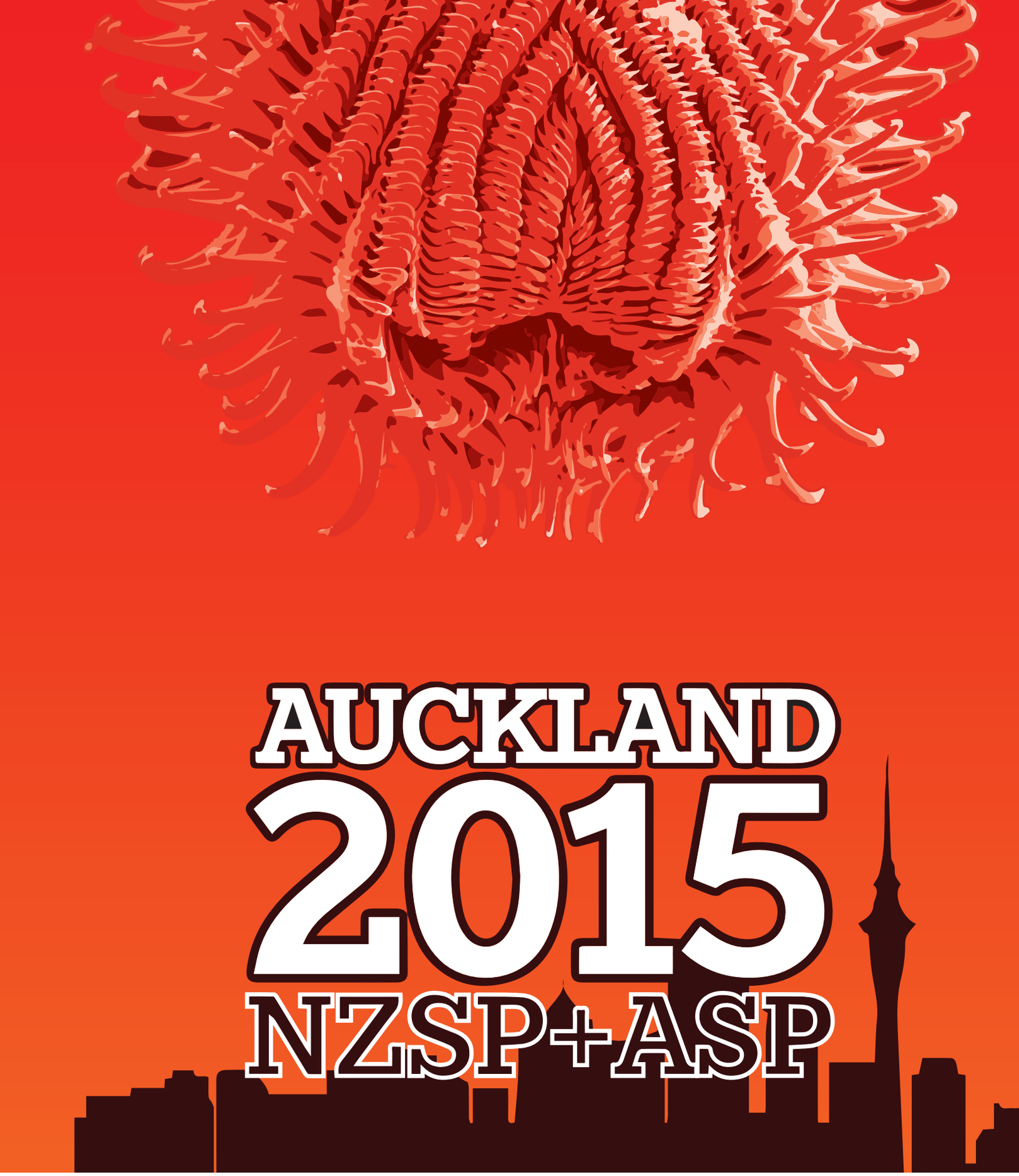

AUCKLAND 2015 NZSP+ASP

Joint Conference of the New Zealand and Australian Societies for Parasitology

Crowne Plaza Auckland, New Zealand, June 29 – July 2, 2015

The Australian Society for Parasitology Inc.

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The ASP and the NZSP acknowledge the generous support of Elsevier Parasitology, the International Journal for Parasitology, IJP: DDR, IJP:PAW, Virbac Animal Health Australia, Bayer Animal Health, Zoetis, New Zealand Veterinary Pathology Ltd, Elanco, Gribbles Veterinary, Merial, PGG Wrightson and New England BioLabs Inc.,who are supporting this conference.

2015 Joint Conference of the New Zealand Society for Parasitology and the Australian Society for Parasitology Inc.

June 29 – July 2, Crowne Plaza Auckland, New Zealand

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2015 Joint Conference of the New Zealand Society for Parasitology and the Australian Society for Parasitology Inc.

June 29 – July 2, Crowne Plaza Auckland, New Zealand

Welcome from the NZSP and ASP and the Conference Organising Committee

Dear Colleague,

On behalf of the NZSP and ASP Councils and the 2015 Conference Organising Committee, we extend a warm welcome to the 2015 NZSP & ASP Annual Conference.

This conference, hosted jointly by the New Zealand Society for Parasitology and Australian Society for Parasitology, celebrates the best Australian and New Zealand parasitology research and the programme includes an outstanding mix of quality international, New Zealand and Australian scientists.

The Conference, at Crown Plaza Auckland, will begin Monday 29 June and culminate, with our Conference Banquet, on Thursday 2 July. We will be holding a special symposium *Marine Parasitology & Aquaculture: Attribute to Associate Professor Ian Whittington* on the first morning of the conference.

The success of our conference is, as always, dependent on our supporters and we would like to thank sincerely the following organisations for their generous support; **Elsevier Parasitology, the International Journal for Parasitology, IJP: DDR, IJP: PAW, Virbac Animal Health Australia, Bayer Animal Health, Zoetis, New Zealand Veterinary Pathology Ltd, Elanco, Gribbles Veterinary, Merial, PGG Wrightson and New England BioLabs Inc**., who are supporting this conference.

We also would like to thank you, the NZSP and ASP Membership, for supporting our Societies and this joint Conference so enthusiastically.

Dr Victoria Chapman
President, NZSP

Prof. Robin Gasser
President, ASP

2015 Joint Conference of the New Zealand Society for Parasitology and the Australian Society for Parasitology Inc.

June 29 – July 2, Crowne Plaza Auckland, New Zealand

Programme

Date: Monday, 29/Jun/2015	
5:00pm - 7:00pm	**Welcome Reception**
ARIA Restaurant	Session Chair: **Victoria Chapman**, Zoetis Conference delegates are invited to Welcome Drinks in Aria Restaurant & Bar Auckland in the ground floor of the Crowne Plaza, Auckland.
Date: Tuesday, 30/Jun/2015	
7:00am - 9:00am	**Early Career Researchers and Students Breakfast Event**
Plenary Room	Session Chair: **Nick Smith**, James Cook University
9:00am - 10:30am	**Opening Plenary**
Plenary Room	Session Chair: **Victoria Chapman**, Zoetis Session Chair: **Robin Gasser**, University of Melbourne NZSP Presidential Address ASP Presidential Address Presentation of ASP Fellowship
10:30am - 11:00am	**Morning Tea Tuesday**
Foyer	
11:00am - 11:30am	**Symposium 1: Marine Parasitology & Aquaculture 1: A Tribute to Ian Whittington**
Plenary Room	Session Chair: **Lesley Warner**, South Australian Museum **Economic impact of aquatic parasites on Asian and global mariculture** **Andrew P. Shinn[1,2], Jarunan Pratoomyot[3], James E. Bron[2], Giuseppe Paladini[2], Esther E. Brooker[2], Adam J. Brooker[2]** [1]Fish VetGroup Asia Limited, Bangkok, Thailand; [2]Institute of Aquaculture, University of Stirling, Stirling, United Kingdom; [3]Institute of Marine Science, Burapha University, Chonburi, Thailand
11:30am - 12:30pm	**CP 1: Marine Parasitology & Aquaculture 1 Contributed Papers**
Plenary Room	Session Chair: **Lesley Warner**, South Australian Museum **Five intriguing facts about the harmful fish ectoparasite *Neobenedenia* sp.** **Kate Suzanne Hutson[1], Alexander Karlis Brazenor[1], Terry Bertozzi[2,3], Terry L. Miller[1], Alejandro Trujillo-González[1], Truong Dinh Hoai[1,4], Thane Austin Militz[1], Ian David Whittington[2]** [1]James Cook University, Australia; [2]The South Australian Museum, Australia; [3]University of Adelaide, Australia; [4]Vietnam National University of Agriculture, Vietnam **Avoidance behaviours of Atlantic salmon (*Salmo salar*) to the ectoparasitic sea lice (*Lepeophtheirus salmonis*)** **S. Bui[1], F. Oppedal[2], T. Dempster[1]** [1]Sustainable Aquaculture Laboratory – Temperate and Tropical, School of BioSciences, University of Melbourne, Australia; [2]Institute of Marine Research, Matredal 5984, Norway **Diversity and effects of digenean trematodes in rocky shore snails: it sucks (less) to have parasites!** **Katie O'Dwyer, Robert Poulin** University of Otago, New Zealand **Occurrence and abundance of zoonotic parasites in selected edible fish from an Australian fish market** **Jaydipbhai Rameshbhai Suthar, Shokoofeh Shamsi** Charles Sturt University, Australia
12:30pm - 1:30pm	**Lunch Tuesday supported by Bayer Animal Health**
ARIA Restaurant	

1:30pm - 2:00pm Symposium Room 1	**Symposium 2: Diagnostics, Detection and Control 1** Session Chair: **Harsha Sheorey**, St Vincent's Hospital, Melbourne **Jetsumon Prachumsri** [1] [1]Mahidol University, Thailand
1:30pm - 2:00pm Symposium Room 2	**Symposium 3: Marine Parasitology & Aquaculture 2** Session Chair: **Kate Hutson**, James Cook University **Parasite source-sink dynamics of giant squid** **Haseeb Sajjad Randhawa** University of Otago, New Zealand
2:00pm - 3:00pm Symposium Room 1	**CP 2: Diagnostics, Detection and Control 1 Contributed Papers** Session Chair: **Harsha Sheorey**, St Vincent's Hospital, Melbourne **Insights into the relationship between blood stage immunity, multiclonal infection, and subsequent clinical outcome.** **Mykola Pinkevych[1], Janka Petravic[2], Sandor Bereczky[3,4], Ingeger Rooth[3], Ann Färnert[3], Miles Davenport[1]** [1]University of New South Wales, Australia; [2]University of Sydney, Australia; [3]Karolinska Institutet, Sweden; [4]Public Health Agency of Sweden **Multiplex real-time PCR monitoring of intestinal helminths in humans reveals widespread polyparasitism in Northern Samar, the Philippines** **Catherine Gordon[1,2], Donald McManus[1], Luz Acosta[3], Remigio Olveda[3], Gail Williams[2], Allen Ross[4], Darren Gray[1,2,5], Geoffrey Gobert[1]** [1]QIMR Berghofer Medical Research Institute, Australia; [2]Discipline of Epidemiology and Biostatistics, School of Population Health, University of Queensland; [3]Department of Immunology, Research Institute of Tropical Medicine, Philippines; [4]Griffith Health Institute, Griffith University; [5]Research School of Population Health, Australian National University **Potential Complications Associated With the Clinical Management of Chagas Disease** **Catherine Perez, Alan Lymbery, RC Andrew Thompson** Murdoch University, Australia **Detection of Cell Free Parasite DNA (CFPD) in human clinical samples as an improved method of diagnosis and evaluation of *Schistosoma japonicum* infection** **Kosala Gayan Weerakoon[1,2,3], Geoffrey Gobert[1], Pengfei Cai[1], Donald McManus[1]** [1]QIMR Berghofer Medical Research Institute; [2]School of Public Health, University of Queensland; [3]Faculty of Medicine and Allied Sciences, Rajarata University of Sri Lanka
2:00pm - 3:00pm Symposium Room 2	**CP 3: Marine Parasitology & Aquaculture 2 Contributed Papers** Session Chair: **Kate Hutson**, James Cook University **Clam (*Austrovenus stutchburyi*) parasite loading in an environment modified by commercial harvesting** **Sorrel O'Connell-Milne** Otago University, New Zealand **How important is host diet for parasite interactions in sharks? Exploring the influence of taxonomic diet breadth on shark tapeworm diversity** **Trent Kevin Rasmussen, Haseeb Sajjad Randhawa** University of Otago, New Zealand **Recommended method of fish examination for infection with anisakid larvae** **Shokoofeh Shamsi, Jaydpbhai Suthar** Charles Sturt University, Australia **Evidence of a cryptic complex of species of *Hamacreadium*, Linton, 1910 (Trematoda: Opecoelidae) and a redefinition of the genus taxonomy, host specifity and composition** **Storm B. Martin[1], Scott C. Cutmore[1], Terrence L. Miller[2], Thomas H. Cribb[1]**

	[1]University of Queensland, Australia; [2]James Cook University, Australia
3:00pm - 3:30pm	**Afternoon Tea Tuesday supported by Elanco**
Foyer	
3:30pm - 4:00pm	**Symposium 4: Protozoan Biology 1** Session Chair: **Katharine Trenholme**, QIMR Berghofer Medical Research Institute
Symposium Room 1	**Ion homeostasis in the malaria parasite: a vulnerable drug target** **Adele M. Lehane, Melanie C. Ridgway, Adelaide S.M. Dennis, James E.O. Rosling, Kiaran Kirk** Australian National University, Australia
3:30pm - 4:00pm	**Symposium 5: Ectoparasites** Session Chair: **Tania Waghorn**, AgResearch
Symposium Room 2	**Investigating the biological roles of scabies mite cysteine proteases and their potential as drug targets** **Simone Louise Reynolds[1], Robert Pike[2], Katja Fischer[1]** [1]QIMR Berghofer Medical Research Institute, Australia; [2]La Trobe University, Australia
4:00pm - 5:00pm	**CP 4: Protozoan Biology 1 Contributed Papers** Session Chair: **Katharine Trenholme**, QIMR Berghofer Medical Research Institute
Symposium Room 1	**Unravelling the molecular systematics of the piroplasms** **Andrea Paparini, Una M. Ryan, Peter J. Irwin** Vector- and Water-Borne Pathogen Research Group, School of Veterinary & Life Sciences, Molecular and Biomedical Sciences, Murdoch University, Australia **Investigating the functional roles of malaria parasite histone deacetylases** **Jessica Engel[1,2], Tina Skinner-Adams[1], Jeffrey Gorman[2], Kathy Andrews[1]** [1]Eskitis Institute for Drug Discovery, Australia; [2]QIMR Berghofer Medical Research Institute, Australia **Characterising the extracellular proteinases in the secretome of *Tritrichomonas foetus* bovine and feline genotypes** **Leah Stroud[1], John Dalton[2], Colin Stack[1]** [1]University of Western Sydney, Australia; [2]Queen's University Belfast, United Kingdom **Investigation of the export pathway of *Plasmodium* parasites utilising small molecule inhibitors of plasmepsin V** **Michelle Gazdik[1,2], Brad E. Sleebs[1,2], Sash Lopaticki[1,2], Matthew T. O'Neill[1,2], Pravin Rajasekaran[1,2], Anthony N. Hodder[1,2], Peter Czabotar[1,2], Kym N. Lowes[1,2], Brian J. Smith[3], Alan F. Cowman[1,2], Justin A. Boddey[1,2]** [1]The Walter and Eliza Hall Institute of Medical Research, Australia; [2]The University of Melbourne, Australia; [3]La Trobe University, Australia
4:00pm - 5:00pm	**CP 5: Ectoparasites Contributed Papers** Session Chair: **Tania Waghorn**, AgResearch
Symposium Room 2	**Immunohistological localisation of scabies mite inactivated cysteine protease paralogues (SMIPP-Cs)** **Waduge Deepani Darshika Fernando, Simone Reynolds, Katja Fischer** Infectious Diseases Department, QIMR Berghofer Medical Research Institute, Australia **Identification of potential endosymbionts in the scabies mite *Sarcoptes scabiei*** **Emily Lau[1], Pearl Swe[1], Rebecca S Waddell[1], Martha Zakrzewski[1], Lutz Krause[2], Katja Fischer[1]** [1]Infectious Diseases Programme, Biology Department, QIMR Berghofer Medical Research Institute, Australia; [2]Translational Research Institute, Australia **A link between scabies mites and *Streptococcus pyogenes* towards host invasion** **Pearl Swe, Lindsay Christian, Kadaba Sri Sriprakash, Katja Fischer** QIMR Berghofer Medical Research Institute, Australia **Phylogenetic analysis of the Australian paralysis ticks and their relatives (*Ixodes (Sternalixodes)*: Ixodidae)** **Mackenzie Lamont Kwak[1], Ian Beveridge[1], Anson Koehler[1], Mali Malipatil[2], Robin Gasser[1], Abdul Jabbar[1]**

	[1]Faculty of Veterinary and Agricultural Sciences, The University of Melbourne, Australia; [2]Biosciences Research, AgriBio, Department of Economic Development, Jobs, Transport & Resources, Australia
5:00pm - 5:30pm	**Pre-poster night drinks**
Foyer	
5:30pm - 6:30pm	**Poster 1: Oral Presentations** Session Chair: **Malcolm Jones**, University of Queensland
Plenary Room	**Investigation into the presence of anthroponotic *Cryptosporidium* sp. in wild and captive Australian grey-headed flying fox (*Pteropus poliocephalus*) populations** **Sabine Eva Schiller, Koa Webster, Michelle Power** Department of Biological Sciences, Macquarie University, Australia **The effects of DNA isolation method on the diversity and composition of flea (Siphonatera) microbial communities resolved from microbiome analysis** **Andrea Lee Lawrence, Cameron Webb, Grant Hill-Cawthorne, Jan Šlapeta** University of Sydney, Australia **Sheep-worm interactions: are historically older sheep more resistant to worm burdens?** **Emily Onizawa[1], Jan Šlapeta[1], David Emery[1], Narelle Sales[2]** [1]Faculty of Veterinary Science, University of Sydney, Australia; [2]The Elizabeth Macarthur Agricultural Institute, NSW Department of Primary Industries, Australia **Characterisation of new and known ascaridoid larvae from marine fish off New Caledonia** **Anita Marie Poupa[1], Shokoofeh Shamsi[1], Jean-Lou Justine[2]** [1]School of Animal and Veterinary Sciences, Charles Sturt University, Australia; [2]ISYEB, Institut de Systématique, Évolution, Biodiversité (UMR7205 CNRS, EPHE, MNHN, UPMC), Muséum National d'Histoire Naturelle, France **Identification of *Miamiensis avidus* from cerebrospinal fluid of Southern bluefin tuna** **Jimena Balli-Garza[1], Natalie Kikidopoulos[2], Andrew Bridle[1], Melanie Leef[1], Barbara Nowak[1], Nathan Bott[2]** [1]Institute for Marine and Antarctic Studies, University of Tasmania, Australia; [2]School of Applied Sciences, RMIT University, Australia **Occurrence and prevalence of parasites of wild canids in southeastern Australia with emphasis on *Linguatula serrata*** **Kate Ashleigh McSpadden, David Jenkins, Shokoofeh Shamsi** Charles Sturt University, Australia **Efficacy of a protective vaccine in young sheep** **MD. Shakif-Ul Azam[1,2], Mark Sandeman[2], Waleed Mahmoud Arafa[3], David Piedrafita[1,2]** [1]Monash University, Australia; [2]Federation University, Gippsland Campus, Australia; [3]Beni-Sufe University, Egypt **High-throughput approach for the screening of immunotherapeutics in hookworm excretory/secretory (ES) products** **Stephanie Ryan[1], Darren Pickering[1], Kiril Alexandrov[2], Javier Sotillo[1], Severine Navarro[1], Alex Loukas[1]** [1]James Cook University, Australia; [2]University of Queensland, Australia ***Toxoplasma gondii* infection in selected Australian cases: how helpful is multilocus genotyping and histopathology?** **Madalyn Kate Cooper[1], Shannon Lynn Donahoe[1], Karrie Rose[2], Jan Šlapeta[1], David Norton Phalen[1]** [1]Faculty of Veterinary Science, University of Sydney, Australia; [2]Taronga Conservation Society Australia, Australia

Adaptation of the larval migration inhibition assay for cyathostomins

Anne Maree Beasley[1], Andrew C Kotze[2], Glen T. Coleman[1]
[1]School of Veterinary Science, University of Queensland, Australia.; [2]CSIRO Agriculture Flagship, CAFHS, Australia

Creating liquid cultures of *Neoparamoebae perurans* from various cell media and a commercial antibiotic preparation

Jessica Christine Johnson-Mackinnon, Andrew Bridle, Philip Crosbie, Barbara Nowak
University of Tasmania, Australia

Effects of third generation P-glycoprotein inhibitors on the sensitivity of drug-resistant and –susceptible isolates of *Haemonchus contortus* to anthelmintics *in vitro*

Ali Raza[1,2], Steven Kopp[2], Abdul Jabbar[3], Andrew Kotze[1]
[1]CSIRO Agriculture Flagship, Queensland Bioscience Precinct, University of Queensland, Australia; [2]School of Veterinary Science, University of Queensland, Australia; [3]School of Veterinary Science, University of Melbourne, Australia

Clinical and pathological features of toxoplasmosis in free-ranging common wombats (*Vombatus ursinus*)

Shannon Lynn Donahoe[1], Jan Šlapeta[1], Graeme Knowles[2], David Obendorf[2], Sarah Peck[2], David Norton Phalen[1]
[1]University of Sydney, Australia; [2]Department of Primary Industries, Parks, Water and Environment, Australia

In vitro* activity and therapeutic potential of 20 novel aminoguanidines against *Trypanosoma brucei* and *Leishmania donovani

R.J. Abraham[1], N.L. Bautista-Lopez[3], A.J. Stevens[2], A. McCluskey[2], D. Trott[1], A. Jardim[3], S.W. Page[4], R. O'Handley[1]
[1]School of Animal and Veterinary Sciences, University of Adelaide, Australia; [2]Chemistry, Centre for Chemical Biology, School of Environmental and Life Sciences, The University of Newcastle, Australia; [3]Institute of Parasitology, McGill University and Centre for Host-Parasite Interactions, Canada; [4]Neoculi Pty Ltd, Australia

Diagnostic tests for *Fasciola hepatica* (liver fluke) in ruminant livestock

Tara Louise Cassidy
Charles Sturt University, Australia

Theileriosis: *Theileria* and anaemia in cattle

Sarah Lochore, Margaret Anderson
New Zealand Veterinary Pathology, New Zealand

The first report of *Bonamia ostreae* from New Zealand represents a large geographic range expansion for this important molluscan parasite

Henry Somerset Lane[1,2], Steve Webb[3], Brian Jones[2]
[1]Department of Zoology, University of Otago, New Zealand; [2]Animal Health Laboratory, IDC&R, Ministry for Primary Industries, New Zealand; [3]Cawthron Institute, New Zealand

Towards the discovery of novel sites of anthelmintic action

Samantha Emery[1], Andrew Crombie[2], Daniel Vuong[2], Ernest Lacey[2], Andrew Piggott[1]
[1]Macquarie University, Australia; [2]Microbial Screening Technologies, Australia

Identification of antigenic tegument proteins of *Fasciola hepatica* recognised following immunosloughing of surface proteins by antibody from resistant ITT sheep

Timothy Charles Cameron[1], Hayley Toet[1], David Piedrafita[2], Ira Cooke[1], Pierre Faou[1], Terence Spithill[1]
[1]La Trobe University, Australia; [2]Federation University, Australia

PD-1 dependent exhaustion of $CD8^+$ T cells drives chronic malaria

Deshapriya Karunarathne, Joshua Horne-Debets, Michelle Wykes, Rebecca Faleiro
QIMR Berghofer Medical Research Institute, Australia

Impact of experimental *Haemonchus contortus* infection on the sheep gut microbiota

Md Abdullah Al Mamun[1,2], David Piedrafita[1,2], Mark Sandeman[2], Andrew R. Greenhill[2]
[1]Monash University, Faculty of Science, Australia; [2]Federation University, Faculty of Science and Technology, Australia 3842

The development of a whole *Plasmodium* parasite blood-stage vaccine utilizing apicoplast knockout parasites generated by chemical treatment.

L.M. Low, D.I. Stanisic, M.F. Good
Institute for Glycomics, Griffith University, Australia;

Molecular eco-epidemiology of *Triatoma brasiliensis,* the most important Chagas disease vector in northeastern Brazil: high natural *Trypanosoma cruzi* infection associated with feedings on *Kerodon rupestris* (Rodentia: Caviidae)

Carlos E. Almeida[1,2], Leslie Faucher[2], Morgane Lavina[2], Jane Costa[3], Myriam Harry[2,4]
[1]Laboratório Ecologia Animal, Programa de Pós-Graduação em Ecologia e Monitoramento Ambiental – PPGEMA, Universidade Federal da Paraíba-UFPB; [2]LEGS-UPR9034/UR 072 IRD, France; [3]Laboratório de Biodiversidade Entomológica, Instituto Oswaldo Cruz – Fiocruz, Brasil; [4]Université Paris Sud, France

Regulation of intrinsic apoptosis in cycloheximide-treated macrophages by Sichuan human strain of Chinese *Leishmania* isolates

Jin Zeng[1], Qi-Wei Chen[1], Ze-Ying Yu[1], Jun-Rong Zhang[1], Jian-Ping Chen[1,2]
[1]Sichuan University, People's Republic of China; [2]Animal Disease Prevention and Food Safety Key Laboratory of Sichuan Province, People's Republic of China

Study of experimental infection and comparative proteome analysis of Chinese *Leishmania* Isolates(SC10-H2)

Jun-rong Zhang, Ze-ying Yu, Jin Zeng, Qi-wei Chen, Jian-ping Chen
Sichuan University, People's Republic of China

Disruption of the digestive vacuole of *Plasmodium falciparum* induces phagocytosis by monocytic THP-1 cells

Yan Quan Lee[1,2], Kevin, Shyong Wei Tan[1,2]
[1]Department of Microbiology, Yong Loo Lin School of Medicine, National University of Singapore, Singapore; [2]NUS Graduate School for Integrative Sciences and Engineering, National University of Singapore, Singapore

Investigating the ecology of parasite transmission in fauna translocations and the impact of polyparasitism in translocated woylies (*Bettongia penicillata*).

S. Keatley[1], A. Northover[1], S. Godfrey[1], A. Lymbery[1], A. Wayne[2], R.C.A. Thompson[1]
[1]Murdoch University, Australia; [2]Science Division, Department of Parks and Wildlife, Australia;

Using next generation sequencing to reveal zoonotic pathogens in archived ticks

Telleasha L. Greay, Siew-May Loh, Alexander W. Gofton, Una Ryan, Peter J. Irwin, Charlotte L. Oskam
Murdoch University, Australia

Antibodies to the *Plasmodium falciparum* proteins MSPDBL1 and MSPDBL2 opsonize merozoites, inhibit parasite growth, and predict protection from clinical malaria

C.Y. Chiu[1], A.N. Hodder[1], CS Lin[1], D.L. Hill[1], C.S. Li Wai Suen[1], L. Schofield[1], P.M. Siba[2], I. Mueller[1], A.F. Cowman[1], D.S. Hansen[1]
[1]The Walter and Eliza Hall Institute of Medical Research, Australia [2]Vector Borne Disease Unit, Papua New Guinea Institute of Medical Research, Papua New Guinea

Population genomic structure of *Plasmodium falciparum* in Papua New Guinea

G.L.A. Harrison[1], N. Tessier[1], S. Lee[1], K. Smith[1], L. Tavul[2], M. Manske[3,4], O. Miotto[5], D. Kwiatkowski[3,4], I. Betuela[2], P.M. Siba[2], I. Mueller[1], M. Bahlo[1], A.E. Barry[1]
[1]Walter Eliza Hall Institute for Medical Research, Australia; [2]Papua New Guinea Institute of Medical Research, Papua New Guinea; [3]Wellcome Trust Sanger Institute, United Kingdom; [4]MRC Centre for Genomics and Global Health, University of Oxford, United Kingdom; [5]Mahidol-Oxford Tropical Medicine Research Unit, Mahidol University, Thailand

	Transcriptomic profiling of host skin immune responses to infestation with *Sarcoptes scabiei* in a porcine model. **S.A. Bhat[1], S.F. Walton[1], S.T. Burgess[2], X. Liu[1], M. Nath[2], D.C. Holt[3], B.J. Currie[3], J.S. McCarthy[4], K.E. Mounsey[1]** [1]University of the Sunshine Coast, Australia; [2]Moredun Research Institute, United Kingdom; [3]Menzies School of Health Research, Charles Darwin University, Australia; [4]QIMR Berghofer Medical Research Institute, Australia **Parasitic disease prevalence and control in Sichuan, China** **Yan Huang, Bo Zhong** Sichuan Provincial Centers for Disease Control and Prevention, People's Republic of China **Intestinal parasitosis in relation to CD4+T Cells levels and anemia among HAART initiated and HAART naïve pediatric HIV patients in model ART Center, Addis Ababa, Ethiopia** **Hylemariam Mihiretie Mengist[1], Bineyam Taye Alemu[2], Aster Tsegaye Abebe[2]** [1]Wollega University, Ethiopia; [2]Addis Ababa University, Ethiopia **Magnitude of anemia and associated factors among pediatric HIV/AIDS patients attending Zewditu Memorial Hospital (ZMH) ART Clinic, Addis Ababa, Ethiopia** **Hylemariam Mihiretie Mengist[1], Bineyam Taye Alemu[2], Aster Tsegaye Abebe[2]** [1]Wollega University, Ethiopia; [2]Addis Ababa University, Ethiopia **Incidence of dicrocoeliasis among local and imported Naheemi sheep in Riyadh Region.** **Wafa Abdullah Almegrin** Princess Nora University, Saudi Arabia **Impact of seasonal patterns and parasite asexual stage on *Anopheles gambiae* susceptibility to *Plasmodium falciparum* infection in Burkina Faso** **Awa Gneme[1], Wamdaogo M. Guelbeogo[2], Gustave B. Kabre[1], Michelle M. Riehle[3], N'Falé Sagnon[2], Kenneth D. Vernick[3,4]** [1]Laboratoire de Biologie et Ecologie Animales, Université de Ouagadougou, Burkina Faso; [2]Department of Biomedical Sciences, Centre National de Recherche et de Formation sur la Paludisme, Burkina Faso; [3]Department of Microbiology, University of Minnesota, United States of America; [4]Unit of Insect Vector Genetics and Genomics, Department of Parasites and Insect Vectors, Institut Pasteur, CNRS Unit of Hosts, Vectors and Pathogens (URA3012), France **Results of helminthological examinations of wild hoofed animals after using the preparation "Ivirsalt" for nematodosis (National Park "Losiny Ostrov" /"Elk Island"), Russia, Moscow)** **Nina Samoylovskaya** All-Russian Scientific Research Institute of Fundamental and Applied Parasitology of Animals and Plants named after K.I. Skryabin, Russian Federation
6:30pm - 10:00pm Foyer	**Poster Viewing** Poster viewing night includes stand-up dinner for all conference delegates
Date: Wednesday, 01/Jul/2015	
9:00am - 10:30am Plenary Room	**P2: Elsevier Plenary Lectures** Session Chair: **Alex Loukas**, James Cook University Session Chair: **Andrew Kotze**, CSIRO Session Chair: **Andrew Thompson**, Murdoch University **The ups and downs of life: population expansion and bottlenecks of helminth parasites through their complex life cycle** **Robert Poulin, Clement Lagrue** Zoology Dept, University of Otago, New Zealand **Ecological collision: climate, perturbation and colonization- lessons about assembly of the biosphere** **Eric P. Hoberg** US National Parasite Collection, USDA, Agricultural Research Service, and Smithsonian Institution,

	United States of America **Uncovering the mysteries of anthelmintic resistance: the more we learn the less we seem to know** **Ray M Kaplan** University of Georgia, United States of America
10:30am - 11:00am Foyer	**Morning Tea Wednesday supported by Elsevier Parasitology**
11:00am - 11:30am Symposium Room 1	**Symposium 6: Ecology of Parasitism 1** Session Chair: **Haseeb Randhawa**, University of Otago **Effect of *Toxoplasma gondii* infection on agriculture and wildlife: a New Zealand perspective** **Laryssa Howe, Wendi Roe, Kandarp Patel, Peter Wilson** Massey University, New Zealand
11:00am - 11:30am Symposium Room 2	**Symposium 7: Drug Discovery** Session Chair: **Kathy Andrews**, Griffith University **An image-based platform identifies compounds with novel activity against *Trypanosoma cruzi*** **Melissa Sykes, Vicky Avery** Eskitis Institute for Drug Discovery, Australia
11:30am - 12:30pm Symposium Room 1	**CP 6: Ecology of Parasitism Contributed Papers 1** Session Chair: **Haseeb Randhawa**, University of Otago **Upstream, downstream: spatial and temporal variations of a parasite in its first and second intermediate host** **Tommy Leung, David Rex Mitchell** Zoology, School of Environmental and Rural Science, University of New England, Australia **An apparent case of rapid diversification amongst the fish blood flukes (Aporocotylidae) of Indo-west Pacific Tetraodontiformes** **Russell Q-Y. Yong[1], Thomas H. Cribb[1], Scott C. Cutmore[1], Rodney A. Bray[2], Terrence L. Miller[3], I W.Y. Semarariana[4]** [1]The University of Queensland, Australia; [2]Department of Life Sciences, Natural History Museum, United Kingdom; [3]School of Marine and Tropical Biology, James Cook University, Australia; [4]The Faculty of Veterinary Medicine, Sudirman Campus, Universitas Udayana, Indonesia **Evidence of co-evolution between species of *Cloacina* (Nematoda: Strongylida) and the host *Macropus robustus* (common wallaroo)** **Mary Alys Shuttleworth, Abdul Jabbar, Ian Beveridge, Robin B. Gasser** Faculty of Veterinary and Agricultural Sciences, The University of Melbourne, Australia **Prevalence and molecular characterisation of haemoprotozoan parasites in native mammals from northern Australia** **Amanda Barbosa[1,2], Andrea Reiss[1], Andrea Paparini[1], Kris Warren[1], Peter Irwin[1], Una Ryan[1]** [1]Murdoch University, Australia; [2]CAPES Foundation, Ministry of Education of Brazil, Brazil
11:30am - 12:30pm Symposium Room 2	**CP 7: Drug Discovery Contributed Papers** Session Chair: **Kathy Andrews**, Griffith University **Investigating the antimalarial potential of primary sulfonamide compounds** **G.M. Fisher, D.M.S. Sumanadasa, J. Moeker, M. Lopez, T.S. Skinner-Adams, S-A. Poulsen, K.T. Andrews** Griffith University, Australia **Modified pantothenamides as potential antimalarials targeting the CoA biosynthesis/utilisation pathway** **Vanessa Howieson[1], Elisa Tran[2], Annabelle Hoegl[2], Han Ling Fam[1], Jonathan Fu[1], Kate Sivonen[1], Karine Auclair[2], Kevin Saliba[1]**

	[1]Australian National University, Australia; [2]McGill University, Canada **Epigenetic regulatory enzymes as antimalarial drug targets** **Ming Jang Chua[1], Tina Skinner-Adams[1], David P Fairlie[2], Katherine T. Andrews[1]** [1]Eskitis Institute for Drug Discovery, Griffith University, Australia; [2]Institute for Molecular Bioscience, The University of Queensland, Australia **Antiparasitic drug lead compounds from the medicinal plant, *Pleurospermum amabile*** **Phurpa Wangchuk[1], Michael Smout[1], Mark Pearson[1], Paul Giacomin[1], Sumalee Kamchonwongpaisan[2], Paul Keller[3], Stephen Pyne[3], Alex Loukas[1]** [1]Centre for Biodiscovery and Molecular Development of Therapeutics, Australian Institute of Tropical Health and Medicine, James Cook University, Australia.; [2]Medical Molecular Biology Research Unit, BIOTEC, National Science and Technology Development Agency, Thailand; [3]School of Chemistry, University of Wollongong, Australia
12:30pm - 1:30pm ARIA Restaurant	**Lunch Wednesday supported by Zoetis**
1:30pm - 2:00pm Symposium Room 1	**Symposium 8: Ecology of Parasitism 2** Session Chair: **Tommy Leung**, University of New England **Do parasites spread along host contact networks? Empirical and experimental insights from reptilian host-parasite systems.** **Stephanie Godfrey[1], Caroline Wohlfeil[2], Michael Gardner[2], Michael Bull[2]** [1]Murdoch University, Australia; [2]Flinders University, Australia
1:30pm - 2:00pm Symposium Room 2	**Symposium 9: Diagnostics, Detection and Control 2** Session Chair: **Katja Fischer**, QIMR Berghofer Medical Research Institute **Characterisation and detection of *Cryptosporidium* using platform technologies** **Una Ryan, Andrea Paparini, Rongchang Yang, Josephine Ng-Hublin, Garth Maker, Robert Trengove** Murdoch University, Australia
2:00pm - 3:00pm Symposium Room 1	**CP 8: Ecology of Parasitism 2 Contributed Papers** Session Chair: **Tommy Leung**, University of New England **A novel putative species-complex found in the platypus poses new challenges on the systematics of the piroplasms** **Andrea Paparini[1], Una M Ryan[1], James Macgregor[2], Peter J. Irwin[1]** [1]Vector- and Water-Borne Pathogen Research Group, School of Veterinary & Life Sciences, Molecular and Biomedical Sciences, Murdoch University, Australia; [2]College of Veterinary Medicine, School of Veterinary and Life Sciences, Murdoch University, Australia **Host-parasite relationships and life histories of wildlife trypanosomes in Australia** **Crystal Cooper[1], Peta Clode[1], Adriana Botero[2], Andrew Thompson[2]** [1]Centre for Microscopy, Characterisation and Analysis, University of Western Australia, Australia; [2]School of Veterinary and Biomedical Sciences, Murdoch University, Australia **Acanthocephalan taxonomy and New Zealand birds – problems and solutions** **Bronwen Presswell[1], Lesley Smales[2]** [1]University of Otago, New Zealand; [2]South Australian Museum, Australia **Review of neosporosis in wildlife** **Shannon Lynn Donahoe, David Norton Phalen, Scott Lindsay, Mark Krockenberger, Jan Šlapeta** University of Sydney, Australia
2:00pm - 3:00pm Symposium Room 2	**CP 9: Diagnostics, Detection and Control 2 Contributed Papers** Session Chair: **Katja Fischer**, QIMR Berghofer Medical Research Institute **Novel approach to detect hookworm ova from wastewater matrices** **Pradip Gyawali[1,2], Jatinder Sidhu[1,2], Warish Ahmed[2], Paul Jagals[1], Simon Toze[1,2]**

	[1]The University of Queensland, Australia; [2]CSIRO Land and Water, Australia **Prevalence and molecular characterization of *Cryptosporidium* species in animals inhabiting Sydney water catchments** **Alireza Zahedi Abdi[1], Andrea Paparini[1], Fuchun Jian[2], Brendon King[3], Paul Monis[3], Andrew Ball[4], Ian Robertson[1], Una Ryan[1]** [1]Murdoch University, Australia; [2]Henan Agricultural University, China,; [3]Australian Water Quality Centre, Australia; [4]Sydney Catchment Authority, Australia **Molecular-based monitoring of *Cryptosporidium* and *Giardia* in animals in Melbourne water catchments** **Anson Koehler[1], Shane Hayden[2], Melita Stevens[2], Aaron Jex[1], Robin Gasser[1]** [1]University of Melbourne, Australia; [2]Melbourne Water Corporation, Australia **Sequenom MassARRAY Platform as a high throughput tool for detection and differentiation of human hookworm species in stool** **Stacey Llewellyn[1], James McCarthy[1], Tawin Inpankaew[2], Rebecca Traub[3]** [1]Clinical Tropical Medicine Laboratory, QIMR Berghofer Medical Research Institute, Australia; [2]Department of Parasitology, Faculty of Veterinary Medicine, Kasetsart University, Thailand; [3]Faculty of Veterinary and Agricultural Science, The University of Melbourne, Australia
3:00pm - 3:30pm Foyer	**Afternoon Tea Wednesday supported by Gribbles Veterinary**
3:30pm - 4:00pm Symposium Room 1	**Symposium 10: Helminth Biology 1** Session Chair: **Dave Cole**, Cole Consulting **Effective immunity to *Haemonchus contortus* worm infection in sheep - clear as mud?** **David Piedrafita[1], Jorge Gonzalez[2], Sarah Preston[3], Els Meeusen[4]** [1]Federation University, Australia; [2]Las Palmas University, Gran Canaria; [3]Melbourne University, Australia; [4]Monash University, Australia
3:30pm - 4:00pm Symposium Room 2	**T1CP11: Theileriosis Contributed Papers** Session Chair: **Abdul Jabbar**, The University of Melbourne **Epidemiology of theileriosis in cattle in Victoria, Australia: 2010 to present** **Grant Thomas Rawlin[1], Laura MacFarlane-Berry[1], Abdul Jabar[3], Roger Paskin[2]** [1]DEDJTR, Victorian Government, Australia; [2]PISA, Australia; [3]University of Melbourne, Faculty of Veterinary Science, Australia **Investigating the first outbreak of oriental theileriosis in cattle in South Australia using multiplexed tandem PCR** **Hagos Gebrekidan Gebremikael, Robin B Gasser, Piyumali K Perera, Abdul Jabbar** The University of Meolbourne, Australia
4:00pm - 5:00pm Symposium Room 1	**CP 10: Helminth Biology 1 Contributed Papers** Session Chair: **Dave Cole**, Cole Consulting **Identification of a GPI-linked tegument protein fraction of the liver fluke *Fasciola hepatica*** **Hayley Michelle Toet, Terence W Spithill** Department of Animal, Plant and Soil Sciences, AgriBio: Centre for AgriBioScience, La Trobe University, Australia **Functional characterization of novel Kunitz type protease inhibitors from *Echinococcus* and *Schistosoma*** **Shiwanthi L Ranasinghe[1,2], Geoffrey N Gobert[1], Katja Fischer[1], Donald P McManus[1]** [1]QIMR Berghofer Medical Research Institute, Australia; [2]School of Public Health, University of Queensland, Australia **Are both species of *Angiostrongylus* in Australia able to cause meningitis in humans and companion animals in Eastern Australia?**

	Mahdis Aghazadeh[1,2], Rebecca Traub[3], Simon Reid[4], Kieran Aland[5], Helen Owen[1], Namitha Mohandas[3], James McCarthy[2], Robbin Gasser[3], Malcolm Jones[1,2] [1]School of Veterinary Scinece, Universuty of Queensland, Australia; [2]QIMR Berghofer Medical Research Institute, Australia; [3]Faculty of Veterinary and Agricultural Sciences, The University of Melbourne, Australia; [4]School of Public Health, University of Queensland, Australia; [5]Queensland Museum and Science Centre, Australia ***Caenorhabditis elegans*: the model worm to study anthelmintic activities of traditional medicinal plant extracts and their activities** **Rasika Kumarasingha[1], Jill Shaw[2], Enzo Palombo[2], T.C. Yeo[3], D.S.L Lim[3], C.L Tu[3], Peter Robert Boag[1]** [1]Department of Biochemistry and Molecular Biology, Monash University, Australia; [2]Department of Chemistry and Biotechnology, Faculty of Science, Engineering and Technology, Swinburne University of Technology, Australia; [3]Sarawak Biodiversity Centre, Malaysia
4:00pm - 5:00pm Symposium Room 2	**CP 11: Theileriosis Contributed Papers** Session Chair: **Abdul Jabbar**, The University of Melbourne **Application of novel PCR assays for the detection and differentiation of *Theileria orientalis* genotypes in New Zealand** **Piyumali K. Perera[1], Robin B. Gasser[1], David J. Pulford[2], Simon M. Firestone[1], Mark A. Stevenson[1], Andrew M.J. Mcfadden[2], Abdul Jabbar[1]** [1]Faculty of Veterinary and Agricultural Sciences, The University of Melbourne, Australia; [2]Ministry for Primary Industries, New Zealand **Establishment and application of a semi-quantitative multiplexed tandem PCR for the detection and differentiation of *Theileria orientalis* genotypes in Australia** **Piyumali K. Perera[1], Robin B. Gasser[1], Simon M. Firestone[1], Lee Smith[2], Elizabeth Read[3], Jakob Malmo[4], Florian Roeber[2], Grant Rawlin[5], Terry W. Spithill[3], Abdul Jabbar[1]** [1]Faculty of Veterinary and Agricultural Sciences, The University of Melbourne, Australia; [2]AusDiagnostics Pty., Ltd., Australia; [3]Department of Agricultural Sciences, Centre for AgriBioscience, La Trobe University, Australia; [4]Maffra Veterinary Centre, Australia; [5]Department of Environment and Primary Industries, Australia **Quantitative PCR for clinical diagnosis, subpopulation analysis and identification of temporal genotype switching in *Theileria orientalis*** **Daniel Ross Bogema[1,2], Sherin Alex[1,2], Ania Therese Deutscher[2], Shayne Fell[2], Melinda Micallef[2], Damian Collins[2], Steven Djordjevic[1], Graeme John Eamens[2], Cheryl Jenkins[2]** [1]University of Technology, Sydney, Australia; [2]Elizabeth Macarthur Agricultural Institute, NSW Department of Primary Industries, Australia **A putative novel species of *Theileria* isolated from the burrowing bettong (*Bettongia lesueur*)** **Andrea Paparini, Peter J. Irwin, Una M. Ryan** Vector- and Water-Borne Pathogen Research Group, School of Veterinary & Life Sciences, Molecular and Biomedical Sciences, Murdoch University, Australia
5:00pm - 5:30pm Foyer	**Pre-AGM drinks**
5:30pm - 6:30pm Symposium Rooms 1 and 2	**AGM: Australian Society for Parasitology** Session Chairs: **Robin Gasser**, University of Melbourne, **David Piedrafita**, Federation University and **Aaron Jex**, University of Melbourne **AGM: New Zealand Society for Parasitology** Session Chair: **Victoria Chapman**, Zoetis
Date: Thursday, 02/Jul/2015	
9:00am - 10:30am Plenary Room	**P3: Plenary Lectures – Immunity, Inflammation and Immunopathology supported by Virbac Animal Health** Session Chair: **Terry Spithill**, La Trobe University **Microparticles - contributors to the pathogenesis of cerebral malaria and potential biomarkers?** **Natalia Tiberti[2], Fatima El-Assaad[2], Anna Zinger[2], Amy Cohen[2], Sharissa Latham[2], Georges Grau[2], Valery Combes[1,2]**

	[1]University of Technology, Sydney, Australia; [2]The University of Sydney, Australia **Regulation of immunity and inflammation during parasitic helminth infections** **Paul Robert Giacomin** James Cook University, Australia **Exploring the immune response in scabies: pathways to diagnostics and therapy** **Shelley Walton** University of the Sunshine Coast, Australia
10:30am - 11:00am Foyer	**Morning Tea Thursday supported by Virbac Animal Health**
11:00am - 11:30am Symposium Room 1	**Symposium 12: Veterinary Parasitology 1 supported by Virbac Animal Health** Session Chair: **Glenn Anderson**, Virbac (Australia) **Chasing the end of the rainbow: a history of the 55 years of development, technology transfer and commercialisation of a vaccine to protect grazing animals against *Echinococcus granulosus.*** **David Duncan Heath[1], Marshall William Lightowlers[2]** [1]AgResearch New Zealand Limited, Hopkirk Research Institute, New Zealand; [2]University of Melbourne, Veterinary Clinical Centre, Australia
11:00am - 11:30am Symposium Room 2	**Symposium 13: Population Genetics** Session Chair: **Aaron Jex**, University of Melbourne **Malaria Elimination in the Asia-Pacific: Addressing the *P. vivax* challenge** **Ivo Mueller[1,2]** [1]Walter + Eliza Hall Institute, Australia; [2]ISGlobal, Barcelona Centre for International Health, Barcelona, Spain;
11:30am - 12:30pm Symposium Room 1	**CP 12: Veterinary Parasitology 1 Contributed Papers supported by Virbac Animal Health** Session Chair: **Glenn Anderson**, Virbac (Australia) **Structural and functional recognition mechanisms of galectin-11 of domestic sheep (*Ovis aries*)** **Dhanasekaran Sakthivel[1,2,3], Adam Shahine[2], MD Shakif-Ul-Azam[1], Dene Littler[2], Sally Troy[2], Matthew Johnson[2], Jamie Rossjohn[2,3], David Piedrafita[1], Travis Beddoe[2,4]** [1]Monash University, Australia; [2]Department of Biochemistry and Molecular Biology, Monash University, Australia; [3]Institute of Infection and Immunity, School of Medicine, Cardiff University, United Kingdom; [4]Department of Animal, Plant and Soil Science and Centre for AgriBioscience (AgriBio), La Trobe University, Australia **Creating a live attenuated veterinary vaccine against schistosomiasis** **Marina Harvie, Oliver Creagh, Najju Ranjit, Don McManus** QIMR Berghofer Medical Research Institute, Australia **Reverse vaccinology for parasitic diseases of livestock** **John Ellis, Stephen Goodswen, Joel Barratt, Paul Kennedy** University of Technology Sydney, Australia **Impact of parasitism on the health, development and production of buffalo in Pakistan** **Thomas Michael Williams** Charles Sturt University, Australia
11:30am - 12:30pm Symposium Room 2	**CP 13: Population Genetics Contributed Papers** Session Chair: **Aaron Jex**, University of Melbourne ***Lucilia cuprina* genome and transcriptomes – critical resources to underpin biological investigations and biotechnological outcomes** **Clare Alayne Anstead[1], Pasi K. Korhonen[1], Neil D. Young[1], Ross S. Hall[1], Aaron R. Jex[1], Shwetha C. Murali[2], Daniel S.T. Hughes[2], Siu F. Lee[3], Trent Perry[3], Andreas J. Stroehlein[1],**

	Brendan R.E. Ansell[1], Bert Breugelmans[1], Andreas Hofmann[4], Jiaxin Qu[2], Shannon Dugan[2], Sandra L. Lee[2], Hsu Chao[2], Huyen Dinh[2], Yi Han[2], Harsha V. Doddapaneli[2], Kim C. Worley[2], Donna M. Muzny[2], Panagiotis Ioannidis[5], Robert M. Waterhouse[5], Evgeny M. Zdobnov[5], Peter J. James[6], Neil H. Bagnall[7], Andrew C. Kotze[7], Richard A. Gibbs[2], Stephen Richards[2], Philip Batterham[3], Robin B. Gasser[1] [1]Faculty of Veterinary and Agricultural Sciences, University of Melbourne, Australia; [2]Department of Human and Molecular Genetics, Baylor College of Medicine, United States of America; [3]School of Biosciences, University of Melbourne, Australia; [4]Eskitis Institute, Griffith University, Australia; [5]Department of Genetic Medicine and Development, University of Geneva & Swiss Institute of Bioinformatics, Switzerland; [6]Queensland Alliance for Agriculture and Food Innovation, University of Queensland, Australia; [7]CSIRO Agriculture Flagship, Queensland Bioscience Precinct, Australia; **Cryptosporidiosis in New Zealand: cyclical ecology and zoonotic link** **Alex Grinberg** Massey University, New Zealand **Integrated morphological and molecular identification of cat fleas (*Ctenocephalides felis*)and dog fleas (*Ctenocephalides canis*)vectoring *Rickettsia felis* in central Europe** **Andrea Lee Lawrence[1], Sze-Fui Hii[2,3], Dagmar Jirsová[4], Lucia Panáková[5], Angela Ionică[6], Katrina Gilchrist[1], David Modrý[4,7], Andrei Mihalca[6], Cameron Webb[1], Rebecca Traub[3], Jan Šlapeta[1]** [1]University of Sydney, Australia; [2]University of Queensland, Australia; [3]University of Melbourne, Australia; [4]University of Veterinary and Pharmaceutical Sciences, Czech Republic; [5]University of Veterinary Medicine, Austria; [6]University of Agricultural Sciences and Veterinary Medicine, Romania; [7]Institute of Parasitology, Academy of Sciences of the Czech Republic **Diversity of *Cryptosporidium* and *Giardia duodenalis* in threatened brush-tailed rock-wallabies (*Petrogale penicillata*)** **Elke Tilly Vermeulen[1], Mark Eldridge[2], Michelle Power[1]** [1]Department of Biological Sciences, Macquarie University, Australia; [2]Australian Museum, Australia;
12:30pm - 1:30pm ARIA Restaurant	**Lunch Thursday supported by Virbac Animal Health**
1:30pm - 2:00pm Symposium Room 1	**Symposium 14: Veterinary Parasitology 2 supported by Virbac Animal Health** Session Chair: **Robert Dempster**, Virbac **Antiparasite immunity, worm burdens and illthrift in adult sheep?** **Dave Malcolm Leathwick** AgResearch, New Zealand
1:30pm - 2:00pm Symposium Room 2	**Symposium 15: Protozoan Biology 2** Session Chair: **Denise Doolan**, QIMR Berghofer Medical Research Institute **Differential stimulation of *Giardia duodenalis* trophozoites between host soluble signals and host cell attachment during *in vitro* interactions** **Samantha J. Emery[1], Mehdi Mirzaei[1], Daniel Vuong[2], Dana Pascovi[3], Ernest Lacey[2], Paul A. Haynes[1]** [1]Macquarie University, Australia; [2]Microbial Screening Technologies, Australia; [3]Australian Proteome Analysis Facility (APAF), Macquarie University, Australia
2:00pm - 3:00pm Symposium Room 1	**CP 14: Veterinary Parasitology 2 Contributed Papers supported by Virbac Animal Health** Session Chair: **Robert Dempster**, Virbac **The occurrence of *Linguatula serrata* and *Taenia* metacestodes in domestic livestock in southeastern Australia** **Sara Claire Baker, David Jenkins, Shokoofeh Shamsi** School of Animal and Veterinary Sciences, Charles Sturt University, Australia **Low cost whole-organism compound screening method** **Sarah Preston[1], Abdul Jabbar[1], Cameron Nowell[2], Anja Joachim[3], Baerbel Ruttkowski[3], Jonathan Baell[2], Tony Cardno[2], Pasi Korhonen[1], David Piedrafita[4], Brendan Ansell[1], Aaron Jex[1], Andreas Hofmann[5], Robin Gasser[1]** [1]Faculty of Veterinary and Agricultural Sciences, The University of Melbourne, Australia; [2]Medicinal

	Chemistry, Monash University Institute of Pharmaceutical Sciences (MIPS), Monash University, Australia; [3]Institute of Parasitology, Department of Pathobiology, University of Veterinary Medicine Vienna, Austria; [4]Faculty of Science and Technology, School of Applied and Biomedical Sciences, Federation University, Australia; [5]Structural Chemistry Program, Eskitis Institute, Griffith University, Australia **Are abomasal incubations needed when assessing the efficacy of anthelmintics against abomasal burdens of adult Ostertagiinae in deer?** **P.C. Mason[1], D.M. Leathwick[2], D.W. Lawrence[3], J.T. MacGibbon[4], G. Williams[5]** [1]Mason Consulting, New Zealand; [2]AgResearch, New Zealand; [3]Tikana, New Zealand; [4]Northern Southland Veterinary Services, New Zealand; [5]Landcorp Farming Limited, New Zealand **Confirmation of macrocyclic lactone resistance in *Ostertagia ostertagi* from cattle in New Zealand** **Tania Susanne Waghorn, Dave Leathwick** AgResearch, New Zealand
2:00pm - 3:00pm Symposium Room 2	**CP 15: Protozoan Biology 2 Contributed Papers** Session Chair: **Denise Doolan**, QIMR Berghofer Medical Research Institute **RNA-seq analysis confirms that extracellular tachyzoites of virulent and avirulent strains of *Neospora caninum* are transcriptionally distinct** **Stephen Bush, Joel Barratt, John Ellis** University of Technology, Sydney, Australia **Characterisation of *Toxoplasma gondii* NBP35 in iron-sulfur cluster biosynthesis** **Yi Tong Vincent Aw[1], Azadeh Seidi[1], Jiwon Lee[2], Melanie Rug[2], Giel van Dooren[1]** [1]Research School of Biology, Australian National University, Australia; [2]Centre for Advanced Microscopy, Australian National University, Australia **Does *Toxoplasma gondii* infection affect mouse personality?** **Amanda R. Worth[1], Patricia A. Fleming[1], R.C. Andrew Thompson[1], Alan J. Lymbery[1,2]** [1]School of Veterinary and Life Sciences, Murdoch University, Australia; [2]Fish Health Unit, Murdoch University, Australia **Leishmaniasis vaccine development using machine learning algorithms** **Webster Itai Nyakudya[1,3], Joel Barratt[1], Paul Kennedy[2], John Ellis[1]** [1]School of Medical and Molecular Biosciences, University of Technology, Sydney, Australia; [2]School of Software, Faculty of Engineering and Information Technology, University of Technology, Sydney, Australia; [3]Department of Microbiology, Royal North Shore Hospital, Australia
3:00pm - 3:30pm Foyer	**Afternoon Tea Thursday supported by Virbac Animal Health**
3:30pm - 4:00pm Symposium Room 1	**Symposium 16: Veterinary Parasitology 3 supported by Virbac Animal Health** Session Chair: **Ian Sutherland**, AgResearch Ltd **Veterinary parasitology in a diagnostic laboratory - a Queensland perspective** **Louise Jackson** Department of Agriculture and Fisheries, Australia
3:30pm - 4:00pm Symposium Room 2	**Symposium 17: Helminth Biology 2** Session Chair: **Nick Smith**, James Cook University **Of monkeys and men: immunomic profiling of sera from humans and non-human primates resistant to schistosomiasis reveals novel potential vaccine candidates** **Mark Simon Pearson[1], Luke Becker[1], Patrick Driguez[2], Xiao-Hong Li[3], Denise Doolan[2], Don McManus[2], Alan Wilson[4], Francisca Mutapi[5], Alex Loukas[1]** [1]Australian Institute of Tropical Health and Medicine, James Cook University, Australia; [2]QIMR Berghofer Medical Research Institute, Australia; [3]National Institute of Parasitic Diseases, China; [4]University of York, United Kingdom; [5]University of Edinburgh, United Kingdom
4:00pm - 5:00pm Symposium Room 1	**CP 16: Veterinary Parasitology 3 Contributed Papers supported by Virbac Animal Health** Session Chair: **Ian Sutherland**, AgResearch Ltd

	Revamping veterinary parasitology teaching for the tech-savvy student **Anne Maree Beasley, Lyn Knott, Malcolm Jones, Justine Gibson, Marnie Holt** University of Queensland, Australia **Evidence for *Toxoplasma gondii* as a cause of abortion in farmed deer in New Zealand** **Kandarp Khodidas Patel[1], Peter Raymond Wilson[1], Laryssa Jane Howe[1], Cord Heuer[1], Geoffrey Asher[2]** [1]Institute of Veterinary, Animal, and Biomedical Sciences, Massey University, New Zealand; [2]AgResearch, Invermay Agricultural Centre, New Zealand **Establishing the prevalence of liver fluke infections in dairy cattle in the Macalister, Goulburn Valley and Upper Murray irrigation districts in Victoria** **Jane Michele Kelley[1], Timothy Peter Elliott[1], Grant Rawlin[2], Terry W. Spithill[1]** [1]Department of Animal, Plant and Soil Sciences, Centre for AgriBioscience, La Trobe University, Australia; [2]Department of Economic Development, Jobs, Transport and Resources, Centre for AgriBioscience, LaTrobe University, Australia **A 'specific' issue: The use of universal primers to detect *Coxiella* sp. in the brown dog tick (*Rhipicephalus sanguineus*)** **Telleasha L. Greay, Charlotte L. Oskam, Alexander W. Gofton, Peter J. Irwin** Murdoch University, Australia
4:00pm - 5:00pm Symposium Room 2	**CP 17: Helminth Biology 2 Contributed Papers** Session Chair**: Nick Smith**, James Cook University **Defining the *Schistosoma haematobium* kinome as a basis for the prediction and prioritisation of kinases as anti-schistosome drug targets** **Andreas J. Stroehlein[1], Neil D. Young[1], Paul W. Sternberg[2], Aaron R. Jex[1], Peter R. Boag[3], Andreas Hofmann[1,4], Robin B. Gasser[1]** [1]Faculty of Veterinary and Agricultural Sciences, The University of Melbourne, Australia; [2]HHMI, Division of Biology, California Institute of Technology, United States of America; [3]Faculty of Medicine, Nursing and Health Sciences, Monash University, Australia; [4]Structural Chemistry Program, Eskitis Institute, Griffith University, Australia **Genomic resources for *Schistosoma haematobium* to support post-genomic discoveries** **Neil D. Young, Pasi K. Korhonen, Robin B. Gasser** Faculty of Veterinary and Agricultural Sciences, The University of Melbourne, Australia; **Suppression of the insulin receptors in adult *Schistosoma japonicum* impacts on parasite growth and development: further evidence of vaccine potential** **Hong You, Geoffrey Gobert, Pengfei Cai, Donald McManus** QIMR Berghofer Medical Research Institute, Australia **A granulin growth factor secreted by the carcinogenic liver fluke, *Opisthorchis viverrini*, and its role in wound healing and carcinogenesis** **Michael J. Smout[1], Javier Sotillo[1], Thewarch Laha[2], Banchob Sripa[2], Jason Mulvenna[3], Gabriel Rinaldi[4], Paul R. Giacomin[1], Paul J. Brindley[4], Alex Loukas[1]** [1]Centre for Biodiscovery and Molecular Development of Therapeutics, Australian Institute of Tropical Health and Medicine, James Cook University, Australia; [2]Department of Parasitology, Khon Kaen University, Thailand; [3]QIMR Berghofer Medical Research Institute, Australia; [4]Department of Microbiology, Immunology and Tropical Medicine, and Research Center for Neglected Diseases of Poverty, George Washington University, United States of America
6:30pm - 10:30pm Plenary Room	**Conference Dinner**

2015 Joint Conference of the New Zealand Society for Parasitology and the Australian Society for Parasitology Inc.

June 29 – July 2, Crowne Plaza Auckland, New Zealand

Presentations

Symposium 1

Marine Parasitology & Aquaculture 1: A Tribute to Ian Whittington

Time: Tuesday, 30/Jun/2015: 11:00am - 11:30am
Session Chair: Lesley Warner, South Australian Museum

Economic impact of aquatic parasites on Asian and global mariculture

Andrew P. Shinn[1,2], Jarunan Pratoomyot[3], James E. Bron[2], Giuseppe Paladini[2], Esther E. Brooker[2], Adam J. Brooker[2]
[1]Fish VetGroup Asia Limited, Thailand; [2]Institute of Aquaculture, University of Stirling, United Kingdom; [3]Institute of Marine Science, Burapha University, Thailand

The production, sustainability and economic viability of global aquaculture enterprises can be significantly impacted upon by a broad spectrum of obligate or opportunistic parasite pathogens. Parasite infections and their impacts can, according to pathogen and context, be considered to be either unpredictable/sporadic or predictable/regular in nature. While these infections may result in the direct loss of stock and incur costs associated with the control and management of infections once established, for predictable infections there are also costs associated with mitigation, prophylactic treatment and management. Estimation of the true cost of each parasitosis event is, however, complicated by the intricate interplay of numerous factors that can extend from direct losses in production to the wider, downstream socio-economic impacts on livelihoods and satellite industries associated with the primary producer. In this presentation, we review the major marine and brackish water aquaculture production industries with a focus on those throughout Asia and provide estimates of the economic cost of some notable parasite-related mortality events and discuss the lessons learned from such events. For this we will draw on both historical and contemporary events impacting on the key aquaculture species reared in Asia. In estimating the global cost of parasitism to aquaculture, the talk will provide an overview of production for a number of key species, including those reared in fresh, brackish and marine waters, as the basis for providing some initial estimates of the impact that parasites impose. Finally, the talk goes on to examine some specific problematic parasites affecting cultured species reared in Asian waters.

This talk is dedicated to the memory of Dr Ian Whittington: an exceptional and inspirational scientist and friend.

CP 1: Marine Parasitology & Aquaculture 1 Contributed Papers

Time: Tuesday, 30/Jun/2015: 11:30am - 12:30pm · *Location:* Plenary Room
Session Chair: Lesley Warner, South Australian Museum

Five intriguing facts about the harmful fish ectoparasite *Neobenedenia* sp.

Kate Suzanne Hutson[1], Alexander Karlis Brazenor[1], Terry Bertozzi[2,3], Terry L. Miller[1], Alejandro Trujillo-González[1], Truong Dinh Hoai[1,4], Thane Austin Militz[1], Ian David Whittington[2]
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This presentation showcases the Marine Parasitology Laboratory's most exciting research discoveries on the ecology, behaviour and biology of the ectoparasitic fish monogenean, *Neobenedenia* sp. Species in this genus are harmful pests in ornamental and food fish aquaculture globally. A monoculture of *Neobenedenia* sp. maintained in the laboratory over the past four years has enabled exploration of research hypotheses on cryptic parasite species, global distribution, microhabitat selection, reproductive mechanisms and management strategies for infested captive fishes. This research revealed: 1) *Neobenedenia* sp. exhibits low host-specificity and is distributed globally; 2) *Neobenedenia* sp. exhibits morphological plasticity which could be influenced by host fish species; 3) parasites migrate to distinct microhabitats on the host body surface during development; 4) hermaphroditic *Neobenedenia* sp. reproduce in isolation and exhibit egg laying and egg hatching rhythms and; 5) *Neobenedenia* sp. can be strategically managed using scheduled treatments and biocontrols. This examination of parasite behaviour, ecology and biology has emphasised the fascinating and diverse adaptations of marine parasites in their environment and has enabled applied research outcomes to reduce production loss and mortality in aquaculture.

Avoidance behaviours of Atlantic salmon (*Salmo salar*) to the ectoparasitic sea lice (*Lepeophtheirus salmonis*)

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The primary defence of hosts to the threat of parasite infection is behavioural avoidance, in order to resist the deleterious effects of being infected without incurring the physiological cost of an immune response. Identifying and quantifying such behaviours in the context of farming is essential in understanding existing capabilities of farmed animals in avoiding infection. Sea lice (*Lepeophtheirus salmonis*) are the most problematic ectoparasite in salmon aquaculture, causing critical issues in health management and extensive farm production losses. Given the severe pathophysiological consequences of infection, we

expected salmon to exhibit strong avoidance behaviours. We investigated the effect of salmon anti-parasite behaviours on sea louse attachment success. We engineered a behavioural phenotype using intramuscular injections of ketamine hydrochloride to reduce host sensitivity to parasite encounters. After an infection challenge in tanks, higher parasite loads were found on treated fish compared with untreated and procedural control fish. Alongside increased parasite loads, treated fish exhibited elevated swimming activity and burst swimming behaviour, and reduced jumping activity. The difference in the level of behaviours between treatment groups indicates the efficacy of such behaviours in reducing parasite attachment success, drawing implications for disease and health management in salmon aquaculture.

Diversity and effects of digenean trematodes in rocky shore snails: it sucks (less) to have parasites!

Katie O'Dwyer, Robert Poulin
University of Otago, New Zealand

We investigated, for the first time, the digenean parasites of three species of Southern Hemisphere rocky shore periwinkles: *Austrolittorina antipodum* and *A. cincta* in New Zealand, and *A. unifasciata* in Australia. First, our work uncovered multiple previously unrecorded digenean species parasitising these snails. We carried out detailed morphological descriptions of their cercariae and intramolluscan stages. We also characterised each species molecularly and analysed family-level phylogenetic trees for the relationships between our new species and those previously investigated. Secondly, because attachment strength is a key determinant of survival for rocky shore gastropods, we tested experimentally whether digenean infection reduced the suction-mediated attachment strength of two of the snail species. Using a mechanical lifting device, we found that for a given snail mass, infected snails were easier to detach from the substrate than uninfected ones, although this pattern was only significant for one species, the larger of the two snail species used. Our findings show that Southern Hemisphere littorinid snails are an important first intermediate host to various trematode species Also, our study demonstrates that parasitism can weaken snail attachment, and indirectly increase snail mortality, on exposed rocky shores, suggesting a new way in which parasites can affect host population dynamics.

Occurrence and abundance of zoonotic Parasites in selected edible fish from an Australian fish market

Jaydipbhai Rameshbhai Suthar, Shokoofeh Shamsi
Charles Sturt University, Australia

Seafood is considered to be a healthy source of nutrition and is highly recommended by medical researchers. However there is a huge gap in our knowledge regarding the occurrence of seafood borne parasites in Australia. The aim of the present study was to determine the occurrence of zoonotic parasites in selected Australian edible fish. Four species of fish, including Tiger Flathead (n=43), Blue Mackerel (n=117), Snapper (n=11) and School Whiting (n=90) were purchased from a fish market in New South Wales. Four main groups of helminthic parasites were found, including nematoda, acanthocephala, trematoda and cestoda. The focus of this presentation will be on nematode parasites only. Most nematodes were in larval stages and were classified as *Anisakis* type I, *Contracaecum* type III, *Terranova* types I-III, *Hysterothylacium* types III, IV, VIII and X, and *Raphidascaris* type. Two previously undescribed *Hysterothylacium* larval types were also found. Among these parasites, genera *Anisakis*, *Contracaecum* and *Terranova* are of high zoonotic importance. Prevalence of nematode larvae in these fish was 80.05, 64.10, 45.45 and 56.67%, respectively. Due to the high prevalence of zoonotic parasites it is highly recommended the current policy regarding seafood safety be revised and educational campaigns for people involved with seafood be established.

Symposium 2: Diagnostics, Detection and Control 1

Time: Tuesday, 30/Jun/2015: 1:30pm - 2:00pm · *Location:* Symposium Room 1
Session Chair: Harsha Sheorey, St Vincent's Hospital, Melbourne

Jetsumon Prachumsri
Mahidol University, Thailand

Symposium 3: Marine Parasitology & Aquaculture 2

Time: Tuesday, 30/Jun/2015: 1:30pm - 2:00pm · *Location:* Symposium Room 2
Session Chair: Kate Hutson, James Cook University

Parasite source-sink dynamics of giant squid

Haseeb Sajjad Randhawa
University of Otago, New Zealand

Trophically-transmitted parasites infecting intermediate hosts that are not part of the food chain of their definitive hosts are trapped in a sink. However, these “dead-end hosts” may harbour other parasite species and act as a parasite source for other predators. The ecological role of the deep-sea giant squid *Architeuthis dux* in the trophic transmission of parasites remains a mystery. Molecular characterisation of the D2 region of the large subunit ribosomal DNA (*c.*600bp) for 27 tapeworm larvae recovered from *A. dux* identified five tapeworm species: three tetraphyllideans (*Clistobothrium* cf. *montaukensis*, *Monorygma* sp. and “Phyllobothriidae” Gen. sp.); one rhinebothriid (*Anthocephalum* sp.); and one trypanorhynch (*Grillotia patagonica*). This giant squid species likely acts as a sink for *C.* cf. *montaukensis*, *Anthocephalum* sp. and *G. patagonica* as these are parasites of pelagic sharks (in the case of the former) or small shallow water or shelf-specialist skates (in the case of the latter two). However, *A. dux* is likely a source of *Monorygma* sp. for sleeper sharks, a confirmed predator of giant squid. Juvenile *A. dux* begin their lives in pelagic waters, picking up tapeworm infective stages along the way. Once young adult *A. dux* migrate to the depths, they become a sink to those parasites acquired during their pelagic phase. Hence, ontogenetic shifts in habitat likely contribute to the parasite source-sink dynamics of *A. dux*.

CP 2: Diagnostics, Detection and Control 1 Contributed Papers

Time: Tuesday, 30/Jun/2015: 2:00pm - 3:00pm · *Location:* Symposium Room 1
Session Chair: Harshvardhan (Harsha) Sheorey, St Vincent's Hospital, Melbourne

Insights into the relationship between blood stage immunity, multiclonal infection, and subsequent clinical outcome

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[1]University of New South Wales, Australia; [2]University of Sydney, Australia; [3]Karolinska Institutet, Sweden; [4]Public Health Agency of Sweden

Infection with genetically distinct clones of *Plasmodium falciparum* is very common in high transmission areas and the frequency of multiclonal infection also varies with age. Recent studies have shown that the number of clones increases with age until late childhood and then decreases. A number of studies have also suggested that multiclonal infection predicts the risk of subsequent clinical malaria. However the mechanism that determines the multiplicity of infection with age, and how this might relate to clinical outcome is not completely understood. In the current study we combined field study data with mathematical modeling to provide novel insights into the relationships between blood-stage immunity, multiclonal infection, and subsequent clinical outcome. Our modeling demonstrates that the observed patterns of multiclonal infection with age are consistent with increasing immunity and hence decreased parasite growth that in turn influence the duration of the detectable parasitaemia. We compared our modelling predictions with the observed clonal structure in data from a study of multiclonal infection in Tanzania. Our results suggest that both the distribution of multiclonal infection and its relationship with clinical outcome can be explained by a single factor – decreased parasite growth rate with age that is a result of increased blood-stage immunity.

Multiplex real-time PCR monitoring of intestinal helminths in humans reveals widespread polyparasitism in Northern Samar, the Philippines

Catherine Gordon[1,2], Donald McManus[1], Luz Acosta[3], Remigio Olveda[3], Gail Williams[2], Allen Ross[4], Darren Gray[1,2,5], Geoffrey Gobert[1]
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The global socioeconomic importance of helminth parasitic disease is underpinned by the considerable clinical impact on millions of people. While helminth polyparasitism is considered common in the Philippines, little has been done to survey its extent in endemic communities. High morphological similarity of eggs between related species complicates conventional microscopic diagnostic methods which are known to lack sensitivity, particularly in low intensity infections. Multiplex quantitative PCR diagnostic methods can provide rapid, simultaneous identification of multiple helminth species from a single stool sample. We describe a multiplex assay for the differentiation of *Ascaris lumbricoides, Necator americanus, Ancylostoma duodenale, Taenia saginata* and *Taenia solium,* building on our previously published findings for *Schistosoma japonicum.* Of 545 human faecal samples examined, 46.6% were positive for at least three different parasite species. High prevalences of *S. japonicum* (90.64%)*, A. lumbricoides* (58.17%)*, T. saginata* (42.57%) and *A. duodenale* (48.07%) were recorded. Neither *T. solium* nor *N. americanus* were found to be present. The utility of molecular diagnostic methods for monitoring helminth parasite prevalence provides new information on the extent of polyparasitism in the Philippines municipality of Palapag. These methods and findings have potential global implications for the monitoring of neglected tropical diseases and control measures.

Potential complications associated with the clinical management of Chagas Disease

Catherine Perez, Alan Lymbery, R.C. Andrew Thompson
Murdoch University, Australia

Chagas Disease (CD), a chronic infection caused by *Trypanosoma cruzi*, is endemic within South America, where transmission naturally occurs via the triatomine vector. Due to increasing rates of global migration, CD is now present within countries previously thought to be non-endemic, such as Australia and Japan, and has global public health implications. The lack of knowledge regarding CD and level of awareness of clinicians in non-endemic areas is alarming, particularly with the identification of several members of the vector genus *Triatoma* within non-endemic areas such as southeastern Asia, Australia and Africa. The murine CD model has proven integral worldwide in building our understanding of host-parasite interactions and the dynamics of parasite-parasite interactions within co-infections. We have developed a murine model, using the tulahuen strain, which has allowed us to study disease progression and drug efficacy. A variety of genetically different strains have been selected for *in vitro* and *in vivo* study so as to elucidate key phenotypic differences. Additionally polyparasitism, re-infection and disease reactivation are phenomena that, along with parasite genetics, have the potential to alter disease progression. Results of *in vitro* and *in vivo* co-infections demonstrate synergistic interactions which will impact on the choice of therapeutic interventions.

Detection of cell-free parasite DNA (CFPD) in human clinical samples as an improved method of diagnosis and evaluation of *Schistosoma japonicum* infection

Kosala Gayan Weerakoon[1,2,3], Geoffrey Gobert[1], Pengfei Cai[1], Donald McManus[1]
[1]QIMR Berghofer Medical Research Institute, Australia; [2]School of Public Health, University of Queensland, Australia; [3]Faculty of Medicine and Allied Sciences, Rajarata University of Sri Lanka, Sri Lanka

Morbidity reduction and eventual elimination are the focus of current schistosomiasis control programs, for which precise diagnosis of infection has a pivotal role. Microscopic detection of parasitic eggs in fecal or urine samples is the current gold standard method. Detection of schistosome DNA by PCR-based techniques is a promising adjunct to parasitological and serological diagnostic tests for accurate schistosomiasis diagnosis. Attempts have been made to detect *Schistosoma* cell-free parasite DNA (CFPD) in human body fluids. CFPD is released to the circulation, originating from different stages of

schistosome and is uniformly distributed in plasma, unlike schistosome eggs in faeces or urine. Thus CFPD may overcome one of the major limitations of egg DNA PCR, the potential for sampling errors. Our current study aims to optimize the detection of CFPD in non-invasive human clinical samples by digital PCR amplification of sensitive retrotransposon genes, *SjCHGCS 19* and *SjR2* of *S. japonicum* to help in disease confirmation, severity assessment and evaluation of therapeutic response.

CP 3: Marine Parasitology & Aquaculture 2 Contributed Papers

Time: Tuesday, 30/Jun/2015: 2:00pm - 3:00pm · *Location:* Symposium Room 2
Session Chair: Kate Suzanne Hutson, James Cook Universtiy

Clam (*Austrovenus stutchburyi*) parasite loading in an environment modified by commercial harvesting

Sorrel O'Connell-Milne
Otago University, New Zealand

Parasites can have significant impacts upon their host, interspecific interactions and ecosystem function. However, parasite transmission dynamics are usually strongly dependent on host densities. Commercial fishing often reduces densities and changes age structures of target populations. This research investigates the effect of commercial harvesting on parasite loading within the Otago clam fishery. Clams (*Austrovenus stutchburyi*) have been commercially harvested from Otago since 1982. Parasite loads (numbers of trematode metacercariae per clam) within areas commercially harvested were compared with unharvested areas to assess the effects of harvesting on parasite abundance within clams. At 14 sites within Blueskin Bay and Otago Harbour, a subset of shellfish were analysed for parasite load. Unparasitised juvenile clams were also caged *in situ* over a winter and summer period to monitor spatial and temporal patterns of parasite loading. Finally, the effect of parasite load on clam growth was monitored both *in situ* and in a laboratory experiment. Overall, commercial harvesting resulted in a 25% increase in average parasite load compared with unharvested control areas. Also, high parasite loads were found to negatively affect growth and body condition of clams. Therefore, harvesting has the potential to alter both the local transmission of trematode parasites and their impact on individual hosts.

How important is host diet for parasite interactions in sharks? Exploring the influence of taxonomic diet breadth on shark tapeworm diversity

Trent Kevin Rasmussen, Haseeb Sajjad Randhawa
University of Otago, New Zealand

For host species that acquire parasites via trophic transmission, diet is thought to play a key role in determining parasite diversity. In theory, host species with broad diets should encounter a greater diversity of parasites than species with restricted diets, and consequently, hosts with broad diets should harbour more parasite species. The present study investigated the role of host diet on tapeworm species richness and taxonomic diversity in sharks. This study conducted a comprehensive analysis of literature records to compare host diet and parasite diversity among a large proportion of known shark species. The influence of diet was analysed at multiple taxonomic levels and was assessed relative to other potentially important predictors of parasite diversity, including host size, phylogeny, latitude and depth. Tapeworm species diversity was found to be positively associated with breadth of diet in sharks, and interestingly, host diet accounted for more variation in tapeworm richness than any other host ecological variable considered in previous studies. These findings provide new evidence in identifying shark species as “hot spots” or “cold spots” for tapeworm diversity. In light of rapid global declines in shark populations, the latter information is key to managing the conservation of marine biodiversity.

Recommended method of fish examination for infection with anisakid larvae

Shokoofeh Shamsi, Jaydpbhai Suthar
Charles Sturt University, Australia

The infection of fish with anisakid nematodes is of great interest to many researchers studying seafood safety, human health or when using them as biological tags for stock assessment studies. Therefore, a reliable method for examining fish for infection with anisakid larvae is crucial to have an accurate estimate of their occurrence, abundance and prevalence in their fish hosts. In this presentation we discuss the issues with current common methods of examining fish for infection with anisakids and describe a new method for detecting these parasites. The prevalence, mean intensity and mean abundance of anisakids in 261 fish, belonging to four different species, was significantly higher when the recommended method was employed to examine these fish. The recommended method has several advantages including allowing examination of a large number of fish in a shorter time frame; larval specimens collected are suitable for both morphological and DNA sequencing; and being simple and inexpensive. While the focus of the method is to collect nematode larvae many other parasites including acanthocephalans, trematoda and tapeworms as well as adult nematodes can be also collected using this method.

Evidence of a cryptic complex of species of *Hamacreadium*, Linton, 1910 (Trematoda: Opecoelidae) and a redefinition of the genus taxonomy, host-specifity and composition

Storm B. Martin[1], Scott C. Cutmore[1], Terrence L. Miller[2], Thomas H. Cribb[1]
[1]University of Queensland, Australia; [2]James Cook University, Australia

The Opecoelidae is one of the richest families of trematodes parasitising marine fishes. Many opecoelid genera are suspected to not form natural groups and phylogenetic relationships between genera remain poorly understood. The genus *Hamacreadium*, Linton, 1910, embodies many of the challenges facing taxonomic studies of opecoelids. The type species, *H. mutabile*, Linton, 1910, originally described from *Lutjanus griseus*, collected off Florida, has a reportedly cosmopolitan distribution, an exceptionally low host-specificity and is the only species of the genus reported from Australian waters, whereas most other nominal species are poorly known and inadequately described. We combined analysis of sequence data and morphological examination, together with considerations for host-specificty, biogeography and an extensive review of all past

records of species of *Hamacreadium*. We concluded, contrary to numerous past reports, that *H. mutabile* is restricted to the West Atlantic and that species of *Hamacreadium* are overwhelmingly restricted to shallow-water piscivorous lutjanids. We argued that only three of 41 nominal species can be recognised as belonging to the genus and add two new combinations and four new species. We also consider *Hamacreadium* species to represent a cryptic complex and will discuss the implications of the prevalence of cryptic species for documenting opecoelid biodiversity.

Symposium 4: Protozoan Biology 1

Time: Tuesday, 30/Jun/2015: 3:30pm - 4:00pm · *Location:* Symposium Room 1
Session Chair: Katharine Trenholme, QIMR Berghofer Medical Research Institute

Ion homeostasis in the malaria parasite: a vulnerable drug target

Adele M. Lehane, Melanie C. Ridgway, Adelaide S.M. Dennis, James E.O. Rosling, Kiaran Kirk
Australian National University, Australia

The intraerythrocytic *Plasmodium falciparum* parasite exerts a tight control over its internal ion composition. Several new antimalarial lead compounds, including the spiroindolone KAE609, disrupt Na^+ regulation in the *P. falciparum* parasite, as well as inducing an alkalinisation of the parasite cytosol. It has been proposed that they do so by inhibiting the efflux of Na^+ via PfATP4, a parasite plasma membrane P-type ATPase that is postulated to export Na^+ and import H^+. We have screened hundreds of chemically diverse compounds for an ability to disrupt ion regulation in the parasite and in doing so have uncovered many additional compounds that disrupt parasite ion (Na^+ and pH) regulation in the same manner seen for the antimalarial spiroindolones. Potential explanations for the possibility that multiple compound classes share a common mechanism of action will be discussed. The results of recent investigations of parasite resistance to PfATP4 inhibitors, including an analysis of the fitness and physiological characteristics of PfATP4-mutant parasites, will be presented.

Symposium 5: Ectoparasites

Time: Tuesday, 30/Jun/2015: 3:30pm - 4:00pm · *Location:* Symposium Room 2

Session Chair: Tania Waghorn*, AgResearch*

Investigating the biological roles of scabies mite cysteine proteases and their potential as drug targets

Simone Louise Reynolds[1], Robert Pike[2], Katja Fischer[1]
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Cysteine proteases are important in many parasitic organisms for immune evasion, invasion and destruction of tissues and cells. *Sarcoptes scabiei* has five cysteine proteases (Sar s 1a-e) and localisation studies demonstrated that Sar s 1a-c are present in the mite gut and excreted faeces in the mite burrows. Cysteine protease activity was investigated using a range of synthetic fluorogenic substrates. As we have previously shown that scabies mites release proteins into the skin that block the host's complement system we tested Sar s 1c in degradation assays of complement factors C3 and C5. Consequently Sar s 1c disables complement activation by inhibiting the deposition of C3b, the formation of the C5 convertase complex and the release of the chemoattractant C5a. We propose that Sar s 1c, and possibly the remaining four homologous proteases, contribute to the complement inhibition seen. This may be only one of multiple roles these proteases play in pathogenicity. As the mite's cysteine proteases are likely to have further functions (e.g. in digestion) we assessed whether the cysteine proteases cleave human epidermal or plasma proteins. We also screened against substrate libraries to define the protease specificities to inform the design and synthesis of specific enzyme inhibitors.

CP 4: Protozoan Biology 1 Contributed Papers

Time: Tuesday, 30/Jun/2015: 4:00pm - 5:00pm · *Location:* Symposium Room 1
Session Chair: Katharine Trenholme, QIMR Berghofer Medical Research Institute

Unravelling the molecular systematics of the piroplasms

Andrea Paparini, Una M. Ryan, Peter J. Irwin
Vector- and Water-Borne Pathogen Research Group, School of Veterinary & Life Sciences, Molecular and Biomedical Sciences, Murdoch University, Australia

Piroplasms are ubiquitous tick-borne protozoa infecting mammals and birds. The order Piroplasmida includes the genera *Babesia*, *Theileria* and *Cytauxzoon*, and species of significant medical/economic importance. The 18S rDNA is the most frequently used gene in phylogenetic studies and >3,000 sequences are available in GenBank. Despite this, the molecular systematics of the order is still confused and debated. The present study evaluates the performance of different phylogenetic reconstruction methods and assesses their effect on piroplasms' molecular classification. A comprehensive set of available 18S rDNA sequences was processed in parallel, using different combinations of alignment algorithms, alignment curation options and tree-building methods. The comparison of the outcomes of each workflow clearly demonstrates that each process has the potential to produce plausible tree topologies, characterized by strongly supported clades. On the other hand, critical topological discrepancies were obtained, when different phylogenetic reconstruction criteria were adopted. Our analysis finally demonstrates how the key disagreements in the literature arose, and shows the effects of alternative analytical procedures on the piroplasms' phylogeny. More importantly, the comparison allowed the identification of the most robust workflow and a novel systematics is presented. The application of our analysis to other genes/organisms is also discussed.

Investigating the functional roles of malaria parasite histone deacetylases

Jessica Engel[1,2], Tina Skinner-Adams[1], Jeffrey Gorman[2], Kathy Andrews[1]
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Histone deacetylase (HDAC) enzymes work together with histone acetyltransferases to reversibly acetylate histone and non-histone proteins. As a result they play key roles in regulating chromatin structure and gene expression, as well as other important cellular processes. HDACs are validated drug targets in cancer and are showing promise as novel antimalarial drug targets. In *Plasmodium falciparum* HDACs appear to play a key role in transcriptional regulation however the role these enzymes have on other important pathways is unknown. An improved understanding of the biology of *P. falciparum* HDACs may contribute to ongoing drug discovery efforts. In this study we are investigating the functional role of *P. falciparum* HDACs on non-histone proteins, specifically trying to identify key members of the multi-protein complexes these enzymes form in order to function. Preliminary work has identified *Pf*Hsp90 and *Pf*β-tubulin as potential *Pf*HDAC1 interacting proteins. Here, data will be presented on work underway to confirm these interactions and to identify and characterise novel interactions using a variety of molecular and proteomic approaches.

Characterising the extracellular proteinases in the secretome of *Tritrichomonas foetus* bovine and feline genotypes

Leah Stroud[1], John Dalton[2], Colin Stack[1]
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Tritrichomonas foetus is a protozoan parasite responsible for causing trichomoniasis in cattle and cats. It is an unusual parasite due to the distinct infections caused within each host. In cattle it can lead to abortions, while in cats it results in chronic diarrhoea. As an extracellular parasite attachment to, and interaction with, host cells is vital to pathogenesis. A number of these key interactions are mediated by proteinases secreted by the parasite. In particular, cysteine proteinases (CPs) secreted by *T. foetus* play a role in nutrient acquisition, immune evasion and adhesion. Both CPs and serine proteinases (SPs) were detected in the secretome using mass spectrometry. Enzymatic activity was quantified using fluorescein-labeled DQ-gelatin. The resultant gelatinolytic activity was inhibited up to 88% and 100% with E-64 (300µm, a cysteine proteinase inhibitor), and 86% and 80% with PMSF (5mM, a serine proteinase inhibitor), in bovine and feline strains, respectively, indicating the importance of CPs and SPs. Furthermore we tested if this enzymatic activity could be inhibited using recombinant bovine Cystatin C (an endogenous cysteine proteinase inhibitor). Given the important role(s) these proteinases play in *T. foetus* pathogenesis not only do they represent targets for therapeutic intervention, but also novel biomarkers for diagnostic applications, while recombinant cystatin C could be a potential treatment for trichomoniasis.

Investigation of the export pathway of *Plasmodium* parasites utilising small molecule inhibitors of plasmepsin V

Michelle Gazdik[1,2], Brad E. Sleebs[1,2], Sash Lopaticki[1,2], Matthew T. O'Neill[1,2], Pravin Rajasekaran[1,2], Anthony N. Hodder[1,2], Peter Czabotar[1,2], Kym N. Lowes[1,2], Brian J. Smith[3], Alan F. Cowman[1,2], Justin A. Boddey[1,2]
[1]The Walter and Eliza Hall Institute of Medical Research, Australia; [2]The University of Melbourne, Australia; [3]La Trobe University, Australia

The human malaria parasite *Plasmodium falciparum* exports several hundred proteins into the host cell erythrocyte that are involved in cellular remodelling and severe virulence. The proteins exported to the erythrocyte possess a conserved N-terminal export motif termed the *Plasmodium* export element (PEXEL). In order for proteins to be exported, the PEXEL motif (RxLxE/Q/D) must be processed by an ER-resident aspartic protease called plasmepsin V (PMV). PMV is conserved in all *Plasmodium* spp., including the most virulent human parasites *P. falciparum* and *P. vivax*, and is essential for blood-stage parasite survival. We have developed a PEXEL-mimetic inhibitor, WEHI-842, that potently inhibits both *P. falciparum* and *P. vivax* PMV (IC_{50} of 0.8 nM and 1.6 nM), demonstrating that the export pathway is conserved in *Plasmodium* species. We used the inhibitor to obtain the first X-ray crystal structure of PMV that provides unparalleled insights into the mechanism and inhibition of this enzyme. Treatment of *P. falciparum*-infected erythrocytes with WEHI-842 impairs PEXEL processing and protein export causing parasite death, in multiple stages of the parasites lifecycle, including transmission to the mosquito, reaffirming PMV as a prime antimalarial drug target.

CP 5: Ectoparasites Contributed Papers

Time: Tuesday, 30/Jun/2015: 4:00pm - 5:00pm · *Location:* Symposium Room 2

Session Chair: Tania Waghorn*, AgResearch*

Immunohistological localisation of scabies mite inactivated cysteine protease paralogues (SMIPP-Cs)

Waduge Deepani Darshika Fernando, Simone Reynolds, Katja Fischer
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Scabies infestations affect an estimated 300 million people worldwide including Australian Indigenous communities. Current treatments are suboptimal and emerging drug resistance has been reported. Mite gut proteases are likely essential for parasite survival. Ten variants of scabies mite cysteine proteases homologous to the house dust mite (HDM) group1 allergens have been identified. Five of them are predicted to be proteolytically inactive (SMIPP-Cs) with active site mutations and other unique changes in their amino acid sequences. These are unique to parasitic scabies mites and to date have no counterparts in non-parasitic free living mites. We hypothesise that they are essential for mite survival in the skin and that they may be potential drug targets. It is essential to confirm the presence and to know the location of these molecules *in situ*. Recombinant proteins of three SMIPP-Cs from three different clades in the phylogenetic tree of the SMIPP-C protein family were generated in *E. coli* and antibodies against them were produced in BALB/c mice. Immunohistological localisation studies using sections through infested human skin revealed that SMIPP-Cs are present internally in the gut of *Sarcoptes scabiei* var. *hominis* and externally in their faeces excreted into the mite burrows within the epidermis.

Identification of potential endosymbionts in the scabies mite *Sarcoptes scabiei*

Emily Lau[1], Pearl Swe[1], Rebecca S. Waddell[1], Martha Zakrzewski[1], Lutz Krause[2], Katja Fischer[1]

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The parasitic mite *Sarcoptes scabiei* inflicts a contagious skin disease known as scabies with world-wide prevalence. Infection rates in Indigenous communities of northern Australia are some of the greatest globally. With limited therapeutics for scabies treatment and increasing mite resistance to current drugs, this research is centred on targeting heritable endosymbionts that are essential for the host. Previously we characterised the internal microbiome of scabies to assess whether the mites carry endosymbionts. Here further research is conducted to confirm the presence of endosymbionts; specifically *Streptomyces sp.*, *Wolbachia sp.*, and *Anaplasma sp.* in *S. scabiei.* qPCR will be used to amplify specific DNA sequences present in adult females and eggs collected from scabies-infected pig skin. 16S rDNA primers designed specifically for screening of *Streptomyces sp.* in *S. scabiei* will be utilised. 16S rDNA and P44 primers will be used for the screening of *Anaplasma sp*. 16S rDNA, Cell division protein, Chaperonin GroEL, and Citrate synthase primers will be used in the screening of *Wolbachia sp*. Fluorescence in situ hybridization (FISH) will then be used to visualise the bacterial endosymbionts in *S. scabiei* life stages. This project will lead into the development of treatments and diagnostics specifically targeting mite-associated symbionts.

A link between scabies mites and *Streptococcus pyogenes* towards host invasion

Pearl Swe, Lindsay Christian, Kadaba Sri Sriprakash, Katja Fischer

QIMR Berghofer Medical Research Institute, Australia

Scabies is a contagious skin disease caused by a parasitic mite *Scarcoptes scabiei* var. *homonis*. It is prevalent worldwide and the disease is closely associated secondary *Streptococcus pyogenes* infection. Consequently high incidences of ARF, RHD and PSGN are reported in the scabies-infected population. We reported earlier that scabies mites secret complement inhibiting molecules. We have also shown that a number of these complement inhibitors are secreted into the mite gut and subsequently excreted into the epidermal mite burrows. These inhibitors promoted the growth of *S. pyogenes in vitro* even in the presence of functional complement components. We now study the generality of this effect by testing specifically one of the mite complement inhibitors, namely SMSB4 on various *S. pyogenes* clinical isolates. Recombinant SMSB4 was produced and purified from *Pichia pastoris*. The complement inhibitory function of the purified SMSB4 was confirmed by haemolytic assay with sheep erythrocytes. The effect of SMSB4 on the establishment of *S. pyogenes* against the host complement defence was investigated by enumerating the number of bacteria recovered when fresh human blood samples treated with or without SMSB4 was challenged with 10^4 cuf/ml *S. pyogenes*. Further investigations into the immune evasion mechanisms of SMSB4 such as opsonisation and production of anaphylatoxin were conducted by a series of ELISA assays. Investigation of the tripartite interactions between host, parasite and microbial pathogens could serve as a basis for the development of novel intervention strategies to prevent and treat scabies and streptococcal infections.

Title: Phylogenetic analysis of the Australian paralysis ticks and their relatives (*Ixodes* (*Sternalixodes*): Ixodidae).

Mackenzie Lamont Kwak[1], Ian Beveridge[1], Anson Koehler[1], Mali Malipatil[2], Robin Gasser[1], Abdul Jabbar[1]

[1]Faculty of Veterinary and Agricultural Sciences, The University of Melbourne, Australia; [2]Biosciences Research, AgriBio, Department of Economic Development, Jobs, Transport & Resources, Australia

The Australian paralysis ticks and their relatives (subgenus: *Sternalixodes*) are the most medically important group of ticks in Australasia; yet little is known about their phylogenetics. It has been proposed that these ticks belong to a paraphyletic subgenus based on morphological features; however, this proposal has never been validated. In this study, we collected specimens (n=120) from eight (*Ixodes anatis, I. confusus, I. cordifer, I. cornuatus, I. hirsti, I. holocyclus, I. trichosuri, I. myrmecobii*) of the nine species in the subgenus across Australia, New Zealand and Papua New Guinea, and characterised them using morphological and molecular (using cytochrome *c* oxidase subunit 1 (COX1)) methods. Phylogenetic analyses (using morphological characters and COX1 sequences) were conducted employing Byaesian Inference, Neighbour-joining and Maximum Likelihood methods. This phylogeny of *Sternalixodes* elucidates the evolution and validity of the subgenus and informs questions about its biogeography.

Poster 1: Oral Poster Presentations

Time: Tuesday, 30/Jun/2015: 5:30pm - 6:30pm · *Location:* Plenary Room
Session Chair: Malcolm Jones, University of Queensland

Investigation into the presence of anthroponotic *Cryptosporidium* sp. in wild and captive Australian grey-headed flying fox (*Pteropus poliocephalus*) populations

Sabine Eva Schiller, Koa Webster, Michelle Power
Department of Biological Sciences, Macquarie University, Australia

Bats are known vectors for a range of zoonotic diseases, but reverse pathogen transmission (zooanthroponosis) from humans into bat species has rarely been investigated. To identify potential zooanthroponosis we are testing wild and captive populations of *Pteropus poliocephalus* for the presence of human-borne *Cryptosporidium* species. *Cryptosporidium* is one of the most common causes of enteric illness in humans, with the zoonotic *C. parvum* infecting both humans and other vertebrates. Habitat loss along the east coast of Australia has resulted in *P. poliocephalus* populations seeking shelter in regional and urban centres, increasing contact rates with humans and potentially facilitating spillover events. We propose that captive populations are at increased risk of human-borne *Cryptosporidium* infection as a result of feeding and handling, and reduction in immune function in cases of illness and injury. DNA was extracted from faecal samples collected from wild (n=149, 6 locations) and captive (n=36, 1 location) populations in NSW. Detection and characterisation of *Cryptosporidium* was performed at the 18s rRNA gene. Sequencing data indicates the presence of novel genotypes of *Cryptosporidium* spp. in wild and captive *P. poliocephalus* populationsin NSW. Further genetic analysis is currently being performed to confirm these novel findings.

The effects of DNA isolation method on the diversity and composition of flea (Siphonatera) microbial communities resolved from microbiome analysis

Andrea Lee Lawrence, Cameron Webb, Grant Hill-Cawthorne, Jan Šlapeta
University of Sydney, Australia

Fleas are the most commonly encountered ectoparasite infesting our canine and feline pets around the world. These parasites have been proven to be ubiquitous and cosmopolitan vectors of many zoonotic pathogens including *Bartonella* spp., *Rickettsia* spp. and *Yersina pestis*. Despite their importance to both veterinary and public health, the microbial community dynamics of pathogens and endosymbionts within fleas has been poorly studied. The limited research addressing microbial communities in fleas does not discuss the effect of DNA isolation methods on the results of microbiome sequencing. In this study, two variables of the DNA isolation process were assessed to define their effects on the microbial community of two species of fleas – the cosmopolitan *Ctenocephalides felis felis* from a pet dog in urban NSW and the native Australian flea *Echidnophaga ambulans ambulans* from an echidna from rural NSW. Washing the exterior of the flea with bleach to eliminate surface bacteria was compared with 'unwashed' fleas which underwent DNA isolation immediately from the absolute ethanol storage medium. In addition to this, crushing whole fleas prior to cell lysis and incubation was compared with retaining the exoskeleton of the specimen during cell lysis for taxonomic purposes. The two DNA isolation methods were tested on both species in duplicate. This study aimed to understand how certain sample preparation and DNA isolation methods affect microbiome results. We also discuss the feasibility for using the microbiome approach for the detection of zoonotic pathogens such as *Rickettsia* spp. in flea microbial communities, thus demonstrating their vector potential.

Sheep-worm interactions: are historically older sheep more resistant to worm burdens?

Emily Onizawa[1], Jan Šlapeta[1], David Emery[1], Narelle Sales[2]
[1]Faculty of Veterinary Science, University of Sydney, Australia; [2]The Elizabeth Macarthur Agricultural Institute, NSW Department of Primary Industries, Australia

Gastrointestinal nematodes act as the greatest constraint to the Australian sheep industry and worldwide. Anthelmintic resistance is a rising problem in sheep health and management, therefore alternative methods of control are required. Currently, methods used to combat this issue include nutrition, integrated parasite management and genetics through selective breeding. Although research has been conducted into genetic resistance of nematodes, many farmers avoid this due to detriment in productivity of the flock due to having to incorporate new breeds or strict breeding strategies. The historically old Merino sheep, Camden Park Flock, have been suggested from anecdotal evidence to be more resistant to nematodes. This project uses a modern Australian Merino and a historically in-bred Camden Park Flock that the Australian Merino was largely bred from, to gain a fundamentally new understanding of the host parasite interactions in the gastrointestinal tract. We utilise Faecal Egg Counts (FEC) / Larval Culure (LC) throughout the year in co-grazed flocks in *Haemonchus contortus* prone property. The outcomes inform and improve the way we perceive Australian Merino sheep and manage parasites with opportunities to influence the gastrointestinal metabolism to maintain or improve tolerance to parasites and reduce the impact of parasites on farmers and Australian and world food security.

Characterisation of new and known ascaridoid larvae from marine fish off New Caledonia

Anita Marie Poupa[1], Shokoofeh Shamsi[1], Jean-Lou Justine[2]
[1]School of Animal and Veterinary Sciences, Charles Sturt University, Australia; [2]ISYEB, Institut de Systématique, Évolution, Biodiversité (UMR7205 CNRS, EPHE, MNHN, UPMC), Muséum National d'Histoire Naturelle, France

Here we report occurrence of various morphotypes of ascaridoid type larvae from 58 species of fish and adult nematodes from one species of whale collected from New Caledonian waters. Second internal transcribed spacers (ITS-2) of ribosomal DNA (rDNA) were sequenced and compared to ascaridoid sequences previously deposited in GenBank. So far we found *Anisakis* type I, *Hysterothylacium* type VI and new larval types XIII and XIV, *Raphidascaris* larval type and *Terranova* larval type II in fish. Results are yet to be obtained for many of the specimens. This taxonomic work is essential if further research on these zoonotic parasites is to be effective, including investigations into aspects such as life cycles, impacts on human health and risk assessment for their transmission to humans.

Identification of *Miamiensis avidus* from cerebrospinal fluid of Southern bluefin tuna

Jimena Balli-Garza[1], Natalie Kikidopoulos[2], Andrew Bridle[1], Melanie Leef[1], Barbara Nowak[1], Nathan Bott[2]
[1]Institute for Marine and Antarctic Studies, University Of Tasmania, Australia; [2]School of Applied Sciences, RMIT University, Australia

Scuticociliates are free-living protozoan organisms present either in marine or freshwater habitats that under certain circumstances can behave as opportunistic pathogens able to infect a wide range of hosts. *Uronema nigricans* has been identified as the main causative agent of the disease, swimmer syndrome in Southern bluefin tuna (SBT) ranched in Port Lincoln, South Australia. Recently it has been suggested that *Miamiensis avidus* could also play an important role in swimmer syndrome. Morphometrical identification of scuticociliates can be confusing leading to misidentification of certain species. However, molecular methods such as sequencing of the mitochondrial cytochrome c oxidase 1 gene (Cox1) and small sub-unit ribosomal (SSU rRNA) genes have been proven to be a rapid and effective tool for the identification of scuticociliates, as these genes are highly conserved within a species and there is a growing database for these genes for scuticociliates. Cerebrospinal fluid was collected from SBT with signs similar to swimmer syndrome, amplification and sequence comparison of a partial sequence of Cox1 and the SSU rDNA showed that SBT samples were 100% identical to *M. avidus*. This study suggests that *M. avidus* may be associated with swimmer syndrome in SBT.

Occurrence and prevalence of parasites of wild canids in southeastern Australia with emphasis on *Linguatula serrata*

Kate Ashleigh McSpadden, David Jenkins, Shokoofeh Shamsi
Charles Sturt University, Australia

The red fox, *Vulpes vulpes*, and wild dogs (dingoes, *Canis lupus dingo* and their hybrids, *Canis lupus dingo X Canis familiaris*) are present throughout southeastern Australia. Wild canids not only predate on livestock and native species but also play a key role in transmission of parasites of veterinary and human health importance, such as *Echinococcus granulosus*. *Linguatula serrata* is an obligate arthropod parasite, commonly known as the tongue worm. It utilises canids and vulpids as its definitive host and several herbivorous species as its intermediate hosts. Tongue worms can be zoonotic where humans may act as accidental intermediate or definitive hosts depending on the source of infection. In some Middle Eastern countries, where the prevalence of the parasite is high in stray dogs and livestock, the risk of human infection is significant. In Australia, *L. serrata* has been reported sporadically across southeastern Australia and Queensland over the past two centuries. Of these occurrences, adult tongue worms have been reported in wild and domestic dogs and foxes. Nymphs have been encountered in cattle and rabbits. Results of a survey of *L. serrata* in wild canids and vulpids in south-eastern Australia are presented and discussed.

Efficacy of a protective vaccine in young sheep

MD. Shakif-Ul Azam[1,2], Mark Sandeman[2], Waleed Mahmoud Arafa[3], David Piedrafita[1,2]
[1]Monash University, Australia; [2]Federation University, Australia; [3]Beni-Sufe University, Egypt;

Haemonchus contortus is one of the important parasitic worms causing global production losses in the small ruminant industry. We have previously shown vaccine efficacy (70%) using with a surface larval antigen and the adjuvant, DEAE-dextran; protection was correlated with significant cellular responses in adult sheep [1]. However, young animals are highly susceptible to nematode infections and successful vaccine-induced protection of these animals is often limited. This has been suggested to be due to inadequate immune responsiveness of young animals. In the present study, we tested whether similar correlates of vaccine-induced protection would be detected in young sheep as with our previous efficacious trials with adult sheep. Intradermal injections using known immune mediators were used to quantify innate responses (before vaccination) and specific anti-larval responses (after vaccination), by measuring wheal responses (hypersensitivity reactions) and analyzing cellular recruitment in skin biopsies at the sites of injection. Vaccinated young lambs demonstrated significant differences in total IgG, cytokine and cellular response post-vaccination, but no protective efficacy was seen. This study suggests that lack of protective efficacy in young sheep is not due to a lack of immune reactivity but that vaccination induces different qualitative or quantitative immune responses of young animals to vaccine antigens.

Reference:

[1] Piedrafita D et al. (2013) The Effect of Different Adjuvants on Immune Parameters and Protection following Vaccination of Sheep with a Larval-Specific Antigen of the Gastrointestinal Nematode,*Haemonchus contortus*. PLoS ONE 8(10): e78357.

High-throughput approach for the screening of immunotherapeutics in hookworm excretory/secretory (ES) products

Stephanie Ryan[1], Darren Pickering[1], Kiril Alexandrov[2], Javier Sotillo[1], Severine Navarro[1], Alex Loukas[1]
[1]James Cook University, Australia; [2]University of Queensland, Australia

Parasitic infections place a costly and disproportionate disease burden on developing countries. However, evidence suggests that certain parasites, such as hookworms, offer substantial health benefits, particularly in the treatment of allergy and inflammatory bowel disease. Helminth therapy is gaining momentum in the medical community; however, the use of live therapeutics has drawbacks. An increasing body of evidence suggests a safer option is to harness the immunomodulatory properties of the hookworms' excretory/secretory (ES) products. We have shown that *Ancylostoma caninum* ES protects against inflammation in mouse models of colitis and ES denaturation neutralizes its protective properties against inflammation. Recent transcriptional and proteomic profiling of *A. caninum* has revealed approximately 1500 secreted proteins with ~100 proteins identified in the ES proteome. We have developed a high throughput screen using a cell-free protein expression system that allows us to test recombinant hookworm proteins for *in vitro* and *in vivo* IM activity. Selected proteins will be expressed in cell-based systems to generate larger amounts for further assessment in different models of chronic inflammation. This study identifies untapped potential for novel hookworm immunomodulatory proteins to be incorporated into immunotherapeutics to treat the alarmingly high global burden of inflammatory diseases.

Toxoplasma gondii infection in selected Australian cases: how helpful is multilocus genotyping and histopathology?

Madalyn Kate Cooper[1], Shannon Lynn Donahoe[1], Karrie Rose[2], Jan Šlapeta[1], David Norton Phalen[1]
[1]Faculty of Veterinary Science, University of Sydney, Australia; [2]Taronga Conservation Society Australia, Australia

Toxoplasma gondii is a cyst-forming, apicomplexan parasite that can infect all warm-blooded vertebrates. The distribution and impact of toxoplasmosis in Australian mammals is not yet clearly defined, but it is linked to severe encephalitis, myocarditis and retinitis in some species. Genotyping strains of *T. gondii* is an important tool that will facilitate epidemiological studies and supplement our understanding of lethal toxoplasmosis in Australian host species. Genetic characterisation of *T. gondii* samples from cases of acute and sub-acute, lethal disease in the Risso's dolphin (*Grampus griseus*), peach-faced lovebird (*Agapornis rosiecollis*) and bilby (*Macrotis lagotis*) will utilise a combination of multilocus nested PCR of B1, SAG1 , altSAG2, SAG3, BTUB, GRA6, C22-8, C29-2, L358, PK1 and Apico DNA markers and virtual RFLP. Genotyping results will be coupled with clinical and pathological features of the disease, where the lesions seen are typical of those previously described in worldwide toxoplasmosis investigations. This poster aims to reveal links between toxoplasmosis-associated mortality events and the presence of specific strain types, and discuss the pros and cons of some diagnostic methods used in animal disease investigation.

Adaptation of the larval migration inhibition assay for cyathostomins.

Anne Maree Beasley[1], Andrew C. Kotze[2], Glen T. Coleman[1]
[1]School of Veterinary Science, University of Queensland, Australia.; [2]CSIRO Agriculture Flagship, CAFHS, Australia

Resistance to the Macrocyclic Lactone drug family among important equine parasites such as cyathostomins is an emerging global problem and there is an urgent need for both quality surveillance of resistance and the development of better tools for detection. The Faecal Egg Count Reduction Test (FECRT), which is considered the gold standard for measuring resistance, lacks sensitivity and is complicated by various factors as it is applied to horses and so attention has recently been directed toward the potential use of in vitro techniques. The larval migration inhibition assay (LMIA) has been used successfully to measure differences in drug susceptibility between isolates of *Haemonchus contortus*, an important gastrointestinal nematode of sheep, however, it has not been sufficiently validated for use with cyathostomins. A modification of the 96-well plate LMIA format, developed by Kotze and co-workers (2006), was tested on various cyathostomin populations in our laboratory. IC50 values of individual populations showed a high level of repeatability between assays on the same day, however showed some inconsistency across time, indicating an effect of pre-assay storage time. The LMIA was able to demonstrate a significant difference in Ivermectin sensitivity between two cyathostomin isolates, which was not detectable via FECRT. The results from this work provide preliminary support for the potential use of the LMIA as a useful tool for the early detection of resistance in cyathostomin populations.

Creating liquid cultures of *Neoparamoebae perurans* from various cell media and a commercial antibiotic preparation

Jessica Christine Johnson-Mackinnon, Andrew Bridle, Philip Crosbie, Barbara Nowak
University of Tasmania, Australia

Amoebic gill disease is a prevalent marine disease worldwide effecting farmed Atlantic salmon (*Salmo salar).* AGD has been particularly problematic in Tasmania and is now present globally, with large scale and recurring outbreaks reported in Ireland, Scotland, France, Spain, Norway and the United States of America. It is caused by the facultative parasite, *Neoparamoeba perurans,* which is a ubiquitous marine amoebae. *N. perurans* can be successfully isolated from the gills of infected fish and grown on malt yeast agar plates with a seawater overlay. These cultures are easy to contaminate, hard to axenize and often produce less than optimal growth conditions. This study tested a dilution series of the commercially available Penacillin-Steptomycin-Neomycine (PSN). Amoebae showed the highest levels of amoebae growth in 5XPSN, though bacterial growth was still detected at the end of the 5 day time trial. No bacterial growth was achieved in 10XPSN after 2 days, however shortly after 3 days the amoebae numbers declined sharply. In addition this study compared media types (malt yeast seawater and L-15) with various putative growth factors (Serum, filtered fish mucus, and filtered dead amoebae). 5xPSN in L-15 with 10% serum in colloidal silver seawater and formalin killed bacteria showed the best growth over time.

Effects of third generation P-glycoprotein inhibitors on the sensitivity of drug-resistant and –susceptible isolates of *Haemonchus contortus* to anthelmintics *in vitro*

Ali Raza[1,2], Steven Kopp[2], Abdul Jabbar[3], Andrew Kotze[1]
[1]CSIRO Agriculture Flagship, Queensland Bioscience Precinct, University of Queensland, Australia; [2]School of Veterinary Science,University of Queensland, Australia; [3]School of Veterinary Science, University of Melbourne, Australia

P-glycoproteins (P-gps) have been implicated in resistance in a number of anthelmintics, particularly for macrocyclic lactones. Hence, inhibition of nematode P-gps has been suggested as a means of reversing some types of anthelmintic resistance. The present study aimed to investigate the ability of the most recently developed group of P-gp inhibitors to increase the sensitivity of *Haemonchus contortus* larvae to various anthelmintics *in vitro*. Larval migration and development assays were used to measure the sensitivity of larvae to anthelmintics alone, or in combination with P-gp inhibitors. Several of the inhibitors increased the sensitivity of both the drug-resistant and –susceptible isolates, while others had significant effects on the resistant isolate only. Findings of this study suggest that some of the inhibitors interact with P-gps representing intrinsic pathways present across nematode populations, while other inhibitors interact with P-gps of resistant nematodes only, thereby suggesting an acquired resistance mechanism. The study highlights the potential of the third generation of P-gp inhibitors to increase the sensitivity of nematodes to anthelmintics.

Clinical and pathological features of toxoplasmosis in free-ranging common wombats (*Vombatus ursinus*)

Shannon Lynn Donahoe[1], Jan Šlapeta[1], Graeme Knowles[2], David Obendorf[2], Sarah Peck[2], David Norton Phalen[1]
[1]University of Sydney, Australia; [2]Department of Primary Industries, Parks, Water and Environment, Australia

This study describes the clinical and pathological features of eight cases of toxoplasmosis in free-ranging common wombats in Tasmania and New South Wales (NSW) from 1992 to 2013, including a morbidity and mortality event investigated in the Southern Highlands NSW in 2010. The diagnosis of *T. gondii* infection was confirmed using either immunohistochemistry, molecular diagnostics, or both. Genetic characterization of two *T. gondii* strains identified a nonarchetypal type II-like strain (ToxoDB PCR-RFLP genotype #1) and an atypical type II-like strain (ToxoDB PCR-RFLP genotype #3) to be the causal agents of toxoplasmosis in wombats from the 2010 morbidity and mortality event. This study suggests that *T. gondii* may act as a significant disease threat to free-ranging wombats. Our findings indicate neurologic signs are a very common clinical presentation in common wombats with toxoplasmosis and that *T. gondii* infection should be considered as a likely differential diagnosis for any wombat exhibiting signs of blindness, head tilt, circling, and changes in mentation.

Diagnostic tests for *Fasciola hepatica* (liver fluke) in ruminant livestock

Tara Louise Cassidy
Charles Sturt University, Australia

The common liver fluke, *Fasciola hepatica,* is one of the most important internal parasites of livestock in many regions around Australia. Egg sedimentation from faecal samples has been the most common detection test for liver fluke infestation in live animals for several decades. However this test is very time consuming and has a low sensitivity, detecting up to only about 60-70% of infected animals (Palmer et al*.,* 2014). This project will investigate and validate a modified sedimentation technique aiming for an increased sensitivity. It will also investigate the diagnostic value for sheep of a commercially available faecal antigen ELISA test including examining how testing using pooled sheep faecal samples compares with testing individual faecal samples. The ability to test pooled faecal samples will increase the appeal of the ELISA test for commercial diagnostic testing for sheep producers.

Theileriosis: *Theileria* and anaemia in cattle

Sarah Lochore, Margaret Anderson
New Zealand Veterinary Pathology, New Zealand

In the spring of 2012, New Zealand's approach to the presence of *Theileria* changed dramatically with the introduction of a new strain, *Theileria orientalis* ikeda, that showed an increase in pathogenicity from the strain already harbored in New Zealand. This created an increased importance in the testing for this parasite. Laboratories across the country joined forces with MPI and the veterinary community to first establish the prevalence of the parasite, then map the spread of disease. This poster gives a quick overview of the diagnostic aspects of *Theileria* testing at New Zealand Veterinary Pathology.

The first report of *Bonamia ostreae* from New Zealand represents a large geographic range expansion for this important molluscan parasite

Henry Somerset Lane[1,2], Steve Webb[3], Brian Jones[2]
[1]Department of Zoology, University of Otago, New Zealand; [2]Animal Health Laboratory, IDC&R, Ministry for Primary Industries, New Zealand; [3]Cawthron Institute, New Zealand

This is the first New Zealand report of the Haplosporidian parasite *Bonamia ostreae* in the New Zealand flat oyster *Ostrea chilensis.* The genus *Bonamia* contain protistan (Haplosporidian) parasites that infect the haemocytes of oysters. Until now, *B. ostreae* has been restricted to the Northern Hemisphere, including Europe, the United Kingdom and eastern United States of America. There*, B. ostreae* has caused substantial losses in production of the European flat oyster *O. edulis.* In New Zealand *Bonamia exitiosa* is considered endemic in the New Zealand flat oyster, *O. chilensis,* and has been responsible for large epizootics within the Foveaux Strait flat oyster fishery. In 2014, samples of *O. chilensis* sampled from the Marlborough Sounds, were submitted to the Cawthron Institute for processing. Histological examination of these samples revealed heavy haemocyte infiltration, with *Bonamia* microcells present within the haemocyte cytoplasm and free within the connective tissue. DNA sequencing of a 300bp portion of the 18S rDNA produced a DNA sequence match of 100% to *B. ostreae.* All DNA sequenced products also produced an expected PCR-RFLP profile of *B. ostreae.* This is the first report of *B. ostreae* from New Zealand and is representative of a large geographical range expansion of this OIE-listed parasite.

Towards the discovery of novel sites of anthelmintic action

Samantha Emery[1], Andrew Crombie[2], Daniel Vuong[2], Ernest Lacey[2], Andrew Piggott[1]
[1]Macquarie University, Australia; [2]Microbial Screening Technologies, Australia

The widespread use of anthelmintics has inevitably led to an increase in the prevalence of poly-anthelmintic resistance in parasitic nematodes. This situation is compounded by the paucity of novel anthelmintic candidates arising from synthetic chemistry, leaving researchers in an evolutionary arms race that only mitigates, rather than solves, increasing drug resistance. Consequently, there is an increasing urgency to utilise unexplored chemistries in the search for new anthelmintic compounds. Microbial natural products offer a diverse range of novel compounds, with leads to many new chemical classes. After the successes of avermectin and derquantel, it is time to take another leaf out of Nature's playbook. Microbes have evolved nematocides over eons, yet resistance has never occurred in nature. In this presentation, we report the discovery of maniwamycins as inhibitors of *in vitro* larval development against poly-resistant and susceptible *Haemonchus contortus* (barber's pole worm). The maniwamycins inhibited development L_1 to L_2 larval transition, independent of resistance status. These metabolites offer a valuable new lead in the hunt for a novel site of anthelmintic action.

Identification of antigenic tegument proteins of *Fasciola hepatica* recognised following immunosloughing of surface proteins by antibody from resistant ITT sheep

Timothy Charles Cameron[1], Hayley Toet[1], David Piedrafita[2], Ira Cooke[1], Pierre Faou[1], Terence Spithill[1]

[1]La Trobe University, Australia; [2]Federation University, Australia

Infection of livestock with *Fasciola hepatica* causes serious economic losses worldwide. The parasite sheds tegumental proteins from its surface as a precipitate when protein antigens are bound by an antibody, potentially suppressing the ability of the host immune effector cells to attack the parasite by ADCC mechanisms. The aim of this experiment was to determine which fluke proteins are shed by the parasite to uncover surface antigens. Live adult *F. hepatica* were harvested from experimentally infected rats and incubated for 1 hour in the presence of purified immune (week 4) or pre-immune (week 0) IgG taken from an experimental infection of Indonesian Thin-Tail sheep, which have previously been shown to express acquired immunity to *F. gigantica* infection. The sloughed precipitate from each parasite was collected, washed, analysed by MS/MS and the peptide hits were screened through *F. hepatica* databases. 21 *Fasciola* proteins were identified to have a significantly higher intensity of peptide hits ($p<0.05$) in the immune pellet when compared to the pre-immune pellet, while 2 proteins showed significantly lower intensity. An additional 29 proteins of interest were identified only in the immune precipitate. This is the first report of antigens immunosloughed from adult flukes.

PD-1 dependent exhaustion of $CD8^+$ T cells drives chronic malaria

Deshapriya Karunarathne, Joshua Horne-Debets, Michelle Wykes, Rebecca Faleiro

QIMR Berghofer Medical Research Institute, Australia

Malaria, caused by *Plasmodium* parasites, is a highly prevalent and devastating disease that can persist for years. There has been considerable difficulty in developing a malaria vaccine, highlighting our incomplete understanding of immunity against this disease. Antibodies and $CD4^+$ T cells are thought to protect against blood-stage infections. We used an experimental rodent malaria model, to show that programmed death-1 (PD-1) mediates a 95% reduction in numbers and functional capacity of parasite-specific $CD8^+$ T cells during acute malaria, driving chronic disease. Furthermore, we demonstrated PD-1 also affect $CD4^+$ T cell function that, improved effector $CD4^+$ and $CD8^+$ T cell function during the chronic phase of infection, compared with wild-type mice. Importantly, in contrast to widely held views, parasite-specific $CD8^+$ T cells are required to control both acute and chronic blood-stage disease even when parasite-specific antibodies and $CD4^+$ T cells are present. Our findings provide a molecular explanation for chronic malaria which will be relevant to future malaria-vaccine design and may need consideration when vaccine development for other infections is problematic.

Impact of experimental *Haemonchus contortus* infection on the sheep gut microbiota

Md Abdullah Al Mamun[1,2], David Piedrafita[1,2], Mark Sandeman[2], Andrew R. Greenhill[2]

[1]Monash University, Faculty of Science, Australia; [2]Federation University, Faculty of Science and Technology, Australia

The gut microbiota is an integral part of host physiology and contributes to immune system development. In recent years, interest in the response of host gut microbiota during host–parasite interactions has increased. However, little is known on the impact of the harmful parasite *Haemonchus contortus* on the gut microbiota of sheep. We used a rapid, low-cost community fingerprinting technique known as Automated Ribosomal Intergenic Spacer Analysis (ARISA) to determine the differences in composition and relative abundances of faecal microbiota of sheep (n=28) with known genetic traits for parasite resistance, before and following *H. contortus* infection. We found evidence of changes in microbial community structure following infection; coinciding with a minor increase in microbial species richness, and slight decreases in relative abundance and frequency of detection of dominant microbial species. Based on genetic information and faecal egg counts, there is no clear correlation between gut microbiota and resistance to *H. contortus*; however, sheep resistant to *H. contortus* infection appear to have a more stable gut microbiota pre- and post-challenge relative to susceptible sheep. We are yet to elucidate a clear link between the gut microbiota of sheep (using faecal pellets) and resistance to infection, but our data do suggest slight perturbation of the gastrointestinal flora due to *H. contortus* infection which may be more prominent in susceptible sheep. Ongoing data analysis, and 16S metagenomics on faecal specimens and samples from the gastrointestinal tract, will further improve our understanding of the relationship between *H. contortus* infection and the sheep gut microbiota.

The development of a whole *Plasmodium* parasite blood-stage vaccine utilizing apicoplast-knockout parasites generated by chemical treatment

L.M. Low, D.I. Stanisic, M.F. Good

Institute for Glycomics, Griffith University, Australia

Malaria is an infectious disease that causes significant morbidity and mortality worldwide. The dependency of the malaria parasite on the apicoplast provides another avenue for vaccine development. Published work has shown *Plasmodium falciparum* can be chemically rescued from apicoplast-inhibitors (doxycycline) using isopentenyl pyrophosphate (IPP)(1). This project aims to investigate the use of chemically rescued parasites as a whole parasite blood-stage vaccine approach. Published *in vitro* methodology is being optimized in different strains of *P.falciparum.* Short-term assays (144h) indicated optimal concentrations of 2uM doxycycline and 100uM IPP; however longer culture periods suggest incomplete apicoplast-knockout and need for increased attenuation time with doxycycline. A rodent model is being established to investigate the generation of apicoplast-knockout rodent *Plasmodia in vitro* and *in vivo.* We determined all rodent *Plasmodia* as doxycycline sensitive and are investigating *in vitro* assays by examining viability of cultured *P.chabaudi* over a 24h period for comparison with *in vitro* doxycycline-treated parasites.A pilot study conducted to generate apicoplast-knock out *P.chabaudi* in mice indicated the need for the development of a LC/MS assay to examine the pharmacokinetics of IPP. The use of an apicoplast-knockout parasite as a vaccine is a novel approach and yet to be attempted in an *in vivo* model.

Molecular eco-epidemiology of *Triatoma brasiliensis,* the most important Chagas disease vector in Northeastern Brazil: high natural *Trypanosoma cruzi* infection associated with feedings on *Kerodon rupestris* (Rodentia: Caviidae)

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A molecular-based multi-source approach over a small geographic scale in Caicó city, Rio Grande do Norte, Brazil was conducted to assess the epidemiological importance of 297 *Triatoma brasiliensis* collected in distinct sites and ecotopes. First, we explored the vector genetic structure by using both cytochrome b (cytb) and microsatellite markers. Second, we determined the *Trypanosoma cruzi* natural infection prevalence and parasite diversity in bugs; and third, we identified *T. brasiliensis* natural feeding sources in distinct ecotopes by using the blood meal content, via vertebrate *cytb* analysis. Potential reservoirs were inferred by detecting the feeding sources and natural *T. cruzi* infection in the same insect population. Genetic structure revealed similarities between the domiciliary and peridomiciliary *T. brasiliensis* populations, indicating that the peridomicile may serve as sources for domiciliary re-colonizations. What is of concern, is that the peridomiciliary population was also related to a sylvatic, suggesting that insecticide spraying in houses is unlikely to be totally effective in eliminating this vector. High *T. cruzi* infection rates (53-79%) and two co-occurring strains were found in sylvatic environments. We suggest that *Kerodon rupestris* rodent is the primary *T. cruzi* reservoir due to its high index of blood meals detected with *T. cruzi* infection. *Galea spixii* rodent seems to be the secondary reservoir because it is found as a *T. brasiliensis* feeding source in sylvatic and peridomiciliary areas, likely linking sylvatic and domiciliary *T. cruzi* cycles.

Regulation of intrinsic apoptosis in cycloheximide-treated macrophages by Sichuan human strain of Chinese *Leishmania* isolates

Jin Zeng[1], Qi-Wei Chen[1], Ze-Ying Yu[1], Jun-Rong Zhang[1], Jian-Ping Chen[1,2]

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Leishmania spp. are able to survive and proliferate inside mammals' mononuclear phagocytes causing a spectrum of leishmaniasis. Previous studies have pointed out that regulation of apoptosis in host cells by these parasites may contribute to their immune evasion. However, results from the latest research remain controversial and the regulation effect of *Leishmania* has been found to be species- and strain-dependent. The aim of this study was to investigate whether the Sichuan isolates of Chinese *Leishmania* (SC10H2) could alter the process of intrinsic apoptosis induced by cycloheximide in different types of macrophage cell lines and to determine in which steps of the whole signaling pathway the parasites are involved. Human THP-1 and mouse RAW264.7 macrophages were infected by SC10H2 promastigotes followed by cycloheximide stimulation and alteration of intrinsic apoptosis was assessed. Results indicated that infection of SC10H2 to human THP-1 macrophages could promote the initiation of intrinsic apoptosis. Interestingly, totally opposite results were found in mouse RAW264.7 macrophages. Nevertheless, expression of Bcl-2 and the ratio of DNA fragmentation had not been changed by infection of SC10H2, neither in THP-1 nor in RAW264.7 cells. This study suggested that SC10H2 promastigote infection was able to promote apoptosis induced by cycloheximide in THP-1 macrophages and delay apoptosis induced by cycloheximide in RAW264.7 macrophages, revealing that regulation of intrinsic apoptosis in host cells by SC10H2 *in vitro* was in a species-dependent manner. Data from this study might play a significant role in furthering understanding of the relationship between Chinese *Leishmania* isolates and different host cells.

Study of experimental infection and comparative proteome analysis of Chinese *Leishmania* Isolates(SC10-H2)

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Leishmania, the causative agent of leishmaniases, is an intracellular parasite of macrophages. Knowledge of the differential expression of *Leishmania* between promastigotes and amastigotes could lead to further understanding of its virulence and invasion mechanism. The aim of this study was to conduct the optimal condition to gain amastigates and to investigate the different protein expression between promastigotes and amastigotes. Two different macrophages, Human THP-1 and mouse RAW264.7 macrophages, were be used in this study. Both were infected by promastigotes in series ratios at different incubation times. Morphology changes of *Leishmania* were observed by light microscopy and the amastigotes were confirmed by transmission electron microscopy. The different extraction proteins of amastogotes and promastogotes were identified by SDS-PAGE and western-blot analyses. The results show that although the proliferation cycle varies with different cells, amastigotes in both cells can be observed in 72 hours. Our study harvest the amastigotes at the ratio of 10:1 after culture for 120 hours. SDS-PAGE and western-blot analyses show that there exists a 70KD protein in amastigotes which is not found in proteigotes. The conclusion is that we have conducted the infection model and there exist differences between the proteins which are expressed by the two stages of *Leishmania*.

Disruption of the digestive vacuole of *Plasmodium falciparum* induces phagocytosis by monocytic THP-1 cells

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In *Plasmodium falciparum* infection, malaria manifests at the erythrocytic stage and this is typically the point when clinical intervention occurs. Upon invading an erythrocyte, *P. falciparum* matures and develops a distinctive digestive vacuole (DV) in which hemoglobin is digested and the toxic heme byproduct sequestered as hemozoin. Recent work in our laboratory showed that upon permeabilization of this vacuole, certain apoptosis-like features are induced. Interestingly, these phenotypes were mitigated by pretreatment with a Ca^{2+} chelator, BAPTA, or a clan CA cysteine protease inhibitor. Similarly, human erythrocyte

programmed cell death (eryptosis) is mediated by cytosolic Ca^{2+} and activation of calpain, a clan CA protease. Given the parallels in food vacuole disruption-induced death and eryptosis, we set out to investigate if permeabilization of the vacuole can result in eryptosis and subsequent phagocytosis, possibly providing a therapeutic strategy for the rapid clearance of parasitemia. Post-treatment, late-stage parasites were stained with dihydroethidium and coincubated with the monocytic cell line THP-1. Unphagocytosed erythrocytes were lysed and the remaining THP-1 cells analyzed by flow cytometry; coculture with DV-disrupted parasites resulted in increased dihydroethidium uptake. Interestingly, pretreatment of parasites with BAPTA-AM but not BAPTA salt or EGTA suppressed the apparent phagocytosis.

Investigating the ecology of parasite transmission in fauna translocations and the impact of polyparasitism in translocated woylies (*Bettongia penicillata*)

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The critically endangered woylie (*Bettongia penicillata*) once occupied regions across the mainland, however is now confined to just a few sites southwest of Western Australia. Although fauna translocations provide an invaluable tool to help alleviate declining populations, there is limited understanding of parasite transmission in translocated populations, and the incidence of polyparasitism within those individual hosts. This project addresses these uncertainties by investigating how fauna translocations impact the transmission of parasites in the woylie and what consequences this has for translocated hosts and other cohabiting species. In June 2014, 182 woylies were translocated from Perup Sanctuary into two unfenced sites within Western Australia. Blood, ectoparasites and faecal samples were collected at source and destinations sites, pre- and post-translocation. Anti- parasite treatment was also assessed to see if it has an effect on the translocated host and the recipient ecosystem. In each destination site, cohabiting species were sampled to quantify parasite transmission between species post-translocation. Using molecular analyses, we have observed changes to the predominant species of *Trypanosoma* in woylies pre- and post-translocation, and that anti-parasite treatment has had an effect on both target and non-target parasites of the translocated hosts.

Using next generation sequencing to reveal zoonotic pathogens in archived ticks

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Implicated in transmitting a greater variety of pathogenic microorganisms than any other arthropod group, ticks (Acari: Ixodida) are the latest ectoparasites to have their viral and bacterial communities characterised through the use of next generation sequencing (NGS) techniques. Ticks and other micropredators archived in museum collections are a previously untapped source of investigating infectious diseases, and could provide valuable data from such molecular advances. The aim of this study was to identify the presence or emergence of pathogenic bacteria in ticks over the past Century using NGS. To demonstrate the viability of the bacterial profiling approach, arDNA successfully isolated from 19 ticks (*Haemaphysalis longicornis*, n=2; *Ixodes cornuatus*, n=2; *I. holocyclus*, n=10; *I. tasmani*, n=5) acquired from the Australian National Insect Collection, CSIRO Canberra, were amplified using the universal bacterial 16S rRNA gene (V1-2) and sequenced using the Ion Torrent semiconductor NGS platform. Preliminary results revealed both environmental and pathogenic bacteria preserved in the archived ticks. Bacterial genera of particular animal and human health interest were *Francisella* sp., *Rickettsiella* sp. and *Rickettsia* sp. This pilot study suggests that archived ticks provide a means to document the emergence of infectious diseases in Australia.

Antibodies to the *Plasmodium falciparum* proteins MSPDBL1 and MSPDBL2 opsonize merozoites, inhibit parasite growth, and predict protection from clinical malaria

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Increasing evidence suggests that antibodies against merozoite surface proteins (MSPs) play an important role in clinical immunity to malaria. Merozoite surface protein duffy binding-like (MSPDBL)1 and MSPDBL2, have been shown to be extrinsically associated to MSP-1 on the parasite surface. In addition to a secreted polymorphic antigen associated with merozoite (SPAM) domain characteristic of MSP-3 family members, they also contain Duffy binding–like (DBL) domain and were found to bind to erythrocytes, suggesting that they play a role in parasite invasion. Antibody responses to these proteins were investigated in a treatment-reinfection study conducted in an endemic area of Papua New Guinea to determine their contribution to naturally acquired immunity. Antibodies to the SPAM domains of MSPDBL1 and MSPDBL2 as well as the DBL domain of MSPDBL1 were found to be associated with protection from Plasmodium falciparum clinical episodes. Moreover, affinity-purified anti-MSPDBL1 and MSPDBL2 were found to inhibit in vitro parasite growth and had strong merozoite opsonizing capacity, suggesting that protection targeting these antigens results from ≥2 distinct effector mechanisms. Together these results indicate that MSPDBL1 and MSPDBL2 are important targets of naturally acquired immunity and might constitute potential vaccine candidates.

Population genomic structure of *Plasmodium falciparum* in Papua New Guinea

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Papua New Guinea (PNG) has the highest burden of malaria outside of Africa with intense year-round transmission. The country's extremely diverse biogeography contributes to variable parasite population dynamics and transmission. Recently, we

have shown that the population structure of *Plasmodium falciparum* on the north coast of PNG is fragmented. Should population fragmentation and structure be observed throughout PNG then mapping of this geographical diversity will enable the monitoring of population changes, identification of migration routes, predict drug resistance spread, and pinpoint the source of outbreaks. Such knowledge is invaluable for malaria elimination and control programmes. Using microsatellite, mitochondrial, and genome wide single nucleotide polymorphism (SNP) data, we are investigating *P. falciparum's* genome dynamic nature, and demographic structure, exploring fundamental biological questions regarding the genetic history. In addition, we are working towards defining a high-resolution map of parasite population networks and migration patterns throughout PNG using a panel of geographically informative SNPs and a national cross-sectional *P. falciparum* dataset of isolates. These results will have direct translational benefits by identifying isolated populations to target for elimination, and will provide a database of genotypes to map the origins of imported infections and outbreaks in areas where malaria is normally absent.

Transcriptomic profiling of host skin immune responses to infestation with *Sarcoptes scabiei* in a porcine model.

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Scabies is one of the most prevalent skin diseases affecting over 100 million globally. The prevailing knowledge of the disease processes and host immune response mechanisms is limited, and to identify novel vaccine and drug targets a better understanding of the host-parasite relationship is essential. The objective of this study was to perform gene expression analysis of the skin immune response to infestation with *Sarcoptes scabiei* in a porcine model to gain a better understanding of the mechanisms and signalling pathways involved. Transcriptomic analysis was performed with the Agilent Porcine Gene Expression Microarray platform and differential gene expression was determined in Partek. Work is ongoing and so far we have found that in crusted vs ordinary scabies, 1854, 1461, 3101, 227 and 982 genes were found to be significantly differentially expressed at weeks 0, 1, 2, 4 and 8 post-infestation, respectively. To further elucidate the mechanisms and signalling pathways involved we will utilize a network/pathway based analysis representing all differentially expressed genes using the Ingenuity Pathway Analysis program. To verify the differential gene expression, qRT- PCR confirmation will be carried out for selective genes from the final list. The outcome of this study will enable the elucidation of the temporal patterns of gene expression through which the host response is regulated.

Parasitic disease prevalence and control in Sichuan, China

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Sichuan Province is located in southwestern China, occupying an area of 485,000 km2, with a total population of more than 80,760 million. The major parasitic diseases are the following. (1) Schistosomiasis is mainly prevalent in hilly and mountain areas distributed across 11 cities (prefectures) and 63 counties in Sichuan. There were 1794 patients in an advanced stage of infection at the end of 2014. But no acute-stage patient nor infected snails have been found for 10 years; no locally infected patient nor cattle were reported in 5 years. (2) Echinococcosis is dominantly distributed in 35 counties across the Qing-Tibet plateau area. A large number of dogs and a nomadic production style maintain the transmission of echinococcus worms between dogs and domestic animals. An epidemiological survey showed the prevalence of echinococcosis (cystic and alveolar) was 1.08% in humans. Dogs were asked to be treated with Praziquantel monthly and the infection was monitored by coproantigen detection. (3) Malaria was serious 50 years ago. But no locally infected patient has been found since 2011. All prevalent areas should achieve the goal of elimination in 2017. (4) The infection of soil-transmitted nematodes in humans was 40.85% in 2004. After implementing interventions including Albendazole treatment, health education, water supply and sanitation improvement, the average infection of hookworm, pinworm, roundworm and whipworm was 7.66%, 0.66%, 0.29% and 7.79%, respectively, in 2014. In control, comprehensive measures have been implemented focusing on a government-dominated multi-sectoral cooperation model. Usually, the central government funds the control project while the local government is asked to provide the counterpart funding.

Intestinal parasitosis in relation to CD4+T cells levels and anemia among HAART initiated and HAART naïve pediatric HIV patients in model ART Center, Addis Ababa, Ethiopia

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The aim of the study was to determine the prevalence of intestinal parasites in relation to CD4+ T cells levels and anemia among HAART initiated and HAART naïve pediatric HIV patients in a model ART center in Addis Ababa, Ethiopia. A comparative cross-sectional study was conducted among HAART initiated and HAART naive pediatric HIV/AIDS patients attending a model ART center 180 (79 HAART initiated and 101 HAART naïve) children were enrolled consecutively. Stool specimen and a socio-demographic data and associated risk factors were collected. Logistic regressions were applied to assess any association between explanatory factors and outcome variables. The overall prevalence of IPs was 37.8% where 27.8% of HAART initiated and 45.5% of HAART naive pediatric HIV/AIDS patients were infected ($p<0.05$). The overall prevalence of anemia was 10% in HAART and 31.7% in non-HAART groups. *Hook worm*, *S. stercoralis* and *H. nana* were helminthes significantly associated with anemia in non-HAART patients [AOR, 95% CI: 4.5(1.3, 15.2), $P< 0.05$]. The prevalence of IPs in non-HAART patients was significantly associated with eating unwashed/raw fruit [AOR, 95%CI: 6.3(1.2, 25.6), $P<0.05$], open field defecation [AOR, 95%CI: 9.3(1.6, 53.6), $P<0.05$] and diarrhea [AOR, 95%CI: 5.2(1.3, 21.3), $P<0.05$]. IPs significantly increased in rural residents [AOR, 95%CI: 0.4(0.1, 0.9, $P<0.05$)]. The overall prevalence of intestinal parasites significantly differed by HAART status and *Cryptosporidium* species were found only in HAART naïve patients with low CD4+ T cell counts. Anemia was also more prevalent and significantly associated with IPs in non-HAART patients.

Incidence of dicrocoeliasis among local and imported Naheemi sheep in Riyadh Region

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Dicrocoelium dendriticum is a common liver fluke of sheep and other herbivorous animals. Examination of sheep livers for *D. dendriticum* worms revealed the infection rate reached to 22.3%. This rate was decreased to 14.86% ($p<0.01$) after diagnoses of infection in the same animals via detection of eggs by fecal examination. The rate of infection considered to be low in local Naheemi sheep (6%) in comparison with the same sheep type imported from Turkey as the rate reached 16.3%. There is an indirect relationship between the increase in the rate of infection and age of the examined sheep. The high rate of infection (52.9%) was recorded among sheep of 25-36 months old, followed by that of 13- 24 month olds (18.4%) and the lowest rate of infection (9.6%) was recorded in sheep aged 6-12 months ($p< 0.01$) The seasonal distribution of dicrocoeliosis indicated a higher percentage of infection in Winter and Autumn (19.2%, 18.5%, respectively) compared with Spring and Summer (13.3%, 9.3%, respectively). The infection with dicrocoeliasis only was 8% while dicrocoeliasis with other heminthic worms (*Fasciola gigantica, Moniezia expansa, Strongyloides papillosus, Trichuris globulosa, Nematodirus spathiger, Haemonchus contortus, Ostertagia circumcincta, Marshallagia marshalli*) was 6.86%.

Impact of seasonal patterns and parasite asexual stage on *Anopheles gambiae* susceptibility to *Plasmodium falciparum* infection in Burkina Faso

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Transmission reduction is a key component of global efforts to control and eliminate malaria. A wide range of novel transmission-reducing drugs and vaccines are currently under development. Currently, it is unclear how the densities of the parasite stages or the season influence the infection rate and its intensity. Here, we highlighted the importance of the *Plasmodium falciparum* stages seasonal pattern in *Anopheles gambiae* infections success. For that, gametocyte carriers' infectiousness to mosquitoes was determined at the peak and end of wet season and dry season via membrane feeding assay. Infection prevalence and intensity were determined 1 week after feeding. About 28,062 mosquitoes offered blood meal and 29.6% fed and survived until dissection. The average number of dissected mosquitoes 75 (range 18 – 207) was similar according to the assay period. In 71.8% (79/110) of feeding experiments, at least one mosquito was infected. The median percentage of infected mosquitoes per infectious experiment was 15.7% (IQR: 07.3- 89.2 %) with a median oocyst number of 2 (range 1 – 101). The prevalence of infected blood meal was similar across season (70.0%, 72.7% to 70.1% at the dry, the peak, and the end of the wet season. Mosquitoes' infection rates did not show any significant variation within season. The infection success was higher for asexual parasites carriers (91%) than non-carriers (9%). However, mosquitoes' infection rates and oocyst loads did not significantly vary according to the asexual forms carriage. This highlights the need to carefully interpret evaluations, regarding asexual parasites and transmission season for malaria control programs.

Results of helminthological examinations of wild hoofed animals after using the praparation "Ivirsalt" at nematodosis (National Park "Losiny Ostrov"/"Elk Island"), Russia, Moscow)

Nina Samoylovskaya
All-Russian Scientific Research Institute of Fundamental and Applied Parasitology of Animals and Plants named after K.I. Skryabin, Russian Federation

Elks and dappled deer infested with helminthes were used in this study. The purpose of this work was to study the efficacy of a new antiparasitic drug "Ivirsalt" used for prevention of helminth infections in wild hoofed animals. The therapeutic efficacy of the new anthelmintic drug "Ivirsalt" used for treatment of nematodosis in wild hoofed animals was tested on 120 dappled deer, 7 elks and 1 roe deer in the National Park "Losiny Ostrov". "Ivirsalt" is in the form of briquettes (licks) with a mass of 5 kg containing the active ingredient ivermectin and sodium chloride in the proportion 0.1: 99.9. Salt lick briquettes were put in the feed-troughs at feeding places and saline soils based on the average daily salt consumption. The preparation was given within 14 days, taking into account that the animals approach salt lick briquettes not less that once per week. To determine the efficacy of the preparation using coproscopy, the fecal samples were collected before and every 10 days after distribution of the salt lick briquettes. Standard life-time and post-mortem helminthological examinations of animals were performed (coproovoscopy, K.I. Skryabin method of full post-mortem helminthological examination, 1928). The intensity of gastrointestinal nematode infestations in dappled deer aged 1.5 to 3 years decreased by 5.4 times and in deer older than 3 years, by 3.1 times.

In vitro activity and therapeutic potential of 20 novel aminoguanidines against *Trypanosoma brucei* and *Leishmania donovani*

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Trypanosomatids are a significant cause of human morbidity and mortality worldwide with an estimated 1.3 million new infections occurring annually. Each year *Leishmania* sp. alone are thought to account for ~30 000 deaths in tropical and subtropical regions; while *Trypanosoma brucei* threatens the welfare and productivity of ~ 66 million people in developing countries. Current therapies for these organisms are limited and have notable toxic side effects. Therefore it is important that new therapeutic agents be developed for treatment of these diseases. In this study, a series of 20 novel aminoguanidines were evaluated for efficacy against the procyclic stage of *T. brucei* and the promastigote stage of *L. donovani* using a resazurin reduction assay. Active compounds were also examined for cytotoxicity in murine macrophages. Of the 20 compounds tested, 6 showed ≥80% inhibition against *T. brucei* at 10 µM while 14 showed similar inhibition against *L. donovani.* The IC_{50} of the most active compounds ranged from 1.3 – 4.1 µM and 0.29 – 6.48 µM against *T. brucei* and *L. donovani,* respectively. Based on this study, some highly efficacious and selective compounds were identified which will be further characterised using the amastigote stage of *L. donovani* before evaluation of the *in vivo* efficacy.

P2: Elsevier Plenary Lectures

Time: Wednesday, 01/Jul/2015: 9:00am - 10:30am · *Location:* Plenary Room
Session Chair: Alex Loukas, James Cook University
Session Chair: Andrew Kotze, CSIRO
Session Chair: Andrew Thompson, Murdoch University

The ups and downs of life: population expansion and bottlenecks of helminth parasites through their complex life cycle

Robert Poulin, Clement Lagrue
Zoology Dept, University of Otago, New Zealand

The fundamental assumption underpinning adaptations shown by parasites with complex life cycles is that huge losses are incurred by infective stages during transmission. However, the magnitude of transmission losses or changes in the standing crop of parasites passing from upstream (source) to downstream (target) hosts have never been quantified in nature. We aimed to address this knowledge gap. Using field data from pairs of successive upstream-downstream life stages, from distinct populations representing 10 freshwater parasite species, we calculated the total size of successive life cohorts. We show that clonal amplification of trematodes in their first intermediate host leads to an average 4-fold expansion of numbers of individuals at the next life stage across multiple trematode taxa in the field. In contrast, trophic transmission to the definitive host results in little numerical change for trematodes, but in large decreases for acanthocephalans and nematodes. We also found a positive association between upstream and downstream cohort sizes for transmission involving free-swimming cercariae in trematodes, suggesting a simple output-recruitment process, but not for trophic transmission. These first quantitative estimates of ontogenetic rises and falls in numbers under natural conditions provide new insights into the selective pressures acting on parasites with complex cycles.

Ecological collision: climate, perturbation and colonization - lessons about assembly of the biosphere

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Complexity characterizes the structure and assembly of the biosphere across space and time, yet our explanatory universe has focused on processes that traditionally emanate from long-term stability. Over the past century ideas about cospeciation (association by descent) have dominated and constrained parasitological thinking, in the face of strong empirical evidence of a more tumultuous, intricate and complex world beyond our windows. Through Earth-history the world has been under dynamic change driving macroevolutionary processes, patterns of diversification and often rapidly shifting or expanding host and geographic distributions. Interacting mechanisms related to climate and ecological perturbation represent a thread of equivalent processes that have, to a considerable extent, determined mosaic faunal assembly in a continuum linking evolutionary and ecological time. That cospeciation is not a dominant driver is significant, contrasting with current concepts that a potential for host switching and emergent patterns of disease may be constrained by narrow evolutionary dependence among parasites on a limited spectrum of related hosts unless influenced by evolution of novel capacities for host exploitation. We can readily recognize that parasites are resource specialists, but concurrently the extensive nature of host colonization is evident. This *Parasitological Paradox* is resolved through interacting mechanisms- *Ecological Fitting* providing opportunities for rapid host switching in changing environments; *Oscillation* leading to alternation in the evolution of generalists and specialists; *Geographic Mosaic Theory of Coevolution* in addressing the generation of novel combinations of interacting species over time; and *Taxon Pulses* whichestablish an episodic context for perturbation as a driver of host and geographic colonization. A paradigm encompassing the pervasive nature of colonization predicts that emerging diseases will be common rather than rare and isolated events during a regime of accelerating climate change and ecological perturbation.

Uncovering the mysteries of anthelmintic resistance: the more we learn the less we seem to know

Ray M. Kaplan
University of Georgia, United States of America

A major shift in the paradigm of modern parasite control began in 1961 with the introduction of thiabendazole. More benzimidazole (BZ) compounds soon followed, and over the next 20 years the membrane depolarizer and avermectin/milbemycin (macrocyclic lactone; ML) classes of anthelmintics were discovered and marketed. Administration of these drugs at frequent intervals to the entire herd provided great health and productivity gains, and rapidly became the new model for parasite control. However, with the introduction of each new anthelmintic class, reports of resistance soon followed. By the early 1990's the mechanism of resistance (MOR) to BZ was elucidated, and molecular diagnostic assays for detecting BZ-resistance were developed soon thereafter. Given this accomplishment, and the exciting new technologies available, many parasitologists shared optimistic expectations that discovery of the MOR and the development of molecular diagnostic assays for the other major anthelmintic classes would soon follow. However, it is now quite clear that these expectations were overly optimistic; 30 years after the first report of ivermectin resistance in *Haemonchus contortus*, we still know quite little about the mechanisms responsible. For many years we thought that the ML exerted their anti-nematodal effects by binding to glutamate-gated chloride channels, leading to pharyngeal and somatic muscular paralysis and worm death. However, we now know that these drugs have additional MOA. Abamectin has recently been shown to antagonize some subtypes of nematode nAChR, and ivermectin recently was shown to have profound inhibitory effects on chemosensory behavior. If we are only discovering these novel mechanisms now after decades of research, how many more might there be that we have not yet discovered? This is especially humbling when one considers that we don't know the function of >40% of all nematodes genes. Another contradiction to established dogma is the development of ML resistance in dog heartworm in the region of the United States of America with the highest levels of refugia, and relatively low treatment coverage. The only reasonable conclusion is that the more we learn about anthelmintic resistance in parasitic nematodes, the more we realize how little we actually know.

Symposium 6: Ecology of Parasitism 1

Time: Wednesday, 01/Jul/2015: 11:00am - 11:30am · *Location:* Symposium Room 1
Session Chair: Haseeb Sajjad Randhawa, University of Otago

Effect of *Toxoplasma gondii* infection on agriculture and wildlife: a New Zealand perspective

Laryssa Howe, Wendi Roe, Kandarp Patel, Peter Wilson
Massey University, New Zealand

Toxoplasma gondii is a parasite of significant medical and veterinary importance worldwide and infects approximately 43% of New Zealanders with prevalence increasing with age. *T. gondii* infection can be life-threatening in immune-suppressed or congenitally infected patients, may alter personality attributes and is also a risk factor for the development of schizophrenia and depression in humans. Over the last 5 years, we have identified both fatal and chronic infections in the endangered Hector's dolphins and several species of native birds. In addition, current studies are suggesting the *T. gondii* is playing a significant role in poor reproductive performance in farmed deer. Highlights of these studies and additional *T. gondii* prevalence data in domestic cats and shellfish will be presented. The possible role of feral domestic cats and contamination of fresh and marine environments resulting in decreased reproductive performance of livestock and mortality in wildlife will be discussed.

Symposium 7: Drug Discovery

Time: Wednesday, 01/Jul/2015: 11:00am - 11:30am · *Location:* Symposium Room 2
Session Chair: Kathy Andrews, Griffith University

An image-based platform identifies compounds with novel activity against *Trypanosoma cruzi*

Melissa Sykes, Vicky Avery
Eskitis Institute for Drug Discovery, Australia

Chagas disease, caused by the protozoan parasite, *Trypanosoma cruzi,* has been recognized by the World Health Organization (WHO) as one of the world's 17 most neglected tropical diseases. Treatment of Chagas disease is limited to two drugs, benznidazole and nifurtimox, which have demonstrated side effects and variable efficacy against the chronic phase of the disease. In an aim to identify new compounds with activity against *T. cruzi*, a phenotypic, high-content, 384-well image-based assay was developed to estimate the effect of compound treatment on *T. cruzi* amastigote infected 3T3 mouse fibroblasts. In the same well, the effect of compound activity on host cells could also be determined. The high-throughput assay has been utilised to profile the activity of a collection of 25,000 chemically diverse compounds, optimised for lead-like properties. From this library, two compounds were identified with selective activity against the parasite, with estimated IC_{50} values for compound 1 of 0.77µM and compound 2 of 4.2µM with selectivity indexes in relation to the host cell of between >95 and >18, respectively. Compound 1 exhibited a sub- optimal plateau (74% removal of parasites) following 48 hours exposure, however compound 2 removed over 96% of the parasite population. The effect of incubation time on the efficacy of these compounds will be discussed, along with testing against an alternative mammalian cell line and the trypomastigote life cycle form of the parasite. These compounds are novel hits against the parasite and serve as promising starting points for further biological and chemical evaluation.

CP 6: Ecology of Parasitism Contributed Papers 1

Time: Wednesday, 01/Jul/2015: 11:30am - 12:30pm · *Location:* Symposium Room 1
Session Chair: Haseeb Sajjad Randhawa, University of Otago

Upstream, downstream: spatial and temporal variations of a parasite in its first and second intermediate host

Tommy Leung, David Rex Mitchell
Zoology, School of Environmental and Rural Science, University of New England, Australia

Parasite abundance varies considerably over both spatial and temporal scales. Such variations are shaped by a multitude of factors including host distribution, host density, and the parasite's dispersal ability. Parasite abundance can also be influenced by seasonal and climatic variations that affect their infectivity, reproductive output, and lifespan of infective stages. For parasites with multi-host life-cycle, changes in a parasite's abundance in one host species can also have direct consequences on their abundance in downstream hosts. We investigated the fine spatial and seasonal variations in the abundance of a microphallid trematode in its first intermediate host, the snail *Posticobia brazieri*, and its second intermediate host, the glass shrimp *Paratya* sp. Snails and shrimps from the Gwydir River in New South Wales, Australia were collected over the course of 5 months and their infection levels were quantified. We detected significant seasonal and fine scale spatial variations in parasite abundance in both the snail and shrimp hosts. Additionally, infection prevalence in snails and intensity in shrimps were both correlated with host body size. I will be discussing the potential implications of such infection patterns for the life cycle of this microphallid trematode in its first and second intermediate hosts.

An apparent case of rapid diversification amongst the fish blood flukes (Aporocotylidae) of Indo-west Pacific Tetraodontiformes

Russell Q-Y. Yong[1], Thomas H. Cribb[1], Scott C. Cutmore[1], Rodney A. Bray[2], Terrence L. Miller[3], I W.Y. Semarariana[4]
[1]The University of Queensland, Australia; [2]Department of Life Sciences, Natural History Museum, United Kingdom; [3]School of Marine and Tropical Biology, James Cook University, Australia; [4]The Faculty of Veterinary Medicine, Sudirman Campus, Universitas Udayana, Indonesia

Investigations into the fish blood flukes of the tropical Indo-west Pacific region revealed three new species in fishes of the order Tetraodontiformes, from the waters off Bali, Indonesia. One species infected the narrow-lined puffer *Arothron manilensis* and the spiny blaasop *Tylerius spinosissimus*, whereas the other two infected the reticulated puffer, *A. reticularis*. The three taxa shared several potentially synapomorphic features, but also differed dramatically from each other, particularly in the morphology and number of testes. Analysis of the partial 28S and ITS2 rDNA regions indicated the formation of a clade including the three new taxa and the two other tetraodontid-infecting aporocotylids for which sequences are known, to the exclusion of all others. The morphological disparity between taxa in this clade is at odds with the molecular divergence between them, suggesting an episode of rapid morphological diversification. This is in contrast to what is observed in other aporocotylid clades, which display retention of morphological features despite higher levels of genetic divergence. This issue of morphological diversity versus molecular similarity has implications for the generic-level classification for the taxa in this clade; should they be classified in separate genera, as suggested by morphology, or in a single genus as indicated by genetics?

Evidence of co-evolution between species of *Cloacina* (Nematoda: Strongylida) and the host *Macropus robustus* (common wallaroo)

Mary Alys Shuttleworth, Abdul Jabbar, Ian Beveridge, Robin B. Gasser
Faculty of Veterinary and Agricultural Sciences, The University of Melbourne, Australia

The Australian nematode genus *Cloacina*, found within a multitude of macropod species, is typically host-specific, providing an opportunity to investigate co-speciation of parasite and host. We investigated *Cloacina* species of the common wallaroo (*Macropus robustus*) and its mainland subspecies, as this host provides a novel opportunity to investigate parasitic speciation within a currently speciating host. Sixteen species of *Cloacina* endemic to *M. robustus* were analysed using a molecular-phylogenetic approach, using the first and second internal transcribed spacer regions (ITS-1 and ITS-2, respectively) of the nuclear ribosomal DNA. To assess phylogeography, the phylogeny of nematodes was mapped against the Australian continent and host location. Results showed variation in all species of *Cloacina* in at least one ITS region. Analysis of parasitic phylogeny against host range indicates that there is a correlation between parasitic speciation and host speciation. Further studies should aim to investigate the genetic variation within the host to further determine if this is an example of co-evolution between parasite and host.

Prevalence and molecular characterisation of haemoprotozoan parasites in native mammals from northern Australia

Amanda Barbosa[1,2], Andrea Reiss[1], Andrea Paparini[1], Kris Warren[1], Peter Irwin[1], Una Ryan[1]
[1]Murdoch University, Australia; [2]CAPES Foundation, Ministry of Education of Brazil, Brazil

Little is known about the prevalence of blood-borne protozoans in northern Australian native mammals and the role they play in population decline events. This research aimed to determine the prevalence and genetic diversity of potential pathogenic haemoprotozoans infecting native mammals from the Northern Territory. A total of 221 blood samples from four target species (brush-tailed possums, northern brown bandicoots, northern quolls and brush-tailed rabbit-rats) were tested by PCR at the 18S rDNA locus for trypanosomes and piroplasms. Overall, 27.6% of the animals were positives for at least one haemoprotozoan species. The prevalence of trypanosomes was 17.6%; of these *Trypanosoma vegrandis* comprised 13.5%, while the remaining 4.1% were positive for a *Trypanosoma sp.* previously reported in possums from Western Australia. This is the first report of *T. vegrandis* in northern brown bandicoots and first report of the possum-*Trypanosoma sp.* in possums from the Northern Territory. The prevalence of *Babesia sp.* and *Hepatozoon sp.* was 5% respectively and phylogenetic analysis revealed a novel *Babesia* species and two novel *Hepatozoon sp* species. Further investigation is required to determine the potential clinical impacts of these parasites upon their hosts and whether they are contributing to population declines in northern Australia.

CP 7: Drug Discovery Contributed Papers

Time: Wednesday, 01/Jul/2015: 11:30am - 12:30pm · *Location:* Symposium Room 2
Session Chair: Kathy Andrews, Griffith University

Investigating the antimalarial potential of primary sulfonamide compounds

G.M. Fisher, D.M.S. Sumanadasa, J. Moeker, M. Lopez, T.S. Skinner-Adams, S-A. Poulsen, K.T. Andrews
Griffith University, Australia

Malaria remains one of the world's most important infectious diseases causing ~600,000 deaths annually. Malaria eradication is being hampered by parasite drug resistance, prompting the need for new antimalarial drugs with novel modes of action to existing drugs to help limit potential cross-resistance. Primary sulfonamides have a proven track record of efficacy and safety in many clinical applications and are a potential new antimalarial chemotype. To investigate the antimalarial potential of primary sulfonamides, a panel of clinically used and novel compounds were screened against *Plasmodium falciparum* drug sensitive and resistant malaria parasites. Five compounds were found to have IC_{50}s between 0.9 - 4 μM for both parasite lines and >50 fold selectivity for *P. falciparum* versus mammalian cells. The most potent compound was used to generate a resistant parasite line to facilitate target identification studies. These resistant parasites were shown to have no cross-resistance with several other antimalarial drugs and the multi-drug resistance transporter (*Pfmdr1*) gene was not amplified. Genome sequencing studies are currently underway to identify possible genetic alterations that may be associated with *P. falciparum* resistance to this primary sulfonamide compound.

Modified pantothenamides as potential antimalarials targeting the CoA biosynthesis/utilisation pathway

Vanessa Howieson[1], Elisa Tran[2], Annabelle Hoegl[2], Han Ling Fam[1], Jonathan Fu[1], Kate Sivonen[1], Karine Auclair[2], Kevin Saliba[1]

[1]Australian National University, Australia; [2]McGill University, Canada

During its intraerythrocytic stage, *Plasmodium falciparum* requires an extracellular supply of vitamin B_5 (pantothenate) in order to grow and multiply. Pantothenate is converted into coenzyme A (CoA), an essential cofactor in many cellular processes. The metabolism of pantothenate to CoA and the utilisation of CoA in essential biochemical pathways represent a promising drug target for a much-needed novel antimalarial. We have been investigating pantothenamides, pantothenate analogues bearing amides, as potential antimalarials. The most potent pantothenamide reported to date has an IC_{50} value of 20 nM; an antiplasmodial potency equivalent to that of chloroquine. Unfortunately, a serum enzyme called pantetheinase easily degrades pantothenamides, rendering them inactive. In this study we describe a series of modified pantothenamides that are active in the presence of pantetheinase, some with sub-micro molar IC_{50} values. The compounds target CoA biosynthesis and/or utilisation and interact with *P. falciparum* pantothenate kinase, the first enzyme involved in the conversion of pantothenate to CoA.

Epigenetic regulatory enzymes as antimalarial drug targets

Ming Jang Chua[1], Tina Skinner-Adams[1], David P. Fairlie[2], Katherine T. Andrews[1]

[1]Eskitis Institute for Drug Discovery, Griffith University, Australia; [2]Institute for Molecular Bioscience, The University of Queensland, Australia

Malaria remains one of the worlds' most devastating infectious diseases and is a major public health problem in many regions. Most malaria-related mortality is due to infection with *Plasmodium falciparum*. The lack of a licensed malaria vaccine and increasing concern about the emergence of parasites resistant to the gold standard drug for treatment of *P. falciparum*, artemisinin-based combination therapies (ACTs), is driving the development of new drugs with novel modes of action. Epigenetic regulatory enzymes, such as histone deacetylases (HDACs) and histone methyltransferases (HMT), are involved in many essential processes in eukaryotic cells and are potential new antimalarial drug targets. In this project, the *in vitro* and *in vivo* antimalarial activity of inhibitors designed to target eukaryotic epigenetic regulatory molecules, in particular HDAC inhibitors, is being investigated. Studies also include profiling the *in vitro* mode of action of HDAC inhibitors in order to try to identify compounds with *P. falciparum* HDAC isoform selectivity.

Antiparasitic drug lead compounds from the medicinal plant, *Pleurospermum amabile*

Phurpa Wangchuk[1], Michael Smout[1], Mark Pearson[1], Paul Giacomin[1], Sumalee Kamchonwongpaisan[2], Paul Keller[3], Stephen Pyne[3], Alex Loukas[1]

[1]Centre for Biodiscovery and Molecular Development of Therapeutics, Australian Institute of Tropical Health and Medicine, James Cook University, Australia; [2]Medical Molecular Biology Research Unit, BIOTEC, National Science and Technology Development Agency, Thailand.; [3]School of Chemistry, University of Wollongong, Australia

An assessment of databases of drug regulatory authorities, WHO, and the clinical trial registries reveals a relatively devoid antiparasitic drug pipeline. In our study involving James Cook University and University of Wollongong in Australia and the BIOTEC governmental agency in Thailand, we tested crude extracts and purified phytochemicals of the Bhutanese medicinal plant, *Pleurospermum amabile*, against *Plasmodium falciparum* malaria, African trypanosomiasis, trichuriasis and schistosomiasis using microdilution radioisotope technique, Anti-*Trypanosoma brucei rhodesiense* assay, and the xCELLigence worm motility assay, respectively. Four crude extracts of *P. amabile* and its essential oil showed varying antiparasitic activities with dichloromethane and chloroform extracts having the best antimalarial and anti-trypanosome effects. From these crude extracts, 10 compounds were isolated and their structures determined using MS and NMR. Among all the compounds tested, (*E*)-isoapiol, isoimperatorin, isopimpinellin, oxypeucedanin hydrate and oxypeucedanin methanolate exhibited antimalarial activities with oxypeucedanin methanolate being the best activity against *P. falciparum* (K1CB1-antimalarial multidrug resistant strain and TM4-chloroquine and antifolate sensitive strain). JCU X and Y showed nematocidal effects against *T. muris* and trematocidal activity against *S. mansoni*. JCU X, which showed the best trematocidal and nematocidal activities at micromolar concentration, has potential to be a novel antiparasitic drug lead candidate.

Symposium 8: Ecology of Parasitism 2

Time: Wednesday, 01/Jul/2015: 1:30pm - 2:00pm · *Location:* Symposium Room 1
Session Chair: Tommy Leung, University of New England

Do parasites spread along host contact networks? Empirical and experimental insights from reptilian host-parasite systems

Stephanie Godfrey[1], Caroline Wohlfeil[2], Michael Gardner[2], Michael Bull[2]

[1]Murdoch University, Australia; [2]Flinders University, Australia

The influence of host behaviour on parasite transmission in now recognised as having an important role in generating heterogeneities in the spread of parasites through host populations. Network models have provided an ideal framework for quantifying the epidemiological consequences of host behaviour, and have enabled empirical comparisons of network models and infection patterns. However, our understanding of the importance of networks in the transmission of pathogens is limited by a lack of experimental testing of network transmission models. In this study, we experimentally tested the importance of host behaviour in the transmission of ticks in a sleepy lizard (*Tiliqua rugosa*) population. We released genetically distinct larval ticks on donor lizards and recaptured them as adults in the study population. Specifically, we asked what factors best predicted the transmission of experimentally released ticks from donor lizards to recipients? We compared the influence of social contact, refuge sharing and spatial spread in the transmission of ticks, to determine which factor (or combination of factors)

were most influential in the transmission of ticks in this host-parasite system. Using network modeling approaches, we provide new insights into the role of animal behaviour in the transmission of parasites.

Symposium 9: Diagnostics, Detection and Control 2

Time: Wednesday, 01/Jul/2015: 1:30pm - 2:00pm · *Location:* Symposium Room 2
Session Chair: Katja Fischer, QIMR Berghofer MRI

Characterisation and detection of *Cryptosporidium* using platform technologies

Una Ryan, Andrea Paparini, Rongchang Yang, Josephine Ng-Hublin, Garth Maker, Robert Trengove
Murdoch University, Australia

Cryptosporidium is considered the second greatest cause of diarrhoea and death in children after rotavirus. With treatment options limited, control relies on improved detection and knowledge of the biology, biochemistry and transmission dynamics of *Cryptosporidium* species. Comparisons between droplet digital PCR and quantitative PCR-based analyses and between Sanger sequencing and high-throughput sequencing (HTS) on an Ion Torrent platform, were conducted and analysed for their sensitivity and accuracy in detecting and characterising *Cryptosporidium* isolates at multiple loci. An alternative technology, metabolomics, was also analysed. Metabolomics may be useful for the diagnosis of *Cryptosporidium* infections, as it allows for detection based on metabolite differences caused by the infection rather than detecting oocysts in faeces by PCR, where sensitivity is limited by both the numbers of oocysts present and the intermittent shedding of oocysts. Metabolomics analysis of human and mice-infected *Cryptosporidium*-positive faecal samples revealed that despite differences in faecal metabolite profiles between these two hosts, metabolomic analysis in both studies was still able to clearly differentiate between infected and uninfected hosts, as well as providing information on the metabolic activity of the parasite during the infection based on faecal metabolite profiles.

CP 8: Ecology of Parasitism 2 Contributed Papers

Time: Wednesday, 01/Jul/2015: 2:00pm - 3:00pm · *Location:* Symposium Room 1
Session Chair: Tommy Leung, University of New England

A novel putative species-complex found in the platypus poses new challenges on the systematics of the piroplasms

Andrea Paparini[1], Una M. Ryan[1], James Macgregor[2], Peter J. Irwin[1]
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Piroplasms are tick-transmitted apicomplexan parasites included in the genera *Theileria*, *Babesia* and *Cytauxzoon*. This group of protozoa comprises species of significant global socio-economic importance, some of which are potentially lethal to companion/production–animals and humans. However, the order Piroplasmida show a puzzling and debated systematics characterized by multiple clades, poorly resolved taxa and paraphyletic or polyphyletic genera. In the present study, screening of Tasmanian platypuses (*Ornithorhynchus anatinus*), was performed to investigate the parasite molecular phylogeny, prevalence and pathogenicity. DNA was extracted from blood (n=28), ectoparasites (n=13) and tick eggs. Phylogenetic reconstructions were based on the 18S rRNA– and hsp70–genes. All blood samples and four adult ticks were positive by PCR, but no particular clinical signs were observed. In blood smears, highly pleomorphic intra-erythrocytic organisms, also forming tetrads and extra-erythrocytic schizonts, were morphologically consistent with previously described *Theileria ornithorhynchi* Mackerras, 1959. The present study shows for the first time the phylogenetic position of *T. ornithorhynchi*, but also reveals a novel monophyletic species complex, basal to most piroplasms' clades currently known. More importantly, compared to previous studies, the topology of our tree appears as one of the most robust and complete, produced up to now for the order.

Host-parasite relationships and life histories of wildlife trypanosomes in Australia

Crystal Cooper[1], Peta Clode[1], Adriana Botero[2], Andrew Thompson[2]
[1]Centre for Microscopy, Characterisation and Analysis, University of Western Australia, Australia; [2]School of Veterinary and Biomedical Sciences, Murdoch University, Australia

Trypanosomes are an important group of flagellate blood parasites in both livestock and humans, yet Australian wildlife trypanosomes remain largely understudied. Recent investigations into Australian trypanosomes in native marsupials observed a genotype of *Trypanosoma copemani* in the brush-tailed bettong (*Bettongia pencillata*) that invades mammalian cells [1]. Few trypanosomes have been observed to infect mammalian cells, with *T. cruzi*, the causative agent of Chagas disease in humans being the most widely studied. Additionally, a trypanosome isolated from a kangaroo - *T.* sp. H25 - was found to be genetically similar to *T. cruzi* and *T.* sp. H25 has since been found in other West Australian marsupials. Using a combination of *in vitro* methods, molecular analyses, and live cell and high resolution imaging tools, new insights into the host-parasite relationships and life histories of various Australian wildlife trypanosomes have been discovered. The most significant of these concern their pathogenicity in vulnerable Australian wildlife, and the identification of possible biosecurity hazards associated with the transmission of *T. cruzi* by Australian marsupials.

[1] Botero, A Thompson, CK Peacock, C Clode, PL Nicholls, PK Wayne, AF Lymbery, AJ Thompson, RCA 2013, Trypanosomes genetic diversity, polyparasitism and the population decline of the critically endangered Australian marsupial, the brush tailed bettong or woylie (*Bettongia penicillata*), *International Journal for Parasitology: Parasites and Wildlife*, vol. 2, pp. 77–89.

Acanthocephalan taxonomy and New Zealand birds – problems and solutions

Bronwen Presswell[1], Lesley Smales[2]
[1]University of Otago, New Zealand; [2]South Australian Museum, Australia

Reports of acanthocephalan parasites in New Zealand are rare, and in fish-eating seabirds even rarer. Of the 13 species of shag listed by NZ Birds online, only 6 have records of parasites in the literature and only one is reported to host an acanthocephalan species. We have necropsied a number of spotted and Stewart Island shags and little blue (fairy) penguins, in which we have found quantities of acanthocephalans of the *Corynosoma* type, a genus known from pinnipeds, and *Andracantha*, their sister genus found in phalacrocoracid birds. The first species, found in large numbers in both shag species, appear to be conspecific with *Corynosoma hannae*, a species that occurs in New Zealand fur seals and which has also been found in yellow-eyed penguins from Otago peninsula. As the birds are accidental hosts for this species, we find only immature specimens. The second species appears, from CO1 sequences and comparative morphology, to be a species of *Andracantha* not yet described in the literature. The third species appear to form a sister clade to the other two genera, with genetic distances of around 20%. This could indicate that a new genus should be erected for them.

Review of neosporosis in wildlife

Shannon Lynn Donahoe, David Norton Phalen, Scott Lindsay, Mark Krockenberger, Jan Šlapeta
University of Sydney, Australia

Neospora caninum is an apicomplexan parasite that is the etiologic agent of neosporosis, a devastating infectious disease regarded as a major cause of reproductive loss in cattle and neuromuscular disease in dogs worldwide. To date, an extensive number of wildlife species have been investigated for their possible role in the *N. caninum* life cycle and many have been implicated as intermediate hosts on the basis of serologic and/or molecular evidence. However, the occurrence and importance of disease due to infection in these nondomestic animals remains poorly understood. Most reports of positive *N. caninum* exposure in wildlife are in asymptomatic animals and, in many instances, investigations of possible associated morbidity, mortality, and pathology have been neglected. In order to improve our understanding of the significance of *N. caninum* infection in nondomestic species, we review the surprisingly low number of cases of clinical neosporosis reported in wildlife. While current data would suggest *N. caninum* infection does not adversely impact wildlife populations, there is a need for greater international awareness and uniformity in the diagnosis of *N. caninum* infection and neosporosis in nondomestic species in order to assess the true consequences of parasite infection.

CP 9: Diagnostics, Detection and Control 2 Contributed Papers

Time: Wednesday, 01/Jul/2015: 2:00pm - 3:00pm · *Location:* Symposium Room 2
Session Chair: Katja Fischer, QIMR Berghofer MRI

Novel approach to detect hookworm ova from wastewater matrices

Pradip Gyawali[1,2], Jatinder Sidhu[1,2], Warish Ahmed[2], Paul Jagals[1], Simon Toze[1,2]
[1]The University of Queensland, Australia; [2]CSIRO Land and Water, Australia

Rapid, sensitive and specific detection of hookworm ova is important to assess the potential public health hazard associated with wastewater and sludge reuse. Treated wastewater, raw wastewater and sludge samples were collected from two wastewater treatment plants (WWTPs). Known numbers of hookworm ova were seeded into the samples. Ova were recovered from treated wastewater samples using membrane filtration and from raw wastewater and sludge samples using floatation methods. A newly developed real-time PCR method was used to detect the ova from the samples. The sensitivity of the method was determined to be < 1 ova for treated wastewater. However, sensitivity of the method was one order of magnitude lower for the raw wastewater and sludge samples from both WWTPs. The range of detection limits obtained for the hookworm ova were treated wastewater > raw wastewater > sludge samples from both WWTPs. Significant differences ($p>0.05$) were observed for the treated wastewater with raw wastewater and sludge samples for both WWTPs. The more sensitive detection limits for the treated wastewater is potentially due to the possible higher recovery of ova via membrane filtration method. Conversely, the flotation method used to recover ova from raw wastewater and sludge samples involves multiple steps with potential losses of ova in each step. Overall, this detection method is rapid and sensitive. The result can be obtained within 6-8 h compared to traditional methods which may take up to 2 weeks. Further studies are required to enable the discrimination of non-viable ova from viable ova in wastewater matrices.

Prevalence and molecular characterization of *Cryptosporidium* species in animals inhabiting Sydney water catchments

Alireza Zahedi Abdi[1], Andrea Paparini[1], Fuchun Jian[2], Brendon King[3], Paul Monis[3], Andrew Ball[4], Ian Robertson[1], Una Ryan[1]
[1]Murdoch University, Australia; [2]Henan Agricultural University, China,; [3]Australian Water Quality Centre, Australia; [4]Sydney Catchment Authority, Australia

Cryptosporidiosis is one of the most common zoonotic waterborne parasitic diseases worldwide and represents the major public health concern of water utilities in developed nations. As animals in catchments can shed human-infectious *Cryptosporidium* oocysts, determining the potential role of animals in dissemination of zoonotic *Cryptosporidium* to drinking water sources is crucial. As a part of an ongoing two-year comprehensive quantitative survey of genotypes of *Cryptosporidium* in different catchments and states in Australia, a total of 615 animal faecal samples from Sydney's drinking water catchments were screened for the presence of *Cryptosporidium* using a quantitative PCR (qPCR). *Cryptosporidium* species were detected in 2.8% (14/499) of kangaroos (95%CI: 1.5%-4.7%), 11.5% (6/52) of cattle (95%CI: 4.4%-23.4), 5% (1/44) of sheep (95%CI: 0.1%-24%) and 9.1% (4 /20) of rabbit samples (95%CI: 2.5%-21.7%) screened. Sequence analysis identified *C. macropodum* and *C. hominis* in 4 and 10 isolates from kangaroos respectively, *C. hominis* and *C. parvum* in 3 isolates each from cattle, *C. ubiquitum* in 1 isolatefrom a sheep and *C. cuniculus* in 4 isolates from rabbits. The public health implications of the identification of zoonotic *Cryptosporidium* species in animals in Sydney's drinking water catchments will be discussed.

Molecular-based monitoring of *Cryptosporidium* and *Giardia* in animals in Melbourne water catchments

Anson Koehler[1], Shane Hayden[2], Melita Stevens[2], Aaron Jex[1], Robin Gasser[1]
[1]University of Melbourne, Australia; [2]Melbourne Water Corporation, Australia

In a joint industry-linked program, we have been conducting a long-term molecular epidemiological survey of the waterborne protists *Cryptosporidium* and *Giardia* in catchments supplying the City of Melbourne and environs (Victoria, Australia) with drinking water. Here, we explore the genetic composition of these genera in faecal samples from various animals in nine reservoir areas, collected over a period of six years. We are using PCR-based single-strand conformation polymorphism (SSCP) and phylogenetic analyses of sequence data for loci in the small subunit of ribosomal RNA (p*SSU*) and 60-kDa glycoprotein (*gp60*) genes to detect and characterise *Cryptosporidium*, and another locus (p*tpi*) in the triose-phosphate isomerase (*tpi*) gene for *Giardia*. *Cryptosporidium* was detected in 2.0% of the 5,313 samples tested, and included *C. canis*, *C. cuniculus, C. fayeri, C. hominis*, *C. macropodum, C. ryanae, C. suis* and *C. ubiquitum* as well as at least six new genotypes. Of note was the first molecular characterisation of *Cryptosporidium* in wombats and *C. cuniculus* in kangaroos. In addition, *Giardia* was identified in 1.5% of the samples; all sequence types defined represent variants of *Giardia duodenalis* assemblage A. The implications of the findings and future focus will be discussed.

Sequenom MassARRAY Platform as a high throughput tool for detection and differentiation of human hookworm species in stool

Stacey Llewellyn[1], James McCarthy[1], Tawin Inpankaew[2], Rebecca Traub[3]
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Three species of hookworm are capable of producing patent infections in humans, namely *Necator americanus*, *Ancylostoma duodenale* and *Ancylostoma ceylanicum.* All three hookworms produce morphologically identical eggs in faeces, making PCR-based tests the only diagnostic option currently available to reliably differentiate between them. As all three species differ in their life cycle, epidemiology, host specificity and pathogenicity, accurate speciation has important implications on approaches to design and implementation of intervention programs. Two Sequenom MassARRAY assays targeting SNPs in the Internal Transcribed Spacer 2 (ITS2) gene were developed to detect and differentiate eggs of the three hookworm species from gDNA extracted from stool. The assays were validated on 218 stool samples collected from an epidemiological survey in northern Cambodia and compared to results of a previously published multiplex real-time PCR and a conventional PCR-RFLP assay. The Sequenom MassARRAY assay provided near perfect agreement (0.92-1.0) with the three assays in terms of differentiation of the hookworms to a genus and species level. Through its ability to provide cost-effective, high-throughput screening for hookworms to the species level in epidemiological surveys in a single step reaction, the Sequenom MassARRAY assay provides a significant advantage over current molecular diagnostics.

Symposium 10: Helminth Biology 1

Time: Wednesday, 01/Jul/2015: 3:30pm - 4:00pm · *Location:* Symposium Room 1
Session Chair: Dave Cole, Cole Consulting

Effective immunity to *Haemonchus contortus* worm infection in sheep - clear as mud?

David Piedrafita[1], Jorge Gonzalez[2], Sarah Preston[3], Els Meeusen[4]
[1]Federation University, Australia; [2]Las Palmas University, Gran Canaria; [3]Melbourne University, Australia; [4]Monash University, Australia

One of the characteristics of worm parasites is they often have multiple developmental stages within the host. The third stage larvae of *H. contortus,* has been considered a major target of effective immunity in sheep. We have suggested two major mechanisms of immune rejection against these third stage larvae. Our recent studies suggest poorly defined effective immune responses directed at other larval and adult stages of this parasite may be equally important. Galectin-11 has been found to preferentially bind the L4 and adult stages, not the L3 stage. Galectin-11 inhibits the *in vitro* development and growth of L4 in vitro, and expressed at high levels in immune sheep. Immunity against adult stages has been established in comparative studies between sheep breeds in the Canary Islands, where significant differences in worm burden, length and fecundity were found. This mechanism is likely to target immature adult stages involving gammadelta T cells, eosinophils and mucosal IgA. In this presentation, potential mechanisms of immunity to multiple developmental stages of the parasite will be presented and the implications for future *H. contortus* multi-stage vaccination discussed.

CP 10: Helminth Biology 1 Contributed Papers

Time: Wednesday, 01/Jul/2015: 4:00pm - 5:00pm · *Location:* Symposium Room 1
Session Chair: Dave Cole, Cole Consulting

Identification of a GPI-linked tegument protein fraction of the liver fluke *Fasciola hepatica*

Hayley Michelle Toet, Terence W. Spithill

Department of Animal, Plant and Soil Sciences, AgriBio: Centre for AgriBioScience, La Trobe University, Australia

It has been demonstrated that juvenile flukes are susceptible to killing *in vitro* by antibody-dependent cell cytotoxicity (ADCC) in rats (*Fasciola hepatica*) and Indonesian Thin Tail (ITT) sheep (*F. gigantica*). However, the immune mechanisms targeting juvenile fluke in cattle are currently unknown and it has been hypothesised that cattle may also produce an ADCC mediated response. Given these observations, it is likely that proteins found on the surface tegument of juvenile and/or immature flukes may be the targets of ADCC. Further analysis of the juvenile and immature surface proteomes are required. The total proteome of the adult *F. hepatica* tegument membrane fraction has been previously reported and further research is required to determine the surface exposure, organisation and interactions of the identified proteins. A subset of tegument proteins have been shown to be GPI-linked on the surface of schistosomes using enzyme shaving techniques. Preliminary data using phosphatidylinositol-specific phospholipase C (PiPLC) to extract GPI-linked proteins from the surface of adult *F. hepatica* identified six proteins based on differential band patterns of treated and untreated worms by SDS-PAGE and MS/MS analysis. Identification of the total PiPLC released fraction is underway. These data will assist in identifying surface exposed proteins on the tegument of *F. hepatica* that may be potential targets of ADCC.

Functional characterization of novel Kunitz type protease inhibitors from *Echinococcus* and *Schistosoma*

Shiwanthi L. Ranasinghe[1,2], Geoffrey N. Gobert[1], Katja Fischer[1], Donald P. McManus[1]

[1]QIMR Berghofer Medical Research Institute, Australia; [2]School of Public Health, University of Queensland, Australia

Kunitz type serine protease inhibitors have been identified from almost all living species including plants. They are involved in diverse biological roles and previous studies on parasite Kunitz type inhibitors have indicated they play critical roles in providing protection from host proteases. We have identified and functionally characterized two novel Kunitz proteins from *Echinococcus granulosus* (EgKI1 and EgKI2) and one each from *Schistosoma mansoni* (SmKI) and *Schistosoma japonicum* (SjKI). They all exhibited protease inhibitory activities and may be involved in host immune evasion mechanisms. EgKI2 is a typical trypsin inhibitor. EgKI1 is a potent neutrophil elastase inhibitor as well as a neutrophil chemotaxis inhibitor, thus exhibiting anti-inflammatory properties. Both SmKI and SjKI possess anti-inflammatory and anti-coagulatory properties. SjKI is the first identified coagulation inhibitor from *S. japonicum*. A pilot vaccine trial with SmKI resulted in reduced total worm burdens and reduced numbers of faecal eggs emphasising the importance of this protein in the biology of *S. mansoni*. Overall, these novel Kunitz type protease inhibitors play a significant role in the host parasite interplay and may prove important novel drug/vaccine candidates.

Are both species of *Angiostrongylus* in Australia able to cause meningitis in humans and companion animals in eastern Australia?

Mahdis Aghazadeh[1,2], Rebecca Traub[3], Simon Reid[4], Kieran Aland[5], Helen Owen[1], Namitha Mohandas[3], James McCarthy[2], Robbin Gasser[3], Malcolm Jones[1,2]

[1]School of Veterinary Scinece, Universuty of Queensland, Australia; [2]QIMR Berghofer Medical Research Institute, Australia; [3]Faculty of Veterinary and Agricultural Sciences, The University of Melbourne, Australia; [4]School of Public Health, University of Queensland, Australia; [5]Queensland Museum and Science Centre, Australia

There are currently two species of *Angiostrongylus* occurring in Australia; *A. cantonensis* present in the introduced rat species and the Australian native species *A. mackerrasae*, found mainly in native rats, *Rattus fuscipes*. Although *A. mackerrasae* has never been reported from humans, it has been recently recovered from the lung of a flying fox. Since *A. mackerrasae* has a similar lifecycle to *A. cantonensis*, there is strong potential for this native species to also be pathogenic to humans. It remains uncertain whether this species is distinct from *A. cantonensis*. In this study, the geographical distribution of *Angiostrongylus* spp. was explored by obtaining rat samples from Brisbane area as well as Cairns and surrounds in northern Queensland. Adult *A. mackerrasae* and *A.cantonensis* were recovered from trapped native and introduced rats respectively. Following morphological identification of the worms, the entire mitochondrial genome of *A. mackerrasae* was amplified and sequenced using next generation sequencing. The sequence analysis results confirm that *A. cantonensis* and *A. mackerrasae* are closely related. Moreover, the pathogenicity of *A. mackerrasae* was studied for the first time in non-permissive host including mice and guinea pigs. The results from this study confirm that *A. mackerrasae* can potentially cause meningitis in humans.

Caenorhabditis elegans: the model worm to study anthelmintic activities of traditional medicinal plant extracts and their activities

Rasika Kumarasingha[1], Jill Shaw[2], Enzo Palombo[2], T.C. Yeo[3], D.S.L Lim[3], C.L. Tu[3], Peter Robert Boag[1]

[1]Department of Biochemistry and Molecular Biology, Monash University, Australia; [2]Department of Chemistryand Biotechnology, Faculty of Science, Engineering and Technology, Swinburne University of Technology, Australia; [3]Sarawak Biodiversity Centre, Malaysia

Resistance to anthelmintics is widespread in worm populations and therefore there is a continuous need for the next novel anthelmintic. However, the cost of screening for new anthelmintic compounds is high and has a very low success rate. Using the knowledge of traditional healers from Borneo Rainforests, Sarawak, Malaysia, we have previously shown that traditional medicinal plants are a rich source of potential new anthelmintic drug candidates. Furthermore, we demonstrated that *C. elegans* is a reliable model for preliminary screening for anthelmintic compounds. We then characterized the stress responses causing by plant extracts using *C. elegans* stress reporter GFP strains. Now we have fractionated the most effective plant extracts (*Picria fel-terrae* Lour. whole plant), and tested fractions on *C. elegans*. The anthelmintic activity was determined to exist in a single fraction which killed 90% of *C. elegans* adults. Analysis of gene expression of selected genes by RT-PCR

confirmed the stress reporter strain findings and gave a clear idea about the timing of gene expression changes. Transcriptome-wide analysis of gene expression by next-generation sequencing is currently being undertaken. Our findings show that *C. elegans* is not only a good tool for preliminary screening, but may also be useful for examining the effects of compounds on nematodes and to understand mechanism of action of the compounds.

T1CP11: Theileriosis Contributed Papers

Time: Wednesday, 01/Jul/2015: 3:30pm - 5:00pm · *Location:* Symposium Room 2
Session Chair: Abdul Jabbar, The University of Melbourne

Epidemiology of theileriosis in cattle in Victoria, Australia: 2010 to present

Grant Thomas Rawlin[1], Laura MacFarlane-Berry[1], Abdul Jabar[3], Roger Paskin[2]
[1]DEDJTR, Victorian Government, Australia; [2]PISA, Australia; [3]University of Melbourne, Faculty of Veterinary Science, Australia

Theileriosis is a recently emerged clinical problem of cattle in Australia. Caused by the protozoan *Theileria orientalis*, theileriosis is recognised usually by clinical animals exhibiting regenerative anaemia and pyrexia. Infection is usually sub-clinical and our work in an affected dairy herd has shown that there is fast transmission within an infected herd under the right conditions, leading to a herd immunity, however severe anaemia and death are seen particularly in animals around calving. The first report of the clinical disease in Victoria was in central north Victoria in 2010. Over the next years clinical cases were increasingly reported in the higher rainfall areas (predominantly dairy farming country) of Victoria. The timing of disease reports were highly seasonal with mainly Spring occurrence and a lesser peak in Autumn. Climate and vegetation overlays have been useful in defining the 'at-risk' areas in Victoria. Disease peaked in 2011/12 with reports of disease from about 150 herds. Reports of disease have decreased markedly since 2012 both in the number of herds affected and the number of animals within each herd clinically infected. With experience gained, the success of treatment of clinical cases is now common.

Investigating the first outbreak of oriental theileriosis in cattle in South Australia using multiplexed tandem PCR

Hagos Gebrekidan Gebremikael, Robin B. Gasser, Piyumali K. Perera, Abdul Jabbar
The University of Meolbourne, Australia;

This study investigated the first outbreak of oriental theileriosis in a herd of beef cattle in South Australia using a newly established multiplexed tandem PCR (MT-PCR) to identify, differentiate and quantitate the four genotypes (*buffeli*, *chitose*, *ikeda* and *type* 5) of *Theileria orientalis*. Following clinical diagnosis of this disease (based on clinical signs, laboratory findings and *post mortem* examination), 155 blood samples were collected from individual cows (*n*=85) and calves (*n*=70), and tested by MT-PCR. In total, 117 (75.48%) cattle were shown to be test-positive for *T. orientalis*. All four genotypes were detected, and *ikeda* had the highest prevalence (90.6%; 106/117), followed by *buffeli* (83.8%; 98/117), *chitose* (18.8%; 22/117) and *type* 5 (5.1%; 6/117). Mixed infections with genotypes *buffeli* and *ikeda* had a higher prevalence (55.5%; 65/117) than any other combination of genotypes. The prevalences of *buffeli* and *ikeda* were significantly higher ($p<0.005$) than those of *chitose* and *type* 5. The average intensity of infection with genotype *ikeda* (329,775 DNA copies) was significantly higher ($p<0.0001$) than *buffeli* (212,843) and *chitose* (125,462). This study reinforces the utility of MT-PCR for rapidly investigating oriental theileriosis outbreaks and for preventing the introduction of this disease into non-endemic regions.

Application of novel PCR assays for the detection and differentiation of *Theileria orientalis* genotypes in New Zealand

Piyumali K. Perera[1], Robin B. Gasser[1], David J. Pulford[2], Simon M. Firestone[1], Mark A. Stevenson[1], Andrew M.J. Mcfadden[2], Abdul Jabbar[1]
[1]Faculty of Veterinary and Agricultural Sciences, The University of Melbourne, Australia; [2]Ministry for Primary Industries, New Zealand

Oriental theileriosis is an emerging tick-borne disease in New Zealand caused by *Theileria orientalis* complex. This study used multiplexed tandem (MT) PCR to assess the prevalence and infection intensity of four *T. orientalis* genotypes (*buffeli*, *chitose*, *ikeda* and *type* 5) in this country. The MT PCR results were then compared with those obtained using PCR-based high resolution melting (PCR-HRM) analysis for *T. orientalis* and a TaqMan® qPCR assay for *ikeda* genotype. Blood samples were tested from cattle involved in theileriosis outbreaks (Group 1; *n*=154) and cattle from a region where no outbreaks had been reported (Group 2; *n*=88). In Group 1, 99.4% (153/154) of cattle were test-positive for *T. orientalis* using both MT PCR and PCR-HRM. The apparent prevalence of genotype *ikeda* in Group 1 was 87.6% (134/153) and 87.7% (135/154) using MT PCR and Ikeda TaqMan® qPCR, respectively. Using MT PCR, all four genotypes of *T. orientalis* were reliably detected. Infection intensity estimated for genotype *ikeda* was significantly higher ($p=0.009$) in severely anaemic cattle than those without anaemia. Future studies should focus on using quantitative diagnostic tools to investigate oriental theileriosis.

Establishment and application of a semi-quantitative multiplexed tandem PCR for the detection and differentiation of *Theileria orientalis* genotypes in Australia

Piyumali K. Perera[1], Robin B. Gasser[1], Simon M. Firestone[1], Lee Smith[2], Elizabeth Read[3], Jakob Malmo[4], Florian Roeber[2], Grant Rawlin[5], Terry W. Spithill[3], Abdul Jabbar[1]
[1]Faculty of Veterinary and Agricultural Sciences, The University of Melbourne, Australia; [2]AusDiagnostics Pty., Ltd., Australia; [3]Department of Agricultural Sciences, Centre for AgriBioscience, La Trobe University, Australia; [4]Maffra Veterinary Centre, Australia; [5]Department of Environment and Primary Industries, Australia

Oriental theileriosis is a tick-borne disease of bovines caused by *Theileria orientalis* complex. Some methods to detect *T. orientalis* have limitations, such as low specificity and sensitivity. This study established and validated a multiplexed tandem PCR (MT PCR) assay for the simultaneous detection and semi-quantification of four common genotypes (*buffeli*, *chitose*, *ikeda* and *type* 5) of *T. orientalis* and employed it to assess the prevalence and infection intensity of these genotypes. Analytical specificity, sensitivity and repeatability of the assay were evaluated. The results revealed that MT PCR specifically and

reproducibly detected the expected genotypes and reliably differentiated them. Subsequently, the assay was employed to test 448 cattle following outbreaks of oriental theileriosis in Victoria. In Victoria, the *buffeli* genotype had the highest prevalence (80.5%), while *ikeda* had the highest infection intensity (55,277 DNA copies). The *ikeda* genotype had a significantly higher infection intensity than *buffeli* in symptomatic cattle ($p<0.001$), and symptomatic cattle had a higher intensity of *ikeda* than asymptomatic cattle ($p=0.004$). The MT PCR assay is a reliable diagnostic tool that should assist epidemiological studies of oriental theileriosis in Australia and other countries.

Quantitative PCR for clinical diagnosis, subpopulation analysis and identification of temporal genotype switching in *Theileria orientalis*

Daniel Ross Bogema[1,2], Sherin Alex[1,2], Ania Therese Deutscher[2], Shayne Fell[2], Melinda Micallef[2], Damian Collins[2], Steven Djordjevic[1], Graeme John Eamens[2], Cheryl Jenkins[2]

[1]University of Technology, Sydney. Australia; [2]Elizabeth Macarthur Agricultural Institute, NSW Department of Primary Industries, Australia

The last decade has seen clinical theileriosis caused by *Theileria orientalis* spread across Australasian cattle herds. Pathogenesis is most often associated with a particular genotype of the parasite (Ikeda). We developed a diagnostic multiplex quantitative PCR to accurately measure total parasite load and detect clinically-relevant *T. orientalis* genotypes. The assay was validated using 318 PCR-positive and negative blood samples. Mean parasite loads of subclinical animals from disease-free, PCR-positive herds were significantly lower than those of clinically-affected cattle ($p<0.001$), allowing the establishment of clinical thresholds to aid laboratory diagnosis, including the first cases inWestern Australia andSouth Australia. Additionally, Ikeda and mixed Ikeda-Chitose infections had significantly higher mean parasite loads than Chitose and Buffeli infections ($p<0.001$). Sequence analysis of the Chitose genotype identified two phylogenetic subpopulations (Chitose A and B). Analysis of 137 cases of Chitose infection revealed that Chitose A almost always co-occurs with Ikeda. Longitudinal analysis of 10 naïve cattle introduced to a property with a history of theileriosis showed mixed infections switched between Ikeda and Chitose, while Buffeli remained at low concentrations. These results confirm that clinical theileriosis is highly-associated with the Ikeda genotype and suggest that Chitose A may exacerbate disease when in combination with Ikeda.

A putative novel species of *Theileria* isolated from the burrowing bettong (*Bettongia lesueur*)

Andrea Paparini, Peter J. Irwin, Una M. Ryan

Vector- and Water-Borne Pathogen Research Group, School of Veterinary & Life Sciences, Molecular and Biomedical Sciences, Murdoch University, Australia

Piroplasms are tick-borne apicomplexan haemoparasites of global socio-economic importance. The order Piroplasmida includes important pathogens (some zoonotic) of humans and companion/production animals. Yet, their molecular classification is still confused and debated. Conservation studies on Australian marsupials have focussed on epidemiology, transmission and pathogenicity. DNA sequence-data obtained from these ancient mammals and geographically isolated populations, however, can prove useful also for resolving the phylogeny and molecular systematics of the Order. In 2012 a novel genotype of Theileria was obtained from a boodie (*Bettongia lesueur*), sheltered in WA. In this original study partial fragments of the 18S rRNA gene were analysed, and the protozoan isolate appeared genetically close to known marsupial parasites from the woylie, the quokka and the long-nosed potoroo. Interestingly, the enhanced phylogenetic reconstruction conducted during the present study suggested the boodie-derived Theileria may actually represent a new species. This novel analysis represents the most comprehensive and robust phylogenetic reconstruction obtained for the piroplasms, to date. The results also show that marsupials are hosts to multiple genera and highly divergent genetic variants of piroplasms, indicating lack of host-parasite co-speciation and suggesting that host switches, parasite extinction or other factors have shaped the host-parasite evolution and ecology.

P3: Plenary Lectures – Immunity, Inflammation and Immunopathology supported by Virbac Animal Health

Time: Thursday, 02/Jul/2015: 9:00am - 10:30am · *Location:* Plenary Room
Session Chair: Terry Spithill, La Trobe University

Microparticles - contributors to the pathogenesis of cerebral malaria and potential biomarkers?

Natalia Tiberti[2], Fatima El-Assaad[2], Anna Zinger[2], Amy Cohen[2], Sharissa Latham[2], Georges Grau[2], Valery Combes[1,2]
[1]University of Technology, Sydney, Australia; [2]The University of Sydney, Australia

Microparticles (MP) are submicron extracellular vesicles involved in various pathways including cell-cell communication. MP numbers are increased in inflammatory diseases and infectious pathologies such as cerebral malaria (CM). Upon infection of mice with *Plasmodium berghei*-ANKA, when fluorescent MP were adoptively transferred into normal or infected recipient mice, they were quickly cleared from the circulation and imaging showed arrested MP lining the endothelium of brain vessels of infected, but not healthy, recipient mice suggesting a role of these MP in the vascular pathology further confirmed when histopathology in uninfected recipient mice was observed after endothelial MP transfer. Of increasing interest is the content these MP carry and can transfer to target cells. By characterising the protein and microRNA cargo of plasma MP we hope to better understand CM pathophysiology and reveal new potential disease biomarkers. We purified MP from the blood of malaria patients from Malawi and from infected mice and analysed their proteome by quantitative proteomics and their miRNA using microarrays. More than 330 proteins were identified in human plasma MP and almost 25% of the quantified proteins were not shared uncomplicated malaria (UCM) and severe anaemia (SMA) patients. Activation of the immune response and migration of immune cells were the most represented and modulated pathways. Among the 281 microRNA detected in human plasma MP, 14% appeared only in CM and 13.5% only in SMA. In the mouse model, LC-MS/MS of MP identified 392 proteins. Analyses highlighted a significant involvement of proteins in actin cytoskeleton regulation and a significant representation of membrane proteins, in addition to proteins involved in the immune response and complement activation. Interestingly, two proteins, S100A8 and S100A9, were also identified as significantly increased in human CM. More than 450 miRNA could be identified in murine MP and 86 were specific to uninfected animals while 24 were specific to CM. The expression of most of these miRNA remained unchanged, while 20-30% were over- or under-expressed during CM. Proteins and miRNA showing a potential association with disease in both human and murine pathology are currently under investigation to confirm this involvement.

Regulation of immunity and inflammation during parasitic helminth infections

Paul Robert Giacomin
James Cook University, Australia

Parasitic helminth infections are an enormous global health problem, particularly in developing, tropical regions of the world. In order to develop effective preventative treatments for helminth infections (i.e. vaccines), more needs to be known about how the immune system controls worm infections. There have been many significant advances in recent years in our understanding of the the immune responses to helminths, in particular our knowledge of the influence of the innate immune system. However, it is clear that helminths have evolved strategies to manipulate these responses, which can have beneficial effects for both the host and the parasite. Consequently, there has been interest in harnessing the immunosuppressive capabilities of parasitic helminths for the development of novel therapies for autoimmune, allergic or inflammatory diseases that have become more prevalent in the developed world. Proof-of-principle studies involving deliberate exposure of people to these infectious agents have yielded some promising results in a variety of inflammatory disorders. However, there is much work still to do before helminth- or helminth secreted protein-based treatments can become mainstream therapies, including more detailed analyses of the impact of helminths on local inflammatory and commensal microbe responses that could mediate their immunoregulatory capabilities in humans.

Exploring the immune response in scabies: pathways to diagnostics and therapy

Shelley Walton
University of the Sunshine Coast, Australia

Scabies is a skin infection caused by the mite *Sarcoptes scabiei*. Scabies mites and the house dust mites (HDM) are members of the same suborder Psoroptidia. Immunodiagnostic studies have revealed high levels of specific IgE antibodies in individuals with scabies to the *S. scabiei* allergen Sar s 14 with minimal cross-reactivity to the house dust mite *Dermatophagoides pteronyssinus* homologue Der p 14. However we have also documented *exceptionally* high titres of IgE in the same individuals to HDM allergens Der p 4 and Der p 20. Future testing for scabies and HDM allergy may need to use HDM and scabies mite allergen panels rather than skin prick tests (which use whole mite extract) to accomplish diagnostic sensitivity. Such observations will enable more appropriate treatment and prevention efforts for those individuals at risk of allergy and asthma, especially in vulnerable populations. Crusted scabies is the severely debilitating form of the disease involving substantial hyper-proliferation of mites, thickening and depigmentation of skin. The underlying mechanisms of why crusted scabies develops are largely unknown. Enhanced T helper 2 immune responses are evident alongside increased levels of interleukin-(IL) 17**.** IL-17 is a potent pro-inflammatory cytokine that amplifies ongoing inflammation in epithelial cells as well as keratinocytes and fibroblasts. Anti-IL-17 is proposed as a novel adjunct therapy for the treatment of crusted scabies.

Symposium 12: Veterinary Parasitology 1 supported by Virbac Animal Health

Time: Thursday, 02/Jul/2015: 11:00am - 11:30am · *Location:* Symposium Room 1
Session Chair: Glenn Anderson, Virbac (Australia)

Chasing the end of the rainbow: a history of the 55 years of development, technology transfer and commercialisation of a vaccine to protect grazing animals against *Echinococcus granulosus*

David Duncan Heath[1], Marshall William Lightowlers[2]
[1]AgResearch New Zealand Limited, Hopkirk Research Institute, New Zealand; [2]University of Melbourne, Veterinary Clinical Centre, Australia

The New Zealand hydatid control research programme started in 1958. Gemmell published in 1966 that protective antigens did occur in the oncosphere or the developing cyst. By 1970, Heath and Smyth had developed the methodology for in vitro culture of oncospheres. In 1975 a dog isolation unit was built in New Zealand that safely supplied *E. granulosus* eggs for the next 30 years. By 1994 the antigenic polypeptides of *E. granulosus* had been analysed and tested for protective ability, after a large scale analysis of adjuvants. In Marshall Lightowler's laboratory various recombinant iterations were created and then tested in New Zealand. One clone, EG95, showed the best protection, and this was sequenced and patented. The world-first antiparasitic vaccine was published in Nature in 1996, using QuilA as the adjuvant. Best technology for 10 litre production using GMP was followed by 1000 litre production of the vaccine in New Zealand, and registration of the vaccine for commercial use. From 1997 field trials were conducted in Xinjiang, China, using vaccine made in New Zealand. By 2004 the first large-scale production of vaccine occurred in Beijing. Safety testing of the Chinese vaccine was completed by 2006 and then the registration process began, ultimately receiving the registration certificate in 2007. A new factory was built in Chongqing in 2011 and vaccine was produced ready for commercial use. Heath provided vaccine for testing in Chile in 1996 and Lightowlers provided laboratory vaccine for a field trial in Argentina in 1999 and again in 2007 and 2009. The vaccine technology was taken up by Tecnovax, Buenos Aires in 2007. The Argentine Government has prepared an action plan for hydatid control including the vaccine. Peru is keen to use the vaccine for the highland sheep farmers. Large scale field use of the vaccine is planned for the Pehuenche Indian tribes of Chile. Sixty-six other authors have contributed to this project. After 55 years the initial biological trials have been transformed into preliminary commercial use in the field.

Symposium 13: Population Genetics

Time: Thursday, 02/Jul/2015: 11:00am - 11:30am *Location:* Symposium Room 2
Session Chair: Aaron Jex, University of Melbourne

Malaria Elimination in the Asia-Pacific: Addressing the *P. vivax* challenge

Ivo Mueller[1,2]
[1]Walter + Eliza Hall Institute, Australia; [2]ISGlobal, Barcelona Centre for International Health, Barcelona, Spain;

After a decade of significant successes in malaria control, the East Asian leaders have committed themselves in 2014 to a malaria-free Asia Pacific by 2030. P. vivax is now the predominant parasite throughout the region and its elimination will the major challenge in meeting this ambitious deadline. It high transmissabilty and ability to relapse from long-lasting liverstages render P. vivax significantly more resistant to elimination than *P. falciparum.* Our studies in PNG and Thailand have shown that relapses cause up 80% of *P. vivax* bloodstage infections and that even submicroscopic, asymptomatic *P. vivax* infections can successfully infect mosquitoes. A rapid path to elimination will thus require a direct attacking on the hidden hypnozoite reservoir with mass-drug administration (MDA). Given the challenges of MDA with an 8-aminoquinoline, novel methods to determine population at risk and individual that carry hypnozoites are urgently needed.

CP 12: Veterinary Parasitology 1 Contributed Papers supported by Virbac Animal Health

Time: Thursday, 02/Jul/2015: 11:30am - 12:30pm · *Location:* Symposium Room 1
Session Chair: Glenn Anderson, Virbac (Australia)

Structural and functional recognition mechanisms of galectin-11 of domestic sheep (*Ovis aries*)

Dhanasekaran Sakthivel[1,2,3], Adam Shahine[2], MD Shakif-Ul-Azam[1], Dene Littler[2], Sally Troy[2], Matthew Johnson[2], Jamie Rossjohn[2,3], David Piedrafita[1], Travis Beddoe[2,4]
[1]Monash University, Australia; [2]Department of Biochemistry and Molecular Biology, Monash University, Australia; [3]Institute of Infection and Immunity, School of Medicine, Cardiff University, United Kingdom; [4]Department of Animal, Plant and Soil Science and Centre for AgriBioscience (AgriBio), La Trobe University, Australia

Galectins are an evolutionarily conserved family of proteins that translate glycan recognition into cellular effects. To date, 15 galectins have been identified in vertebrates; however the expression of galectin-11 has only been reported in ruminants such as sheep, goats and cattle. Galectin-11 putatively plays a critical role in several important biological processes, such as reproduction and parasite mediated innate immune responses (Dunphy et al., 2000; Dunphy et al., 2002; Gray et al., 2004). Despite the emerging biological significance of galectin-11, no structural information is available, which may unravel the functional mechanisms of galectin-11 activity. Here, we crystallized recombinant Galectin-11 and the resulting crystal structure was determined at a 2.0 Å resolution. The overall structure of Galectin-11 was highly similar to mammalian Galectins 1, 2 and 10. Interestingly, several amino acid variations were observed in Galectin-11 which could have potential roles in inter molecular and cellular attachment. Further studies are underway to explore the molecular basis of glycan-galectin interaction.

Creating a live attenuated veterinary vaccine against schistosomiasis

Marina Harvie, Oliver Creagh, Najju Ranjit, Don McManus
QIMR Berghofer Medical Research Institute, Australia

Schistosomiasis is an infection caused by the trematode parasites from the genus *Schistosoma*. The disease is endemic in Africa, South America and parts of southeastern Asia and is a significant global problem. Praziquantel is the only effective drug treatment available however administration does not prevent re-infection and repeated dosages are required. *S. japonicum* is endemic to southeastern Asia and is unique in that it is a zoonosis; Buffalo and other bovines are heavily infected and act as an infection reservoir. Mathematical modelling suggests that vaccination of bovines, alongside mass drug administration and molluscicide will eliminate schistosomiasis in endemic areas. The most successful attempts to vaccinate bovines to date used live radiation-attenuated cercariae, which confer up to 90% protection. Unfortunately radiation induced attenuation proved to be inconsistent and as such this line of research was abandoned. We hypothesise that using a DNA binding molecule Tafuramycin we will be able to create a successful, consistent live attenuated cercarial vaccine suitable for use in bovines. Our results show that Tafuramycin can bind parasite DNA and also that treatment with Tafuramycin does not kill parasites. Preliminary studies in mice demonstrate a dose dependent relationship between Tafuramycin treatment and interruption of the parasite intra-mammalian life cycle – providing the opportunity for attenuated parasites to elicit a protective immune response, which can protect against future natural infections. Studies are currently being undertaken to quantitate the protective effect of vaccination with chemically attenuated cercariae. Future directions involve adapting this vaccine strategy for use in bovines.

Reverse vaccinology for parasitic diseases of livestock

John Ellis, Stephen Goodswen, Joel Barratt, Paul Kennedy
University of Technology, Sydney, Australia

The increasing volume of “omics” data from economically important veterinary parasites, such as *Toxoplasma gondii* and *Neospora caninum*, is providing an opportunity for an *in silico* approach to the discovery of protein-based vaccines. We have completed a feasibility study on a high-throughput *in silico* vaccine discovery pipeline constructed from freely available prediction programs. The primary challenge was to determine which evidence should be included in reverse vaccinology as the evidence gathered is often in different formats, contradicting, and inaccurate. This considerable uncertainty in the reliability of the evidence arises because an unknown number of the inputs to the pipeline (e.g. protein sequences, database annotations, and predicted evidence itself) are incorrect. Finally, given the available evidence how can a decision be made as to what represents a likely vaccine candidate? Goodswen et al. [1] discuss these and many other issues in detail. Central to our methodology was the development of Vacceed, a linux based pipeline that is organised into two major parts: part A builds a proteome from a genome using gene predictors, and part B predicts vaccine candidates from the proteome with the aid of machine learning algorithms. Vacceed is available from Github along with an extensive installation and user guide. We present an overview of reverse vaccinology and discuss the importance of "hypothetical proteins" within the scheme of vaccine development..

[1] Goodswen SJ, Kennedy PJ, Ellis JT. Discovering a vaccine agasint neosporosis using computers: is it feasible? Trends Parasitol. 2014 30(8):401-11.

Impact of parasitism on the health, development and production of buffalo in Pakistan

Thomas Michael Williams
Charles Sturt University, Australia

Parasitism has a major impact on livestock production worldwide. Many developed agricultural countries consistently struggle with losses in highly managed systems. The impacts of parasites on livestock production in countries with a developing agricultural sector are less well understood. Pakistan’s dairy sector is of high value to this developing nation. It currently provides jobs for 25% of Pakistan’s working population. Milk produced provides a highly valued and important source of nutrition for a hungry nation. It is estimated that 70% of the dairy producers in Pakistan still operate under conditions of subsistence, maintaining herds of less than five animals. Buffalo constitute 62% of Pakistan’s 62.9 million strong milking herd and produce 67% of total milk production. Our study will: (1) identify parasites found commonly in Pakistani buffalo through the use phenotypic and molecular methods; (2) determine parasite prevalence in relation to Agro-Climatic zones; (3) undertake a 2 year controlled infection trial of buffalo under Australian conditions; (4) develop a parasite control and management strategy for Pakistani smallholder farmers.

CP 13: Population Genetics Contributed Papers

Time: Thursday, 02/Jul/2015: 11:30am - 12:30pm · *Location:* Symposium Room 2
Session Chair: Aaron Jex, University of Melbourne

Lucilia cuprina genome and transcriptomes – critical resources to underpin biological investigations and biotechnological outcomes.

Clare Alayne Anstead[1], Pasi K. Korhonen[1], Neil D. Young[1], Ross S. Hall[1], Aaron R. Jex[1], Shwetha C. Murali[2], Daniel S.T. Hughes[2], Siu F. Lee[3], Trent Perry[3], Andreas J. Stroehlein[1], Brendan R.E. Ansell[1], Bert Breugelmans[1], Andreas Hofmann[4], Jiaxin Qu[2], Shannon Dugan[2], Sandra L. Lee[2], Hsu Chao[2], Huyen Dinh[2], Yi Han[2], Harsha V. Doddapaneli[2], Kim C .Worley[2], Donna M. Muzny[2], Panagiotis Ioannidis[5], Robert M. Waterhouse[5], Evgeny M. Zdobnov[5], Peter J. James[6], Neil H. Bagnall[7], Andrew C. Kotze[7], Richard A. Gibbs[2], Stephen Richards[2], Philip Batterham[3], Robin B. Gasser[1]

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Lucilia cuprina is a parasitic blowfly that causes flystrike. This myiasis is a major problem in many countries. In Australasia alone, losses of > $320 million are incurred each year as a result of reduced body and wool growth in sheep as well as costs linked to morbidity and treatment. No vaccine is available and resistance in blowfly to almost all insecticides in current use demands the development of alterative interventions. An improved understanding of the fly could support this quest. In the present study, we sequenced and annotated the 458 Mb draft genome of *L. cuprina*. Analyses of this genome and the 14,544 predicted protein-encoding genes provide first insights into the fly's biology, host interactions and insecticide resistance. These molecular resources shouldunderpin future studies of fly development, parasitism, the pathogenesis of disease, population genetics and drug resistance mechanisms as well as the design of radically new methods for the prevention or control of flystrike.

Cryptosporidiosis in New Zealand: cyclical ecology and zoonotic link

Alex Grinberg

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Until the early 2000s, the *Cryptosporidium* parasites producing round oocysts identified in calves' faeces were collectively classified as *C. parvum* and considered pathogenic and potentially zoonotic. This situation started to change with the use of genotyping in epidemiological research and the discovery of new taxa of unknown clinical and zoonotic impact in cattle. In New Zealand, human *C. parvum* infection rates peak every year in September-October, soon after the calving season. Yet, the impact of the *Cryptosporidium* parasites cycling in cattle on animal and public health is unknown as their genetic makeup has not been studied and comparative molecular data of human and bovine isolates are scarce. In this presentation, the epidemiology of human cryptosporidiosis in New Zealand will be summarised, followed by an account of a country-wide study of *Cryptosporidium* spp. performed in dairy cattle at Massey University. Data indicated a 50.5%. *C. parvum* farm-level prevalence. Multivariable analysis showed a significant contribution of this species to neonatal calf diarrhoea burden. A high degree of genetic similarity between human and bovine *C. parvum* was found, indicating calves are significant amplifiers of potentially zoonotic parasites. Nonetheless, molecular data suggested the presence of infection routes not linked to dairy cattle, which should also be considered in source-attribution studies of cryptosporidiosis.

Integrated morphological and molecular identification of cat fleas (*Ctenocephalides felis*)and dog fleas (*Ctenocephalides canis*)vectoring *Rickettsia felis* in central Europe

Andrea Lee Lawrence[1], Sze-Fui Hii[2,3], Dagmar Jirsová[4], Lucia Panáková[5], Angela Ionică[6], Katrina Gilchrist[1], David Modrý[4,7], Andrei Mihalca[6], Cameron Webb[1], Rebecca Traub[3], Jan Šlapeta[1]

[1]University of Sydney, Australia; [2]University of Queensland, Australia; [3]University of Melbourne, Australia; [4]University of Veterinary and Pharmaceutical Sciences, Czech Republic; [5]University of Veterinary Medicine, Austria; [6]University of Agricultural Sciences and Veterinary Medicine, Romania; [7]Institute of Parasitology, Academy of Sciences of the Czech Republic

Fleas of the genus *Ctenocephalides* are the most common ectoparasites infesting dogs and cats world-wide and are vectors for zoonotic pathogens such as *Rickettsia felis* and *Bartonella* spp. Fleas infesting owned dogs and cats from the Czech Republic (n=97) and Romania (n=66) were subjected to morphological and molecular identification and phylogenetic analysis. Mitochondrial DNA sequencing at the *cox1* gene on a cohort of 40 fleasrevealed the cosmopolitan *C. felis felis* clade represented by *cox1* haplotype 1 is present in the Czech Republic. A new *C. felis felis* clade from both the Czech Republic and Romania is also reported. A high proportion of *C. canis* was observed from dogs and cats in the current study and phylogeny revealed that *C. canis* forms a sister clade to the oriental cat flea *Ctenocephalides orientis* (syn. *C. felis orientis*). Out of 33 fleas, representing *C. felis felis*, *C. canis* and *Ce. gallinae*, 7 (21.2%) were positive for *Rickettsia felis* using real-time PCR targeting the *glt*A gene and a conventional PCR targeting the *omp*B gene. This study confirms high genetic diversity of *C. felis felis* globally and serves as a foundation to understand the implication for zoonotic disease carriage by the flea genus *Ctenocephalides*.

Diversity of *Cryptosporidium* and *Giardia duodenalis* in threatened brush-tailed rock-wallabies (*Petrogale penicillata*)

Elke Tilly Vermeulen[1], Mark Eldridge[2], Michelle Power[1]
[1]Department of Biological Sciences, Macquarie University, Australia; [2]Australian Museum, Australia

Cryptosporidium and *Giardia duodenalis* are significant pathogens of humans and animals, including wildlife. Both Genera comprise species with broad host ranges that are commonly found in humans and wildlife hosts. However, the occurrence of these parasites in Australian wildlife species is largely unknown. The aim of this study was to investigate transmission sources of these parasites to wildlife using a case-study of the threatened brush-tailed rock-wallaby (*Petrogale penicillata*). Faecal samples (n=318) were collected from various sites in New South Wales. Faecal DNAs were initially screened at the 18S rRNA locus, followed by identification at discriminatory loci: *actin* and *gp60* for *Cryptosporidium* and *β giardin* and *gdh* for *Giardia* to confirm species identification. Multi-locus sequencing revealed the presence of *Cryptosporidium fayeri,* a marsupial-specific species*,* and *C. meleagridis*, which has a broad host range, including humans. For *Giardia*, isolates were assigned to the zoonotic sub-assemblages AI and BIV, identified previously in human clinical cases and other animals. The identification of these *Cryptosporidium* species and *Giardia* assemblages suggests transmission pathways from humans or other animals to wildlife may exist. We recommend further study into *Cryptosporidium* and *Giardia* to understand the diversity and epidemiology of these parasites in Australian wildlife.

Symposium 14: Veterinary Parasitology 2 supported by Virbac Animal Health

Time: Thursday, 02/Jul/2015: 1:30pm - 2:00pm · *Location:* Symposium Room 1
Session Chair: Robert Peter Dempster, Virbac

Antiparasite immunity, worm burdens and illthrift in adult sheep?

Dave Malcolm Leathwick
AgResearch, New Zealand

It has often been said that adult ewes under duress have a lower level of immunity to nematode parasites and this results in increased worm burdens and poorer condition in these animals i.e. skinny ewes are skinny because they have worms and they have worms because of reduced immune status. Because of a growing interest in leaving ewes untreated as 'refugia' against the development of anthelmintic resistance, we investigated the relationship between anti-parasite immunity, body condition and parasite load in adult sheep. In an initial series of trials we were unable to find any correlation between ewe weight gain or body condition score and faecal nematode egg count or antibody levels in plasma and saliva. There was no difference in FEC, or antibody levels, between ewes of different body condition scores. Subsequently, in an on-farm investigation of what appeared to be clinical parasitism it was found that ewes of CS 1.0, which were visually 'wormy', had similar FEC to ewes of CS 3.0, which did not look ‘wormy’. Further, all ewes showed a similar liveweight-gain response to treatment with an anthelmintic. In a more recent large scale study on commercial farms there was no interaction between body condition score at treatment (pre-lambing) and response to treatment with anthelmintic i.e. fat ewes responded similarly to skinny ewes. Further, there was no relationship between FEC at the time of treatment and response to the treatment. Therefore, our attempts to show a correlation between body condition score, worm burden as indicated by FEC and immune status in adult sheep have failed. When combined with studies showing that adult ewes show a similar response to anthelmintic treatment regardless of their condition, these data call into question the idea that ewes are skinny because they have more worms than other ewes and that this is a consequence of reduced anti-parasite immunity. While this does not negate the potential benefits of treating skinny ewes with anthelmintic, it does call into question the potential conclusion that worms have caused the problem, and suggests that perhaps we should be looking elsewhere for causes of ewe illthrift.

Symposium 15: Protozoan Biology 2

Time: Thursday, 02/Jul/2015: 1:30pm - 2:00pm · *Location:* Symposium Room 2
Session Chair: Denise Doolan, QIMR Berghofer Medical Research Institute

Differential stimulation of *Giardia duodenalis* trophozoites between host soluble signals and host cell attachment during *in vitro* interactions

Samantha J. Emery[1], Mehdi Mirzaei[1], Daniel Vuong[2], Dana Pascovi[3], Ernest Lacey[2], Paul A. Haynes[1]
[1]Macquarie University, Australia; [2]Microbial Screening TechnologiesAustralia; [3]Australian Proteome Analysis Facility (APAF), Macquarie University, Australia

Giardia duodenalis is the protozoan agent responsible for the majority of parasitic gastroenteritis in humans worldwide. Disease pathology includes malabsorption and maldigestion, small intestinal barrier dysfunction, which occurs in the absence of known toxins, and overt inflammation. We performed the first proteomic analysis of *G. duodenalis* trophozoites interacted with intestinal epithelial cells for 6 hours, and compared it to trophozoites exposed to cell-free fractions of host-soluble signals. This has demonstrated distinct and independent protein cascades are induced by host attachment compared to host soluble signals. We utilised a tandem mass tag approach and found a total of 68 proteins were differentially expressed, of which 47 were up-regulated and 21 down-regulated. Host soluble signals triggered the up-regulation of membrane-associated and secreted proteins, including 26.7% of all variant surface proteins, tenascins, cathepsin B precursor and an unannotated cystatin homologue. Conversely, co-incubation with IECs up-regulated intracellular pathways, including ubiquitination proteins, oxioreducatases and proteins involved in pyridoxamine phosphate or vitamin B6 production. These may present novel metabolic targets for therapeutics. These results indicate that *Giardia* trophozoites are primed to sense soluble host signals independent from attachment, and soluble signals cause up-regulation of known and putative virulence factors.

CP 14: Veterinary Parasitology 2 Contributed Papers supported by Virbac Animal Health

Time: Thursday, 02/Jul/2015: 2:00pm - 3:00pm · *Location:* Symposium Room 1
Session Chair: Robert Peter Dempster, Virbac

The occurrence of *Linguatula serrata* and *Taenia* metacestodes in domestic livestock in South East Australia

Sara Claire Baker, David Jenkins, Shokoofeh Shamsi
School of Animal and Veterinary Sciences, Charles Sturt University, Australia

Parasitic infections are considered to be the most significant and dominant health issues associated with grazing ruminants within Australia. Among parasites affecting livestock, *Linguatula serrata* (the tongue worm)is a parasitic arthropod that utilises herbivorous mammals, such as domestic livestock, as its intermediate host. The larval stage is found most commonly in the mesenteric lymph nodes of herbivores, usually cattle and rabbits. The parasite is found worldwide, including Australia; however the last report of larval *L. Serrata* in an Australian herbivore was in 1936. Other important parasites infecting domestic livestock are intermediate stages of parasites belonging to the family Taeniidae. Transmission occurs through similar predator/prey interaction as for *L. serrata* where definitive hosts consume intermediate hosts infected with the intermediate stage of the parasite. Taeniid cestodes are parasites of considerable public health, veterinary and economic importance. We present data from a study of the occurrence of *L. serrata* and metacestodes of taeniid cestodes in livestock from southeastern Australia.

Low cost whole-organism compound screening method

Sarah Preston[1], Abdul Jabbar[1], Cameron Nowell[2], Anja Joachim[3], Baerbel Ruttkowski[3], Jonathan Baell[2], Tony Cardno[2], Pasi Korhonen[1], David Piedrafita[4], Brendan Ansell[1], Aaron Jex[1], Andreas Hofmann[5], Robin Gasser[1]
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Due to major problems with drug resistance in parasitic nematodes of animals, there is a need to develop new anthelmintics via genomic-guided and/or repurposing approaches. Here, we established a practical and cost-effective whole-organism assay for the in vitro-screening of compounds for activity against parasitic stages of the nematode *Haemonchus contortus*. The assay is based on the use of exsheathed L3 (xL3) and L4 stages of *H. contortus* of small ruminants (sheep and goats). Using this assay, we screened a panel of 522 well-curated kinase inhibitors (GlaxoSmithKline, United States of America; code: PKIS2) for activity against *H. contortus* by measuring the inhibition of larval motility using an automated image analysis system. We identified two chemicals within the compound classes biphenyl amides and pyrazolo[1,5-α]pyridines, which reproducibly inhibit both xL3 and L4 motility and development, with IC_{50}s of 14–47 µM. These compounds fit the Lipinski rule-of-five (including bioavailability), and show promise for hit-to-lead optimisation and repurposing for use against parasitic nematodes. The screening assay established here has some significant advantages over conventional methods, particularly in terms of ease of use, throughput, time and cost.

Are abomasal incubations needed when assessing the efficacy of anthelmintics against abomasal burdens of adult Ostertagiinae in deer?

P.C. Mason[1], D.M. Leathwick[2], D.W. Lawrence[3], J.T. MacGibbon[4], G. Williams[5]
[1]Mason Consulting, New Zealand; [2]AgResearch, New Zealand; [3]Tikana, New Zealand; [4]Northern Southland Veterinary Services, New Zealand; [5]Landcorp Farming Limited, New Zealand

When farming of deer (*Cervus elaphus*) started in New Zealand the only significant internal parasites were lungworm (*Dictyocaulus* sp.). 35 years on gastrointestinal (GI) nematodes have become a much more important challenge to farmed deer health. The most important GI nematodes are Ostertagiinae parasitizing the abomasum. We carried out 6 controlled slaughter trials (236 deer) where we could compare worm counts from abomasal washings, abomasal incubations and total abomasal worm counts in order to assess the efficacy of the anthelmintics being tested. Our concern was whether the extra work involved in carrying out abomasal incubations improved the results. Based separately on paired comparison t-tests and regressing the efficiencies one against another, our findings were that they did not. We conclude that if farmed deer abomasa are thoroughly washed out there is no need for abomasal incubations when assessing the efficacy of anthelmintics against abomasal burdens of adult Ostertagiinae.

Confirmation of macrocyclic lactone resistance in *Ostertagia ostertagi* from cattle in New Zealand

Tania Susanne Waghorn, Dave Leathwick
AgResearch, New Zealand

Although resistance to macrocyclic lactone anthelmintics in *Ostertagia ostertagi* had been suspected in New Zealand, it had never been confirmed. In this study, four suspected cases were investigated after routine anthelmintic testing on commercial farms. Initially a comprehensive faecal egg count reduction test (FECRT) was undertaken using oral formulations of ivermectin (0.2 mg/kg), albendazole (5.0 mg/kg) and levamisole (7.5 mg/kg). The proportions of *O. ostertagi* in the untreated control and post-treatment larval cultures were used to determine efficacy against this species. Subsequently, the isolates from two of the farms were recovered and used to infect 18 six month old calves for each isolate. The efficacy of oral ivermectin and moxidectin, both at 0.2 mg/kg, against these two isolates was determined by slaughter and worm count trial. The efficacy of ivermectin against *O. ostertagi,* based on differentiated FECRT for each of the farms was 45%, 39%, 71% and 0%. Efficacy results from worm counts in the slaughter trial for the first two isolates were 54% and 12% respectively for ivermectin and 100% for both with moxidectin. In addition albendazole, at a dose rate of 5mg/kg, failed to achieve 95% efficacy for two of the

isolates (82 and 85%). These results confirm the presence of macrocyclic lactone resistant *O. osteragi* in cattle in New Zealand and the likely presence of dual resistance, to macrocyclic lactones and albendazole, in some isolates.

CP 15: Protozoan Biology 2 Contributed Papers

Time: Thursday, 02/Jul/2015: 2:00pm - 3:00pm · *Location:* Symposium Room 2
Session Chair: Denise Doolan, QIMR Berghofer Medical Research Institute

RNA-seq analysis confirms that extracellular tachyzoites of virulent and avirulent strains of *Neospora caninum* are transcriptionally distinct

Stephen Bush, Joel Barratt, John Ellis
University of Technology, Sydney, Australia

Different *Neospora caninum* isolates from bovine and canine sources differ in their ability to cause disease in mice and cows. For example, NC-Liverpool is extremely pathogenic and infection of laboratory mice results in death while NC-Nowra is far less virulent. This suggests that there may be intrinsic, genetic differences amongst isolates which await identification. Illumina next generation sequencing was used to compare the extracellular tachyzoite transcriptome from these two *Neospora* isolates. Total RNA was extracted from extracellular tachyzoites of NC-Liverpool and NC-Nowra grown *in vitro* using Trisure reagent, and RNA-seq was conducted. The reads were analysed using workflows in the web-based platform Galaxy. Reads were aligned to the *N. caninum* genome (obtained from ToxoDB). The existence of differentially expressed genes occurring in tachyzoites between NC-Liverpool and NC-Nowra was investigated using a variety of models, including Cufflinks and CuffDiff or HTSeq. The results suggest that as many as 1000 genes may be differentially expressed between these two tachyzoite populations. Annotation of these genes indicates that “ribosome” and “ATP binding” are highly represented gene ontology terms in the list of differentially expressed genes, suggesting that protein synthesis and kinase activity by a tachyzoite is an important contributor to virulence in *N. caninum*.

Characterisation of *Toxoplasma gondii* NBP35 in iron-sulfur cluster biosynthesis

Yi Tong Vincent Aw[1], Azadeh Seidi[1], Jiwon Lee[2], Melanie Rug[2], Giel van Dooren[1]
[1]Research School of Biology, Australian National University, Australia; [2]Centre for Advanced Microscopy, Australian National University, Australia

Iron-sulfur (Fe-S) clusters are prosthetic groups on iron-sulfur proteins, and are essential for survival of all eukaryotes. Studies in model eukaryotes have identified independent Fe-S cluster biosynthesis pathways in the mitochondrion, plastid and cytosol, which produce Fe-S clusters for the respective compartments. Little is known about Fe-S cluster biosynthesis in apicomplexan parasites, the causative agents of diseases such as malaria. NBP35 is the central protein in the synthesis of cytosolic Fe-S clusters, and has a cytosolic localisation in all eukaryotes studied thus far. Unexpectedly, we found the NBP35 homologue of the model apicomplexan *Toxoplasma gondii* (*Tg*NBP35) localised to the mitochondrion. Using a genetically- encoded electron microscopy tagging approach, we demonstrate that *Tg*NBP35 likely localises to the cytosolic face of the outer mitochondrial membrane. *Tg*NBP35 has an N-terminal transmembrane domain that we show is necessary and sufficient for mitochondrial localisation. We generated an anhydrotetracycline-regulatable knockdown mutant in *Tg*NBP35, and found *Tg*NBP35 knockdown leads to a severe parasite growth defect, highlighting the essentiality of *Tg*NBP35 for parasite survival. Knockdown of *Tg*NBP35 leads to defects in the biogenesis of cytosolic Fe-S proteins, but not of mitochondrial Fe-S proteins, consistent with *Tg*NBP35 playing a role in cytosolic Fe-S cluster biosynthesis despite its mitochondrial localisation.

Does *Toxoplasma gondii* infection affect mouse personality?

Amanda R. Worth[1], Patricia A. Fleming[1], R.C. Andrew Thompson[1], Alan J. Lymbery[1,2]
[1]School of Veterinary and Life Sciences, Murdoch University, Australia; [2]Fish Health Unit, Murdoch University, Australia

It is believed that *T. gondii* manipulates rodent behaviour in order to increase transmission to its definitive host. Parasitism may affect host behaviour in subtle ways that have not yet been considered in the *T. gondii*-rodent system. For example, parasitism may influence host personality by altering the repeatability of behavioural traits and/or correlations between behavioural traits. To study this, we assessed behaviour of uninfected female mice in three behavioural tests (the elevated plus maze; EPM, the open field; OF, and a predator odour avoidance arena; POAA), then infected a subset of mice and re-assessed behaviour at four subsequent time points. We characterised mouse personality using exploratory factor analysis and defined two main factors for both the EPM and OF; EPM activity, EPM boldness, OF activity and OF boldness. Results indicate that uninfected mice do show consistent, repeatable behaviour across both time and context, and mice that were more active tended to be more bold. Interestingly, it appears that behavioural traits were more consistent in *T. gondii*-infected mice, and the correlation between activity and boldness was not as strong. Although individuals differed in their response to cat urine, infection with *T. gondii* did not consistently alter this behaviour.

Leishmaniasis vaccine development using machine learning algorithms

Webster Itai Nyakudya[1,3], Joel Barratt[1], Paul Kennedy[2], John Ellis[1]
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Protozoa of the genus *Leishmania* are obligatory intracellular parasites and causative agents of various clinical forms of leishmaniasis. Chemotherapeutics are available but show high toxicity, high costs and are prone to resistance development due to prolonged treatment periods. Recovery from leishmaniasis is associated with life-long resistance to re-infection which implies that vaccination might be a feasible control strategy. However, despite all the efforts and advances there is no vaccine against human leishmaniasis. It is hypothesised that *in silico* selection of antigens from genomic and proteomic data using machine learning algorithms, can facilitate development of an anti-*Leishmania* vaccine. We will discuss the potential

application of Vacceed; a recently developed vaccine prediction tool based on machine learning algorithms, to the development of anti-*Leishmania* vaccines. Vacceed provides a flexible and automated process to predict worthy vaccine candidates for eukaryotes from large volumes of superfluous and noisy genomic, proteomic and transcriptomic data. As input, Vacceed can accept thousands of pathogen derived sequences and the main output is a ranked list of protein candidates determined by a set of machine learning algorithms. In this way, Vacceed has the potential to save time and money by reducing the number of false candidates allocated for laboratory validation.

Symposium 16: Veterinary Parasitology 3 supported by Virbac Animal Health

Time: Thursday, 02/Jul/2015: 3:30pm - 4:00pm · *Location:* Symposium Room 1
Session Chair: Ian Sutherland, AgResearch Ltd

Veterinary parasitology in a diagnostic laboratory - a Queensland perspective

Louise Jackson
Department of Agriculture and Fisheries, Australia

The Biosecurity Science Laboratory (BSL) is the Queensland Government's veterinary diagnostic laboratory and it is located in Brisbane. BSL is accredited with the National Association of Testing Authorities (NATA) for Parasitology (including helminths, arthropods and protozoa) for production animals, production avian species, avian species, wildlife, equine species, companion animals, laboratory animals and zoo animals. The Parasitology section of the laboratory performs standard diagnostic testing including faecal egg counts, faecal culture and larval nematode differentiation, and nematode identification and counts in livestock species and sometimes wildlife and aquatic species. However, other parasitological testing of a more unusual nature is also done, including *Trichinella* testing in pigs and crocodiles, identification of exotic mites of honeybees (including *Varroa* sp.) and acaricide resistance testing of cattle ticks. I will be speaking on the less common parasitological testing performed in the laboratory and some interesting cases where parasites were involved.

Symposium 17: Helminth Biology 2

Time: Thursday, 02/Jul/2015: 3:30pm - 4:00pm · *Location:* Symposium Room 2
Session Chair: Nick Smith, James Cook University

Of monkeys and men: immunomic profiling of sera from humans and non-human primates resistant to schistosomiasis reveals novel potential vaccine candidates

Mark Simon Pearson[1], Luke Becker[1], Patrick Driguez[2], Xiao-Hong Li[3], Denise Doolan[2], Don McManus[2], Alan Wilson[4], Francisca Mutapi[5], Alex Loukas[1]
[1]Australian Institute of Tropical Health and Medicine, James Cook University, Australia; [2]QIMR Berghofer Medical Research Institute, Australia; [3]National Institute of Parasitic Diseases, China; [4]University of York, United Kingdom; [5]University of Edinburgh, United Kingdom

Schistosoma haematobium affects more than 100 million people throughout Africa and is the causative agent of urogenital schistosomiasis. The parasite is strongly associated with urothelial cancer in infected individuals and as such is designated a group I carcinogen by the International Agency for Research on Cancer. Using a protein microarray containing schistosome proteins, we sought to identify antigens that were the targets of protective IgG1 immune responses in *S. haematobium*-exposed individuals that acquire drug-induced resistance (DIR) to schistosomiasis after praziquantel treatment. Numerous antigens with known vaccine potential were identified, including calpain (Smp80), tetraspanins, glutathione-S-transferases and glucose transporters (SGTP1), as well as previously uncharacterized proteins. Reactive IgG1 responses were not elevated in exposed individuals who did not acquire DIR. To complement our human subjects study, we screened for antigen targets of rhesus macaques rendered resistant to *Schistosoma japonicum* by experimental infection followed by self-cure, and discovered a number of new and known vaccine targets, including major targets recognised by our human subjects. This study has further validated the immunomics-based approach to schistosomiasis vaccine antigen discovery and identified numerous novel potential vaccine antigens.

CP 16: Veterinary Parasitology 3 Contributed Papers supported by Virbac Animal Health

Time: Thursday, 02/Jul/2015: 4:00pm - 5:00pm · *Location:* Symposium Room 1
Session Chair: Ian Sutherland, AgResearch Ltd

Revamping veterinary parasitology teaching for the tech-savvy student

Anne Maree Beasley, Lyn Knott, Malcolm Jones, Justine Gibson, Marnie Holt
University of Queensland, Australia

Teaching veterinary parasitology to undergraduate students has traditionally relied upon standard printed material in the form of study guides, and tools like dichotomous keys to assist with parasite identification during practical sessions. Providing a sufficient number of knowledgeable and experienced tutors to assist groups of 120 students or more with these resources can be a limiting factor, highlighting the need for better resources which enable self-directed learning. We report on, and demonstrate, the progress of a new parasitology eBook designed to be a comprehensive teaching aid for our tech-savvy Veterinary Parasitology students as well as a useful reference guide to the graduated Veterinarian or postgraduate student. The main eBook chapters, organised by parasite class, are compilations of interactive lists, charts and keys embedded with high resolution images illustrating morphological features essential for parasite identification. A chapter on diagnostic parasitology contains protocols and demonstrational videos for commonly used laboratory procedures, and an image library allows quick links to all parasite images indexed by genus and species name. Overwhelmingly positive feedback has been

received following preliminary student trials and we anticipate that this modern learning format will enhance the overall learning experience of students and translate into improved performance in practical exams.

Evidence for *Toxoplasma gondii* as a cause of abortion in farmed deer in New Zealand

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Abortions due to *Toxoplasma gondii* infections during pregnancy have been reported previously in New Zealand deer. Abortion rates of 2.8% in rising-two-year-old (R2) and 1.2% in mixed-age (MA) hinds were detected in a two-year fetal wastage study (n=96 farms). The sero-prevelence of *T.gondii* using validated ELISA test (cut-off SP%:18.3) in hinds with and without abortions were 30% (n=86) and 25% (283), respectively in MA group and 31% (n=270) and 22% (n=432), respectively in R2 group. The association between *T.gondii* serostatus and abortion was significant (odds ratio: 1.65, Chisq p=0.004) in R2 hinds and non-significant in MA hinds (Chisq p=0.3). In hinds with abortion, *T.gondii* DNA was detected in 3/20 R2 and 1/10 MA fetal brains, 21/136 (15%) R2 and 3/25 MA myometrium samples, 3/9 R2 placenta samples, 1/13 R2 fetal diaphragms, 2/79 (15%) R2 and 9/50 (18%) MA caruncle samples and 2/18 R2 and 1/10 MA cotyledon samples. Three *T.gondii* positive fetal brains came from R2 hinds seen aborting at scan-1 with one hind also having presence of *Toxoplasma* DNA in myometrium suggesting transplacental transmission and possible early abortions by *Toxoplasma*. The serology and molecular biology findings suggest *T.gondii* may be a cause of abortions in NZ farmed deer.

Establishing the prevalence of liver fluke infections in dairy cattle in the Macalister, Goulburn Valley and Upper Murray irrigation districts in Victoria

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Watt (1979) established that the incidence of fasciolosis in dairy cattle in Victoria is greater in irrigation regions. Elliott *et al.* (2015) recently reported a mean 81% prevalence of fasciolosis on 6 dairy farms in the Macalister irrigation district (MID). In order to gain a deeper understanding of the distribution of fasciolosis in dairy cattle in Victoria, we have now assessed the prevalence of fasciolosis on 42 farms (855 cattle) across three Victorian irrigation districts (MID, the Goulburn Valley and Upper Murray) using the coproantigen faecal ELISA (BioX 201) and liver fluke faecal egg counts (FEC). The mean herd prevalence of liver fluke infections in dairy cattle in each region was: 72% by ELISA and 73% by FEC in the MID, 20% by ELISA and 23% by FEC in the Goulburn Valley; and 51% by ELISA and 57% by FEC in the Upper Murray. Production loss in dairy cattle occurs once the herd prevalence of liver fluke exceeds 25% (Vercruysse and Claerebout 2001), suggesting that producers in the MID and Upper Murray are experiencing significant production losses. Ongoing research is assessing whether the high prevalence of liver fluke on some dairy farms is a result of triclabendazole resistance.

A 'specific' issue: the use of universal primers to detect *Coxiella* sp. in the brown dog tick (*Rhipicephalus sanguineus*)

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The zoonotic bacterium *Coxiella burnetii* (*C. burnetii*) has been detected worldwide in many tick species. The role of the brown dog tick, *Rhipicephalus sanguineus* (*R. sanguineus*), in harbouring and transmitting this pathogen in Australia is currently unknown. This study aimed to detect *C. burnetii* in *R. sanguineus* (*n*=107) from urban Western Australia and the Northern Territory using *C. burnetii*-specific primers targeting the IS1111a transposase element gene. No amplification of the IS1111a gene was detected in the tick samples, while the two positive controls amplified the 498bp region. Subsequently, Next-Generation Sequencing (NGS) was used to evaluate the bacterial microbiome, and to identify *Coxiella* sp. in *R. sanguineus* ticks. Universal bacterial primers targeting the 16S rRNA gene (V1-2) were used for bacterial amplification, and NGS was performed on the Ion Torrent™ semiconductor platform. NGS results revealed *Coxiella* sp. in 53/59 (90%) tick pools. Further analyses showed these sequences had a 100% sequence homology to a *Coxiella*-like sp. previously identified from *R. sanguineus* in the Philippines. This study illustrates the value of using universal primers, rather than species-specific primers, to detect novel bacterial species with NGS methodology. Future investigations could lead to further characterisation of this novel bacterium's genome.

CP 17: Helminth Biology 2 Contributed Papers

Time: Thursday, 02/Jul/2015: 4:00pm - 5:00pm · *Location:* Symposium Room 2
Session Chair: Nick Smith, *James Cook University*

Defining the *Schistosoma haematobium* kinome as a basis for the prediction and prioritisation of kinases as anti-schistosome drug targets

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The blood fluke *Schistosoma haematobium* causes urogenital schistosomiasis, a neglected tropical disease (NTD) that affects at least 110 million people. Treating this disease by targeted or mass administration of a single chemical, praziquantel, bears the risk that drug resistance will develop in this pathogen. Therefore, there is an imperative to search for new drug targets in *S. haematobium* and other schistosomes. In this regard, protein kinases have potential, given their roles in essential biological processes and as targets for drugs already approved by the US Food and Drug Administration (FDA) for use in humans. In this

study, we defined the kinome of *S. haematobium* using a refined bioinformatic pipeline. We classified, curated and annotated predicted kinases, and assessed the transcription profiles of kinase genes in different developmental stages. Then, we prioritised a panel of kinases as target candidates and chemicals inferred to bind to them. Most kinases of *S. haematobium* are very similar to *S. mansoni* orthologs, offering the prospect of designing or repurposing chemicals that kill these and related schistosomes.

Genomic resources for *Schistosoma haematobium* to support post-genomic discoveries

Neil D. Young, Pasi K. Korhonen, Robin B. Gasser

Faculty of Veterinary and Agricultural Sciences, The University of Melbourne, Australia

Urogenital schistosomiasis is a debilitating disease caused by *Schistosoma haematobium* that affects more than 100 million people mainly in sub-Saharan Africa. Disease relates to chronic inflammation and fibrosis mainly of the urinary bladder and/or genital system, and also promotes malignant cancer and HIV/AIDS. Given the limitations of current interventions, international *non-government organisations have committed to* finding next-generation treatments and interventions for this and other neglected diseases. Our perspective has been to support this focus by providing crucial molecular resources. Therefore, within the framework of our genomics program, we characterised the genome and transcriptomes of *S. haematobium*,which are now publicly available to the international research community. This talk will summarise this progress and emphasize recent enhancements to these resources (including non-coding RNAs, alternative splicing and annotation methods) as a basis for many fundamental research areas as well as the development of new and improved methods of diagnosis, treatment and control.

Suppression of the insulin receptors in adult *Schistosoma japonicum* impacts on parasite growth and development: further evidence of vaccine potential

Hong You, Geoffrey Gobert, Pengfei Cai, Donald McManus

QIMR Berghofer Medical Research Institute, Australia

To further investigate the importance of insulin signaling in the growth, development, sexual maturation and egg production of adult schistosomes, we have focused attention on the insulin receptors (SjIRs) of *Schistosoma japonicum*, which we have previously cloned and partially characterised. We now show, by Biolayer Interferometry, that human insulin can bind the L1 subdomain (insulin binding domain) of recombinant (r)SjIR1 and rSjIR2 (designated SjLD1 and SjLD2) produced using the *Drosophila* S2 protein expression system. We have then used RNA interference (RNAi) to knock down the expression of the SjIRs in adult *S. japonicum in vitro* and show that, in addition to their reduced transcription, the transcript levels of other important downstream genes within the insulin pathway, associated with glucose metabolism and schistosome fecundity, were also impacted substantially. Further, a significant decrease in glucose uptake was observed in the SjIR-knockdown worms compared with luciferase controls. In vaccine/challenge experiments, we found that rSjLD1 and rSjLD2 depressed female growth, intestinal granuloma density and faecal egg production in *S. japonicum* in mice presented with a low dose challenge infection. These data re-emphasize the potential of the SjIRs as veterinary transmission blocking vaccine candidates against zoonotic schistosomiasis japonica in China and the Philippines.

A granulin growth factor secreted by the carcinogenic liver fluke, *Opisthorchis viverrini*, and its role in wound healing and carcinogenesis

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Parasitic worms are large, invasive pathogens. To combat the pathology they induce, worms evolved strategies to promote wound repair in infected hosts. The Thai liver fluke, *Opisthorchis viverrini,* induces such extensive immunopathology and protracted wound healing that it causes cancer. We show that the secreted proteins of *O. viverrini* accelerated wound repair in human cholangiocytes, and this repair process was diminished by silencing expression in the fluke-of a gene that encodes for the granulin-like growth factor, *Ov*-GRN-1. Recombinant *Ov*-GRN-1 induced angiogenesis and accelerated wound healing in mice. *Ov*-GRN-1 was internalized by cholangiocytes and induced changes in expression of proteins and mRNAs associated with wound healing and cancer pathways. This is the first description of a pathogen protein that stimulates wound repair and in doing so contributes to the establishment of a tumorigenic environment. *Ov*-GRN-1 holds promise as both a novel wound healing agent and vaccine with anti-parasitic and anti-cancer properties.

2015 Joint Conference of the New Zealand Society for Parasitology and the Australian Society for Parasitology Inc.

June 29 – July 2, Crowne Plaza Auckland, New Zealand

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Aghazadeh, Mahdis	93*	CP 10, Crowne Plaza Symposium Room 1
Almegrin, Wafa Abdullah	3	Poster View, Crowne Plaza Foyer
Almeida, Carlos E.	10*	Poster Oral, Crowne Plaza Plenary Room
Anstead, Clare Alayne	15	CP 13, Crowne Plaza Symposium Room 2
Aw, Yi Tong Vincent	76*	CP 15, Crowne Plaza Symposium Room 2
Azam, MD. Shakif-Ul	51*	Poster Oral, Crowne Plaza Plenary Room
Baker, Sara Claire	44*	CP 14, Crowne Plaza Symposium Room 1
Balli-Garza, Jimena	48*	Poster Oral, Crowne Plaza Plenary Room
Barbosa, Amanda	29*	CP 6, Crowne Plaza Symposium Room 1
Beasley, Anne Maree	40	CP 16, Crowne Plaza Symposium Room 1
Beasley, Anne Maree	71	Poster Oral, Crowne Plaza Plenary Room
Bhat, S.A.	126*	Poster Oral, Crowne Plaza Plenary Room
Bogema, Daniel Ross	55	CP 11, Crowne Plaza Symposium Room 2
Bui, S.	111*	CP 1, Crowne Plaza Plenary Room
Bush, Stephen	107	CP 15, Crowne Plaza Symposium Room 2
Cameron, Timothy Charles	102*	Poster Oral, Crowne Plaza Plenary Room
Cassidy, Tara Louise	88*	Poster Oral, Crowne Plaza Plenary Room
Chiu, C.Y.	124*	Poster Oral, Crowne Plaza Plenary Room
Chua, Ming Jang	47*	CP 7, Crowne Plaza Symposium Room 2
Cooper, Crystal	83*	CP 8, Crowne Plaza Symposium Room 1
Cooper, Madalyn Kate	61*	Poster Oral, Crowne Plaza Plenary Room
Donahoe, Shannon Lynn	81*, 84*	CP 8, Crowne Plaza Symposium Room 1; Poster Oral, Crowne Plaza Plenary Room
Ellis, John	103	CP 12, Crowne Plaza Symposium Room 1
Emery, Samantha	96*, 43*	Poster Oral, Crowne Plaza Plenary Room; Symp 15, Crowne Plaza Symposium Room 2
Engel, Jessica	49*	CP 4, Crowne Plaza Symposium Room 1
Fernando, Waduge Deepani Darshika	63*	CP 5, Crowne Plaza Symposium Room 2

Fisher, G.M.	45*	CP 7, Crowne Plaza Symposium Room 2
Gazdik, Michelle	68*	CP 4, Crowne Plaza Symposium Room 1
Gebremikael, Hagos Gebrekidan	97*	T1CP11, Crowne Plaza Symposium Room 2
Giacomin, Paul Robert	120	P3, Crowne Plaza Plenary Room
Gneme, Awa	46	Poster View, Crowne Plaza Foyer
Godfrey, Stephanie	117	Symp 8, Crowne Plaza Symposium Room 1
Gordon, Catherine	77	CP 2, Crowne Plaza Symposium Room 1
Greay, Telleasha L.	24*, 80*	CP 16, Crowne Plaza Symposium Room 1; Poster Oral, Crowne Plaza Plenary Room
Grinberg, Alex	72	CP 13, Crowne Plaza Symposium Room 2
Gyawali, Pradip	14*	CP 9, Crowne Plaza Symposium Room 2
Harrison, G.L.A.	125	Poster Oral, Crowne Plaza Plenary Room
Harvie, Marina	110	CP 12, Crowne Plaza Symposium Room 1
Heath, David Duncan	18	Symp 12, Crowne Plaza Symposium Room 1
Hoberg, Eric P.	116	P2, Crowne Plaza Plenary Room
Howe, Laryssa	122	Symp 6, Crowne Plaza Symposium Room 1
Howieson, Vanessa	106*	CP 7, Crowne Plaza Symposium Room 2
Huang, Yan	130	Poster Oral, Crowne Plaza Plenary Room
Hutson, Kate Suzanne	65	CP 1, Crowne Plaza Plenary Room
Jackson, Louise	109	Symp 16, Crowne Plaza Symposium Room 1
Johnson-Mackinnon, Jessica Christine	74*	Poster Oral, Crowne Plaza Plenary Room
Kaplan, Ray M.	129	P2, Crowne Plaza Plenary Room
Karunarathne, Deshapriya	104	Poster Oral, Crowne Plaza Plenary Room
Keatley, S.	123	Poster Oral, Crowne Plaza Plenary Room
Kelley, Jane Michele	100*	CP 16, Crowne Plaza Symposium Room 1
Koehler, Anson	52	CP 9, Crowne Plaza Symposium Room 2
Kumarasingha, Rasika	19*	CP 10, Crowne Plaza Symposium Room 1
Kwak, Mackenzie Lamont	82*	CP 5, Crowne Plaza Symposium Room 2
Lane, Henry Somerset	95*	Poster Oral, Crowne Plaza Plenary Room
Lau, Emily	112*	CP 5, Crowne Plaza Symposium Room 2
Lawrence, Andrea Lee	16*, 17*	CP 13, Crowne Plaza Symposium Room 2; Poster Oral, Crowne Plaza Plenary Room
Leathwick, Dave Malcolm	118	Symp 14, Crowne Plaza Symposium Room 1
Lee, Yan Quan	69*	Poster Oral, Crowne Plaza Plenary Room
Lehane, Adele M.	121	Symp 4, Crowne Plaza Symposium Room 1
Leung, Tommy	39	CP 6, Crowne Plaza Symposium Room 1
Llewellyn, Stacey	101	CP 9, Crowne Plaza Symposium Room 2
Lochore, Sarah	94*	Poster Oral, Crowne Plaza Plenary Room

Low, L.M.	115*	Poster Oral, Crowne Plaza Plenary Room
Mamun, Md Abdullah Al	108*	Poster Oral, Crowne Plaza Plenary Room
Martin, Storm B.	37*	CP 3, Crowne Plaza Symposium Room 2
Mason, P.C.	114	CP 14, Crowne Plaza Symposium Room 1
McSpadden, Kate Ashleigh	50*	Poster Oral, Crowne Plaza Plenary Room
Mengist, Hylemariam Mihiretie	7, 8	Poster View, Crowne Plaza Foyer
Nyakudya, Webster Itai	42*	CP 15, Crowne Plaza Symposium Room 2
O'Connell-Milne, Sorrel	99*	CP 3, Crowne Plaza Symposium Room 2
O'Dwyer, Katie	5*	CP 1, Crowne Plaza Plenary Room
Onizawa, Emily	20*	Poster Oral, Crowne Plaza Plenary Room
Paparini, Andrea	56, 57, 59	CP 4, Crowne Plaza Symposium Room: 1; CP 8, Crowne Plaza Symposium Room 1; CP 11, Crowne Plaza Symposium Room 2
Patel, Kandarp Khodidas	85*	CP 16, Crowne Plaza Symposium Room 1
Pearson, Mark Simon	1	Symp 17, Crowne Plaza Symposium Room 2
Perera, Piyumali K.	21*, 22*	CP 11, Crowne Plaza Symposium Room 2; CP 11, Crowne Plaza Symposium Room 2
Perez, Catherine	89*	CP 2, Crowne Plaza Symposium Room 1
Piedrafita, David	58	Symp 10, Crowne Plaza Symposium Room 1
Pinkevych, Mykola	98	CP 2, Crowne Plaza Symposium Room 1
Poulin, Robert	4	P2, Crowne Plaza Plenary Room
Poupa, Anita Marie	41*	Poster Oral, Crowne Plaza Plenary Room
Presswell, Bronwen	113	CP 8, Crowne Plaza Symposium Room 1
Preston, Sarah	30	CP 14, Crowne Plaza Symposium Room 1
Ranasinghe, Shiwanthi L.	35*	CP 10, Crowne Plaza Symposium Room 1
Randhawa, Haseeb Sajjad	90	Symp 3, Crowne Plaza Symposium Room 2
Rasmussen, Trent Kevin	53*	CP 3, Crowne Plaza Symposium Room 2
Rawlin, Grant Thomas	26	T1CP11, Crowne Plaza Symposium Room 2
Raza, Ali	79*	Poster Oral, Crowne Plaza Plenary Room
Reynolds, Simone Louise	32	Symp 5, Crowne Plaza Symposium Room 2
Ryan, Stephanie	60*	Poster Oral, Crowne Plaza Plenary Room
Ryan, Una	31	Symp 9, Crowne Plaza Symposium Room 2
Sakthivel, Dhanasekaran	66*	CP 12, Crowne Plaza Symposium Room 1
Samoylovskaya, Nina	64	Poster View, Crowne Plaza Foyer
Schiller, Sabine Eva	13*	Poster Oral, Crowne Plaza Plenary Room
Shamsi, Shokoofeh	38	CP 3, Crowne Plaza Symposium Room 2
Shinn, Andrew P.	128	Symp 1, Crowne Plaza Plenary Room
Shuttleworth, Mary Alys	34*	CP 6, Crowne Plaza Symposium Room 1
Smout, Michael J.	92	CP 17, Crowne Plaza Symposium Room 2

Stroehlein, Andreas J.	62*	CP 17, Crowne Plaza Symposium Room 2
Stroud, Leah	70*	CP 4, Crowne Plaza Symposium Room 1
Suthar, Jaydipbhai Rameshbhai	36*	CP 1 Crowne Plaza Plenary Room
Swe, Pearl	33	CP 5, Crowne Plaza Symposium Room 2
Sykes, Melissa	91*	Symp 7, Crowne Plaza Symposium Room 2
Tiberti, Natalia	119	P3, Crowne Plaza Plenary Room
Toet, Hayley Michelle	78	CP 10, Crowne Plaza Symposium Room 1
Vermeulen, Elke Tilly	11*	CP 13, Crowne Plaza Symposium Room 2
Waghorn, Tania Susanne	25	CP 14, Crowne Plaza Symposium Room 1
Walton, Shelley	127	P3, Crowne Plaza Plenary Room
Wangchuk, Phurpa	73	CP 7, Crowne Plaza Symposium Room 2
Weerakoon, Kosala Gayan	28*	CP 2, Crowne Plaza Symposium Room 1
Williams, Thomas Michael	75*	CP 12, Crowne Plaza Symposium Room 1
Worth, Amanda R.	87*	CP 15, Crowne Plaza Symposium Room 2
Yong, Russell Q-Y.	2*	CP 6, Crowne Plaza Symposium Room 1
You, Hong	12	CP 17, Crowne Plaza Symposium Room 2
Young, Neil D.	54	CP 17, Crowne Plaza Symposium Room 2
Zahedi Abdi, Alireza	27*	CP 9, Crowne Plaza Symposium Room 2
Zeng, Jin	23*	Poster Oral, Crowne Plaza Plenary Room
Zhang, Jun-rong	67*	Poster Oral, Crowne Plaza Plenary Room

***Student presentation**

2015 Joint Conference of the New Zealand Society for Parasitology and the Australian Society for Parasitology Inc.

June 29 – July 2, Crowne Plaza Auckland, New Zealand

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