are usually of low toxicity to mammals, water soluble, producing non-residual effects and have a low incidence of developing resistant strains. The aim of this study was to evaluate the acaricidal activity of methanolic crude extracts from leaves and stem bark of *Diospyros anisandra* (Enenaceae) against larvae of *R. microplus* (resistant to organophosphates, pyrethroids and amitraz) using the larval immersion test (LIT) and adult immersion test (AIT). In the LIT extracts of leaves from *D. anisandra* evaluated at 10% (100 mg/ml) and 20% (200 mg/ml) concentrations against larvae of *R. microplus* showed acaricidal activity of 45.5±11.0% and 71.9±6.0%, respectively. Extracts of stem bark showed acaricidal activity of both 100% when they were tested at 10% and 20% concentrations. Based on these results, extracts of the stem bark from *D. anisandra* were selected for evaluating against adults of *R. microplus*. In the AIT, the stem bark extracts at 10% and 20% concentrations evaluated against *R. microplus* engorged females showed mortality of 16.6±16.7% and 33.3±16.7%, respectively. The 10% and 20% of these methanolic crude extracts showed 22.1±30.7% and 44.0±15.5% of egg laying inhibition, respectively. Our results showed that the methanolic crude extracts from *D. anisandra* are a promising candidates to control larvae of *R. microplus* multi resistance to acaricides.. In addition *D. anisandra* reduced the ability to lay eggs of engorged females. Further studies are required to identify the active fractions and compound of these crude extracts.

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Session Details:	EPoster Only
Poster Details:	<i>Rhipicephalus (Boophilus) microplus</i> resistance against high concentration ivermectin (630 mcg/kg) in naturally infested cattle
Authors:	Breno Cayeiro Cruz ¹ , Welber Daniel Zanetti Lopes ¹ , João Carlos Pereira ¹ , Flávia Carolina Favero ¹ , Vando Edésio Soares ¹ , Carolina Buzzilini ¹ , Gustavo Felppelli ¹ , Weslen Fabricio Pires Teixeira ¹ , Lucas Vinicius Shigaki de Matos ¹ , Willian Giquelin Maciel ¹ , Alvimar José da Costa ^{1*} ¹ CPPAR - Animal Health Research Center - Faculdade de Ciências Agrárias e Veterinárias, UNESP, Via de acesso Prof. Paulo Donatto Castellane, s/nº, CEP: 14884-900, Jaboticabal, São Paulo – Brazil. +55 (16) 3202-1720. cppar@asbyte.com.br
Poster Number:	110

The efficacy of 630 mcg/kg ivermectin against *Rhipicephalus (B.) microplus* strains was assessed in six experiments that were conducted on different rural properties. In experiment I, two groups of ten bovines, naturally infested with at least 20 ticks measuring between 4.5 and 8 mm on the left side of the animal's body were selected after three consecutive counts (days 3, 2 and 1 before treatment); one group was treated subcutaneously with 630 mcg/kg ivermectin and the other was held as a control. On experiments II, III, IV, V and VI another 20 animals were selected for each trial following the same criteria and the same experimental delineation. In all experiments the parasites were quantified on days 3, 7, 14, 21, 28 post treatment (p. t.) and then weekly, until the efficacy was inferior to 80%, in order to determine the efficacy of the tested formulation, based on the geometric means of the parasite counts. In only one of the six experiments a sufficient efficacy (average of efficacy on days 7 and 14 superior to 90%) was observed. The efficacy of 630 mcg/kg ivermectin was 95.59% in experiment I, the only experiment where it could be considered effective. 630 mcg/kg ivermectin obtained an efficacy of 72.35% in experiment II; 32.14% in experiment III; 51.24% in experiment IV; 78.55% in experiment V and 53.62% in experiment VI. The results from these experiments indicate that the resistance of *R. (B.) microplus* to 630 mcg/kg ivermectin, a high concentration, is widely disseminated in different populations of this parasite.



Session Details:	EPoster Only
Poster Details:	Diagnosis of ivermectin (630 and 700 mcg/kg) resistance of nematodes from necropsied bovines the South and Southeast regions of Brazil
Authors:	Gustavo Felippelli ¹ , João Carlos Melo Pereira ¹ , Roberto Cesar Araújo de Lima ¹ , Thalita Silveira Righi ¹ , Lucas Costa Gomes ¹ , Welber Daniel Zanetti Lopes ¹ , Breno Cayeiro Cruz ¹ , Weslen Fabricio Pires Teixeira ¹ , Gilson Pereira de Oliveira ¹ , Hurzana de Mello ¹ , Alvimar José da Costa ^{1*} ¹ CPPAR - Animal Health Research Center - Faculdade de Ciências Agrárias e Veterinárias, UNESP, Via de acesso Prof. Paulo Donatto Castellane, s/nº, CEP: 14884-900, Jaboticabal, São Paulo – Brazil. +55 (16) 3202-1720. cppar@asbyte.com.br
Poster Number:	100

The specific objectives of the present study were to diagnose high concentration ivermectin (3.15% and 3.5%) resistance in nematodes through parasitological necropsies conducted in bovines originating from eight cities from the states of Minas Gerais, São Paulo and Rio Grande do Sul and provide aid for a better knowledge about the distribution of ivermectin resistance in nematodes throughout different regions of Brazil. To achieve these goals 116 naturally infected animals were used, all selected using the average of three (-3, -2 and -1) eggs per gram of feces (EPG) count, randomized in experimental groups with six or eight repetitions each. Fourteen days after treatment all animals were euthanized and necropsied. Resistance to 3.15% ivermectin (630 mcg/Kg) and 3.5% ivermectin (700 mcg/Kg) was diagnosed by obtaining insufficient therapeutical efficacy (< 80%) when analyzing arithmetic means or by finding at least 1000 specimens that survived in the treated groups: *Haemonchus placei* (0.0-67.00%), *Cooperia punctata* (0.0-26.46%), *Cooperia pectinata* (0.0%), *Cooperia spatulata* (0.0-71.50%), *Oesophagostomum radiatum* (54.93-78.37%) and *Trichuris discolor* (0.0-64.71%). Considering only the statistically analyzed results related to the eight experiments conducted (116 necropsies) it can be inferred that resistance to high concentration ivermectin (630 and 700 µg/Kg) is highly disseminated, especially in *Haemonchus placei*, *Cooperia punctata*, *Cooperia pectinata*, *Cooperia spatulata*, *Oesophagostomum radiatum* and *Trichuris discolor*, parasitizing bovines from the Southeast and South regions of Brazil.



Session Details:	EPoster Only
Poster Details:	Anthelmintic efficacy of moxidectin (200mcg/kg) against ivermectin-resistant (630mcg/kg) nematode strains in cattle naturally infected
Authors:	Welber Daniel Zanetti Lopes ¹ , Flávia Carolina Favero ¹ , João Carlos Melo Pereira ¹ , Breno Cayeiro Cruz ¹ , Thalita Silveira Righi ¹ , Lucas Costa Gomes ¹ , Weslen Fabricio Pires Teixeira ¹ , Hurzana de Mello ¹ , Gilson Pereira de Oliveira ¹ , Alvimar José da Costa ^{1*} ¹ CPPAR - Animal Health Research Center - Faculdade de Ciências Agrárias e Veterinárias, UNESP, Via de acesso Prof. Paulo Donatto Castellane, s/nº, CEP: 14884-900, Jaboticabal, São Paulo – Brazil. +55 (16) 3202-1720. cppar@asbyte.com.br
Poster Number:	101

The anthelmintic efficacy of 200 mcg/kg moxidectin against nematode strains that were resistant to 630 mcg/kg ivermectin in naturally infected cattle was assessed in two experiments that were conducted on different rural properties. In experiment I, two groups of eight cattle naturally infected with populations of the gastrointestinal nematodes *Haemonchus placei*, *Cooperia punctata*, *C. spatulata*, *O. radiatum* and *Trichuris discolor* that were known to be resistant to 200 and 630 mcg/kg ivermectin were studied; one group was treated subcutaneously with 200 mcg/kg moxidectin and the other was held as a control. Twenty-four naturally infected cattle were selected for experiment II and divided into three groups of eight animals each: moxidectin (administered subcutaneously, 200 mcg/kg), 3.15% ivermectin (administered subcutaneously, 630 mcg/Kg) and a control. The gastrointestinal helminths were quantified and identified following a necropsy of all animals on the 14th day post-treatment. Moxidectin was highly effective (arithmetic mean) against the ivermectin-resistant species (experiment I) *H. placei* (97.84%), *C. punctata* (98.51%) and *C. spatulata* (100.00%). Moxidectin was poorly effective against *O. radiatum*. The small number of *T. discolor*-parasitized animals in the control group did not permit a conclusion to be drawn regarding this helminth species. Moxidectin (200mcg/kg) achieved efficacy values of 98.70%, 99.16, 93.80 and 82.97% in ivermectin (630 mcg/kg)-resistant adult *H. placei*, L4 of *H. placei*, *C. punctata*, and adult and L4 of *O. radiatum*, respectively, identified in experiment II. The immature stages of *O. radiatum* (L4) were considered moxidectin-resistant. The results from both experiments indicate that the formulation containing 200 mcg/kg moxidectin administered as described could provide an alternative treatment to control helminth parasites in cattle that are resistant to ivermectin(200 and 630mcg/kg).



Session Details:	EPoster Only
Poster Details:	Effects of fluazuron and fluazuron + abamectin on the reproductive parameters of engorged Rhipicephalus (Boophilus) microplus females naturally detached from experimentally infested cattle
Authors:	Thalita Silveira Righi ¹ , Breno Cayeiro Cruz ¹ , Lucas Costa Gomes ¹ , Carolina Buzzilini ¹ , Lucas Vinicius Shigaki de Matos ¹ , João Carlos Melo Pereira ¹ , Weslen Fabricio Pires Teixeira ¹ , Welber Daniel Zanetti Lopes ¹ , Gilson Pereira de Oliveira ¹ , Alvimar José da Costa ^{1*} ¹ CPPAR - Animal Health Research Center - Faculdade de Ciências Agrárias e Veterinárias, UNESP, Via de acesso Prof. Paulo Donatto Castellane, s/nº, CEP: 14884-900, Jaboticabal, São Paulo – Brazil. +55 (16) 3202-1720. cppar@asbyte.com.br
Poster Number:	102

The present study assessed the deleterious effects of fluazuron 2.5% (2.5 mg/kg) and fluazuron 3% + abamectin 0.5% (3 mg/kg + 500 mcg/kg) on the reproductive parameters of engorged *R. (B.) microplus* females that naturally detached from experimentally infested cattle in two different studies. In experiment I, the pour-on application of fluazuron (2.5 mg/kg) presented an acaricidal efficacy higher than 80% from day 16 post-treatment (p. t.) up until day 45, being above 90% from day 19 to day 32. It also exceeded 80% on days 53 to 59, 63 and 64 p. t. The treated group demonstrated a 36.75% reduction in oviposition, 57.73% reduction in hatchability and fluazuron reproductive efficacy was 65.41%. In experiment II, the association of fluazuron and abamectin (3 mg/kg + 500 mcg/kg) presented acaricidal efficacy higher than 80% from day 16 until day 85. The efficacy was higher than 90% from days 18 to 85 p. t. The formulation percentage of reduction in oviposition of engorged female ticks was 95.47%. It presented a reduction of 100% in hatchability and the percentage of efficacy of this formulation on the reproductive parameters of engorged female ticks also achieved 100%. Comparing both experiments it is possible to observe that the association between fluazuron and abamectin presented highest acaricidal efficacies and more deleterious effects on the reproductive parameters of engorged *R. (B.) microplus* females, when compared to formulation that contain fluazuron 2.5%.





Session Details:	EPoster Only
Poster Details:	Effects of macrocyclic lactones on the reproductive parameters of engorged <i>Rhipicephalus (Boophilus) microplus</i> females naturally detached from experimentally infested cattle
Authors:	Weslen Fabricio Pires Teixeira ¹ , Welber Daniel Zanetti Lopes ¹ , Breno Cayeiro Cruz ¹ , Hurzana de Mello ¹ , Flávia Carolina Favero ¹ , Lucas Costa Gomes ¹ , Thalita Silveira Righi ¹ , Gilson Pereira de Oliveira ¹ , Alvimar José da Costa ^{1*} ¹ CPPAR - Animal Health Research Center - Faculdade de Ciências Agrárias e Veterinárias, UNESP, Via de acesso Prof. Paulo Donatto Castellane, s/nº, CEP: 14884-900, Jaboticabal, São Paulo – Brazil. +55 (16) 3202-1720. cppar@asbyte.com.br
Poster Number:	103

The present study therefore assessed the deleterious effects of MLs (ivermectin, abamectin, doramectin and moxidectin) on the reproductive parameters of engorged *R. (B.) microplus* females that naturally detached from experimentally infested cattle in two experiments. In the experiment I, statistical analysis of the data grouped into 5-day intervals revealed that pour-on application of abamectin (500 mcg/kg) had significantly ($p \leq 0.05$) reduced engorged female weight, egg mass weight and percent hatchability on days 6 to 15, 6 to 20 and 11 to 20 post-treatment (p. t.), compared to the respective data for detached and pre-selected engorged females in the control group. The abamectin, demonstrated 33.41% of reduction in oviposition, 6.77% in hatchability and abamectin efficacy was of 13.99 %. In the experiment II, statistically significant reductions ($p \geq 0.05$) were observed in animals treated subcutaneous with ivermectin (630 mcg/kg), doramectin (700 mcg/kg) and moxidectin (1000 mcg/kg) relative to the control for days 6 to 40, 6 to 48 and 6 to 40 p. t., respectively. Ivermectin reduced hatchability only on days 16 to 20 p. t., whereas doramectin significantly reduced ($p \leq 0.05$) hatchability on days 6 to 10 and 16 to 35 p. t. For moxidectin, deleterious effects on hatchability were observed on days 16 to 35 p. t. The percent reductions in oviposition of engorged female ticks were 46.31 %, 62.17 % and 61.02 % with ivermectin, doramectin and moxidectin treatments, respectively. The percent efficacy of the formulations on the reproductive parameters of engorged female ticks was 21.22 % for ivermectin, 36.03 % for doramectin and 35.45 % for moxidectin. Among the MLs assessed, doramectin and moxidectin had the highest acaricidal efficacies and the most deleterious effects on the reproductive parameters of engorged *R. (B.) microplus* females.



Session Details:	EPoster Only
Poster Details:	Effects of spray formulations on the reproductive parameters of engorged Rhipicephalus (Boophilus) microplus females naturally detached from experimentally infested cattle
Authors:	Hurzana de Mello ¹ , Gustavo Felippelli ¹ , João Carlos Melo Pereira ¹ , Weslen Fabricio Pires Teixeira, ¹ Breno Cayeiro Cruz ¹ , Thalita Silveira Righi ¹ , Lucas Costa Gomes ¹ , Welber Daniel Zanetti Lopes ¹ , Lucas Vinicius Shigaki de Matos ¹ , Carolina Buzzulini ¹ , Gilson Pereira de Oliveira ¹ , Alvimar José da Costa ^{1*} ¹ CPPAR - Animal Health Research Center - Faculdade de Ciências Agrárias e Veterinárias, UNESP, Via de acesso Prof. Paulo Donatto Castellane, s/nº, CEP: 14884-900, Jaboticabal, São Paulo – Brazil. +55 (16) 3202-1720. cppar@asbyte.com.br
Poster Number:	104

The present study assessed the deleterious effects of cypermethrin 15% + chlorpyrifos 25% + citronellal 1%, cypermethrin 8% + ethion 60% and DDVP 60% + chlorpyrifos 20% on the reproductive parameters of engorged *R. (B.) microplus* females that naturally detached from experimentally infested cattle in three different experiments. In experiment I, the spray application of cypermethrin + chlorpyrifos + citronellal presented an acaricidal efficacy higher than 80% starting from day 3 to 9 post-treatment (p. t.), occurring again from days 16 to 30 and being above 90% on days 8, 9, 23, 25, 26 and 29. The treated group demonstrated a 63.23% reduction in oviposition, 10.53% reduction in hatchability and the reproductive efficacy was 64.74%. In experiment II, the association of cypermethrin and ethion presented acaricidal efficacy higher than 80% from day 5 until day 29. The efficacy was higher than 90% from days 7 to 28 p. t. The formulation percentage of reduction in oviposition of engorged female ticks was 73.18%. It presented a reduction of 35.79% in hatchability and the percentage of efficacy on the reproductive parameters of engorged female ticks achieved 70.08%. In experiment III, DDVP associated with chlorpyrifos reached acaricidal efficacy higher than 90% starting on day 2, which lasted until day 25, reaching 100% on day 6 p. t. The percentage of reduction in oviposition was 93.50%. It presented a reduction of 78.79% in hatchability and the efficacy on reproductive parameters of engorged female ticks achieved 96.45%. Comparing the data gathered from these experiments it is possible to observe that the association between DDVP and chlorpyrifos, two organophosphates, presented highest acaricidal efficacy and more deleterious effects on the reproductive parameters of engorged *R. (B.) microplus* females when compared to the associations between organophosphates and synthetic pyrethroids.





Session Details:	EPoster Only
Poster Details:	<i>Eimeria</i> species in young and adult sheep raised under intensive and / or semi-intensive systems in Brazil
Authors:	Rafael Silveira Carvalho, Antonio Campanha Martinez ¹ , Lucas Costa Gomes ¹ , Breno Cayeiro Cruz ¹ , Thalita Silveira Righi ¹ , Lucas Vinicius Shigaki de Matos ¹ , Willian Giquelin Maciel ¹ , Weslen Fabricio Pires Teixeira ¹ , Maycon Araujo Ruivo ¹ , Welber Daniel Zanetti Lopes ^{1*} , Fernando de Almeida Borges ¹ , Gilson Pereira de Oliveira ¹ ¹ Universidade Estadual de Maringá (UEM) – Campus Regional de Umuarama-PR, Departamento de Medicina Veterinária, wdzlopes@hotmail.com
Poster Number:	25

The present study aimed to use traditional methods of diagnosis to identify *Eimeria* species in young and adult sheep that were raised under intensive and / or semi-intensive systems and to classify the types of infections (clinical and / or subclinical) in the herd. Fecal samples were collected directly from the rectal ampullae of 210 sheep and were subjected to laboratory analysis to differentiate the *Eimeria* species. Furthermore, animals were observed daily for 20 days after fecal collection to determine the occurrences of the clinical or subclinical forms of eimeriosis. Of the 210 collected fecal samples, 147 (70%) were positive for *Eimeria* oocysts, and 101 (47.86%) belonged to young animals that were raised under intensive and / or semi-intensive farming systems. All 101 (100%) samples from young lambs were positive for *Eimeria* oocysts. Oocysts from 9 species of *Eimeria* parasites were identified in the sheep at the following prevalence rates: *E. crandallis*, 50.00%; *E. parva*, 21.62%; *E. faurei*, 8.11%; *E. ahsata*, 8.11%; *E. intricata*, 5.41%; *E. granulosa*, 2.70%; *E. ovinoidalis*, 2.03%; *E. ovina*, 1.35%; and *E. bakuensis*, 0.68%. There were no differences regarding the more frequent *Eimeria* species among the different ages of animals or between the different farming management systems. Because there were no clinical cases of eimeriosis, the disease was considered to be subclinical. Based on these data, constant monitoring for specific *Eimeria* oocysts in sheep feces is necessary because the subclinical form of this disease is the most common, which could lead to damage of the infected animals and consequent economic losses for the producers of these small ruminants, due mainly to decreases in the productive performance of the infected animals.



Session Details:	EPoster Only
Poster Details:	Macrocyclic lactones and phenylpyrazoles: There is the possibility of cross-resistance?
Authors:	Carolina Buzullini ¹ , Welber Daniel Zanetti Lopes ¹ , João Carlos Melo Pereira ¹ , Gustavo Felippelli ¹ , Hurzana de Mello ¹ , Breno Cayeiro Cruz ¹ , Willian Giquelin Maciel ¹ Vando Edésio Soares ¹ , Weslen Fabricio Pires Teixeira ¹ , Thalita Silveira Righi ¹ , Flávia Carolina Fávero ¹ , Alvimar José da Costa ^{1*} ¹ CPPAR - Animal Health Research Center - Faculdade de Ciências Agrárias e Veterinárias, UNESP, Via de acesso Prof. Paulo Donatto Castellane, s/nº, CEP: 14884-900, Jaboticabal, São Paulo – Brazil. +55 (16) 3202-1720. cppar@asbyte.com.br
Poster Number:	105

Based on the hypothesis of some researchers about the occurrence of cross-resistance between phenylpyrazoles and macrocyclic lactones, coupled with the fact that there is no “*in vivo*” studies, our objective was to correlate this possible phenomenon. The present study aimed to evaluate the efficacy of fipronil (1mg/kg) against three strains of *Rhipicephalus (Boophilus) microplus* resistant to ivermectin in cattle naturally infested. Were selected three properties, two in the state of Minas Gerais and the other in Sao Paulo, all with a history of inefficiency of the macrocyclic lactones against the cattle tick and low frequency of use of fipronil. In each experiment, the animals were randomized in tree groups of 10 animals each, based on mean of ticks counts performed on days -3, -2 and -1: control (saline), T02: ivermectin (0.63 mg/kg) subcutaneously and T03: fipronil (1mg/kg) pour-on route. All treatment groups received a single dose on day zero. tick counts after treatment were performed on days 3, 7, 14 and every seven days to 49° post-treatment. In three experiments, it was possible to diagnose resistance *R. (B.) microplus ivermectin* (0.63 mg/kg). The maximum efficacy (arithmetic means) obtained by ivermectin was 64.29% in experiment II. Moreover, the formulation containing fipronil (1mg/kg) reached high values of efficiency (≥ 97%) in all experiments. Therefore, based on the results obtained in the three studies conducted in different properties from Brazil, in cattle naturally infested, it was not possible to diagnose cross-resistance between fipronil and ivermectin against *Rhipicephalus (Boophilus) microplus*.



Session Details:	EPoster Only
Poster Details:	Nematode resistance to ivermectin pour-on (500mcg/kg) in cattle from the states of São Paulo and Minas Gerais, Brazil
Authors:	João Carlos Melo Pereira ¹ , Gustavo Felippelli ¹ , Welber Daniel Zanetti Lopes ¹ , Weslen Fabricio Pires Teixeira ¹ , Breno Cayeiro Cruz ¹ , Willian Giquelin Maciel ¹ , Carolina Buzzulini ¹ , Lucas Vinicius Shigaki de Matos ¹ , Flávia Carolina Fávero ¹ , Gilson Pereira de Oliveira ¹ , Alvimar José da Costa ^{1*} ¹ CPPAR - Animal Health Research Center - Faculdade de Ciências Agrárias e Veterinárias, UNESP, Via de acesso Prof. Paulo Donatto Castellane, s/nº, CEP: 14884-900, Jaboticabal, São Paulo – Brazil. +55 (16) 3202-1720. cppar@asbyte.com.br
Poster Number:	106

This study aimed to evaluate the efficacy of anthelmintic to ivermectin administered via pour-on at dose of 500mcg/kg, against nematodes of cattle naturally infected, from state of São Paulo and Minas Gerais, Brazil . For each study, 12 naturally infected calves were selected using the mean of three consecutive counts of eggs per gram of feces (EPG, days -3, -2 and -1). Subsequently, the animals in each experiment were randomized into two groups of six animals each, one treated via pour-on ivermectin (500mcg/kg) in volume 1mL/10Kg body weight, and other kept as a control (solution saline). All animals were euthanized on day 14 after treatment. Based on the results found in this study, in four experiments conducted “in vivo” in naturally infested cattle from different regions of Brazil, it can be concluded that all four strains of *Haemonchus placei* and *Cooperia punctata* evaluated, are resistant to ivermectin, administered by pour-on, the dose of 500mcg/kg. Against *O. radiatum* was possible to observe this formulation resistance in two of the four strains involved in the study. For the other helminths species found (*Haemonchus similis*, *Cooperia pectinata*, *C. spatulata*, *Trichostrongylus axei*, *T. colubriformis*, *Trichuris discolor*, *Capillaria bovis*, *Strongyloides papillosus* and *Bunostomum phobotomum*), the low number of cattle in the control group parasitized did not permit conclusions to be made regarding the efficacy results or statistical analyses of the ivermectin (500mcg/kg) against theses helminth species.



Session Details:	EPoster Only
Poster Details:	Ineffectiveness of ivermectin and abamectin, administered at different doses and routes against <i>Cochliomyia hominivorax</i> (myiasis) in the scrotum of newly castrated cattle from different regions of Brazil
Authors:	Lucas Costa Gomes ¹ , Flávia Carolina Favero ¹ , Breno Cayeiro Cuz ¹ , Carolina Buzzulini ¹ , Gustavo Felippelli ¹ , Welber Daniel Zanetti Lopes ¹ , Vando Edésio Soares ¹ , Lucas Vinicius Shigaki de Matos ¹ , Weslen Fabricio Pires Teixeira ¹ , Willian Giquelin Maciel ¹ , Alvimar José da Costa ^{1*} ¹ CPPAR - Animal Health Research Center - Faculdade de Ciências Agrárias e Veterinárias, UNESP, Via de acesso Prof. Paulo Donatto Castellane, s/nº, CEP: 14884-900, Jaboticabal, São Paulo – Brazil. +55 (16) 3202-1720. cppar@asbyte.com.br
Poster Number:	107

The present study aimed to evaluate the preventive efficacy of ivermectin and abamectin administered in different routes (subcutaneous, intramuscular and pour-on) and doses (200 to 500mcg/kg) against *Cochliomyia hominivorax* (myiasis) in the scrotal sac of cattle after castration. Were used animals from six farms in the state of São Paulo and Minas Gerais, Brazil. For each study, were selected 30-45 bulls, depending on the experiment. On day zero, each animal was bloody orquiectomizado method. Concomitantly the process of orchiectomy animals were treated. In two experiments, the T01 was kept as a control, the T02 and T03 received abamectin and ivermecitna, respectively, both via pour-on, at a dose of 500mcg/kg. In two other studies, the T01 was the control, the T02 and T03 abamectin and ivermectin, respectively, both subcutaneously 200mcg/kg. Two other experiments, the T01 was kept as a control and T02 received abamectin (200mcg/kg), intramuscularly. The results obtained by these two macrocyclic lactone (ML) in all six experiments, regardless of the route and dose were similar. Preventive efficacy values higher (0.0% - 87.50%) were observed by abamectin days following the process orchiectomy animals (3 and 4 days post-treatment), compared to ivermectin (0.0% - 62.50%). Moreover, as the challenge by myiasis increased in the animals not treated (control) values of both efficacy LM, in six experiments decreased, and in five experiments, these active ingredients were ineffective (0.0%) before the 10th day after treatment. Therefore, the results from six studies conducted in different regions of Brazil, allow concluding that either ivermectin as abamectin were ineffective in preventing scrotal myiasis in cattle newly castrated, regardless of the route and dose administered.





Session Details:	EPoster Only
Poster Details:	Therapeutic efficacy of a new formulation in cattle naturally and experimentally infested with <i>Rhipicephalus (Boophilus) microplus</i>
Authors:	Rafael Rodriguez Corrêa ¹ , Flávia Carolina Favero ¹ , Breno Cayeiro Cruz ¹ , Vando Edésio Soares ¹ , Gustavo Felippelli ¹ , Welber Daniel Zanetti Lopes ¹ , Weslen Fabricio Pires Teixeira ¹ , Lucas Vinicius Shigaki de Matos ¹ , Willian Giquelin Maciel ¹ , Alvimar José da Costa ^{1*} ¹ CPPAR - Animal Health Research Center - Faculdade de Ciências Agrárias e Veterinárias, UNESP, Via de acesso Prof. Paulo Donatto Castellane, s/nº, CEP: 14884-900, Jaboticabal, São Paulo – Brazil. +55 (16) 3202-1720. cppar@asbyte.com.br
Poster Number:	108

Two trials were conducted in order to evaluate the anti-ixodidae efficacy of a new formulation containing 15% cypermethrin + 30% chlorpyriphos + 15% fenthion, administered topically (spray), in bovines naturally and experimentally infested by *R. (B.) microplus*. For the study involving natural infestation, female tick counts were conducted on days -3, -2, -1, 3, 7, 14 and weekly until the 28th day post-treatment (p. t.). On the study conducted with artificial infestations ('stall test'), female ticks that detached from the animals in two experimental groups were quantified daily until the 44th day p. t. In both studies, the animals were randomized, by the means of tick counts on days -3, -2 and -1, in two groups of ten animals each, being: GI - control and GII - 15% cypermethrin + 30% chlorpyriphos + 15% fenthion, administered topically (spray). The association reached an anti-ixodidae efficacy superior to 95% on days 7, 14 and 21 p. t. on naturally infested bovines. The maximum efficacy was 97.38% in the 14th day p. t., falling to 74.97% in the 28th day p. t. The counts of female ticks in the treated group (GII) were significantly ($P\leq0.05$) lower to those of the control group (GI) in all experimental dates (day 1 to day 28 p. t.). in artificially infested bovines ('stall test'), it could be verified that the tested formulation reached an efficacy superior to 90% from the 3rd to the 36th days p. t. From days 5 to 33 p. t., the anti-ixodidae efficacy was superior to 95%. On the first 23 days p. t., the average of efficacy was 96.32%. Therefore, the results obtained in the two conducted trials enable to recommend the aforementioned formulation, in the correct dosage and administration route, for the treatment and control of *R. (B.) microplus* parasitizing bovines.



Session Details:	EPoster Only
Poster Details:	Rhipicephalus (Boophilus) microplus resistance against injectable and pour-on ivermectin formulations (200 mcg/kg and 500 mcg/kg) in naturally infested cattle
Authors:	Breno Cayeiro Cruz ¹ , Weslen Fabricio Pires Teixeira ¹ , Flávia Carolina Favero ¹ , Vando Edésio Soares ¹ , Welber Daniel Zanetti Lopes ¹ , Carolina Buzzulini ¹ , Gustavo Felppelli ¹ , Lucas Vinicius Shigaki de Matos ¹ , João Carlos Pereira ¹ , Willian Giquelin Maciel ¹ , Alvimar José da Costa ^{1*} ¹ CPPAR - Animal Health Research Center - Faculdade de Ciências Agrárias e Veterinárias, UNESP, Via de acesso Prof. Paulo Donatto Castellane, s/nº, CEP: 14884-900, Jaboticabal, São Paulo – Brazil. +55 (16) 3202-1720. cppar@asbyte.com.br
Poster Number:	109

The efficacies of 200 mcg/kg and 500 mcg/kg ivermectin against *Rhipicephalus (B.) microplus* strains were assessed in four experiments that were conducted on different rural properties. In experiment I, two groups of ten bovines, naturally infested with at least 20 ticks between 4.5 and 8 mm on the left side of the body were selected after three consecutive counts (days 3, 2 and 1 before treatment); one group was treated subcutaneously with 200 mcg/kg ivermectin and the other was held as a control. On experiments II, III and IV another 20 animals were selected for each trial following the same criteria, and divided in two groups of ten animals, one being hold as a control group and the other being treated with a pour-on formulation of 500 mcg/kg ivermectin. In all experiments the parasites were quantified on days 3, 7, 14, 21 and 28 post treatment (p. t.) in order to determine the efficacy of the tested formulations, based on the geometric means of the parasite counts. In none of the four experiments a sufficient efficacy (average of efficacy on days 7 and 14 superior than 90%) was observed. The efficacy of 200 mcg/kg ivermectin was 72.04%. 500 mcg/kg ivermectin reached an efficacy of 79.03% in experiment II; 85.93% in experiment III; and 52.08% in experiment IV. The results from these experiments indicate that the resistance of *R. (B.) microplus* to ivermectin is widely disseminated, not only against 200 mcg/kg ivermectin, but against 500 mcg/kg as well.



Session Details:	EPoster Only
EPoster Details:	Helminth fauna of sheep from the northwestern region of the state of São Paulo, Brazil
Authors:	João Carlos Melo Pereira ¹ , Gustavo Felippelli ¹ , Welber Daniel Zanetti Lopes ¹ , Weslen Fabricio Pires Teixeira ¹ , Breno Cayeiro Cruz ¹ , Willian Giquelin Maciel ¹ , Carolina Buzzulini ¹ , Lucas Vinicius Shigaki de Matos ¹ , Flávia Carolina Fávero ¹ , Thais Rabelo dos Santos ¹ , Gilson Pereira de Oliveira ¹ , Alvimar José da Costa ^{1*} ¹ CPPAR - Animal Health Research Center - Faculdade de Ciências Agrárias e Veterinárias, UNESP, Via de acesso Prof. Paulo Donatto Castellane, s/nº, CEP: 14884-900, Jaboticabal, São Paulo – Brazil. +55 (16) 3202-1720.cppar@asbyte.com.br
Poster Number:	188

We evaluated the prevalence and intensity of parasitism of different species of helminths in sheep from the northwest region of São Paulo. Sixty-six naturally infected animals were necropsied, four to 36 months of age, reared in extensive, belonging to different properties in the area above. The results of necropsy revealed the presence of seven genera and 12 species with the following prevalence and average intensity of infection: *Haemonchus contortus*: 100.00% and 2947.20; *Trichostrongylus colubriformis*: 90.90% and 3048.82; *Cooperia curticei*: 256.52 and 56.06%; *Oesophagostomum columbianum*: 48.48% and 36.00; *Cooperia punctata*: 30.30% and 94.53; *Trichostrongylus axei*: 22.72% and 26.56; *Strongyloides papillosus*: 19.69% and 83.09; L4 stage of *H. contortus*: 7.58% and 17.29; *Cooperia pectinata*: 10.60% and 12.97; *Trichuris ovis*: 10.60% and 0.67; *Cooperia spatulata* 4.54% and 0.35, *Capillaria bovis*: 4.54% and 0.09. The parasite mean was 6524.77 per animal. *Haemonchus contortus* (adults and L4) and *Trichostrongylus colubriformis* corresponded to 45.43% and 46.73% of mean total of parasite load, respectively. We observe that 86.37% of sheep were infected with two to six helminth species. Only 9.09% of parasitized hosts showed up with seven or eight different species of helminths in your digestive tract. Additionally, six animals that were infected with seven or eight species of helminths contained a mean of *H. contortus* and *T. colubriformis* relatively minor when compared to other sheep diagnosed with a six species of nematodes. It can be concluded that the two species of helminths most frequent and abundant, in the region studied, were *Trichostrongylus colubriformis* and *Haemonchus contortus*, which accounted for 92.16% of total helminth diagnosed in 66 necropsied sheep.



Session Details:	EPoster Only
EPoster Details:	Aspects of Anaplasma marginale infection in cattle experimentally infected
Authors:	Gustavo Felippelli ¹ , Welber Daniel Zanetti Lopes ^{1*} , João Carlos Melo Pereira ¹ , Flavia Carolina Favero ¹ , Breno Cayeiro Cruz ¹ , Vando Edésio Soares ¹ , Thalita Silveira Righi ¹ , Lucas Vinicius Shigaki de Matos ¹ , Weslen Fabricio Pires Teixeira ¹ João Ricardo Martins ¹ ¹ CPPAR - Animal Health Research Center - Faculdade de Ciências Agrárias e Veterinárias, UNESP, Via de acesso Prof. Paulo Donatto Castellane, s/nº, CEP: 14884-900, Jaboticabal, São Paulo – Brazil. +55 (16) 3202-1720. cpar@asbyte.com.br ² Instituto de Pesquisas Desidério Finamor – IPVDF, Eldorado do Sul/RS.
Poster Number:	178

This study aimed to evaluate the clinical, hematological, parasitological aspects and the effectiveness of long-acting oxytetracycline against *Anaplasma marginale* in experimentally infected cattle. Six 10-month-old animals seronegative by indirect immunofluorescence reaction (IFAT) were obtained. On day -9 of the study, three animals were splenectomized, and on day zero all six animals were inoculated with about 1x10⁶ by *Anaplasma marginale* parasitized erythrocytes. Rectal temperature was measured from the 1st to the 35th day post-inoculation (DPI). The packed cell volume (VG - microhematocrit) and calculation of parasitemia was obtained from 10^o to 35^o DPI. The experimental animals received first pecific treatment (oxytetracycline LA) when they presented hyperthermia (≥39.2°C) and parasitemia ≥2.0%, and received new treatments until clinical and parasitological stabilization occurred. The results revealed that on 21^o DPI parasitemia was present in the six animals, and from this day on the VG decreased. Their rectal temperature reached ≥39.2°C from 23^o DPI on, when the parasitemia was on the rise. In general, the specific treatment against *A. marginale* had to be performed about three days after the haemoparasite is identified in the blood. The animals received one to four specific treatments against *A. marginale* to obtain clinical and parasitological stabilization. The parasite was not totally eliminated after the treatments. Based on the experimental model used in this study, one can conclude that the specific treatment required against *A. marginale* had to start about 72 hours after detection of the parasite on the cover slips. One to four treatments were required for clinical recovery of the animals and parasitological reduction of the infection. The incubation period for the disease was on average 21 days; however, this period may extend more, according to the amount of inoculum or the route of administration used to infect the cattle.

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Session Details:	EPoster Only
EPoster Details:	Aspects of infection by Babesia bigemina and Babesia bovis in cattle experimentally infected
Authors:	Carolina Buzzulini ¹ , Gustavo Felippelli ¹ , Flavia Carolina Favero ¹ , Breno Cayeiro Cruz ¹ , Thalita Silveira Righi ¹ , Welber Daniel Zanetti Lopes ^{1*} , Weslen Fabricio Pires Teixeira ¹ , Lucas Vinicius Shigaki de Matos ¹ , João Carlos Melo Pereira ¹ , João Ricardo Martins ¹ ¹ CPPAR - Animal Health Research Center - Faculdade de Ciências Agrárias e Veterinárias, UNESP, Via de acesso Prof. Paulo Donatto Castellane, s/nº, CEP: 14884-900, Jaboticabal, São Paulo – Brazil. +55 (16) 3202-1720. cppar@asbyte.com.br ² Instituto de Pesquisas Desidério Finamor – IPVDF, Eldorado do Sul/RS.
Poster Number:	179

The present study aimed to evaluate the clinical, hematological, parasitological, and the effectiveness of imidocarb dipropionate against *Babesia bigemina* and *Babesia bovis* in cattle experimentally infected. The temperature, packed cell volume (VG) and parasitemia were measured from 1 to 25 days post-inoculation (DPI). Cattle infected with *B. bigemina*, have showed hyperthermia from 9th to 11th DPI, while the fever peak, observed in four animals inoculated with *B. bovis* was the 7th to 11th DPI. In the remaining two animals, this hyperthermia occurred at 16 and 17 DPI. Cattle inoculated with *B. bigemina*, showed a drop in VG ($\pm 32\%$ to $\pm 22\%$) between the 9th to the 13th DPT. Only a slight decrease of VG was observed in animals infected with *B. bovis*. It was observed that the pre-patent period of *B. bigemina* was 6 to 9 days, while for *B. bovis* was 7 to 16 days post-inoculation. Forty-eight to 72 hours after administration of imidocarb, it was not possible view evolutive stage of *B. bigemina* and/or *B. bovis* in peripheral blood of animals. In summary, the pre-patent period of *Babesia bovis* and *B. bigemina* diagnosed in this study were 8 to 16 and 6 to 9 days, respectively. However, these periods may be different if these agents are transmitted by *Rhipicephalus (Boophilus) microplus*. It was shown also that a single administration of imidocarb was sufficient to eliminate these protozoa blood circulation, about 48-72 hours post treatment.





Session Details:	EPoster Only
EPoster Details:	Efficiency of sulfadoxine + trimethoprim compared to management measures for the control of Eimeria parasitism in naturally infected and clinically asymptomatic sheep that were maintained in a feedlot
Authors:	Rafael Silveira Carvalho, Welber Daniel Zanetti Lopes ¹ , Antonio Campanha Martinez ¹ , Breno Cayeiro Cruz ¹ , Valdomiro Pereira ¹ , Thalita Silveira Righi ¹ , Gabriel Henrique Campos Guse ¹ , Willian Giquelin Maciel ¹ , Weslen Fabricio Pires Teixeira ¹ , Gilson Pereira de Oliveira ¹ ¹ Universidade Estadual de Maringá (UEM) – Campus Regional de Umuarama-PR, Departamento de Medicina Veterinária,
Poster Number:	149

The efficiency of sulfadoxine + trimethoprim in comparison to management measures for the control of *Eimeria* parasitism was studied in naturally infected sheep that were raised in a feedlot. The groups were formed with 15 animals/group: T01, control animals that received saline solution and maintenance of the same management measures that were performed before the study; T02, two intramuscular doses of sulfadoxine (20 mg/kg) + trimethoprim (4 mg/kg) with a 14-day interval; T03, two intramuscular doses of sulfadoxine (20 mg/kg) + trimethoprim (4 mg/kg) with a 14-day interval plus management measures (wood shaving bedding was changed every Monday, and 30 g of ammonium sulfate were applied to the bedding and other facilities were performed every Thursday, 10 mL/20 L of water), and T04, animals that received only the management measures described for the previous group. The highest efficiency rates (arithmetic mean) for the T02 group (sulfadoxine + trimethoprim at days 0 and 14) were 21.04% and 21.98% on the 14th and 28th days after the first treatment (DAFT), respectively. However, the treatment showed efficiency rates below 17% and was totally ineffective from the 70th DAFT to the end of the study. In both the T03 (chemical treatment + management) and T04 (management only) groups, a significant ($P\leq0.05$) reduction of oocyst shedding per gram of feces was observed in the animals from the 14th DAFT in comparison to the control group; however, an efficiency rate above 90% was observed from the 28th DAFT. Thus, it is possible to conclude that the two-dose sulfadoxine + trimethoprim treatment, given with a 14-day interval, had little or no effect on the protozoan. Moreover, the adopted management measures were enough to cause a decrease in the ingestion of *Eimeria* sporulated oocysts by sheep, which consequently caused a significant decrease in the animal parasite loads.



Session Details:	EPoster Only
EPoster Details:	Survey of <i>Toxoplasma gondii</i> in the reproductive system of cats (<i>Felis catus domesticus</i>) experimentally infected (preliminary data)
Authors:	Weslen Fabricio Pires Teixeira ¹ , Julia Cestari Pierucci ¹ , André Cayeiro Cruz ¹ , Flávia Favero ¹ , Carolina Buzzilini ¹ , Gustavo Felippelli ¹ , Lucas Vinicius Shigaki de Matos ¹ , Willian Giquelin Maciel ¹ , Alvimar José da Costa ^{1*} ¹ CPPAR - Animal Health Research Center - Faculdade de Ciências Agrárias e Veterinárias, UNESP, Via de acesso Prof. Paulo Donatto Castellane, s/nº, CEP: 14884-900, Jaboticabal, São Paulo – Brazil. +55 (16) 3202-1720. cppar@asbyte.com.br
Poster Number:	153

The present study’s objective was to evaluate the elimination of *Toxoplasma gondii* in experimentally infected feline breeders. Six feline breeders were selected, all of which were serologically negative (IFAT) for *T. gondii*, and randomized in two groups (GI and GII). The first group (GI) was formed by four animals inoculated with 600 cysts originated from the encephalon of mice bearing toxoplasmosis (P strain) and the second group (GII) was formed by two animals inoculated with physiological solution. On the 7th, 14th, 28th, 42nd, 56th and 70th days after inoculation, all animals were anaesthetized with intramuscular administration of a Tiletamine + Zolazepam association (0.15 mL/kg) in order to collect blood samples (venipuncture) and semen samples (electroejaculation). All blood samples were centrifuged, in order to analyze the sera with IFAT. Semen samples collected from the felines were submitted to a *T. gondii* research, being one aliquot inoculated in mice (bioassay) after previous dilution in buffer solution (PBS) with a 7.2 pH, autoclaved and treated with antibiotics (ampicillin, 1 mg/mL). The remaining aliquot was used for the PCR analysis. All animals from the first group (GI) seroconverted (titles superior to 1:64) after the seventh or fourteenth days post-inoculation. None of the mice inoculated with the semen samples of experimental felines (both groups) tested positive for the presence of brain cysts of *T. gondii*. This test was conducted with the aid of optical microscopy or research of antibodies (IgG) against *T. gondii* (IFAT). With the aid of the PCR technique the DNA of the parasite was not identified in the semen samples collected from the feline breeders in different experimental dates. In short, the obtained results make possible to conclude that, unlike most species of domestic animals, cats do not eliminate *Toxoplasma gondii* in their semen.



Session Details:	EPoster Only
EPoster Details:	Occurrence of <i>Ancylostoma</i> spp. and <i>Toxocara canis</i> in dogs from Jaboticabal, state of São Paulo, Brazil
Authors:	Lucas Vinicius Shigaki de Matos ¹ , Flavia Carolina Favero ¹ , Thalita Silveira Righi ¹ , Lucas Costa Gomes ¹ , Carolina Buzzulini ¹ , Hurzana de Mello ¹ , João Carlos Melo Pereira ¹ , Willian Giquelin Maciel ¹ , Gilson Pereira de Oliveira ¹ , Alvimar José da Costa ^{1*} ¹ CPPAR - Animal Health Research Center - Faculdade de Ciências Agrárias e Veterinárias, UNESP, Via de acesso Prof. Paulo Donatto Castellane, s/nº, CEP: 14884-900, Jaboticabal, São Paulo – Brazil. +55 (16) 3202-1720. cppar@asbyte.com.br
Poster Number:	150

Ancylostomiasis and toxocariasis, responsible for hookworm and “visceral larva migrans” infections in humans, have dogs and cats as their definitive hosts, and have gained more importance throughout the world lately. The present study aimed to identify the occurrence of *Ancylostoma* spp. and *Toxocara* spp. in dogs originated from the region of Jaboticabal, state of São Paulo, Brazil. Twenty-six dogs that came to death were selected, based on the counts of eggs per gram of feces (EPG), from municipal kennels in the regions. The animals were also classified according to age: sixteen of them were less than three months old, and ten were more than four months old. The helminthological results in dogs older than four months revealed the following occurrence and amplitude of nematodes: *Ancylostoma caninum* (80% - 0-95), *Ancylostoma braziliense* (80% - 0-19) and *Toxocara canis* (40% - 0-17). For dogs under three months old, the following frequency and amplitude was observed: *A. caninum* (56.25% - 0-113), *A. braziliense* (50% - 0-13), *T. canis* (81.25% - 0-119). Based on the results obtained in this study, it is possible to conclude that, even though *Ancylostoma* spp. and *Toxocara canis* were found in animals from both ages described in this research, a higher prevalence of *Ancylostoma* spp. Was observed in dogs older than four months and *Toxocara canis* was more frequent in animals with less than three months of age.





Session Details:	EPoster Only
EPoster Details:	Helminthic fauna of cats from the northwestern region of the state of São Paulo, Brazil
Authors:	Willian Giquelin Maciel ¹ , Gustavo Felippelli ¹ , Weslen Fabricio Pires Teixeira ¹ , Thalita Silveira Righi ¹ , Lucas Costa Gomes ¹ , Carolina Buzzulini ¹ , Hurzana de Mello ¹ , João Carlos Melo Pereira ¹ , Gilson Pereira de Oliveira ¹ , Alvimar José da Costa ^{1*} ¹ CPPAR - Animal Health Research Center - Faculdade de Ciências Agrárias e Veterinárias, UNESP, Via de acesso Prof. Paulo Donatto Castellane, s/nº, CEP: 14884-900, Jaboticabal, São Paulo – Brazil. +55 (16) 3202-1720. cppar@asbyte.com.br
Poster Number:	151

The present study had as its objective the evaluation of the prevalence and parasitism intensity of different helminth species in cats originated from the region of Jaboticabal, northwestern of the state of São Paulo. To achieve this, 14 animals, males and females, naturally infected, with ages ranging from four to 36 months, which eventually died from varied causes, were used. The necroscopic results revealed the presence of four genres and five species of helminths, with the following prevalence and mean intensity of infection: *Ancylostoma tubaeforme* (28.57% - 1.90); *Ancylostoma brazilienses* (64.28% - 13.10); *Toxocara cati* (21.42% - 2.10); *Dipylidium caninum* (28.57% - 10.80) and *Physaloptera praeputialis* (21.42% - 2.40). The total parasite load found in the 14 animals was of 425 helminths, with an average load of 6.10 parasites per animal. *Ancylostoma braziliense* and *Dipylidium caninum* corresponded to 43.10% and 35.50% of the total parasite load, respectively. It was observed that 57.14% of the animals (eight cats) were infected by only one helminth specie. Three other animals (21.42%) were parasitized with two helminth species and the remaining cats (21.42%) presented three different helminth species. Based on the results obtained, it is possible to conclude that the most frequent helminth specie in cats from the region of Jaboticabal, São Paulo, is *A. braziliense*, followed by *D. caninum* and *A. tubaeforme*. These three species totaled 84.90% of the helminths diagnosed in domestic felines.



Session Details:	EPoster Only
EPoster Details:	Prevalence and intensity of endoparasites infections in equines from Brazil
Authors:	Weslen Fabricio Pires Teixeira ¹ , Gustavo Felippelli ¹ , Breno Cayeiro Cruz ¹ , Willian Giquelin Maciel ¹ , Lucas Vinicius Shigaki de Matos ¹ , João Carlos Pereira, Welber Daniel Zanetti Lopes ¹ , Carolina Buzulini ¹ , Gilson Pereira de Oliveira ¹ , Alvimar José da Costa ^{1*} ¹ CPPAR - Animal Health Research Center - Faculdade de Ciências Agrárias e Veterinárias, UNESP, Via de acesso Prof. Paulo Donatto Castellane, s/nº, CEP: 14884-900, Jaboticabal, São Paulo – Brazil. +55 (16) 3202-1720. cppar@asbyte.com.br
Poster Number:	152

The objective of this study was to evaluated the helminthic fauna of equines from the Center-West region of the Minas Gerais state, 25 animals, bearing an infection greater than 500 eggs per gram of feces (EPG) were selected. By means of parasitological necropsies and collection of the specimens present in the digestive tract with the aid of a stereomicroscope, all helminths were, posteriorly, identified by optical microscopy, allowing the classification of twelve species, as well as the Cyathostominae sub-family. This last group presented higher incidence, followed by *Trichostrongylus axei*, *Oxyuris equi*, *Triodontophorus serratus*, *Strongyloides westeri*, *Strongylus edentatus*, *Habronema muscae*, *Parascaris equorum*, *Probstmayria vivípara*, *Strongylus vulgaris*, *Gasterophilus nasalis*, *Anoplocephala magna* and *Anoplocephala perfoliata*. In the present study, if we do not consider the *Probstmayria vivipara* in the prevalence, a benign specie of helminth for horses, the frequency of Cyathostominae family is equivalent as 94,85%. This research allowed to detect and identify different helminth species in equines, as well as to confirm the huge diversity and occurrence of helminthic infections in horses from Brazil, specially the higher prevalence of Cyathostominae family. Besides, it was possible to consider this family one of the most important in equines, from an epidemiological and clinical point of view.





Session Details:	EPoster Only
EPoster Details:	Poisoning of sheep that received two applications of closantel in therapeutic dosage (7.5 mg/kg), with an interval of 28 days
Authors:	Rafael Silveira Carvalho, Gustavo Felippelli ¹ , Antonio Canpanha Martinez ¹ , Welber Daniel Zanetti Lopes ^{1*} , Valdomiro Pereira ¹ , Weslen Fabricio Pires Teixeira ¹ , Breno Cayeiro Cruz ¹ , Willian Giquelin Maciel ¹ , Gabriel Henrique Campos Guse ¹ , Maycon Araujo Ruivo ¹ , Walter Antonio G. Junior ¹ ¹ Universidade Estadual de Maringá (UEM) – Campus Regional de Umuarama-PR, Departamento de Medicina Veterinária, wdzlopes@hotmail.com
Poster Number:	210

This study notifies the poisoning of sheep receiving two applications of closantel in therapeutic dosage (7.5 mg/kg) at intervals of 28 days. The interval between applications was predetermined by the efficacy of the formulation used. Referring to the results of effectiveness was observed high percentage (above 90% - arithmetic means) after the first and second treatment. Approximately 72 hours after administration of the second dose (D +30), three animals that received a second dose of closantel showed mild depression, anorexia, diarrhea and bilateral blindness and with no reaction pupils were dilated. For reasons of animal welfare, and based of knowing the history of animals in this study, coupled with several reports regarding the clinical poisoning of domestic animals by closantel, we chose not to sacrificing the three animals to perform autopsies. But, in another hand, these three sheep were observed for about 250 days after the second administration of the treatment, and bilateral blindness not regressed. The numerous reports of animals poisoned by closantel in literature emphasize that overdose and / or nutritional status of the animals, are determining factors for the occurrence of poisoning animals, from administration closantel. However, in the present work, the signs of intoxication (mild depression, anorexia, diarrhea and ophthalmic) observed in the three clinically healthy sheep, occurred when they received two applications closantel (7.5 mg/kg), with the interval of 28 days , highlighting the fact that performing two treatments in therapeutic dosage, with the interval of one month between them, can also be a predisposing factor for sheep to demonstrate irreversible signs of intoxication active principle in question.



Session Details:	EPoster Only
EPoster Details:	Acute poisoning by triclofon in goats given a therapeutic dose
Authors:	Welber Daniel Zanetti Lopes ^{1*} , Rafael Silveira Carvalho ¹ , Antonio Campanha Martinez ¹ , Breno Cayeiro Cruz ¹ , Carolina Buzzulini ¹ , Hurzana de Mello ¹ , Walter Antonio G. Junior ¹ , Valdomiro Pereira ¹ , João Carlos Pereira ¹ , Lucas Vinicius Shigaki de Matos ¹ , Willian Giquelin Maciel ¹ ¹ CPPAR - Animal Health Research Center - Faculdade de Ciências Agrárias e Veterinárias, UNESP, Via de acesso Prof. Paulo Donatto Castellane, s/nº, CEP: 14884-900, Jaboticabal, São Paulo – Brazil. +55 (16) 3202-1720. cppar@asbyte.com.br
Poster Number:	210

The present study describes an outbreak of trichlorfon poisoning in goats, that received orally, the therapeutic dosage of this active ingredient (100mg/kg), from the State University of Maringa, campus of Umuarama/PR. Of the 20 goats medicated, about 40 minutes after administration of trichlorfon, eight had the classic clinical signs of ataxia, external lateral decubitus, drooling, tremors, contraction pupils, dyspnea noisy, involuntary urination and defecation, spastic paresis, bloat and tearing. Almost immediately after the detection of these signals, the eight goats were medicated with 1% atropine sulfate 0.5 mg/kg more fluid-therapy. Five of these animals had received new dose of atropine sulfate hour after the first administration on the basis of some clinical signs, such as muscle tremor, still being present. 48 to 72 hours after administration of trichlorfon, three of the five animals died. At necropsy, were observed cyanotic mucous membranes, congestion of liver, spleen and kidneys, mesenteric vessels congested, filled gallbladder, emphysema, lung parenchyma reddish. The results of this study draws attention to the outbreak occurred in adult goats that had good clinical conditions and, above all, they received the therapeutic dosage recommended by the manufacturer label. These results may indicate higher sensitivity of this species to triclofon even at therapeutic dose.



Session Details:	EPoster Only
EPoster Details:	Aspects of <i>Toxoplasma gondii</i> infection on clinical parameters of dogs, cats, pigs, cattle, sheep and goats adults experimentally infected
Authors:	Lucas Vinicius Shigaki de Matos ¹ João Carlos Melo Pereira ¹ , Gustavo Felippelli ¹ , Weslen Fabricio Pires Teixeira ¹ , Breno Cayeiro Cruz ¹ , Willian Giquelin Maciel ¹ , Carolina Buzzulini ¹ , Welber Daniel Zanetti Lopes ¹ , Flávia Carolina Fávero ¹ , Alvimar José da Costa ^{1*} ¹ CPPAR - Animal Health Research Center - Faculdade de Ciências Agrárias e Veterinárias, UNESP, Via de acesso Prof. Paulo Donatto Castellane, s/nº, CEP: 14884-900, Jaboticabal, São Paulo – Brazil. +55 (16) 3202-1720. cppar@asbyte.com.br
Poster Number:	180

This study aimed to evaluate the effect of *Toxoplasma gondii* infection on clinical parameters (rectal temperature, heart rate and breathing), as well as the general physical appearance, behavior and appearance of the feces of adults dogs, cats, pigs, cattle, sheep cousin and goats infected with 2x10⁵ P strain oocysts by oral or subcutaneously with 1x10⁶ tachyzoites of the RH strain of *T. gondii*. In all experiments, one group was kept as a control. Periodically until the 70th day post-inoculation (DPI), were measured clinical parameters, clinical appearance usually described above, and the presence of the parasite by indirect immunofluorescence assay (IFA). All infected animals seroconverted to toxoplasmosis (IFA). Among the eight dogs and four cats inoculated, hyperthermia was observed on the 7th DPI and loose stools at 6 DPI, respectively. In the six experimentally infected pigs, was not observed any change in clinical animals that could be attributed *T. gondii*. Already the 16 cattle positive for toxoplasmosis demonstrated hyperthermia between 3 and 16 DPI, whereas in small ruminants (sheep and goats), besides hiepertermia and loose stools detected in infected animals between 3 and 11 DPI, these also were apathetic during that period. Strains RH and P were responsible by the clinical alterations in dogs and cats, respectively. In cattle there was no difference between the strains in relation to clinical parameters demonstrated by animals. Already in sheep and goats strain P was responsible for the clinical changes observed in these animal species. Based on the results, and the animal species used, it can be concluded that the primary infection with *Toxoplasma gondii* can trigger clinical hyperthermia, loose stools and apathy in these animals in the first three weeks after exposure to parasite in question, which in turn, field causes this important zoonosis go unnoticed by producers and/or veterinarians.



Session Details:	EPoster Only
EPoster Details:	Predilection sites of parasitism by larvae of <i>Dermatobia hominis</i> in naturally infested cattle from Brazil
Authors:	Flávia Favero ¹ , Gustavo Felippelli ¹ , João Carlos Pereira ¹ , Carolina Buzzilini ¹ , Welber Daniel Zanetti Lopes ¹ , Hurzana de Mello ¹ , Breno Cayeiro Cruz ¹ , Lucas Vinicius Shigaki de Matos ¹ , Willian Giquelin Maciel ¹ , Lucas Costa Gomes ¹ , Alvimar José da Costa ^{1**} ¹ CPPAR - Animal Health Research Center - Faculdade de Ciências Agrárias e Veterinárias, UNESP, Via de acesso Prof. Paulo Donatto Castellane, s/nº, CEP: 14884-900, Jaboticabal, São Paulo – Brazil. +55 (16) 3202-1720. cppar@asbyte.com.br
Poster Number:	157

The larvae of *Dermatobia hominis* (botfly), is an ectoparasite of huge importance in cattle industry, being responsible for initiating a furuncular myiasis (dermatobiosis) in several animal species, including humans. 3624 bovines were examined, originating from 16 rural properties from the states of Minas Gerais and São Paulo. Among these animals, 363 bovines, naturally infested by these larvae were selected (at least six nodules each), seeking to evaluate the frequency and predilection sites of the larvae in 15 anatomical regions of the animal's body: head, neck, scapula, arm-forearm, carpus-metacarpus-phalange, back, costal, chest, abdomen side, ventral, sacrum, femoral, leg, tarsus-metatarsus and interscapular. Counts of nodules containing larvae were conducted using moderate compression (tactile-visual inspection). A review was filled representing the distribution of the larvae in each animal. 6507 *D. hominis* larvae were quantified, distributed over the entire body surface of the bovines. The site with the highest parasite count was the scapula with 2298 nodules (35.32%), followed by the back: 2121 nodules (32.6%), costal: 577 (8.87%), arm-forearm: 543 (8.34%), neck: 326 (5.01%), abdomen side: 214 (3.29%) sacrum: 210 (3.23%), femoral: 72 (1.11%), chest: 53 (0.82%), leg: 34 (0.52%), carpus-metacarpus-phalange: 25 (0.38%) ventral: 15 (0.23%), head: 13 (0.19%), interscapular: 6 (0.09%) and tarsus-metatarsus which presented no nodules. There was no significant difference ($P \leq 0.05$) in the total number of nodules containing larvae when the right and left sides of the animal's bodies were compared (3309 – 50.85% and 3198 – 49.15%, respectively). It is possible to conclude that the highest incidence of nodules containing larvae of *Dermatobia hominis* was found in the scapula and back of the animals (67.90%) when compared to the posterior side of their bodies. This could be related, possibly, to the fact that the animal's tail can't reach the anterior portion of its body in order to protect itself against phoretic dipterous.





Session Details:	EPoster Only
EPoster Details:	Survey of <i>Toxoplasma gondii</i> in the reproductive system of cats (<i>Felis catus domesticus</i>) experimentally infected (preliminary data)
Authors:	Weslen Fabricio Pires Teixeira ¹ , Julia Cestari Pierucci ¹ , André Cayeiro Cruz ¹ , Flávia Favero ¹ , Carolina Buzzilini ¹ , Gustavo Felippelli ¹ , Lucas Vinicius Shigaki de Matos ¹ , Willian Giquelin Maciel ¹ , Alvimar José da Costa ^{1*} ¹ CPPAR - Animal Health Research Center - Faculdade de Ciências Agrárias e Veterinárias, UNESP, Via de acesso Prof. Paulo Donatto Castellane, s/nº, CEP: 14884-900, Jaboticabal, São Paulo – Brazil. +55 (16) 3202-1720. cppar@asbyte.com.br
Poster Number:	153

The present study’s objective was to evaluate the elimination of *Toxoplasma gondii* in experimentally infected feline breeders. Six feline breeders were selected, all of which were serologically negative (IFAT) for *T. gondii*, and randomized in two groups (GI and GII). The first group (GI) was formed by four animals inoculated with 600 cysts originated from the encephalon of mice bearing toxoplasmosis (P strain) and the second group (GII) was formed by two animals inoculated with physiological solution. On the 7th, 14th, 28th, 42nd, 56th and 70th days after inoculation, all animals were anaesthetized with intramuscular administration of a Tiletamine + Zolazepam association (0.15 mL/kg) in order to collect blood samples (venipuncture) and semen samples (electroejaculation). All blood samples were centrifuged, in order to analyze the sera with IFAT. Semen samples collected from the felines were submitted to a *T. gondii* research, being one aliquot inoculated in mice (bioassay) after previous dilution in buffer solution (PBS) with a 7.2 pH, autoclaved and treated with antibiotics (ampicillin, 1 mg/mL). The remaining aliquot was used for the PCR analysis. All animals from the first group (GI) seroconverted (titles superior to 1:64) after the seventh or fourteenth days post-inoculation. None of the mice inoculated with the semen samples of experimental felines (both groups) tested positive for the presence of brain cysts of *T. gondii*. This test was conducted with the aid of optical microscopy or research of antibodies (IgG) against *T. gondii* (IFAT). With the aid of the PCR technique the DNA of the parasite was not identified in the semen samples collected from the feline breeders in different experimental dates. In short, the obtained results make possible to conclude that, unlike most species of domestic animals, cats do not eliminate *Toxoplasma gondii* in their semen.



Session Details:	EPoster Only
EPoster Details:	Correlation between the level of helminth infection and eosinophil counts in sheep
Authors:	Maycon Araújo Ruivo ¹ , Gabriel Henrique Campos Guse ¹ , Welber Daniel Zanetti Lopes ^{1*} , Raquel Reis Martins ¹ , Jefferson Leonardo Rocha Alves ¹ , Walter Antônio G. Junior ¹ , Mara Lucia Gravinatti Delgado ¹ , Ana Cristina Zavala Bortolozzo ¹ , Valdomiro Pereira ¹ , Antônio Campanha Martinez ¹ , Gisela Ferraro ¹ , Joaquim Moleirinho ¹ ¹ Universidade Estadual de Maringá (UEM) – Campus Regional de Umuarama-PR, Departamento de Medicina Veterinária, wdzlopes@hotmail.com
Poster Number:	182

Generally, the literature describes that animal with high helminth loads, commonly demonstrated eosinophilia in laboratory tests. The present study aimed to investigate the correlation between the parasitism of gastrointestinal nematodes in sheep naturally infected, untreated more than 90 days, raised to pasture, to the level of eosinophils in the blood of these animals. For this study, 62 stool samples were collected directly from the rectum, and the sequence subjected to quantification of strongyle type eggs, the technique of egg counts per gram of feces (EPG). Animals with EPG between 0 and 450 were considered with a parasite load low or medium, EPG with sheep while over 500 were considered to have a high burden of gastrointestinal nematodes. Concomitantly of the collection feces, blood samples were obtained from these animals for eosinophil count from each sheep. The results were submitted to correlation analysis and Student's T test, 5% significance level. Of the 62 animals involved in the study, 33 contained low / medium parasitism (EPG 0 - 450) and the remaining 29 a high parasite load (EPG 550-13000). Based on the results assessed by Pearson correlation and the T test, was found a negative correlation (-0.3326050) between the results of EPG and eosinophil for animals with low / medium level of helminth infection, in other words, a high eosinophils has been found in animals showed EPG between 0 and 450 (P = 0.0083). No correlation was observed (-0.34011400) between these two variables, for animals with high parasite load (P = 0.1816). This fact may be assigned, probably, to a greater immune response of animals with low levels of EPG, which in turn produce more eosinophils to combat these helminth infections.



Session Details:	EPoster Only
EPoster Details:	Correlation between the level of helminth infection and hematocrit values in sheep
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This study aimed to investigate the correlation between the parasitism of gastrointestinal nematodes in sheep naturally infected, untreated more than 90 days, raised to pasture, to the level of hematocrit (%) in the blood of these animals. Sixty-two stool samples were collected directly from the rectum, and the sequence subjected to quantification of strongyle eggs, the technique of egg counts per gram of feces (EPG). A pool of stool samples underwent culture technique larvae (fecal culture) to diagnose the genera of helminths in these animals. Concomitantly of the collection of feces, blood samples were obtained from these animals for calculating the hematocrit from each sheep. The results were submitted to correlation analysis and Student's T test, 5% significance level. Of the 62 animals involved in the study, 33 contained low / medium parasitism (OPG 0-450) and the remaining 29 harbored a high parasite load (EPG 550-13000). Pool of stool specimens were diagnosed infective larvae (L3) of *Haemonchus* (48.8%), *Trichostrongylus* (24.3%), *Oesophagostomum* (24.1%), *Cooperia* (1.7%) and *Strongyloides* (1.1%). Based on the results assessed by Pearson correlation and the T test, was found a negative correlation (-0.3726756) between the results of EPG and the percentage of hematocrit for animals with high level of helminth infection, in other words, a low hematocrit value ($\pm 25.56\%$) was found in animals which showed EPG between 550 and 13 000 ($P = 0.0028$) as compared to hematocrit values of animals with low helminth infection ($\pm 30.97\%$; 0, 1210518, $P = 0.5093$). This can be attributed to the higher prevalence of genus *Haemonchus* diagnosed in the herd, since these helminths show hematophagism, which in turn may reflect a lower hematocrit percentage of animals with high helminth infection.