2021 Annual Conference of the Australian Society for Parasitology Inc.

Parasitravaganza 2021, June 21 - 25, Online

Index

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Welcome from the ASP President

It is my great pleasure to welcome you to Parasitravaganza 2021 – our online Parasite Fest! This is the second virtual ASP conference. While we would prefer to meet in person, nothing is more important to the ASP than the health and safety of our members, their families, and our communities, so going virtual is an obvious choice during pandemic. As we gather for this meeting virtually and physically dispersed, I would like to reflect on the meaning of place and, in doing so, recognise the First Nation's lands on which we gather today. We acknowledge the Aboriginal and Torres Strait Islander people, the traditional custodians of these lands, and pay respects to their Elders – past, present and emerging - and their Ancestral Spirits, with gratitude and respect.

This meeting wouldn't have been possible without a number of people who volunteered to make it happen. I would like to thank the organising committee: Sarah Preston, Ali Raza, Alireza Zahedi, Shokoofeh Shamsi, Abdul Jabbar, Michelle Clark, Lisa Jones, Nick Smith, Michelle Power and Sonja Frolich for all their enthusiasm, hard work and time they put into making sure that the conference is a success.

The conference includes presentations from BMM 2020 winner Katja Fischer, BMM 2021 winner and Sprent Prize 2020 winner Kathryn Parker. I would like to congratulate the 2021 BMM winner, and also Katja and Kathryn. We are looking forward to their presentations. Early Career Researcher Workshops are on Monday 21st & Tuesday 22nd June 2021 and Scientific Presentations Wednesday 23rd – Friday 25th June 2021. There will be prizes awarded for the best presentations by ASP member students.

Finally, a very warm welcome to those of you attending ASP conference for the first time. This virtual event offers our members and friends a wonderful chance to participate in the conference in the comfort of your own home. If you are not already a member of the ASP, I highly recommend that you join us. Hope to meet you when we can - we can't wait to get together in person next year.

We look forward to seeing you online at the 2021 Annual Conference for the Australian Society for Parasitology.

Professor Barbara Nowak
President, ASP

www.parasite.org.au

Parasitravaganza 2021 Program Overview

Date: Monday, 21/June/2021	
3:00pm - 4:00pm	**ECR1: "Meet the Elsevier Editors"** Session Chair: **Andrew Kotze**, CSIRO Session Chair: **Coralie Boulet**, Burnet Institute Session Chair: **Siobhon Egan**, Murdoch University "Meet the IJP and IJPDDR Editors" during this online panel event. Email your questions for the Editors to secretary@parasite.org.au by Sunday 20th June 2021 or bring your questions along to ask live during this session. Your panel members are IJP Editor-in-chief Brian Cooke (JCU) and IJP DDR Editor Andrew Kotze (CSIRO). The chairs for this session are Coralie Boulet (Burnet Institute) and Siobhon Egan (Murdoch University). They will be able to answer all of your questions about the IJP and IJPDDR journals and anything about publishing and being on Editorial boards. You can read their bios on the Slack channel for this event https://asp2021.slack.com/archives/C023MLXBX6Z
Date: Tuesday, 22/June/2021	
3:00pm - 4:00pm	**ECR: Resilience in Research for Early Career Researchers** Session Chair: **Aleta Knowles**, Virbac 2020 and 2021 have meant that Early Career Researchers need to show even more resilience in research. Join this panel discussion to talk about challenges facing ECRs, especially during the COVID19 pandemic. How can you submit your thesis during a lockdown? How can I deal with career interruptions? What is a good work-life balance and how can I achieve this? How can I take an overseas post-doc position during a pandemic when the borders are closed? Returning to research after maternity or paternity leave and managing family with work commitments. What about career pivots and changes? The "Resilience in Research" panel members are Michelle Power from Macquarie University who will speak on Diversity (in particular LGBTQI+) in the workplace, Katharina Stracke from University of Bergen who will talk about finding a post-doc position and moving overseas during a pandemic, Abdul Ghafar from Melbourne University who will speak on how to finish a PhD during a pandemic, and Joanne Devlin from Melbourne University who will speak about leadership and balancing family life and work. The chair of our session is Aleta Knowles from Virbac. You can read their bios on the Slack channel for this event. https://asp2021.slack.com/archives/C0243BY8J3T
Date: Wednesday, 23/June/2021	
11:00am - 11:05am	**Opening: Opening Day 1 & Acknowledgement of Country** Session Chair: **Barbara Nowak**, University of Tasmania Session Chair: **Cameron Raw**, University of Melbourne
11:05am - 11:45am	**BMM_2021: The Bancroft-Mackerras Medal for Excellence Winner 2021** Session Chair: **Barbara Nowak**, University of Tasmania
11:45am - 12:00pm	**First Break Wed**
12:00pm - 12:45pm	**Symp1: Symposium1** Session Chair: **Alireza Zahedi**, Murdoch University
12:45pm - 1:00pm	**CP1: Contributed Papers 1** Session Chair: **Alireza Zahedi**, Murdoch University
1:00pm - 1:45pm	**Lunch Wed with ZEISS demonstration** Session Chair: **Sonja Frolich**, The University of Adelaide Join us from 1:00 - 1:10pm when Dr. Shannon Das from ZEISS Research Microscopy Solutions will update us on the latest developments in microscopy.
1:45pm - 2:30pm	**Symp2: Symposium 2** Session Chair: **Abdul Jabbar**, University of Melbourne
2:30pm - 2:45pm	**CP2: Contributed Papers 2** Session Chair: **Abdul Jabbar**, University of Melbourne
2:45pm - 3:00pm	**Third Break Wed**
3:00pm - 3:30pm	**Symp3: Symposium3** Session Chair: **Sonja Frolich**, The University of Adelaide
3:30pm - 3:45pm	**CP3: Contributed Papers 3** Session Chair: **Sonja Frolich**, The University of Adelaide
3:45pm - 4:00pm	**Fourth Break Wed**
4:00pm - 5:15pm	**ST: Short talks: 3-minute presentations 3MT style** Session Chair: **Abdul Jabbar**, University of Melbourne Speed Talks! Each presenter has three-minutes to showcase their data. 3MT style presentations, one-slide and three minutes to spruik your research! Check out the abstract uploads for more information from the researcher.
Date: Thursday, 24/June/2021	

11:00am - 11:05am	**OD2: Opening Day 2 & Acknowledgement of Country** Session Chair: **Barbara Nowak**, University of Tasmania
11:05am - 11:45am	**Sprent2020: The John Frederick Adrian Sprent Prize Winner 2020** Session Chair: **Barbara Nowak**, University of Tasmania
11:45am - 12:00pm	**First Break Thurs**
12:00pm - 12:45pm	**Symp4: Symposium4** Session Chair: **Shokoofeh Shamsi**, Charles Sturt University
12:45pm - 1:00pm	**CP4: Contributed Papers 4** Session Chair: **Shokoofeh Shamsi**, Charles Sturt University
1:00pm - 1:45pm	**Lunch Thurs**
1:45pm - 2:30pm	**Symp5: Symposium5** Session Chair: **Sarah Preston**, Federation University
2:30pm - 2:45pm	**CP5: Contributed Papers 5** Session Chair: **Sarah Preston**, Federation University
2:45pm - 3:00pm	**Third Break Thurs**
3:00pm - 3:30pm	**Symp6: Symposium6** Session Chair: **Cibelly Goulart**, University of Technology Sydney
3:30pm - 3:45pm	**CP6: Contributed Papers 6** Session Chair: **Cibelly Goulart**, University of Technology Sydney
3:45pm - 4:00pm	**Fourth Break Thurs**
4:00pm - 5:15pm	**ST2: Short talks: 3-minute presentations 3MT style day 2** Session Chair: **Michelle Power**, Macquarie University Speed Talks! Each presenter has three-minutes to showcase their data. 3MT style presentations, one-slide and three minutes to spruik your research! Check out the abstract uploads for more information from the researcher.
Date: Friday, 25/June/2021	
11:00am - 11:05am	**OD3: Opening Day 3 & Acknowledgement of Country** Session Chair: **Rebecca Traub**, The University of Melbourne Session Chair: **Cameron Raw**, University of Melbourne
11:05am - 11:45am	**BMM_2020: The Bancroft-Mackerras Medal for Excellence Winner 2020** Session Chair: **Rebecca Traub**, The University of Melbourne
11:45am - 12:00pm	**First Break Fri**
12:00pm - 12:45pm	**Symp7: Symposium7** Session Chair: **Deborah Holt**, Charles Darwin University
12:45pm - 1:00pm	**CP7: Contributed Papers 7** Session Chair: **Deborah Holt**, Charles Darwin University
1:00pm - 1:45pm	**Lunch Fri**
1:45pm - 2:30pm	**Symp8: Symposium8** Session Chair: **Clare Anstead**, University of Melbourne
2:30pm - 2:45pm	**CP8: Contributed Papers 8** Session Chair: **Clare Anstead**, University of Melbourne
2:45pm - 3:00pm	**Third Break Fri**
3:00pm - 3:30pm	**Symp9: Symposium9** Session Chair: **Mike Gardner**, Flinders University
3:30pm - 3:45pm	**CP9: Contributed Papers 9** Session Chair: **Mike Gardner**, Flinders University
3:45pm - 4:00pm	**Fourth Break Fri**
4:00pm - 5:15pm	**ST3: Short talks: 3-minute presentations 3MT style day 3** Session Chair: **Michelle Clark**, The Walter and Eliza Hall Institute of Medical Research Speed Talks! Each presenter has three-minutes to showcase their data. 3MT style presentations, one-slide and three minutes to spruik your research! Check out the abstract uploads for more information from the researcher.

Parasitravaganza 2021 Summary Presentations

Symp1: Symposium1

Time: Wednesday, 23/June/2021: 12:00pm - 12:45pm
Session Chair: Alireza Zahedi, Murdoch University

(ID: 175)

Knockdown of PTEX impairs the haemoglobin digestion pathway in *Plasmodium falciparum*

Thorey Jonsdottir[1,2], Brendan Elsworth[1], Simon Cobbold[3], Mikha Gabriela[1,4], Paul Sanders[1], Malcolm McConville[3], Hayley Bullen[1], Brendan Crabb[1,2], Paul Gilson[1]
[1]Burnet Institute; [2]Department of Microbiology and Immunology, University of Melbourne; [3]Bio21 Institute, University of Melbourne; [4]Deakin University

(ID: 111)

A multipronged next-generation sequencing metabarcoding approach unearths hyper-diverse and abundant dog pathogen communities in Cambodia

Lucas Huggins, Anson Koehler, Vito Colella, Rebecca Traub
Faculty of Veterinary and Agricultural Sciences, University of Melbourne, Parkville, VIC 3052, Australia

(ID: 215)

Breakthrough with a new cattle tick vaccine

A.E. Tabor
The University of Queensland, QAAFI, St Lucia, Qld, Australia

CP1: Contributed Papers 1

Time: Wednesday, 23/June/2021: 12:45pm - 1:00pm
Session Chair: Alireza Zahedi, Murdoch University

(ID: 117)

Temporal analysis of cyclised Platelet factor 4 peptide anti-plasmodial activity.

Brendan McMorran[1], Karoline White[1], Dianne Xu[1], Megan Sawbridge[1], Lara Malins[2], Nicole Lawrence[3]
[1]Department of Immunology and Infectious Diseases, John Curtin School of Medical Research, College of Health and Medicine, Australian National University, Acton, Australian Capital Territory 2601, Australia.; [2]Research School of Chemistry, College of Science, Australian National University, Acton, Australian Capital Territory 2601, Australia.; [3]Institute of Molecular Bioscience, University of Queensland, St Lucia, Queensland 4072, Australia

(ID: 222)

Systems-based approaches to antigen discovery: implication for rational malaria vaccine design

Carla Proietti[1], Lutz Krause[2], Angela Trieu[3], Daniel Dodoo[4], Ben Gyan[4], Kwadwo A. Koram[4], William O. Rogers[5], Thomas L Richie[5], Philip L. Felgner[6], Denise Doolan[1]
[1]Centre for Molecular Therapeutics, Australian Institute of Tropical Health and Medicine, James Cook University, Cairns, QLD, Australia; [2]The University of Queensland Diamantina Institute, Brisbane, QLD, Australia; [3]QIMR Berghofer Medical Research Institute, Brisbane, QLD, Australia; [4]Noguchi Memorial Institute for Medical Research, University of Ghana, Ghana; [5]Naval Medical Research Center, Silver Spring, MD, USA; [6]Department of Medicine, Division of Infectious Diseases, University of California Irvine, Irvine, CA, USA

(ID: 149)

High-quality reference genome for *Clonorchis sinensis*

Neil D. Young[1], Andreas J. Stroehlein[1], Liina Kinkar[1], Tao Wang[1], Woon-Mok Sohn[2], Bill Chang[1], Parwinder Kaur[3], David Weisz[4], Olga Dudchenko[4], Erez Lieberman Aiden[4], Pasi K. Korhonen[1], Robin B. Gassser[1]
[1]The University of Melbourne, Australia; [2]Gyeongsang National University, Republic of Korea; [3]University of Western Australia, Australia; [4]Baylor College of Medicine, USA

Symp2: Symposium 2

Time: Wednesday, 23/June/2021: 1:45pm - 2:30pm
Session Chair: Abdul Jabbar, University of Melbourne

(ID: 218)

Designing and delivering a bespoke parasitology subject in an alternative online realm

Karena Waller[1], Abdul Jabbar[2], Daniel Clarke[1]
[1]1) Department of Microbiology and Immunology, The University of Melbourne, The Peter Doherty Institute for Infection and Immunity, 792 Elizabeth Street, Melbourne Victoria 3000, Australia; [2]2) Department of Veterinary Biosciences, Melbourne Veterinary School, The University of Melbourne, 250 Princes Highway, Werribee Victoria 3030, Australia

(ID: 165)

Genomic landscape of diversification, selective sweeps and demographic history in an anthroponotic parasite

Swapnil Tichkule[1], Simone M Cacciò[2], Guy Robinson[3], Rachel M Chalmers[3], Ivo Mueller[1], Melanie Bahlo[1], Daniel Eibach[4], Kevin M Tyler[5], Cock van Oosterhout[5], Aaron R Jex[1]
[1]Walter Eliza Hall Institute, Australia; [2]Istituto Superiore di Sanità, Italy; [3]Swansea University Medical School, UK; [4]Bernhard Nocht Institute for Tropical Medicine, Germany; [5]University of East Anglia, UK

(ID: 221)

Predicting host control of parasite burden following controlled human malaria infection

Denise Doolan[1], Martha Cooper[1], Kelly Trinh[2], Ashley Waardenberg[1], Lachlan Webb[3], Fiona Amante[3], Peter O'Rouke[3], James McCarthy[3,4]
[1]Australian Institute of Tropical Health and Medicine, James Cook University, Cairns, QLD 4878, Australia; [2]College of Science & Engineering, James Cook University, Cairns, QLD 4878, Australia; [3]Infectious Diseases Program, QIMR Berghofer Medical Research Institute, Brisbane, QLD 4029, Australia; [4]Royal Melbourne Hospital and Doherty Institute, University of Melbourne, Melbourne, VIC 3000, Australia

CP2: Contributed Papers 2

Time: Wednesday, 23/June/2021: 2:30pm - 2:45pm
Session Chair: Abdul Jabbar, University of Melbourne

(ID: 185)

Social cognitive factors of dog owners towards canine gastrointestinal parasitism in Greater Brisbane, Australia

Swaid Abdullah, Tu Nguyen, Nicholas Clark, Malcolm Jones, Ricardo Soares Magalhaes
University of Queensland, School of Veterinary Sciences, Gatton, Australia

(ID: 198)

Promoting parasitology through fun and inclusive community science outreach

Rina Wong (Fu)
School of Medical and Health Sciences, Edith Cowan University, Joondalup, WA 6027, Australia

(ID: 195)

The inside scoop on urban foxes; what they harbour and what are the implications

Narelle Dybing[1], Trish Fleming[1], Alan Lymbery[2], Amanda Ash[3]
[1]Centre for Terrestrial Ecosystem Science and Sustainability, Harry Butler Institute, Murdoch University, Australia; [2]Centre for Sustainable Aquatic Ecosystems, Harry Butler Institute, Murdoch University, Australia; [3]Centre for Biosecurity and OneHealth, Harry Butler Institute, Murdoch University, Australia

Symp3: Symposium3

Time: Wednesday, 23/June/2021: 3:00pm - 3:30pm
Session Chair: Sonja Frolich, The University of Adelaide

(ID: 159)

Multi-omic profiling of Australian Paralysis tick, *Ixodes holocyclus*

Amrita Vijay[1], Thomas Karbanowicz[2], Quentin Gouil[1], Balu Balan[1,3], Louise Baker[1], Samantha J Emery-Corbin[1], Stefano Gaiarsa[4], Ala Lew-Tabor[2], Nathan Lo[5], Jan Riemer[6], Fabrizia Stavru[7], Davide Sassera[8], Peter Czabotar[1], Tony Papenfuss[1], Aaron R Jex[1,3]

[1]The Walter and Eliza Hall Institute of Medical Research, Parkville, Victoria, Australia; [2]The University of Queensland, Brisbane, Queensland, Australia; [3]Faculty of Veterinary and Agricultural Sciences, The University of Melbourne, Parkville, Victoria, Australia; [4]Microbiology and Virology unit at Policlinico San Matteo, Fondazione IRCCS, Pavia, Province of Pavia, Italy; [5]School of Life and Environmental Sciences, The University of Sydney, New South Wales,Australia; [6]Department for Chemistry, Institute for Biochemistry, University of Cologne, Cologne, Germany; [7]Unité de Biologie Evolutive de la Cellule Microbienne, Institut Pasteur, Paris, France; [8]Department of Biology and Biotechnology, University of Pavia, Pavia, Italy

(ID: 124)

MicroRNAs Expression Induces Apoptosis of Macrophages in response to Leishmania major (MRHO/IR/75/ER): An InVitro and In-Vivo Study

Mostafa Gholamrezaei, Soheila ROUHANI Rouhani, Mehdi Mohebali, Samira Mohammadi-yeganeh, Mostafa Haji Mollahoseini, Ali Haghighi, Zohreh Lasjerdi, Faezeh Hamidi, Mohammad KAZEM Sharifi-yazdi

Shahid Sadoughi University of medical sciences, Iran, Islamic Republic of

CP3: Contributed Papers 3

Time: Wednesday, 23/June/2021: 3:30pm - 3:45pm
Session Chair: Sonja Frolich, The University of Adelaide

(ID: 202)

PREDNISOLONE AS ADJUVANT IN THE TREATMENT OF EXPERIMENTAL *SCHISTOSOMA HAEMATOBIUM* INFECTION IN MICE

Ogochukwu Chiamah[1], Patience Ubachukwu[2], Fabian Okafor[2]

[1]Alex Ekwueme Federal University Ndufu-Alike Ebonyi State, Nigeria; [2]University of Nigeria, Nsukka, Enugu State, Nigeria

(ID: 121)

Characterisation of egress and invasion inhibitors in blood-stage *Plasmodium falciparum* reveals a potentially unique invasion-blocking compound

Dawson B. Ling[1,2], Madeline G. Dans[1,3], Brendan S. Crabb[1,2], Paul R. Gilson[1]

[1]Burnet Institute, Melbourne, Victoria 3004, Australia; [2]The University of Melbourne, Parkville, Victoria 3010, Australia; [3]Deakin University, Geelong, Victoria 3220, Australia

(ID: 119)

ACT treatment failure and resistance gene variants in African *Plasmodium falciparum*

Colin Sutherland

LSHTM, United Kingdom

ST: Short talks: 3-minute presentations 3MT style

Time: Wednesday, 23/June/2021: 4:00pm - 5:15pm
Session Chair: Abdul Jabbar, University of Melbourne

(ID: 182)

Characterisation of mitochondrial genomes of *Lucilia cuprina* populations in Australia

Shilpa Kapoor[1], Vern Bowles[2], Clare Anstead[2], Trent Perry[1]
[1]Bio21 Molecular Science and Biotechnology Institute. The University of Melbourne, Parkville, Victoria 3010, Australia; [2]Department of Veterinary Biosciences, Melbourne Veterinary School, The University of Melbourne, Parkville, Victoria 3010, Australia

(ID: 172)

Exploring the Antiplasmodial Activity of Thiamine Analogues

Imam Fathoni[1], Alex HY Chan[2], Finian J Leeper[2], Kevin J Saliba[1]
[1]The Australian National University, Australia; [2]University of Cambridge, UK

(ID: 173)

Development of Human Toxo IgG ELISA Kit, and false-positivity of Latex Agglutination Test for the diagnosis of toxoplasmosis

Muhammad Imran Rashid
University of Veterinary and Animal Sciences, Pakistan

(ID: 180)

In vitro antiprotozoal activity of Selected Plant Extracts on *Cryptosporidium parvum* and *Giardia duodenalis*: A preliminary Screening

Sandamalie Ranasinghe, Alan Lymbery, Amanda Ash, Ali Zahedi, Anthony Armson
Murdoch University, Australia

(ID: 203)

Prevalence of Intestinal Parasites in Captive Dingos

Cecil Wheeler[1], Indu Panicker[1], Vito Colella[2], Richard Bradbury[1]
[1]Federation University, Australia; [2]The University of Melbourne, Australia

(ID: 187)

Comparison of four faecal egg counting techniques for the detection of parasites in horses

J King, A Ghafar, G Abbas, CG Gauci, A Jabbar
Department of Veterinary Biosciences, Melbourne Veterinary School, Faculty of Veterinary and Agricultural Sciences, The University of Melbourne, Werribee 3030, VIC, Australia

(ID: 118)

Blood meal analysis to investigate which host are ticks using in Australia

Tatiana Proboste[1], Nicholas Clark[1], Lee McMichael[2], Jenny Seddon[2]
[1]UQ Spatial Epidemiology Laboratory, School of Veterinary Science, the University of Queensland, Gatton 4343, Queensland, Australia; [2]School of Veterinary Science, The University of Queensland, Gatton 4343, Queensland, Australia

(ID: 204)

Molecular characterisation of Monogenea parasitise blue mackerel *Scomber australasicus* (Perciformes: Scombridae) in the Australian waters

Md. Shafaet Hossen[1,2], Diane P. Barton[1], Skye Wassens[3], Shokoofeh Shamsi[1]
[1]School of Animal and Veterinary Sciences & Graham Centre for Agricultural Innovation, Charles Sturt University, Wagga Wagga, NSW 2678, Australia; [2]Department of Fisheries Biology and Genetics, Bangladesh Agricultural University, Mymensingh 2202, Bangladesh; [3]School of Environmental Sciences & Institute of Land, Water and Society, Charles Sturt University, Albury, NSW 2640, Australia

(ID: 211)

Comparing natural resistance to *Haemochus contortus* infection in Wiltshire Horn and Luxton Black sheep

Kate De Witte, Abdul Jabbar, Abdul Ghafar, Charles Gauci
University of Melbourne, Australia

(ID: 223)

Immunomics-guided discovery and validation of serum and urine antibody biomarkers for urogenital schistosomiasis

Mark Pearson[1], Bemnet Tedla[1], Carla Proietti[2], Luke Becker[1], Rie Nakajima[3], Bemnet Tedla[3], Gebeyaw Mekonnen[1], Denise Doolan[1], Abena Amoah[4], Stefanie Knopp[5,6], David Rollinson[6], Said Ali[6], Cornelius Hokke[1], Akim Adegnika[1], Matt Field[1], Govert van Dam[1], Paul Corstjens[1], Takafira Mduluza[1], Francisca Mutapi[1], Claude Oeuvray[1], Beatrice Greco[1], Sujittra Chaiyadet[1], Thewarach Laha[1], Pengfei Cai[1], Donald McManus[1], Maria Elena Bottazzi[1], Philip Felgner[1], Javier Sotillo[1], Alex Loukas[1]

[1]James Cook University, Australia; [2]James Cook University, Australia; [3]James Cook University, Australia; [4]James Cook University, Australia; [5]James Cook University, Australia; [6]James Cook University, Australia

(ID: 130)

Novel 3D compounds to fight malaria in a time of drug resistance

Liana Theodoridis[1], Derek Wong[1], Adjoa Ampem-Lassen[2], Pallavi Sharma[2], Teresa Carvalho[1]

[1]Molecular Parasitology Laboratory, Department of Physiology, Anatomy and Microbiology, La Trobe University, Bundoora, VIC, 3086, Australia; [2]La Trobe Institute for Molecular Science, La Trobe University, Bundoora, VIC, 3086, Australia

(ID: 208)

A GRA2 minimal ¬promoter improves the efficiency of TATi conditional regulation of gene expression in *Toxoplasma gondii*

Mohammad Farouq Sharifpour[1], Shadi Khadiv[1], Markus Meissner[2], Milton McAllister[1]

[1]School of Animal and Veterinary Sciences, The University of Adelaide, Adelaide, South Australia, Australia.; [2]Institute for Experimental Parasitology, Faculty of Veterinary Medicine, Ludwig-Maximilians-Universität Munich, Bavaria, Germany.

(ID: 129)

Induction of heterologous protection using a novel whole parasite liposomal *Babesia* vaccine

Danielle Stanisic[1], Hanan Al-Nazal[1], Emily Cooper[1], Mei Fong Ho[1], Sharareh Eskandari[1], Victoria Majam[2], Ashwini Kumar Giddam[1], Waleed Hussein[3], Md. Tanjir Islam[3], Mariusz Skwarczynski[3], Istvan Toth[3,4,5], Sanjai Kumar[2], Ali Zaid[1], Michael Batzloff[1], Michael Good[1]

[1]Institute for Glycomics, Griffith University Gold Coast Campus, Southport, 4215, Australia; [2]Laboratory of Emerging Pathogens, Division of Emerging and Transfusion Transmitted Diseases, CBER, FDA, Rockville, 20852, USA.; [3]The University of Queensland, School of Chemistry and Molecular Biosciences, St Lucia, 4067, Australia.; [4]The University of Queensland, School of Pharmacy, St Lucia, 4067, Australia.; [5]The University of Queensland, Institute for Molecular Bioscience, St Lucia, 4067, Australia.

(ID: 104)

Near-term forecasting of companion animal tick paralysis incidence: an iterative ensemble model

Nicholas Clark[1], Tatiana Proboste[1], Guy Weerasinghe[2], Ricardo Soares Magalhaes[1]

[1]Spatial Epidemiology Laboratory, School of Veterinary Science, University of Queensland, Australia; [2]Department of Agriculture, Water and the Environment, GPO Box 858, 2601, Canberra, Australian Capital Territory, Australia

(ID: 197)

Parasites of the Tasmanian devil

Di Barton[1], Vanessa Lee[1], Lesley Smales[2], Xiaocheng Zhu[1,3], Shokoofeh Shamsi[1,4]

[1]School of Animal & Veterinary Sciences, Charles Sturt University, Wagga, NSW; [2]Parasitology Section, South Australian Museum, Adelaide, South Australia; [3]NSW Department of Primary Industries, Wagga, NSW; [4]Graham Centre for Agricultural Innovation, Charles Sturt University, Wagga, NSW

(ID: 194)

Multiple anthelmintic resistance in small strongyles of Australian Thoroughbred horses

Ghazanfar Abbas[1], John Hurley[2], Jenni Bauquier[1], Anne Beasley[3], Edwina Wilkes[4], Caroline Jacobson[5], Charles El-Hage[1], Lucy Cudmore[6], Peter Carrigan[6], Brett Tennent-Brown[1], Kris J. Hughes[4], Ian Beveridge[1], Abdul Jabbar[1]

[1]Melbourne Veterinary School, The University of Melbourne, Werribee, Australia; [2]Swettenham Stud, Nagambie, Australia; [3]School of Veterinary Science, University of Queensland, Gatton, Australia; [4]School of Animal and Veterinary Sciences, Charles Sturt University, Wagga Wagga, Australia; [5]School of Veterinary & Life Sciences, Murdoch University, Murdoch, Australia; [6]Scone Equine Hospital, Scone, Australia

(ID: 152)

Accurate assessment of lesions suspected of being caused by *Taenia solium* in body organs of pigs with naturally acquired porcine cysticercosis

Charles Gauci, Meritxell Donadeu, Marshall Lightowlers

University of Melbourne, Australia

(ID: 200)

In vitro culture of *Cryptosporidium parvum* using a novel gut-on-a-chip

Samantha Gunasekera[1], Brendon King[2], Paul Monis[2], Benjamin Thierry[3], Jill Carr[4], Abha Chopra[5], Mark Watson[5], Mark O'Dea[6], Una Ryan[1]
[1]Murdoch University, Australia; [2]South Australian Water Corporation, Australia; [3]Future Industries Institute, University of South Australia, Australia; [4]College of Medicine and Public Health, Flinders University, Australia; [5]Institute for Immunology and Infectious Diseases, Murdoch University, Australia; [6]Department of Primary Industries and Regional Development, Australia

(ID: 177)

Not gone but forgotten: *Tritrichomonas foetus* in extensively-managed bulls from Australia's Northern Territory

Nichola Calvani[1,2,3], Jan Slapeta[2], Emily Onizawa[3], Kieran Eamens[3], Cheryl Jenkins[3], Mark Westman[3]
[1]Molecular Parasitology Laboratory, The National University of Ireland, Galway, Ireland; [2]Sydney School of Veterinary Science, The University of Sydney, Australia; [3]Elizabeth Macarthur Agricultural Institute, New South Wales Department of Primary Industries and Environment, Australia

(ID: 178)

Fasciola species introgression: Just a fluke or something more?

Nichola Calvani[1,2], Jan Slapeta[2]
[1]The National University of Ireland, Galway, Ireland; [2]Sydney School of Veterinary Science, The University of Sydney, Australia

(ID: 123)

Comparative pathogenicity of drug-resistant *Trypanosoma brucei* and *Trypanosoma congolense* infections in dogs

Chukwunonso Obi, Michael Okpala, Davinson Anyogu, Nnenna Emejuo, Ikenna Ezeh, Romanus Ezeokonkwo
University of Nigeria, Nsukka, Nigeria, Nigeria

Symp4: Symposium4

Time: Thursday, 24/June/2021: 12:00pm - 12:45pm
Session Chair: Shokoofeh Shamsi, Charles Sturt University

(ID: 214)

Investigating the Zoonotic Potential of Pig Parasites Within Small Holder Farming Communities in Lao PDR

A.M. Peck
School of Veterinary and Life Sciences, Murdoch University, Murdoch, Perth 6150 Australia

(ID: 157)

TriTOX: A new *Trichomonas* sp. assay for high-throughput screening of compound libraries

Alexander Y.F. Lam[1,5], Daniel Vuong[2], Aaron R. Jex[1,3,5], Andrew M. Piggott[4], Ernest Lacey[2,4], Samantha J. Emery-Corbin[1,5]
[1]Population Health and Immunity Division, The Walter and Eliza Hall Institute of Medical Research, Melbourne, VIC, Australia; [2]Microbial Screening Technologies, Smithfield, NSW, Australia; [3]Department of Veterinary Biosciences, Melbourne Veterinary School, Faculty of Veterinary and Agricultural Sciences, The University of Melbourne, Parkville, VIC, Australia; [4]Department of Molecular Sciences, Faculty of Science and Engineering, Macquarie University, North Ryde, NSW, Australia; [5]Department of Medical Biology, The University of Melbourne, Parkville, VIC, Australia

(ID: 176)

The sulfonylpiperazine MMV020291 prevents red blood cell invasion through interference with actin-1/profilin dynamics in the malaria parasite *Plasmodium falciparum*

Madeline Dans[1,2], William Nguyen[3], Somya Mehra[1,2], Zahra Razook[1,2], Sujaan Das[4], Molly Schneider[1], Thorey Jonsdottir[1,5], Mikha Gabriela[1,2], Chris Tonkin[3], Vanessa Mollard[6], Geoff McFadden[6], Danny Wilson[7], Alyssa Barry[1,2], Brad Sleebs[3], Brendan Crabb[1,5], Tania de Koning-Ward[2], Paul Gilson[1]
[1]Burnet Institute, Melbourne, Victoria 3004, Australia; [2]Deakin University, Geelong, VIC, Australia; [3]Walter and Eliza Hall Institute, Parkville, Victoria 3052, Australia; [4]Faculty of Veterinary Medicine, Experimental Parasitology, Ludwig Maximilian University, Munich, Germany; [5]Department of Microbiology and Immunology, University of Melbourne, Melbourne, Australia; [6]School of BioSciences, University of Melbourne, Australia; [7]The University of Adelaide, Adelaide, South Australia 5005, Australia

CP4: Contributed Papers 4

Time: Thursday, 24/June/2021: 12:45pm - 1:00pm
Session Chair: Shokoofeh Shamsi, Charles Sturt University

(ID: 120)

A phase 1b clinical trial to assess safety and efficacy of an attenuated hookworm larvae vaccine

Alex Loukas
James Cook University, Australia

(ID: 110)

Are you ready for this jelly? A multiomic characterisation of two Kudoa spp. causing “jellymeat” and macroscopic cysts in high-value commercial fish

Jessica Bolin[1,2,3], Scott Cummins[1,3], Shahida Mitu[1,3], David Schoeman[1,4], Karen Evans[2], Kylie Scales[1]
[1]School of Science, Technology and Engineering, University of the Sunshine Coast, Sippy Downs, QLD 4556 Australia; [2]CSIRO Oceans and Atmosphere, Hobart, Tasmania, Australia; [3]Genecology Research Centre, University of the Sunshine Coast, Sippy Downs, QLD 4556 Australia; [4]Centre for African Conservation and Ecology, Nelson Mandela University, Port Elizabeth, South Africa

(ID: 183)

Validating the phylogeny of the nematode subfamily Phascolostrongylinae (Nematoda: Strongyloidea) using mitochondrial protein coding genes

Tanapan Sukee, Ian Beveridge, Anson Koehler, Robin Gasser, Abdul Jabbar
Department of Veterinary Biosciences, Melbourne Veterinary School, Faculty of Veterinary and Agricultural Sciences, University of Melbourne, Victoria, Australia

Symp5: Symposium5

Time: Thursday, 24/June/2021: 1:45pm - 2:30pm
Session Chair: Sarah Preston, Federation University

(ID: 192)

Teaching Parasitology in times of change: the story remains the same.

Malcolm Jones
University of Queensland, Australia

(ID: 150)

CRISPR/Cas9 Mutagenesis Causes Putative Deletion in *Schistosoma mansoni*

Xiaofeng Du[1,2], Donald McManus[1,2], Juliet French[3], Malcolm Jones[4], Hong You[1]
[1]Immunology Department, QIMR Berghofer Medical Research Institute, Herston, Brisbane, Queensland, Australia; [2]Faculty of Medicine, The University of Queensland, Herston, Brisbane, Queensland, Australia; [3]Genetics & Computational Biology Department, QIMR Berghofer Medical Research Institute, Herston, Brisbane, Queensland, Australia; [4]School of Veterinary Science, The University of Queensland, Gatton, Australia

(ID: 160)

Exploring *Ascaris* chemosensation and its importance in infection

Pradip Roy[1,2], Joy Liu[1], Peter Thurgood[3], Balu Balan[1,2], Samantha J Emery-Corbin[1], Verena Wimmer[1], Khashayar Khoshmanesh[3], Aaron R Jex[1,2]
[1]The Walter and Eliza Hall Institute of Medical Research, Parkville, Melbourne, Australia; [2]Faculty of Veterinary and Agriculture Science, The University of Melbourne, Melbourne, Australia; [3]School of Engineering, RMIT University, Melbourne, Victoria, Australia

CP5: Contributed Papers 5

Time: Thursday, 24/June/2021: 2:30pm - 2:45pm
Session Chair: Sarah Preston, Federation University

(ID: 136)

Establishment of RNAi in *Sarcoptes scabiei* eggs to identify novel therapeutic targets

Deepani D Fernando[1], Robin B Gasser[1], Katja Fischer[2]
[1]QIMR Berghofer Medical Research Institute, Australia; [2]Faculty of Veterinary and Agriculture Sciences, University of Melbourne, Australia

(ID: 141)

Parasite galectin inhibits mast cell degranulation

Michael Stear[1], Marta Maruszewska-Cheruiyot[2], Katarzyna Donskow-Łysoniewska[2]
[1]La Trobe University, Australia; [2]Laboratory of Parasitology, General Karol Kaczkowski Military Institute of Hygiene and Epidemiology, Kozielska 4, 01-163 Warsaw, Poland

(ID: 174)

The *Plasmodium falciparum* parasitophorous vacuole protein P113 interacts with the parasite protein export machinery and maintains normal vacuole architecture.

Hayley Bullen[1], Paul Sanders[1], Madeline Dans[1], Thorey Jonsdottir[1], Jo-Anne Chan[1], David Riglar[2], Catherine Palmer[3], Betty Kouskousis[1], Sarah Charnaud[4], Tony Triglia[4], Mikha Gabriela[1], Molly Parkyn Schneider[1], Tania de Koning-Ward[5], Jake Baum[2], James Beeson[1], Alan Cowman[4], Paul Gilson[1], Brendan Crabb[1]
[1]Burnet Institute, Australia; [2]Imperial College London; [3]Bio21; [4]Walter and Eliza Hall Institute; [5]Deakin University

Symp6: Symposium6

Time: Thursday, 24/June/2021: 3:00pm - 3:30pm
Session Chair: Cibelly Goulart, University of Technology Sydney

(ID: 205)

Uncovering the lipid 'scavengome' in *Toxoplasma gondii* parasites

Serena Shunmugam[1], Sheena Dass[1], Laurence Berry[2], Christophe-Sebastien Arnold[1], Nicholas Katris[1], Samuel Duley[1], Fabien Pierrel[3], Marie-France Cesbron-Delauw[1], Yoshiki Yamaryo-Botte[1], Cyrille Botte[1]

[1]Apicolipid Team, Institute for Advanced Biosciences, CNRS UMR5309, Université Grenoble Alpes, INSERM U1209, Grenoble, France,; [2]Laboratory of Pathogen Host Interactions, UMR 5235, Université de Montpellier, France.; [3]Université Grenoble Alpes, CNRS, Grenoble INP, TIMC-IMAG, 38000 Grenoble, France

(ID: 217)

ANTIOXIDANT ENZYME AND CYTOKINE LEVEL RELATIONSHIPS DURING SEVERE AND UNCOMPLICATED MALARIA INFECTION IN URBAN GHANAIAN CHILDREN

Richard Asmah[2], Daniel Squire[1], Selorme Adukpo[5], Eric Kyei-Baafour[6], Ebenezer Aidoo[4], Patrick Ayeh-Kumi[3]

[1]Department of Medical Laboratory Science, School of Allied Health Sciences, University of Health and Allied Sciences, Ho, Ghana; [2]School of Basic and Biomedical Sciences, University of University of health and Allied Sciences, Ho, Ghana; [3]College of Health Sciences, University of Ghana, Accra, Ghana; [4]Accra psychiatric hospital, Ghana health service; [5]School of Pharmacy, University of Ghana, Ghana; [6]Department of Immunology, Noguchi Memorial Institute for Medical Research, University of Ghana, Ghana

CP6: Contributed Papers 6

Time: Thursday, 24/June/2021: 3:30pm - 3:45pm
Session Chair: Cibelly Goulart, University of Technology Sydney

(ID: 115)

Comparison of the egg recovery rates and limit of detection for soil-transmitted helminths using the Kato-Katz thick smear, faecal flotation and quantitative real-time PCR in human stool.

Patsy A. Zendejas-Heredia, Vito Colella, Sze Fui Hii, Rebecca Traub

Faculty of Veterinary and Agricultural Sciences, University of Melbourne, Parkville, VIC, Australia

(ID: 132)

L672H mutation in the *P. falciparum* flavokinase confers resistance to roseoflavin and 8-aminoriboflavin

Ayman Hemasa[1], Kevin Saliba[1,2]

[1]Research School of Biology, Australian National University, Canberra, ACT, Australia; [2]Medical School, Australian National University, Canberra, ACT, Australia

(ID: 164)

Geospatial analysis of pre-intervention prevalence of onchocerciasis in Ethiopia

Himal Shrestha[1], Karen McCulloch[1,2], Shannon M Hedtke[1], Sindew M Feleke[1,3], Warwick N Grant[1]

[1]Department of Physiology, Anatomy and Microbiology, School of Life Sciences, La Trobe University, Bundoora, Australia; [2]WHO Collaborating Centre for Viral Hepatitis, Victorian Infectious Diseases Reference Laboratory, Royal Melbourne Hospital, and Department of Infectious Diseases, University of Melbourne, at the Peter Doherty Institute for Infection and Immunity, Australia; [3]Ethiopian Public Health Institute, Addis, Ethiopia

ST2: Short talks: 3-minute presentations 3MT style day 2

Time: Thursday, 24/June/2021: 4:00pm - 5:15pm
Session Chair: Michelle Power, Macquarie University

(ID: 206)

Rapid *Schistosoma* DNA detection using a dipstick with LAMP assay

Oyime Aula[1,2], Donald McManus[1], Malcolm Jones[3], Catherine Gordon[1]
[1]QIMR Berghofer Medical Research Institute, Australia; [2]School of Public Health, Faculty of Medicine, The University of Queensland, Australia; [3]School of Veterinary Science, Faculty of Science, The University of Queensland, Queensland, Australia

(ID: 145)

The potential effects of host origin on attachment and engorgement of two parapatric ticks

Mike Gardner[1,2], Sophie Hammond[1], Gerrut Norval[1], Bob Sharrad[1], Steph Godfrey[3]
[1]Flinders University, Australia; [2]South Australian Museum; [3]The University of Otago, NZ

(ID: 170)

*Tg*MPODD and the quest for the missing membrane anchor of Succinate Dehydrogenase in *Toxoplasma gondii*

Soraya M. Zwahlen, Jenni A. Hayward, Giel G. Van Dooren
Australian National University, Canberra

(ID: 193)

Ticks and tick-borne diseases of bovines in smallholder dairy farms

Abdul Ghafar[1], Robin B Gasser[1], Tariq Abbas[2], Abdul Rehman[3], Abdul Jabbar[1]
[1]Department of Veterinary Biosciences, Melbourne Veterinary School, Faculty of Veterinary and Agricultural Sciences, The University of Melbourne, Werribee 3030, VIC, Australia; [2]Department of Epidemiology and Public Health, Cholistan University of Veterinary and Animal Sciences, Bahawalpur, Punjab, Pakistan; [3]Department of Epidemiology and Public Health, University of Veterinary and Animal Sciences, Lahore, Punjab, Pakistan

(ID: 186)

Parasitism in the black-spotted croaker: analysis of species infection dynamics against environmental factors

Megan Porter[1,2], Diane Barton[1,2], Shokoofeh Shamsi[1,2,3]
[1]Charles Sturt University, Australia; [2]Charles Sturt University School of Animal and Veterinary Sciences; [3]Charles Sturt University Graham Centre for Agricultural Innovation

(ID: 190)

Thermal stability proteomics identifies protein targets for antimalarial compounds

Matthew P. Challis[1], Ghizal Siddiqui[1], Amanda De Paoli[1], Raymond S. Norton[2], Peter J. Scammells[2], Sheena McGowan[3], Shane M. Devine[2], Darren J. Creek[1]
[1]Monash Institute of Pharmaceutical Sciences, Drug Delivery, Disposition and Dynamics, Monash University, Parkville, VIC 3052; [2]Monash Institute of Pharmaceutical Sciences, Medicinal Chemistry, Monash University, Parkville, VIC 3052; [3]Department of Microbiology, Biomedicine Discovery Institute, Monash University, Clayton, VIC 3800, Australia.

(ID: 142)

Plasmodium vivax malaria serological exposure markers: assessing the presence and implications of potential cross-reactivity with *P. knowlesi*

Rhea Longley[1], Matthew Grigg[2], Kael Schoffer[1], Stephanie Hyslop[1], Ramin Mazhari[1], Bridget Barber[2], Kim Piera[2], Timothy William[3], Nick Anstey[2], Ivo Mueller[1]
[1]WEHI, Australia; [2]Menzies School of Health Research and Charles Darwin University, Australia; [3]Infectious Diseases Society Kota Kinabalu Sabah, Malaysia

(ID: 189)

Detection and characterization of *Coccidian* parasites in wild dogs and foxes from south-east Australia

Jose L. Huaman[1], Mikaeylah J. Davidson[1], Corey Pollock[1], Carlo Pacioni[2,3], Teresa G. Carvalho[1]
[1]Department of Physiology, Anatomy and Microbiology, School of Life Sciences, La Trobe University, Melbourne, VIC, Australia; [2]Arthur Rylah Institute for Environmental Research, Department of Environment, Land, Water and Planning, 123 Brown Street, Heidelberg, VIC, Australia; [3]Murdoch University, Environmental and Conservation Sciences, South Street, Murdoch, WA, Australia

(ID: 140)

β-triketones - A new prospective scabicide

Nirupama Nammunige[1], Kylie Agnew-Francis[2], Deepani Fernando[1], Sara Taylor[1], Hieng Lu[1], Craig Williams[2], Robin Gasser[3], Katja Fischer[1]
[1]Cellular and Molecular Biology Department, Infectious Diseases Program, QIMR Berghofer Medical Research Institute, Brisbane, Australia; [2]School of Chemistry and Molecular Biosciences, University of Queensland, Brisbane, Australia; [3]Faculty of Veterinary and Agricultural Sciences, University of Melbourne, Melbourne, Australia

(ID: 143)

Investigating the mode of action of the antimalarial drug proguanil

Yunan Qian[1], Gillian Fisher[1], Darren Creek[2], David Fidock[3,4], Tina Skinner-Adams[1], Katherine Andrews[1]
[1]Griffith Institute for Drug Discovery, Griffith University Nathan Campus, Queensland 4111, Australia; [2]Department of Biochemistry and Molecular Biology, University of Melbourne, Parkville, VIC, Australia; [3]Department of Microbiology and Immunology, Columbia University Irving Medical Center, New York, NY 10032, USA; [4]Division of Infectious Diseases, Department of Medicine, Columbia University Irving Medical Center, New York, NY 10032, USA

(ID: 166)

Descriptive Comparison of ELISAs for the Detection of *Toxoplasma gondii* Antibodies in Animals: A Systematic Review

Tharaka Liyanage, Jasmin Hufschmid, Abdul Jabbar, Anke Wiethoelter
Department of Veterinary Biosciences, Melbourne Veterinary School, Faculty of Veterinary and Agricultural Sciences, The University of Melbourne, Werribee, VIC 3030, Australia

(ID: 153)

Fast-tracking gastrointestinal nematode speciation in livestock

Emily Francis, Jan Slapeta
The University of Sydney, Australia

(ID: 188)

Spatial variation in prevalence of hookworm infection in pet dogs in dog parks of GreaterBrisbane, Australia

Swaid Abdullah, Yishu Zhang, Tu Nguyen, Nicholas Clark, Malcolm Jones, Ricardo Soares Magalhaes
The University of Queensland, School of Veterinary Sciences, Gatton, Australia

(ID: 113)

The Development of a Novel Antimalarial Class with Antimalarials with Slow Acting Erythrocytic Stage Activity

Brodie Bailey[1,2], Brad Sleebs[1,2], Alan Cowman[1,2], William Nguyen[1,2], Paul Jackson[3]
[1]WEHI, Australia; [2]University of Melbourne, Australia; [3]Janssen Pharmaceuticals, California, USA

(ID: 147)

The exotic snake mite (*Ophionyssus natricis*), a neglected parasite of significant veterinary concern in Australia

Gerrut Norval[1], Bruce Halliday[2], Robert D. Sharrad[1], Michael G. Gardner[1]
[1]Flinders University, Australia; [2]Australian National Insect Collection, CSIRO, Australia

(ID: 135)

Investigating the antimicrobial effect of emerging scabicides on scabies associated pathogens

Sara Taylor[1], Deonne Walther[2], Kylie Agnew-Francis[2], Deepani D. Fernando[1], Craig Williams[2], Katja Fischer[1]
[1]QIMR Berghofer Medical Research Institute, Brisbane, Australia; [2]University of Queensland, Brisbane, Australia

(ID: 138)

Abametapir – a potential new scabicide targeting metalloproteases in *S. scabiei* mites and eggs.

Gangi R Samarawickrama[1], Deepani D Fernando[1], Vern M Bowles[2], Katja Fischer[1]
[1]QIMR Berghofer Medical Research Institute, Brisbane, Australia; [2]2Centre for Animal Biotechnology, The University of Melbourne, Melbourne, Australia

(ID: 161)

Ultrastructure and functions of nuclear microtubules in *Plasmodium falciparum* gametocytes

Jiahong Li[1], Gerry Shami[1], Boyin Liu[1], Eric Hanssen[2], Matt Dixon[3], Leann Tilley[1]
[1]Department of Biochemistry and Pharmacology, The University of Melbourne, Australia; [2]Melbourne Advanced Microscopy Facility & Bio21 Molecular Science & Biotechnology Institute, The University of Melbourne; [3]Department of Infectious Diseases, The University of Melbourne, Australia

(ID: 137)

Investigating the antiplasmodial activity and mode of action of the natural product alstonine

Jacinta Macdonald[1], Megan Arnold[1], Madeline Luth[2], Ronald Quinn[1], Elizabeth Winzeler[2], Tina Skinner-Adams[1], Katherine Andrews[1], Gillian Fisher[1]

[1]Griffith Institute for Drug Discovery, Australia; [2]University of California

(ID: 209)

Quantifying appetite suppression in livestock during nematode infection

Fazel Almasi, Michael Stear

Agribio, Department of Animal, Plant and Soil Sciences, 5 Ring Road, La Trobe University, Bundoora, Victoria 3086, Australia

(ID: 207)

Exploring novel insights of the *Plasmodium vivax* sporozoite proteome

Caitlin Bourke[1,2], Samantha Emery-Corbin[1,2], Anthony Ruberto[3], Amélie Vantaux[4], Benoit Witkowski[4], Ivo Mueller[1,2], Aaron Jex[1,2]

[1]WEHI, Australia; [2]Department of Medical Biology, University of Melbourne, Australia; [3]Malaria: Parasites and Hosts, Institut Pasteur, France; [4]Institut Pasteur du Cambodge, Kingdom of Cambodia

(ID: 126)

Prevalence and molecular characterization of cattle ticks in Burundi: First report on the presence of the invasive *Rhipicephalus microplus* tick

Lionel Nyabongo[1], David Odongo[1], Gad Milton[2], Eunice Machuka[3], Patrick Vudriko[4], Roger Pelle[3], Esther Kanduma[5]

[1]School of Biological Sciences, University of Nairobi, Nairobi, Kenya; [2]Tick Unit, International Livestock Research Institute, Nairobi, Kenya; [3]Biosciences eastern and central Africa-International Livestock Research Institute (BecA-ILRI) Hub, Nairobi, Kenya; [4]College of Veterinary Medicine, Animal Resources and Biosecurity, Makerere University, Uganda; [5]Department of Biochemistry, School of Medicine, University of Nairobi, Nairobi, Kenya

(ID: 125)

Development of highly sensitive one step-PCR for improved detection of *B. bigemina* and *B. bovis*.

Martina Paoletta[1], Sofía de la Fournière[1], Eliana Guillemi[1], Néstor Sarmiento[2], Pablo Donati[3], Silvina Wilkowsky[1], Marisa Farber[1]

[1]Instituto de Agrobiotecnología y Biología Molecular (IABIMO) INTA - CONICET; [2]Estación Experimental Agropecuaria Mercedes, INTA; [3]Departamento de Anestesiología y manejo del dolor, Facultad de Ciencias Veterinarias, Universidad de Buenos Aires

Symp7: Symposium7

Time: Friday, 25/June/2021: 12:00pm - 12:45pm
Session Chair: Deborah Holt, Charles Darwin University

(ID: 127)

A kinase that coordinates nuclear abscission in the malaria parasite *Plasmodium falciparum*.

Ben Liffner, Sabrina Absalon
Indiana University School of Medicine, Department of Pharmacology and Toxicology, United States of America

(ID: 155)

Apicoplast derived metabolites are essential for the biosynthesis of glycophosphatidylinositol anchors and egress of asexual stage *Plasmodium falciparum*.

Michaela Bulloch, Kit Kennedy, Julie Ralton, Long Huynh, Malcolm McConville, Stuart Ralph
University of Melbourne, Australia

(ID: 219)

CRISPR gene knockout targeting *Ov*-GRN-1 in the carcinogenic liver fluke, *Opisthorchis viverrini*, reducing hamster pathogenesis

Michael Smout
JCU, Australia

CP7: Contributed Papers 7

Time: Friday, 25/June/2021: 12:45pm - 1:00pm
Session Chair: Deborah Holt, Charles Darwin University

(ID: 151)

Cross-predicting essential genes between two model eukaryotic species using machine learning

Tulio Campos, Pasi Korhonen, Neil Young
Department of Veterinary Biosciences, Melbourne Veterinary School, Faculty of Veterinary and Agricultural Sciences

(ID: 191)

Understanding antigen diversity and immune selection targets of leading *Plasmodium vivax* vaccine candidates and sero-surveillance markers

Paolo Bareng[1,2], Myo Naung[1,2,3,4], Somya Mehra[1,2], Alyssa Barry[1,2,3,4]
[1]Institute for Mental and Physical Health and Clinical Translation (IMPACT), School of Medicine, Deakin University, Geelong, Victoria, Australia; [2]Life Sciences Discipline, Burnet Institute, Melbourne, Victoria, Australia; [3]Division of Population Health and Immunity, Walter and Eliza Hall Institute of Medical Research, Parkville, Victoria, Australia; [4]Department of Medical Biology, University of Melbourne, Carlton, Victoria, Australia

(ID: 184)

The identification of addiction to a human kinase inhibitor in *Plasmodium falciparum*

Tayla Williamson[1], Jack Adderley[1], Sarah Jackson[2], Chrsitian Doerig[1]
[1]Centre for Chronic Infectious and Inflammation Disease, Biomedical Sciences Cluster, School of Health and Biomedical Sciences, RMIT University, Bundoora VIC 3083, Australia; [2]Infection and Immunity Program, Biomedicine Discovery Institute and Department of Microbiology, Monash University, Clayton VIC 3800, Australia

Symp8: Symposium8

Time: Friday, 25/June/2021: 1:45pm - 2:30pm
Session Chair: Clare Anstead, University of Melbourne

(ID: 216)

Development and use of 360-degree imaging and a virtual reality interface for veterinary education

Stuart Barber
Melbourne Veterinary School, Faculty of Veterinary and Agricultural Science, University of Melbourne, Australia

(ID: 112)

Con-FeS-ions of *Tg*ApiCox13, a novel iron-sulfur protein of the mitochondrial electron transport chain of *Toxoplasma gondii*

Jenni Hayward, Rachel Leonard, Giel van Dooren
Research School of Biology, Australian National University, Canberra, ACT, Australia

(ID: 114)

Schistosoma mansoni cercariae tegument-anchored proteins that facilitate host interaction and infection

Conor Fogarty[1], Tianfang Wang[1], Scott Cummins[1], Russell Wyeth[2], Donald McManus[3], Mary Duke[3]
[1]University of the Sunshine Coast, Australia; [2]St. Francis Xavier University; [3]QIMR Berghofer Medical Research Institute

CP8: Contributed Papers 8

Time: Friday, 25/June/2021: 2:30pm - 2:45pm
Session Chair: Clare Anstead, University of Melbourne

(ID: 213)

In vitro selection of *Giardia duodenalis* for Albendazole resistance identifies a β-tubulin mutation at amino acid E198K

Qiao Su[1,2], Samantha J. Emery-Corbin[1], Swapnil Tichkule[1,2], Louise Baker[1,3], Ernest Lacey[1,4], Aaron Jex[1,3]
[1]Population Health and Immunity Division, The Walter and Eliza Hall Institute of Medical Research, Melbourne, VIC, Australia; [2]Faculty of Medicine, Dentistry and Health Science, University of Melbourne, Parkville, Victoria, Australia; [3]Faculty of Veterinary and Agricultural Science, University of Melbourne, Parkville, Victoria, Australia; [4]Department of Chemistry and Biomolecular Sciences, Faculty of Science, Macquarie University, North Ryde, NSW, Australia

(ID: 128)

The conduct of acaricide efficacy trials in Australia with highlight on the Australian Paralysis Tick (*Ixodes holocyclus*)

Florian Roeber
Invetus Pty Ltd, Australia

(ID: 100)

Parasites Online!

Lisa Jones[1], Sarah Preston[2], Coralie Boulet[3], Rina Fu[4], Michelle Power[5], Katherine Andrews[6], Shokoofeh Shamsi[7], Danny Wilson[8], Juan Miguel Balbin[8], Tina Skinner-Adams[6], Cameron Raw[9], Katja Fisher[10], Christina Spry[11]
[1]Australian Society for Parasitology; [2]Federation University; [3]Burnet Institute; [4]Edith Cowan University; [5]Macquarie University; [6]Griffith University; [7]Charles Sturt University; [8]University of Adelaide; [9]University of Melbourne; [10]QIMR Berghofer; [11]Australian National University

Symp9: Symposium9

Time: Friday, 25/June/2021: 3:00pm - 3:30pm
Session Chair: Mike Gardner, Flinders University

(ID: 131)

Parasitic diseases in a climate crisis

Coralie Boulet
Burnet Institute, Australia

(ID: 122)

From lumping to splitting and back again: on the evolution of species delineation philosophy in marine trematodes

Daniel Huston
CSIRO, Australia

CP9: Contributed Papers 9

Time: Friday, 25/June/2021: 3:30pm - 3:45pm
Session Chair: Mike Gardner, Flinders University

(ID: 169)

Decloaking the blackbox: Interpretable machine learning and parasites

Nicholas Fountain-Jones
University of Tasmania, Australia

(ID: 146)

Super-resolved view of PfCERLI1, a rhoptry associated protein essential for *Plasmodium falciparum* merozoite invasion of erythrocytes

Sonja Frolich
The University of Adelaide, Australia

(ID: 103)

Shifts in genetic diversity of *Cryptosporidium* species in WA patients over the last decade: Four major outbreaks, three different stories.

Alireza Zahedi, Kamil Braima, Josephine Ng-Hublin, Una Ryan
Murdoch University, Australia

ST3: Short talks: 3-minute presentations 3MT style day 3

Time: Friday, 25/June/2021: 4:00pm - 5:15pm
Session Chair: Michelle Clark, The Walter and Eliza Hall Institute of Medical Research

(ID: 134)

Antibodies as Serological Markers of *Plasmodium vivax* Infections in Moderate Transmission Settings

Yanie Tayipto[1,2], Jason Rosado[3], Donicia Gamboa[4], Herbert Opi[5], James Beeson[5], Leanne Robinson[1,5], Ivo Mueller[1,2,3], Rhea Longley[1,2]

[1]Population Health and Immunity Division, Walter and Eliza Hall Institute of Medical Research, Melbourne, Victoria, Australia; [2]Department of Medical Biology, University of Melbourne, Melbourne, Victoria, Australia; [3]Unité Malaria: Parasites et Hôtes, Département Parasites et Insectes Vecteurs, Institut Pasteur, Paris, France; [4]Laboratorio ICEMR-Amazonia, Laboratorios de Investigación y Desarrollo, Facultad de Ciencias y Filosofía, Universidad Peruana Cayetano Heredia, Lima, Peru; [5]Burnet Institute, Melbourne, Australia

(ID: 167)

Impact of *Trypanosoma cruzi* strain on the *in vitro* activity of compounds

Melissa Louise Sykes, Vicky Marie Avery
Discovery Biology, Griffith University, Australia

(ID: 162)

Determinants of parasite diversity and community structure in waterbirds

Atsuhiro Ueda[1], Amanda Ash[2], Alan Lymbery[3]
[1]Murdoch University, Australia; [2]Centre for Biosecurity and One Health, Harry Butler Institute, Murdoch University, Australia; [3]Centre for Sustainable Aquatic Ecosystem, Harry Butler Institute, Murdoch University, Australia

(ID: 154)

Investigating macrocyclic lactone resistance in *Dirofilaria immitis* from Australia

Rosemonde Power, Jan Šlapeta
The University of Sydney, Australia

(ID: 116)

Zoonotic soil-transmitted helminths in free-roaming dogs from Kiribati, Western Pacific

Patsy A. Zendejas-Heredia[1], Allison Crawley[2], Helen Byrnes[3], Rebecca Traub[1], Vito Colella[1]
[1]Faculty of Veterinary and Agricultural Sciences, University of Melbourne, Parkville, VIC, Australia; [2]Independent researcher; [3]Vets Beyond Borders, Brisbane, Queensland, Australia

(ID: 144)

The role of wild deer in the transmission of parasites to livestock in Australia

David Jenkins, Diane Barton
Charles Sturt University, Australia

(ID: 212)

Immune responses to strongyles in equines with pituitary *pars intermedia* dysfunction

Adelaina Horner[1], Nicholas Bamford[2], Michael Stear[3], David Piedrafita[1], Sarah Preston[1]
[1]Federation University, Australia; [2]Melbourne University; [3]La Trobe University

(ID: 181)

Membranes, monocytes, and malaria: *Plasmodium*-induced breakdown of phospholipid asymmetry leads to phagocytosis of infected erythrocytes

Merryn Fraser[1,2], Weidong Jing[1], Stefan Bröer[1], Florian Kurth[3,4], Leif-Erik Sander[3], Kai Matuschewski[2], Alexander G. Maier[1]
[1]The Australian National University, Canberra, Australia; [2]Humboldt University, Berlin, Germany; [3]Charité, Berlin, Germany; [4]Bernhard Nocht Institute for Tropical Medicine, Hamburg, Germany

(ID: 199)

Interactions of pro-coagulatory *Sarcoptes scabiei* pseudo-cysteine proteases with human dermatopontin.

Deonne Walther[1,2], Deepani Fernando[1], Katja Fischer[1]
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(ID: 156)

Development of a diagnostic index to identify nematode-resistant cattle

Asfiya Mansuri, Michael Stear
La trobe University, Australia

(ID: 133)

Field application of a novel multiplex qPCR assay reveals the occurrence of the zoonotic hookworm *Ancylostoma braziliense* in Nigerian dogs

Luca Massetti[1], Joshua Kamani[2], Anke Wiethoelter[1], Phillip McDonagh[3], Vito Colella[1], Rebecca J Traub[1]
[1]Univeristy of Melbourne, Australia; [2]Parasitology Division, National Veterinary Research Institute (NVRI), PMB 01, Vom, Plateau State, Nigeria; [3]Boehringer Ingelheim Animal Health Australia, North Ryde, New South Wales 2113, Australia

(ID: 171)

Immunomodulatory properties of *Schistosoma mansoni* egg-derived exosomes in food allergy

Madeleine Rogers[1,2], Severine Navarro[1,3,4], Yan Lu[1], Athena Andreosso[1]
[1]QIMR Berghofer Medical Research Institute, Australia; [2]University of Queensland; [3]Woolworth Centre for Childhood Nutrition Research; [4]Children's Hospital Foundation

(ID: 163)

Four polyopisthocotyleans (Platyhelminthes: Monogenea) from carangid fishes in the Mediterranean, off the Algerian coasts

Chahinez Bouguerche[1,4], Fadila Tazerouti[1], Delphine Gey[2,3], Jean-Lou Justine[4]
[1]Université des Sciences et de la Technologie Houari Boumediene, Faculté des Sciences Biologiques, Laboratoire de Biodiversité et Environnement: Interactions – Génomes, BP 32, El Alia, Bab Ezzouar, 16111 Alger, Algérie; [2]Service de Systématique Moléculaire, UMS 2700 CNRS, Muséum National d'Histoire Naturelle, Sorbonne Universités, 43 Rue Cuvier, CP 26, 75231 Paris Cedex 05, France; [3]UMR7245 MCAM, Muséum National d'Histoire Naturelle, 61, Rue Buffon, CP52, 75231 Paris Cedex 05, France; [4]Institut Systématique Évolution Biodiversité (ISYEB), Muséum National d'Histoire Naturelle, CNRS, Sorbonne Université, EPHE, Université des Antilles, 57 Rue Cuvier, CP 51, 75231 Paris Cedex 05, France

(ID: 179)

In vitro acaricidal activity of some plant extracts against *Rhipicephalus microplus*

Manaswini Dehuri, Manas Dalei, Santwana Palai, Bijayendranath Mohanty
Odisha university of agriculture and technology, India

(ID: 158)

First molecular characterisation of the haemogregarine parasite *Hemolivia mariae* in the stump-tailed lizard tick (*Amblyomma albolimbatum*) in Western Australia

Samuel Elliot, Jill Austen, Siobhon Egan, Ruby McKenna, Amanda Barbosa, Charlotte Oskam
Centre for Biosecurity and One Health, Murdoch University, Australia

(ID: 108)

INTESTINAL PARASITES PRESENT IN THE MISQUITA INDIGENOUS ETHNIC, LIVING IN GRACIAS A DIOS, HONDURAS DURING THE YEAR 2019-2020.

Wendy Valladares[1,2], Bryan Tinoco[1]
[1]Department of Parasitology, School of Microbiology, National Autonomous University of Honduras, Honduras; [2]Parasitology Research Group, Microbiology Research Institute, UNAH, Honduras.

(ID: 109)

Intestinal parasitosis in patients admitted to the Juan Manuel Gálvez Hospital. Gracias Lempira, Honduras

Wendy Valladares[1,2], Nelsy Perez[1]
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(ID: 105)

Global prevalence of hydatidosis in Equidae family, a systematic and meta-analysis review article

Elham Moghaddas[1], Mahya Razmi[2], Davood Anvari[3], Behzad Kiani[4], Seyed Aliakbar Shamsian[1]
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(ID: 106)

Evaluation of zoonotic platyhelminthe infections identified in slaughtered livestock in Iran, 2015-2019

Behzad Kiani[1], Elham Moghaddas[2], Christine M. Budke[3], Ebrahim Shams Abadi[4], Soheil Hashtarkhani[1], Amene Raouf Rahmati[2], Mostafa AkbarPour[5], Mehdi Zarean[2], Bibi Razieh Hosseini Farash[2], Fatemeh Kiani[1]

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(ID: 107)

World-wide prevalence of *Anisakis* larvae in fish and its relationship to human allergic Anisakiasis: A systematic review

Elham Moghaddas[1], Amene Raouf Rahmati[1], Behzad Kiani[2], Asma Afshari[3], Michelle Williams[4], Shokoofeh Shamsi[4]

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(ID: 210)

Australian Tick Microbiomes: What We've Learnt & Where to Next

Telleasha Greay

Murdoch University, Australia

Parasitravaganza 2021 Presentations

Symp1: Symposium1

Time: Wednesday, 23/June/2021: 12:00pm - 12:45pm
Session Chair: Alireza Zahedi, Murdoch University

(ID: 175)

Knockdown of PTEX impairs the haemoglobin digestion pathway in *Plasmodium falciparum*

Thorey Jonsdottir[1,2], Brendan Elsworth[1], Simon Cobbold[3], Mikha Gabriela[1,4], Paul Sanders[1], Malcolm McConville[3], Hayley Bullen[1], Brendan Crabb[1,2], Paul Gilson[1]

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During its blood-stage the human malaria parasite *Plasmodium falciparum* resides within the red blood cell (RBC). The parasite deploys its own translocation machinery called PTEX to export hundreds of proteins across the parasite's encasing vacuole membrane and into the RBC compartment to establish host cell modifications. Conditional knockdown of PTEX core components, HSP101, PTEX150 and EXP2, results in rapid growth arrest. Interestingly, parasite cells with depleted PTEX150, HSP101, or EXP2 have accumulation of undigested haemoglobin (Hb) inside the parasite, suggesting that proteolytic processing of this metabolite is impaired. This suggests that PTEX might also be involved in the trafficking of Hb proteases. Early-acting Hb proteases are trafficked to the parasite surface where they enter Hb containing vesicles en route to the food vacuole. We looked specifically into one of these proteases, FP2a with regards to PTEX association and trafficking. We found that FP2a food vacuole targeting relies on two superficially-distinct steps involving (i) delivery of FP2a to the parasite plasma membrane, and (ii) extraction into the parasitophorous vacuole space appears to be HSP101-dependent. This study therefore indicates that PTEX might play an intermediate step in the trafficking route of these Hb proteases expanding PTEX's current role in protein translocation.

(ID: 111)

A multipronged next-generation sequencing metabarcoding approach unearths hyper-diverse and abundant dog pathogen communities in Cambodia

Lucas Huggins, Anson Koehler, Vito Colella, Rebecca Traub

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Recent surveys in Southeast Asia, including Cambodia, have identified canine vector-borne pathogens (VBPs), including those with zoonotic potential, as highly endemic. The lack of veterinary care alongside close associations semi-domesticated dogs have with humans in the region exacerbates these zoonotic risks. We utilised a previously validated, next-generation sequencing (NGS) based metabarcoding protocol to charcaterise the bacterial, apicomplexan and kinetoplastid blood-borne pathogens of free-roaming dogs from across Cambodia. From 467 dogs in five field sites, at least 62% were infected with one of eight confirmed pathogens; *Anaplasma platys* (32%), *Ehrlichia canis* (20%), *Hepatozoon canis* (18%), *Babesia vogeli* (14%), *Mycoplasma haemocanis* (13%), *Bartonella clarridgeiae* (3%), *Candidatus* Mycoplasma haematoparvum (0.2%) and *Trypanosoma evansi* (0.2%). Coinfections of between two and four VBPs were also common (28%). In addition, DNA from putatively infectious agents belonging to the bacterial family and genera *Coxiella, Mycobacterium*, *Neisseria*, Rickettsiaceae, *Treponema* and two uncharacterised *Mycoplasma* species were identified in addition to protozoan genera *Colpodella, Parabodo* and *Bodo.* This study represents the first time NGS metabarcoding has been used to holistically detect the bacterial and protozoan haemoparasite communities of canines through a country-wide survey, highlighting the power of NGS to unearth a wide spectrum of pathogenic organisms in an unbiased manner.

(ID: 215)

Breakthrough with a new cattle tick vaccine

A.E. Tabor

The University of Queensland, QAAFI, St Lucia, Qld, Australia

Cattle ticks (*Rhipicephalus (Boophilus) microplus* species complex) cost Australian cattle industries approximately $161M per annum in economic losses through decreased production, hide damage, tick fever transmission, and the cost of chemical treatments. TickGARD was discontinued in 2010 due to the requirement of 4 boosts per annum and ticks are managed through the application of chemicals or through the infusion of *Bos indicus* genetics into tick susceptible *Bos taurus* breeds. Beef CRC research (2005-2012) identified 20 vaccine components which were trialled in an MLA project (2014-2017) leading to full patent submissions in 2018. A dual vaccination of 2 proteins (6 cattle/group) following vaccination and boost after one month demonstrated a 90% efficacy after the 2nd tick challenge 6 months after vaccination, with an 86% efficacy overall. Under the same conditions, one of these 2 proteins had an efficacy of 82% which was higher than Bm86 at 70%. The dual vaccine is promising as the efficacy increased following a second tick challenge and the adult ticks obtained were black and did not lay viable eggs. A new cattle tick vaccine with greater >80% efficacy and a minimum requirement of 2 boosts per year will improve management of ticks in northern Australia.

CP1: Contributed Papers 1

Time: Wednesday, 23/June/2021: 12:45pm - 1:00pm
Session Chair: Alireza Zahedi, Murdoch University

(ID: 117)

Temporal analysis of cyclised Platelet factor 4 peptide anti-plasmodial activity.

Brendan McMorran[1], Karoline White[1], Dianne Xu[1], Megan Sawbridge[1], Lara Malins[2], Nicole Lawrence[3]
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We have developed small, cyclised peptides with anti-plasmodial activity that replicate the antimicrobial domain of the Platelet factor 4 protein. These peptides, named Platelet Derived Internalisation Peptides (PDIP) due to their ability to translocate inside infected but not uninfected erythrocytes, kill parasites by selective binding and disruption of membrane enclosing the digestive vacuole (DV) and thereby exposing the organelle's proteolytic and cytotoxic contents. In this study, we found using live video microscopy that PDIP caused the parasite to rapidly swell in size – a maximal size increase of 20-40% occurred after only 5 minutes. In contrast, erythrocytes harbouring these parasites as well as their uninfected counterparts were unaffected. PDIP treatment of parasites expressing GFP-tagged Plasmepsin-II, which normally localises within the DV, caused redistribution of GFP fluorescence into the parasite cytosol (indicative of DV destruction). This occurred over a similarly short timeframe and immediately prior to the size increase, suggesting a direct relationship between the phenomena. We also tested several antimalarial drugs and 100 anti-plasmodial compounds from the Malaria Box collection and found none affected the DV or parasite size. PDIP molecules therefore act against parasites by a novel and unique mode of action and may be amenable for drug development.

(ID: 222)

Systems-based approaches to antigen discovery: implication for rational malaria vaccine design

Carla Proietti[1], Lutz Krause[2], Angela Trieu[3], Daniel Dodoo[4], Ben Gyan[4], Kwadwo A. Koram[4], William O. Rogers[5], Thomas L Richie[5], Philip L. Felgner[6], Denise Doolan[1]
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The OMICs revolution has resulted in unprecedented opportunities to identify important targets for vaccines or immunodiagnostics. We have generated unique omics-scale datasets of IgG and T-cell reactivity to *P. falciparum* which provide unique insights into host-parasite responses. Unexpectedly, only 30% of the *Plasmodium* proteome is targeted by antibody or T cell responses. By analysing responses during a longitudinal study on a proteome-wide scale, we showed that individual immune profiles comprise either high reactivity to a low number of antigens, or low reactivity to a high of antigens. A wide range of computational tools, Artificial Intelligence and machine learning technologies were the applied to analyse the synergetic interactions and identify predictive signatures of immunity. We defined a set of 15 *P. falciparum* antigens that could accurately predict an individual's immune status for the following malaria season with high accuracy. We also integrated immunological reactivity with genomics determinates and identified a set of molecular and structural features that predicted the preferential type of immune response associated with a given antigen on a genome–wide scale. Our findings have direct implications for the development of a rationally designed malaria vaccine or immunodiagnostic to identify individuals at high risk of clinical disease

(ID: 149)

High-quality reference genome for *Clonorchis sinensis*

Neil D. Young[1], Andreas J. Stroehlein[1], Liina Kinkar[1], Tao Wang[1], Woon-Mok Sohn[2], Bill Chang[1], Parwinder Kaur[3], David Weisz[4], Olga Dudchenko[4], Erez Lieberman Aiden[4], Pasi K. Korhonen[1], Robin B. Gassser[1]
[1]The University of Melbourne, Australia; [2]Gyeongsang National University, Republic of Korea; [3]University of Western Australia, Australia; [4]Baylor College of Medicine, USA

The Chinese liver fluke, *Clonorchis sinensis*, causes the disease clonorchiasis, affecting ~ 35 million people in regions of China, Vietnam, Korea and the Russian Far East. Clonorchiasis causes cholangitis and can induce a malignant cancer, called cholangiocarcinoma, in the biliary system. Control in endemic regions is challenging, and often relies largely on chemotherapy with one anthelmintic, called praziquantel. Routine treatment carries a significant risk of inducing resistance to this anthelmintic in the fluke, such that the discovery of new interventions is considered important. It is hoped that the use of molecular technologies will assist this endeavour by enabling the identification of drug or vaccine targets involved in crucial biological processes in the parasite. Although draft genomes of *C. sinensis* have been published, their assemblies are fragmented. In the present study, we tackle this genome fragmentation issue by utilising advanced DNA sequencing and informatic approaches to build a high-quality reference genome for *C. sinensis*, with chromosome-level contiguity and curated gene models. This substantially-enhanced genome provides a resource that could accelerate fundamental and applied molecular investigations of *C. sinensis*, clonorchiasis and/or cholangiocarcinoma, and assist in the discovery of new interventions against what is a highly significant, but neglected disease-complex.

Symp2: Symposium 2

Time: Wednesday, 23/June/2021: 1:45pm - 2:30pm
Session Chair: Abdul Jabbar, University of Melbourne

(ID: 218)

Designing and delivering a bespoke parasitology subject in an alternative online realm

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In Semester two of 2020, despite the need to pivot to online learning in response to the COVID-19 pandemic, our academic teaching team commenced the delivery of a brand-new, bespoke parasitology subject to third year Bachelor of Biomedicine and Bachelor of Science students at the University of Melbourne. This purposefully designed subject, *Medical Microbiology: Parasitology,* which is comprised of lectures, practical classes and active learning sessions, was developed in collaboration with internationally renowned parasitologists and global health researchers to take a broad, multi-disciplinary approach to student learning in the field. This worked to introduce and engage students in the exciting, complex and diverse world of medically important parasites, including key examples of protists, helminths and arthropods. In this presentation, we will describe our approach to curriculum design, and our experiences in and reflections on delivering this subject wholly online. Additionally, we will outline the initial impressions taken from the qualitative subject evaluation, as well as feedback from the perspective of both teaching staff and students.

(ID: 165)

Genomic landscape of diversification, selective sweeps and demographic history in an anthroponotic parasite

Swapnil Tichkule[1], Simone M Cacciò[2], Guy Robinson[3], Rachel M Chalmers[3], Ivo Mueller[1], Melanie Bahlo[1], Daniel Eibach[4], Kevin M Tyler[5], Cock van Oosterhout[5], Aaron R Jex[1]

[1]Walter Eliza Hall Institute, Australia; [2]Istituto Superiore di Sanità, Italy; [3]Swansea University Medical School, UK; [4]Bernhard Nocht Institute for Tropical Medicine, Germany; [5]University of East Anglia, UK

Cryptosporidium hominis is the primary cause of human cryptosporidiosis, which is the second leading cause of death due to diarrhoea worldwide. Sequence analyses of the highly polymorphic 60-kilodalton glycoprotein gene (*gp60*) found distinct *gp60* subtypes in the developed and developing world, however, this observation has not yet been confirmed at the genomic level. Here, we undertake detailed analysis of *C. hominis* genomes from Europe, Asia and Africa. These analyses identify discrete genetic populations that may represent two diverging sub-species, with one (the IbA10G2 subtype) predominating in Europe, and other in Asia and Africa. We find genomic signatures suggesting that the *C. hominis* population size might be contracting in low-income countries, and expanding in high-income countries. We examine other processes that could explain this genomic signature, including selective sweeps and a recent peri- or parapatric speciation event. Furthermore, we show that the limited gene flow between these parasite populations is localized largely to telomeric regions of the genome and may reflect selection of markers for increased virulence. Finally, we find that *gp60* and its surrounding genomic region is a major hotspot for recombination, further indicating this marker may not be suitable for evaluating population structure.

(ID: 221)

Predicting host control of parasite burden following controlled human malaria infection

Denise Doolan[1], Martha Cooper[1], Kelly Trinh[2], Ashley Waardenberg[1], Lachlan Webb[3], Fiona Amante[3], Peter O'Rouke[3], James McCarthy[3,4]

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Infection with the *Plasmodium* spp parasite that causes malaria induces a wide spectrum of disease manifestations ranging from asymptomatic to mild disease to severe disease to death. There is substantial heterogeneity between individuals in immune responses and capacity to control parasite burden, but the mechanisms underlying this inter-individual heterogeneity remain largely unknown. We are taking advantage of a Controlled Human Malaria Infection model to understand and predict host factors associated with parasite control. This model allows us to keep parasite factors and vector factors constant and focus in on what defines differences in host immune responses. By analyzing and integrating from various whole transcriptome studies, we identified distinct host molecular signatures that associate with parasite control. Differences in parasite multiplication rate and parasite burden between individuals were significantly associated with specific microRNAs, mRNAs and lncRNAs, suggesting that these expression profiles may determine an individual's ability to control *Plasmodium*. Importantly, transcriptomic signatures of miRNA, mRNA and lncRNA that predict the host response following infection could be identified at the pre-infection baseline. We anticipate that this systems-based approach with controlled human infection will facilitate the development of new strategies to combat the *Plasmodium* parasite and eradicate malaria.

CP2: Contributed Papers 2

Time: Wednesday, 23/June/2021: 2:30pm - 2:45pm
Session Chair: Abdul Jabbar, University of Melbourne

(ID: 185)

Social cognitive factors of dog owners towards canine gastrointestinal parasitism in Greater Brisbane, Australia

Swaid Abdullah, Tu Nguyen, Nicholas Clark, Malcolm Jones, Ricardo Soares Magalhaes
University of Queensland, School of Veterinary Sciences, Gatton, Australia

Studies in Australia indicate that parasitic infections in dogs are common and there is variability in the awareness of its zoonotic risks among pet owners. It is thus essential to understand the perception of the pet owners towards pet parasites and their beliefs about the benefits of parasite control in pets. In this study, we surveyed a total of 281 dog owners in and around Brisbane city between April and March 2020 and the relationship between dog owners' perception of risk of GI parasite infection was assessed using an adaptation of the Health Belief Model, social cognitive framework for health protection. The model investigated the role of dog owners' demography on their perceived severity and susceptibility to zoonotic canine parasites and their likelihood of performing actions associated with worm control. Our results indicate that owners' perceptions about parasitic disease severity in their pets was 26% higher in female dog owners compared to males, in respondents owning dogs over 10 years (27% higher than those owning a dog < 3 years). Our study indicates that the perceptions of pet owners towards zoonotic canine parasites varies demographically and owner education is important to prevent infection among dogs and possible zoonotic transmission.

(ID: 198)

Promoting parasitology through fun and inclusive community science outreach

Rina Wong (Fu)
School of Medical and Health Sciences, Edith Cowan University, Joondalup, WA 6027, Australia

Although parasites have co-existed with human and animal hosts for thousands of years, the average person in the community has little awareness of what parasites are and mistakenly classify them as another virus or bacteria. From 2018 to 2021, a parasitologist created a series of interactive workshops, demonstrations, songs, and stage shows that put parasites in the spotlight for people of all ages and abilities. Audiences included toddlers aged two-and-a-half to pre-schoolers, primary year one to six, and secondary school students. Furthermore, university students were engaged both within their microbiology and haematology courses as well as offered extra-curricular opportunities to participate in communicating parasitology. These students connected with children of lower socio-economic standing, the elderly, and those in regional areas. Tailored activities were also designed and successfully delivered to children with special needs including those who are hard of hearing, on the autism spectrum (verbal and non-verbal, with/without intellectual disabilities), inattentive type ADHD, and generalised anxiety. Illustration work is underway for a new parasitology focused children's picture science storybook entitled "My Mummy's Pet Parasites" due for publishing in 2022.

(ID: 195)

The inside scoop on urban foxes; what they harbour and what are the implications

Narelle Dybing[1], Trish Fleming[1], Alan Lymbery[2], Amanda Ash[3]
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With increased spread of urbanisation across the globe, the interface between wild animals with livestock, domestic pets and humans has been intensified. Consequently, the opportunity for transmission of many important pathogens has become increasingly apparent. After domestic cats and dogs, the red fox (*Vulpes vulpes*) is the world's most widespread carnivore. Foxes have established in many cities across the world. To date there is very little known of the risk that urban foxes may pose as reservoirs for parasitic diseases in Australia. This pilot study investigated the prevalence of endoparasites and ectoparasites within the urban fox community of Perth, Western Australia. Fox carcasses (n=44) were sourced through urban pest management programs, necropsied, and examined for parasites, while blood samples were screened for heartworm using the commercial SNAP 4Dx antigen test. A total of eight ectoparasite species and nine endoparasite species were identified. Antigens for *Dirofilaria immitis* (heartworm) were detected in blood samples from 7 foxes (16.7%). This pilot study demonstrates that urban foxes are capable of harbouring parasites of zoonotic importance as well as parasites that can infect domestic pets and native wildlife. This is the first study documenting heartworm in a reservoir host in Western Australia.

Symp3: Symposium3

Time: Wednesday, 23/June/2021: 3:00pm - 3:30pm
Session Chair: Sonja Frolich, The University of Adelaide

(ID: 159)

Multi-omic profiling of Australian Paralysis tick, *Ixodes holocyclus*

Amrita Vijay[1], Thomas Karbanowicz[2], Quentin Gouil[1], Balu Balan[1,3], Louise Baker[1], Samantha J Emery-Corbin[1], Stefano Gaiarsa[4], Ala Lew-Tabor[2], Nathan Lo[5], Jan Riemer[6], Fabrizia Stavru[7], Davide Sassera[8], Peter Czabotar[1], Tony Papenfuss[1], Aaron R Jex[1,3]

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Ixodes holocyclus, the Australian Eastern Paralysis tick, is a socioeconomically important parasite impacting on human and veterinary health. Current treatment of paralysis is restricted to a paralysis anti-serum, administered after the development of clinical signs. Despite the importance of this parasite, its molecular study is severely limited by a lack of genomic, transcriptomic, and proteomic resources. One of the major obstacles to the study of tick genomes, including *I. holocyclus*, is their large size (~1-7 gigabases) and highly repetitive sequence regions. We overcame this obstacle using a hybrid sequencing approach combining long Oxford-Nanopore and short Illumina sequence reads and generated a 1.9 Gb draft genome predicted to represent at least 91.3% of the euchromatin and with at least 50% of the genome in scaffolds larger than 1.37 Mb. We complimented this with a long-read transcriptome to develop better gene models and map alternate spliced variants. We then performed tissuespecific proteomics using high resolution mass spectrometry. Together, this first multiplatform, multi-omics reference of *I. holocyclus* provides a foundation for exploring tick evolution, biology and tick-host interaction, and supports opportunities to develop new therapeutics.

(ID: 124)

MicroRNAs Expression Induces Apoptosis of Macrophages in response to Leishmania major (MRHO/IR/75/ER): An InVitro and In-Vivo Study

Mostafa Gholamrezaei, Soheila ROUHANI Rouhani, Mehdi Mohebali, Samira Mohammadi-yeganeh, Mostafa Haji Mollahoseini, Ali Haghighi, Zohreh Lasjerdi, Faezeh Hamidi, Mohammad KAZEM Sharifi-yazdi

Shahid Sadoughi University of medical sciences, Iran, Islamic Republic of

We aimed to investigate the effect of miR-15a mimic and inhibitor of miR-155 expression on apoptosis induction in macrophages infected with Iranian strain of *Leishmania major* in-vitro and in-vivo. RAW 264.7 cells were infected with *L. major* promastigotes, and then were treated with miRNAs. For in-vivo experiment, BALB/c mice were inoculated with *L. major* promastigotes, and then they were treated with miRNAs. For evaluation of miRNA therapeutic effect, in-vitro and in-vivo studies were performed using quantitative Real-time PCR, Flow cytometry, lesion size measurement, and Limiting Dilution Assay (LDA).
In-vitro results of flow cytometry showed that using miR-15a mimic, miR-155 inhibitor or both of them increased apoptosis of macrophages. In in-vivo, size of lesion increased during experiment in control groups ($P<0.05$) while application of both miR-155 inhibitor and miR-15a mimic inhibited the increase in the size of lesions within 6 wk of experiment ($P=0.85$). LDA results showed that microRNA therapy could significantly decrease parasite load in mimic or inhibitor receiving groups compared to the control group ($P<0.05$).
miR-155 inhibitor and miR-15a mimic in L. major infected macrophages can induce apoptosis and reduce parasite burden. Therefore, miRNA-based therapy can be proposed as new treatment for cutaneous leishmaniasis.

CP3: Contributed Papers 3

Time: Wednesday, 23/June/2021: 3:30pm - 3:45pm
Session Chair: Sonja Frolich, The University of Adelaide

(ID: 202)

PREDNISOLONE AS ADJUVANT IN THE TREATMENT OF EXPERIMENTAL *SCHISTOSOMA HAEMATOBIUM* INFECTION IN MICE

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In this study, mice were infected with 300 *Schistosoma haematobium* cercaria. Thirteen weeks post infection, groups of mice were treated with 300mg/kg praziquantel in divided doses for two consecutive days (PZQ), 0.5mg/kg prednisolone for 7days (PRED), and 0.5mg/kg prednisolone for 7days + 300mg/kg PZQ in divided doses for 2 consecutive days (PZQ+PRED). Another groups of mice were the normal (N), infected untreated (IU), and uninfected treated with prednisolone (UP). Fourteen days post treatment; mice were killed and perfused to recover worms. Liver, spleen and bladder sections processed for histopathological examination. Worm reductions were observed in the PZQ (85.7%) and PZQ+PRED (80.3%) groups. The tissue sections of the NC mice showed normal histology. Hepatocyte degeneration/necrosis, hypertrophy of kupffer cells were seen in liver sections of the IU mice. Liver sections of the PZQ+PRED mice showed mild hepatocyte degenerations, with little mononuclear leucocyte infiltration compared to the PRED and PZQ groups. Spleen section of the IU mice showed a red pulp with moderate hemosiderin pigments. Spleen sections of the treated groups showed inflammatory changes, with mild reactions to worm presence observed in the PZQ+PRED group. Results suggest that prednisolone in combination with praziquantel may help suppress inflammatory reactions in *S. haematobium* infection.

(ID: 121)

Characterisation of egress and invasion inhibitors in blood-stage *Plasmodium falciparum* reveals a potentially unique invasion-blocking compound

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Malaria remains a deadly human disease, with parasite resistance emerging against frontline, artemisinin-combination treatments. The development of new antimalarial drugs against the deadly *Plasmodium falciparum* parasite is therefore critical. Symptomatic malaria manifests during the blood-stage cycle of the parasite, in which the parasite invades, grows, and replicates and then egresses from the body's red blood cells (RBCs) to invade new cells. To identify *P. falciparum* blood-stage egress and invasion inhibitors, the Medicines for Malaria Venture library of 400 antimalarial compounds was screened by Subramanian et. al. (2018), and 26 compounds were identified. To investigate their mechanisms of action (MoA) with greater precision, the specific activity of nine of these compounds was studied in parasites expressing a bioluminescent Nanoluciferase reporter. The compounds MMV006172 and MMV665878 were found to be the most potent and specific invasion and egress inhibitors, respectively. Live-cell microscopy of MMV006172-treated parasites indicated the parasites were unable to successfully invade RBCs due to a defect in resealing the RBC membrane behind them, which caused the parasites to exit the RBC. The target enzyme of MMV006172 is currently being sought with the aim of developing the compound into a future anti-malarial medicine.

(ID: 119)

ACT treatment failure and resistance gene variants in African *Plasmodium falciparum*

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As we near the end of a second decade of widespread artemisinin combination therapy (ACT) use for treating human malaria, there are signs of waning efficacy in some African settings. Evidence to date suggests the parasite factors linked to ACT treatment failure in Asia, such as K13 variants and markers of piperaquine drug failure, have not themselves spread to Africa. Rather, a suite of variant *Plasmodium falciparum* loci, experimentally linked to reduced artemisinin susceptibility *in vitro*, are under scrutiny in African parasite populations. These include not only *pfk13* variants, but also variant alleles of *pfcoronin*, *pfk10*, *pfubp1* and *pfap2mu*. I will present recent molecular, epidemiological and *in vitro* data and attempt to provide some mechanistic insights that could help us understand the emerging complexity of the genetic polymorphisms underlying reduced artemisinin susceptibility. Finally, the importance of such variant loci in resistance surveillance will be considered.

ST: Short talks: 3-minute presentations 3MT style

Time: Wednesday, 23/June/2021: 4:00pm - 5:15pm
Session Chair: Abdul Jabbar, University of Melbourne

Speed Talks! Each presenter has three-minutes to showcase their data. 3MT style presentations, one-slide and three minutes to spruik your research! Check out the abstract uploads for more information from the researcher.

(ID: 182)

Characterisation of mitochondrial genomes of *Lucilia cuprina* populations in Australia

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The Australian sheep blowfly, *Lucilia cuprina*, is a parasite of global socioeconomic importance. In this study, *Lucilia* spp. blowflies were collected from across five Australian states and their genomes sequenced to understand the species level evolution in these closely related individuals. Bioinformatic tools were used to assemble and annotate the complete mitochondrial genomes of these blowflies and a phylogenetic analysis performed to compare the mitochondrial genomes of *Lucilia* spp. with other dipteran species. The mitochondrial genomes were approximately 15 mb in size and consisted of 13 protein-coding genes, 2 ribosomal RNAs, 22 transfer RNAs and a control region. Comparative analyses of the complete mitochondrial sequences showed that flies collected from the sheep properties from Tasmania clustered within the clade of the genus *L. sericata*. The flies from urban properties of QLD were more closely related to *L. sericata* and represented the subspecies *L. cuprina cuprina,* whereas the flies collected from NSW, VIC and WA represented subspecies *L. cuprina dorsalis.* Phylogenetic analyses supported previously demonstrated paraphyly of *L. cuprina* with respect to *L. sericata*. The complete mitochondrial genomes of *Lucilia* spp. therefore supports their potential as ideal markers for species-level identification of *Lucilia* from different geographical regions across Australia.

(ID: 172)

Exploring the Antiplasmodial Activity of Thiamine Analogues

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Plasmodium requires several different vitamins for biochemical processes, including thiamine (vitamin B_1). Thiamine is converted into its active form, thiamine pyrophosphate (TPP), by the enzyme thiamine pyrophosphokinase (TPK). TPP is an essential cofactor of several enzymes. Oxythiamine, a thiamine analogue, has been shown to be converted by TPK into the oxythiamine pyrophosphate (OxPP) within the parasite, and goes on to inactivate at least two TPP-dependent enzymes and kill the parasite. In an attempt to identify more potent antiplasmodial thiamine analogues, ten commercially-available thiamine analogues and ten triazole-modified analogues were tested against *Plasmodium* species. Four of the commercially-available compounds, fursultiamine, cycotiamine, allithiamine, and ethyl thiamine, were active against *P. falciparum* and *P. knowlesi*, but were not as potent as oxythiamine. Six ester and one ether of triazole-modified thiamine analogues also showed antiplasmodial activity, one with an IC_{50} value of 2.2 ± 0.2 µM. This compound was only active against human foreskin fibroblasts at much higher concentrations (selectivity index of 44.6). Unexpectedly, the antiplasmodial activity of these analogues is unlikely to be related to thiamine metabolism in the parasite because their antiplasmodial activity could not be altered by varying the extracellular concentration of thiamine.

(ID: 173)

Development of Human Toxo IgG ELISA Kit, and false-positivity of Latex Agglutination Test for the diagnosis of toxoplasmosis

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Toxoplasma gondii is an intracellular zoonotic parasite that causes infection in a wide range of warm-blooded animals and humans. The main aim of this study was to assess the diagnostic value of the recombinant SAG1 antigen (rSAG1) for *T. gondii*-IgG screening through Human Toxo IgG ELISA Kit (K). Total of 400 human sera were tested by LAT and K. One hundred and twenty two (30.5 %) sera were found positive by LAT and eighty nine (22.25 %) sera were found positive by K. Out of 400 samples, 80 were selected to evaluate the performance of K through commercial *Toxoplasma gondii* IgG ELISA Kit (C). The cutoff value for K was 0.398 and it was calculated through Receiver Operator Characteristic (ROC) curve. The ELISA plates were coated at optimized concentration of rSAG1= 0.125 µg/ml, and the test was performed by diluting the sera at 1:50. The sensitivity and specificity of K were observed to be 98.5 % and 100 %, respectively. The six sera (K-L+) were found positive through LAT and these human sera were later evaluated by Western Blot (WB) analysis. These sera did not produce a band equivalent to 35 kDa on WB analysis thus, LAT produced false-positive results.

(ID: 180)

In vitro antiprotozoal activity of Selected Plant Extracts on *Cryptosporidium parvum* and *Giardia duodenalis*: A preliminary Screening

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Murdoch University, Australia

Giardia duodenalis and *Cryptosporidium* spp. are the most common cause of protozoal diarrhoea, worldwide. Several classes of drugs with good efficacy are available for *G. duodenalis*, but reduced compliance and drug resistance are evident. There is no effective specific chemotherapeutic intervention for *Cryptosporidium*. This study aims to identify potential compounds from plant extracts that provide evidence for efficacy against *Giardia duodenalis* and *C. parvum*. The initial compound screening for activity against *G. duodenalis* was evaluated by resazurin reduction assay. Compound efficacy against *C. parvum* was

detected and quantified by using quantitative-PCR (q-PCR) method. Preliminary results indicated that none of the extracts out of 13 plant compounds demonstrated antigiardial efficacy at the screened concentration. However, potential candidates have been identified for *C. parvum* which need to be further validated at higher concentrations. Further examination of compounds at higher doses will produce dose-response curves allowing for IC_{50} values to be ascertained.

(ID: 203)

Prevalence of Intestinal Parasites in Captive Dingos

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Dingos have the ability to carry zoonotic parasites however, the prevalence of *Strongyloides stercoralis* is uncertain. The aim of the study was to assess the prevalence of *S. stercoralis* and other intestinal parasites in a sample of captive dingos. Forty faecal samples were assessed for parasites using Sheather's sucrose solution egg flotation tests, *Strongyloides*/hookworm agars and the Baermann technique. Flotation tests showed eggs of *Toxocara canis* (15%), *Trichuris vulpis* (2.5%), hookworm (10%), Taeniids (7.5%), Strongylid eggs (5%) and oocysts of *Cytoisospora canis* (17.5%) and another *Cytoisospora* spp. (8%). The *Strongyloides*/hookworm agar plates and Baermann's sedimentation recovered hookworm larvae but did not identify the Strongylids. The addition of 10mg/L of amphotericin B to the *Strongyloides*/hookworm agar was effective in preventing fungal overgrowth and allowed recovering of larvae. The standard Baermann was found to be more effective at recovering hookworm larvae than the modified method. Further investigations using PCR and sequencing to confirm species and larger sample numbers will assist in clarifying the dingo's status as an intestinal parasite reservoir.

(ID: 187)

Comparison of four faecal egg counting techniques for the detection of parasites in horses

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Strongylids and ascarids are the two most significant types of gastrointestinal nematodes of horses, with ascarids posing a large risk to foals under 6 months of age while strongylids are ubiquitous that can affect all ages of grazing horses. Faecal egg counting (FEC) method is currently the most commonly used technique for diagnosing gastrointestinal nematodes of horses and determining when treatment with antiparasitic drugs is necessary as well as to monitor anthelmintic resistance. This study is aimed at the comparison of four faecal egg counting techniques, including FECPAK®, Parasight®, Mini-FLOTAC® and McMaster, in terms of their precision and accuracy. Validation of methods will utilise both spiked and naturally acquired infection samples to assess the techniques' repeatability, analytical sensitivity, diagnostic sensitivity and diagnostic specificity. This study will provide data for the selection of a sensitive, user friendly, accurate and precise method diagnosing parasites in horses.

(ID: 118)

Blood meal analysis to investigate which host are ticks using in Australia

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The development of new molecular techniques is providing us with new opportunities to elucidate host-parasite interactions in blood-feeding arthropods. Identify the DNA of the previous host is now possible and affordable. However, the potential of molecular tools to understand parasite's host preferences, are still poorly developed. This study aimed to evaluate the applicability of the blood meal analysis using a short barcode for two Australian ixodid tick species. We analysed host DNA of 57 questing ixodid ticks (*I. holocyclus* and *Haemaphysalis* sp.) collected from 19 sites in Brisbane. Using a new mammalian-specific cytochrome *b* primers, we identified three marsupial species and cattle as hosts in four (12%) of the *I. holocyclus,* and a marsupial species in two (8%) of *Haemaphysalis* sp. This study provides preliminary guidelines for future blood-sucking parasite research to expand this method to identify host DNA from nymph blood meals in ticks in Australia. Moreover, the primers developed have the potential to help not only parasite related stud but molecular research on Australian mammals.

(ID: 204)

Molecular characterisation of Monogenea parasitise blue mackerel *Scomber australasicus* (Perciformes: Scombridae) in the Australian waters

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This study describes the occurrence and molecular characterisation of Monogenea from blue mackerel *Scomber australasicus*, an edible Australian fish. A total of 50 fish, sourced from the waters off the south-eastern Australian coastline, were examined for Monogenean infection. The overall prevalence, intensity, and abundance were 64%, 2.22, and 1.42, respectively. Monogenea were initially classified as five different species under two families. Family Mazocraeidae was represented by *Kuhnia scombri*, *K. scombercolias* and *Pseudokuhnia minor* and family Gastrocotylidae by *Gastrocotyle kurra* and *Allogastrocotyle bivaginalis*. Molecular identification was conducted through sequencing of the mitochondrial cytochrome *c* oxidase subunit 1 (*cox*1) gene. The host *S. australasicus* was also barcoded (*cox*1). There was no comparable sequence available in GenBank for *K. scombercolias*. Also, limited sequences were available in GenBank for the Gastrocotylid Monongenea. The phylogenetic tree of *cox*1 sequences clustered the Monogenea according to their familial groups of Mazocraeidae and Gastrocotylidae. *Gastrocotyle kurra* and *A. bivaginalis*, two Gastrocotylid species, were identified for the

first time in *S. australasicus*. This study has provided the first evidence for the exploration of *cox*1 region for *K. scombercolias*. The findings of this study provide a basis for future Monogenean research in Australian waters and on other *Scomber* spp.

(ID: 211)

Comparing natural resistance to *Haemochus contortus* infection in Wiltshire Horn and Luxton Black sheep

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Haemonchus contortus is a globally prevalent and economically significant gastrointestinal nematode parasite of small ruminants. Widespread development of anthelmintic resistance has prompted interest in elucidating the immune mechanisms underlying natural resistance to *H contortus* among certain breeds or individual sheep. This study aims to compare natural resistance to *H contortus* between Wiltshire Horn and Luxton Black sheep, both of which are currently absent from available literature pertaining to natural resistance to nematode parasites. Ten sheep of each breed were housed in indoor pens and subject to deworming and a one month acclimatisation period. For each breed, seven sheep were subject to experimental infection with 5000 L3 larvae, with the remaining three kept as uninfected controls. Each week, blood, serum and faecal samples were collected and each animal weighed. Animals were euthanised after 10 weeks in order to carry out a total worm count and histopathological examination of the abomasal tissue. Faecal samples were also collected directly from the farm at weekly intervals for faecal egg counts. Should the resulting data provide evidence of a difference in immune response granting varying levels of natural resistance between breeds, further research may involve investigating the genetic basis of these mechanisms.

(ID: 223)

Immunomics-guided discovery and validation of serum and urine antibody biomarkers for urogenital schistosomiasis

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Sensitive diagnostics are needed for effective schistosomiasis treatment and surveillance to achieve current transmission interruption goals set by the WHO. To respond to this agenda, we screened the *Schistosoma haematobium* interactome for antibody biomarkers, validated their diagnostic performance in endemic populations, and assessed their utility as point-of-care immunochromatographic tests (PoC-ICT) for urogenital schistosomiasis. We first constructed a proteome array with ~1,000 validated and predicted *S. haematobium* proteins and screened it with sera and urine from *S. haematobium*-endemic populations. ELISA was used to test IgG-reactive antigens as well as a subset of antigens from the worm extracellular vesicle proteome that were predicted to be diagnostically informative. Using array probing, it was discovered that 208 and 45 antigens were the targets of significantly increased IgG responses in infected subject serum and urine, respectively. Of the proteins validated by ELISA, *Sh*-TSP-2 and MS3 01370 had the most remarkable overall diagnostic performance in each biofluid and outperformed *S. haematobium* soluble egg antigen in urine. Additionally, *Sh*-TSP-2 and MS3 01370 demonstrated absolute specificity and sensitivities of 75% and 89 %, respectively, when incorporated in separate PoC-ICTs. Thus, *Sh*-TSP-2 and MS3 01370 were identified as sensitive, specific, and field-deployable diagnostics to control and eradicate schistosomiasis.

(ID: 130)

Novel 3D compounds to fight malaria in a time of drug resistance

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Malaria is a significant global health burden for which an efficient vaccine has yet to be developed. Rising antimalarial drug resistance and a plateau in new therapeutic trials, creates an urgent demand for novel antimalarials with structural diversity. We have synthesised novel 3D-spiroheterocycle compounds with chemical connectivities never synthesised or previously studied. The particular spatial conformation of these molecules allows targeting biological domains otherwise inaccessible to relatively flat compounds. Testing of eighteen novel 3D-spirocyclic compounds against human *P. falciparum* parasites *in vitro* revealed that two compounds (compound 24 and compound 25) induce parasite death within 24hrs, while their flat precursors showed no effect on parasite growth. Further, we have shown that the antimalarial activity of both compounds is cytotoxic (i.e. irreversible), and that fluorescently labelled compounds 24 and 25 appear to target the parasite nucleus. *P. falciparum* IC_{50} values of compound 24 and compound 25 were measured in the low micromolar range, and neither compound exhibits toxicity to mammalian cell cultures. Further analysis of these novel drugs is underway to identify their specific parasite target(s). Gathering biological information will allow the synthesis of refined derivatives with higher potency that mirror major antimalarials.

(ID: 208)

A GRA2 minimal ¬promoter improves the efficiency of TATi conditional regulation of gene expression in *Toxoplasma gondii*

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TATi (acronym for **T**rans**A**ctivtor**T**rap **i**dentified) is the only existing transcription system for the model apicomplexan, *Toxoplasma gondii*. While this system is efficient for the regulation of many genes of interest, there has never been an attempt to improve it. Here, we showed significant improvement of TATi regulation by replacing the minimal promoter element of the system. Two alternative minimal promoters, based on the promoters for the dense granule proteins Gra1 and Gra2, were examined to determine if the Signal to Noise Ratio (i.e. induced vs background gene expression) could be improved. Use of Tg GRA1 and Tg GRA2 candidate minimal promoters each led to a significantly greater level ($p < 0.0001$) of TATi-induced expression of an EYFP reporter gene in comparison with the original SAG1 minimal promoter, although the GRA1 minimal promoter induced higher background noise. In comparison with the SAG1 minimal promoter, pooled stable transfectants having the GRA2 minimal promoter had a 23-fold higher Signal to Noise Ratio for EYFP fluorescence in the absence or presence of anhydrotetracycline. Therefore, the performance of TATi for both activation and suppression of transcription can be markedly enhanced by incorporating a GRA2 minimal promoter.

(ID: 129)

Induction of heterologous protection using a novel whole parasite liposomal *Babesia* vaccine

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Babesiosis is a tick-borne infectious disease, caused by *Babesia* parasites. *B. microti* is the most common cause of human babesiosis however, infections may also be caused by other species e.g. *B.divergens* and *B.duncani*. There is currently no human vaccine available, with prevention strategies focused on controlling the tick vector.

We have previously shown that a whole blood-stage parasite liposomal malaria vaccine is able to induce protective immunity in rodent models of the related Apicomplexan parasite, Plasmodium. We have applied this same approach to the development of a Babesia vaccine, using a rodent *B. microti* model. Freshly prepared *B. microti* or *B. divergens* liposomal vaccines induced strong homologous and heterologous protection against *B. microti* challenge. Further studies demonstrated that a freeze-dried *B. microti* liposomal formulation had comparable protection to a fresh formulation.

These results support clinical development of this vaccine approach. We have previously transitioned a whole blood-stage parasite malaria vaccine into human trials, using a cultured *Plasmodium falciparum* cell bank as a source of parasite material. Our data suggest that a cultured *B.divergens* cell bank could be used as a source of parasite material for a broadly protective liposomal Babesia vaccine for humans. This vaccine approach also has veterinary applications.

(ID: 104)

Near-term forecasting of companion animal tick paralysis incidence: an iterative ensemble model

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Tick paralysis is a leading cause of emergency veterinary admissions for Australian pets, often resulting in death if left untreated. Information on periods of increased risk can help reduce exposures to ticks and improve awareness for the need of preventative treatment. Improved awareness of clinicians and pet owners about changes in tick paralysis risk can be assisted by integrating environmental information into time series models. Using an 11-year time series of tick paralysis cases from veterinary clinics in one of Australia's tick paralysis hotspots, we forecasted caseloads over near-term horizons. We fit a series of statistical and generative models using a suite of environmental variables as predictors and combined forecasts into a weighted ensemble to minimise prediction interval error. Our model forecasted cases with exceptional accuracy while preserving interpretability, outperforming a field-leading benchmark. Variables related to temperature anomalies, vegetation moisture and the Southern Oscillation Index were useful for predicting admissions. Using particle filtering to adjust forecast distributions when new data became available, our model adapted to changing conditions and further reduced errors. We expect our pipeline to act as a platform for developing early warning systems to notify clinicians and pet owners about risks of environmentally driven veterinary conditions.

(ID: 197)

Parasites of the Tasmanian devil

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The Tasmanian devil is an endangered carnivorous marsupial, limited to the islands of Tasmania in southern Australia. The parasites of the Tasmanian devil are understudied. This study aimed to increase the knowledge of the parasite fauna of Tasmanian devils. Ten Tasmanian devils were examined for parasites from northern and southern Tasmania. Nematodes that were collected were morphologically characterised as two separate species: the majority were identified as *Baylisascaris tasmaniensis* (verified through molecular sequences). The other species was an unidentified oxyurid nematode, collected from a single Tasmanian devil from the northern part of Tasmania. The most commonly encountered parasite was the cestode *Anoplotaenia dasyuri*. No specimens of *Dasyurotaenia robusta* were collected. The ectoparasite, *Ixodes tasmani*, was also found, although only in Tasmanian devils collected from the southern part of Tasmania. The need to undertake more sampling of the parasites of endangered hosts, such as the Tasmanian devil, to assist with a better understanding of their conservation management, is discussed.

(ID: 194)

Multiple anthelmintic resistance in small strongyles of Australian Thoroughbred horses

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This study aimed to evaluate the efficacy of commonly used anthelmintics against small strongyles (Nematoda: Strongylida) of Australian Thoroughbred horses. Of two farms selected for study, the horses at farm A were treated with single and double-active anthelmintics i.e. oxfendazole (OFZ), abamectin (ABM), abamectin + morantel (ABM + MOR), moxidectin + praziquantel (MOX + PZQ), and oxfendazole + pyrantel (OFZ + PYR). Whereas at farm B, horses only received MOX. Efficacy of moxidectin was checked upon re-testing on both farms at two different time intervals and age groups of horses. Resistance to MOX was found at farm B both times with reduced efficacy of 86.1% (64.3% LCL) and 76.27 % (48.9% LCL) on 14-days post-treatment. Of five dewormers tested at farm A, resistance to three anthelmintics i.e. OFZ, ABM, and OFZ+PYR was found with efficacies of -190.5% (-400.7 LCL), 78.2% (60.6 LCL), 68.8% (50.5 LCL) at day 14 post-treatment, respectively. While shortened ERP of MOX and ABM + MOR was detected after 5 weeks post-treatment and similar results were obtained for the ERP of MOX upon re-testing. The study provides valuable data on multi-drug resistant cyathostomins in Australia and warrants future large-scale studies to assess their prevalence in the country.

(ID: 152)

Accurate assessment of lesions suspected of being caused by *Taenia solium* in body organs of pigs with naturally acquired porcine cysticercosis

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University of Melbourne, Australia

The only currently available method for accurate assessment of the prevalence of porcine cysticercosis is to undertake detailed examination of tissues at necropsy. Most investigations have found that in pigs, *Taenia solium* encysts in the striated muscles and nervous tissue. A previous investigation of porcine cysticercosis in Zambia described 27% of infected pigs as having *T. solium* cysts in the liver, as well some animals having cysts in other unusual tissue locations. We collected lesions from the tissues of pigs derived from *T. solium* endemic areas in Uganda and Nepal. Particular care was taken to avoid cross contamination of specimens with *T. solium* DNA from other tissue sites or from other animals. Control tissue samples were collected from the same organs as lesions were collected, but from sites where no lesion was present. The samples were assessed macroscopically, histologically and by PCR-RFLP and sequencing analysis of DNA isolated from the lesions. Evidence was obtained for lesions in pig tissues other than the striated muscles and nervous tissue as being caused by *Taenia hydatigena*, *Taenia asiatica*, *Echinococcus granulosus* and nematode parasites, however no evidence was found for the presence of any lesion in these tissues being caused by *T. solium*.

(ID: 200)

In vitro culture of *Cryptosporidium parvum* using a novel gut-on-a-chip

Samantha Gunasekera[1], Brendon King[2], Paul Monis[2], Benjamin Thierry[3], Jill Carr[4], Abha Chopra[5], Mark Watson[5], Mark O'Dea[6], Una Ryan[1]

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Cryptosporidium is a major cause of severe diarrhoea-related disease in children in developing countries, but currently no vaccine or effective treatment exists for those who are most at risk of serious illness. This is partly due to the lack of in vitro culturing methods that can support the entire *Cryptosporidium* life cycle, which has led to research in *Cryptosporidium* biology lagging behind other protozoan parasites. Standard culturing methods have only been able to support *Cryptosporidium* growth short-term, however, recently developed three-dimensional intestinal models have shown more promising results. This research aims to establish and sustain *Cryptosporidium parvum* growth in vitro by leveraging recent advancements in microfluidics and organ-on-a-chip technology.

Organ-on-a-chip technology aims to reproduce the key features of the three-dimensional structure and function of specific tissues in the body on a miniaturised scale in vitro. Our research utilises a microfluidic device that represents a rudimentary model of the human gut. Preliminary data indicates that our novel gut-on-a-chip microfluidic device can support the *Cryptosporidium* life cycle for at least one week, and will potentially provide a simplified in vitro culturing system for *Cryptosporidium parvum* with many downstream applications for research and diagnostics.

(ID: 177)

Not gone but forgotten: *Tritrichomonas foetus* in extensively-managed bulls from Australia's Northern Territory

Nichola Calvani[1,2,3], Jan Slapeta[2], Emily Onizawa[3], Kieran Eamens[3], Cheryl Jenkins[3], Mark Westman[3]

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Bovine trichomonosis, caused by infection with the protozoan parasite *Tritrichomonas foetus,* is globally recognised as a cause of reproductive failure in cattle. Maintained in asymptomatic bulls, *T. foetus* infection results in infertility and abortion in infected cows. In Australia's Northern Territory (NT), logistical limitations associated with extensive livestock production inhibit wide-

scale testing and diagnosis allowing the parasite to persist undetected. In the current study, *T. foetus* was detected in 18/109 preputial cultures collected from bulls on a property in the NT with a history of low birth rates and reproductive failure using real-time PCR. Of the *T. foetus* positive samples, 13/18 were genotyped using the internal transcribed spacer regions (ITS-1 and ITS-2) and the 5.8S rDNA unit. Selected samples were further characterised using the protein coding genes of cysteine proteases (CP-1, 2, 4-9) and cytosolic malate dehydrogenase 1 (MDH-1) to determine if the isolates were 'bovine', 'feline' or 'Southern Africa' genotypes. All samples were 100% identical to the *T. foetus* 'bovine' genotype across all markers. This is the first reported case of trichomonosis in Australian cattle since 1988 and is a reminder that *T. foetus* should be considered whenever reproductive failure occurs in extensive cattle systems.

(ID: 178)

Fasciola species introgression: Just a fluke or something more?

Nichola Calvani[1,2], Jan Slapeta[2]

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The threats posed by a range of viral and bacterial zoonotic diseases inevitably receive renewed attention in the wake of global pandemic events due to their overt and devastating impacts on human health and the economy. Parasitic zoonoses, however, many of which affect millions of people each day, are frequently ignored. In the case of fasciolosis, caused by infection with *Fasciola hepatica* or *Fasciola gigantica*, this oversight has allowed the expansion of areas of parasite sympatry and thus increased incidences of hybridisation and possible introgression between the two species. Here we highlight how an increased demand for animal-derived protein, combined with a lack of appropriate tools for detection of these events, is changing the *status quo* of these zoonotic parasites.

(ID: 123)

Comparative pathogenicity of drug-resistant *Trypanosoma brucei* and *Trypanosoma congolense* infections in dogs

Chukwunonso Obi, Michael Okpala, Davinson Anyogu, Nnenna Emejuo, Ikenna Ezeh, Romanus Ezeokonkwo

University of Nigeria, Nsukka, Nigeria, Nigeria

The comparative pathogenicity of drug-resistant and drug-sensitive *Trypanosoma brucei* and *Trypanosoma congolense* infections in dogs were investigated. Twenty Nigerian local dogs were used and were randomly assigned into five groups (A - E) of four dogs each. Group A served as the uninfected-control group while groups B - C were infected with 10^6 drug-sensitive *T. congolense* and *T. brucei* respectively. Groups D and E were infected with 10^6 multidrug-resistant *T. congolense and T. brucei* respectively. The pre-patent period (PPP), clinical signs, level of parasitaemia (LOP), body weight, packed cell volume (PCV), hemoglobin concentration (HbC), total erythrocyte count (TEC), total leucocyte count (TLC) and survivability were assessed. Groups D and E had longer (p<0.05) mean PPP than groups B and C. Also, group E dogs had lower (p < 0.05) mean LOP; longer (p<0.05) mean survivability, and higher (p<0.05) mean body weight, PCV, HbC and TEC than group C dogs. The clinical signs were very severe in group C dogs compared to group E dogs. However, these parameters did not differ statistically amongst groups B and D dogs. Thus, drug-resistant *T. brucei* had low pathogenicity compared to drug-sensitive *T. brucei* while drug-resistant and drug-sensitive *T. congolense* had comparable pathogenicity.

Symp4: Symposium4

Time: Thursday, 24/June/2021: 12:00pm - 12:45pm
Session Chair: Shokoofeh Shamsi, Charles Sturt University

(ID: 214)

Investigating the Zoonotic Potential of Pig Parasites Within Small Holder Farming Communities in Lao PDR

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Soil-transmitted helminths (STHs) are highly prevalent in subtropical and tropical environments, especially South East Asia. In areas where humans live in sympatry with animals, (e.g pigs and dogs), the potential for cross-transmission between hosts is high, especially in communities with free-roaming pigs and dogs; and limited water access, sanitation, and hygiene (WASH). A Previous study in Northern Lao PDR identified a high prevalence of polyparasitism in all host types warranting an investigation into the transmission dynamics within this study site. To achieve this, molecular characterization of the highly prevalent STHs *Ascaris* spp. and *Trichuris* spp. was completed to identify patterns of cross-transmission and potential hybridization.

Phylogenetic analysis demonstrated that humans, pigs, and dogs share the same *Ascaris* genotypes, which is indicative of recent or current cross-transmission. Potential hybrid species were identified which indicate that introgression between *Ascaris* genotypes has or is currently occurring. This finding is likely a result of sympatric living conditions which facilitate parasite cross-transmission. This was further supported by evidence of *Spirocerca vulpis,* a dog parasite, detected in a human sample. These results advocate for the improvement of WASH and emphasise the involvement that pigs and dogs have on the transmission dynamics of human parasite infections.

(ID: 157)

TriTOX: A new *Trichomonas* sp. assay for high-throughput screening of compound libraries

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Trichomonas vaginalis is the most prevalent non-viral sexually transmitted disease, causing 170 million cases of trichomoniasis annually. Current treatment relies solely on nitroheterocyclics, most commonly metronidazole, however due to increasing drug-resistant cases there is an urgent need for novel anti-trichomonals. Historically, the lack of a standardised screening platform restricts anti-trichomonal drug-discovery efforts, and limited surveillance of drug-resistance. Therefore, we have developed a cost-effective chromogenic growth assay amendable to high- and medium-throughput for *T. vaginalis*, but also the related veterinary pathogen *Tritrichomonas foetus*. We demonstrate that pH changes correlated with trichomonad growth, allowing the development of a growth assay based on the pH indicator phenol red in 96- and 384-well microtiter plate formats, which could be quantitively assessed through measuring absorbance values at 570nm, and also qualitatively evaluated by eye. We have demonstrated the utility of this assay by conducting a high-throughput screen of a novel microbial metabolite library (812 compounds), identifying 43 anti-trichomonals. Furthermore, we observed nanomolar inhibition of fumagillin against both trichomonad species, noting this compound has been previously reported to be anti-parasitic. Together, the TriTOX platform is a valuable tool to accelerate drug-discovery efforts and allow drug-resistance surveillance for this neglected parasite.

(ID: 176)

The sulfonylpiperazine MMV020291 prevents red blood cell invasion through interference with actin-1/profilin dynamics in the malaria parasite *Plasmodium falciparum*

Madeline Dans[1,2], William Nguyen[3], Somya Mehra[1,2], Zahra Razook[1,2], Sujaan Das[4], Molly Schneider[1], Thorey Jonsdottir[1,5], Mikha Gabriela[1,2], Chris Tonkin[3], Vanessa Mollard[6], Geoff McFadden[6], Danny Wilson[7], Alyssa Barry[1,2], Brad Sleebs[3], Brendan Crabb[1,5], Tania de Koning-Ward[2], Paul Gilson[1]

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With emerging resistance to frontline treatments, it is vital that new antimalarial drugs are identified to target *Plasmodium falciparum.* A critical process during the parasite's lifecycle is invasion of red blood cells (RBCs), requiring unique parasite proteins that could be exploited as druggable targets. We have recently reported the identification of a compound, MMV020291, as a specific inhibitor of RBC invasion, and successful drug resistance selection was performed. Whole genome sequencing on three MMV020291 resistant populations revealed different non-synonymous single nucleotide polymorphism (SNP); two populations had SNPs in a gene encoding *profilin* (N154Y, K124N) and the third had a SNP present in the *actin-1* gene (M356L). Using CRISPR-Cas9, we engineered these SNPs into wildtype parasites, reproducing parasite resistance to MMV020291. Monomeric actin-1 is polymerised to form filamentous strands, crucial in generating the force required for RBC invasion, with profilin acting to regulate this process by binding monomeric actin-1. MMV020291 appears to inhibit actin polymerisation and we are seeking to understand how the compound engages its target proteins. We have developed a series of MMV020291 analogues, achieving potency with EC_{50}<100 nM, indicating the possible development for invasion blocking drugs and utilised as a research tool to study parasite invasion.

CP4: Contributed Papers 4

Time: Thursday, 24/June/2021: 12:45pm - 1:00pm
Session Chair: Shokoofeh Shamsi, Charles Sturt University

(ID: 120)

A phase 1b clinical trial to assess safety and efficacy of an attenuated hookworm larvae vaccine

Alex Loukas
James Cook University, Australia

Control of human hookworm infection through mass drug administration is impeded by high rates of reinfection, leading to the proposal for a human hookworm vaccine. We hypothesised that percutaneous exposure to *Necator americanus* larvae (L_3) attenuated with ultraviolet C (UVC) light would result in protective immunity. We conducted a phase 1b clinical trial using an attenuated L_3 vaccine delivered via dermal application to healthy human volunteers. Fifteen hookworm-naive volunteers were randomised (1:2) to receive placebo (tabasco sauce) or vaccine (50 attenuated L_3) via dermal application. Two cycles of placebo or vaccine were administered 6 weeks apart, followed 6 weeks later by challenge with 30 unattenuated L_3. Significantly more adverse events (AEs) were observed following vaccination with attenuated larvae compared with placebo (p=0·003), but there was no difference between groups in the frequency of AEs following challenge. Vaccinated participants mounted a robust humoral and cellular response to the vaccine. Significantly fewer larvae were recovered in the vaccinated group than in the placebo group after challenge (p=0·014). Larger studies are required to confirm protective efficacy. Immunomics-based studies are underway to identify the specific antigen targets of protective immunity with a view to ultimate development of a multivalent subunit vaccine.

(ID: 110)

Are you ready for this jelly? A multiomic characterisation of two Kudoa spp. causing “jellymeat” and macroscopic cysts in high-value commercial fish

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Recent anecdotal reports from seafood processors in Eastern Australia have described increased instances of macroscopic cysts (“hoshi”) throughout the musculature of yellowfin tuna, and post-mortem myoliquefaction (“jellymeat”) in broadbill swordfish. Myxozoan parasites of the genus Kudoa are known to occur in economically important fisheries species globally, and cause similar quality-deterioration issues, by secreting an enzyme into the fish tissue post-mortem. However, knowledge of Kudoa spp. epizootiology within Australian tuna and billfish fisheries is poorly understood. To determine the causal agent responsible for this observed quality deterioration, muscle-tissue samples of swordfish and yellowfin tuna from seafood processors in Mooloolaba, Australia, were examined for parasitic infection. Kudoid myxospores were identified from both hosts, and the SSU rDNA sequences from both fish shared >99% homology to Kudoa species. An initial exploration of the transcriptome and secretome reveal metalloproteinases and acid ceramidases are likely secreted by both parasites, suggesting these may be candidate enzymes causing jellymeat. This study provides the first multiomic characterisation of Kudoa thunni in yellowfin tuna, and K. musculoliquefaciens in swordfish harvested from the waters of eastern Australia, expanding the geographical distribution of both parasites and providing new information into the mechanisms underpinning Myxozoan-related quality deterioration in high-value fish.

(ID: 183)

Validating the phylogeny of the nematode subfamily Phascolostrongylinae (Nematoda: Strongyloidea) using mitochondrial protein coding genes

Tanapan Sukee, Ian Beveridge, Anson Koehler, Robin Gasser, Abdul Jabbar
Department of Veterinary Biosciences, Melbourne Veterinary School, Faculty of Veterinary and Agricultural Sciences, University of Melbourne, Victoria, Australia

Australian kangaroos, wallabies (Family Macropodidae) and wombats (family Vombatidae) are parasitised by a diverse group of strongyloid nematodes belonging to the family Cloacinidae. The systematic status of the Cloacinidae has been contentious in previous research due to lack of informative morphological features, and robust molecular phylogenetic framework. The subfamily Phascolostrongylinae found primarily within the large intestines of macropods and wombats was hypothesised to be the basal group within the Cloacinidae. The phylogeny within the Phascolostrongylinae was recently assessed using the internal transcribed spacer (ITS) sequences of the ribosomal DNA. The currrent study validated this phylogeny using amino acid sequences derived from twelve mitochondrial protein coding genes. Preliminary data indicate that the tree derived from the mitochondrial datasets shared some consistencies with the ITS-based phylogeny. The position of Oesophagostomum spp. as a sister group to the genera of Phascolostrongylinae supports the previous hypothesis that strongyloid nematodes in marsupial may have originated from the Chabertiidae. However, the inclusion of additional species from the related subfamily Cloacininae will be necessary to test this hypothesis. This work is part of a larger study which aims to provide a robust molecular phylogenetic framework for future studies into the evolutionary origins of strongyloid nematodes in marsupials.

Symp5: Symposium5

Time: Thursday, 24/June/2021: 1:45pm - 2:30pm
Session Chair: Sarah Preston, Federation University

(ID: 192)

Teaching Parasitology in times of change: the story remains the same.

Malcolm Jones
University of Queensland, Australia

This presentation will be part of the ASP Education in Parasitology Session. The talk will be given from the perspective of one who has witnessed parasitology from the old chalk 'n duster days, through the OHP sheets, the 35 mm slides (that were always back to front and upside down), to the modern era of lecture recordings and blended learning activities. I will share some of the tips in teaching I have picked up along the way, and I will attempt to relate my ideas on how we can continue to captivate and train our young audiences in parasitology- regardless of the teaching methods we use. I will highlight some of my worst mistakes in public speaking, as well as some positive experiences.

(ID: 150)

CRISPR/Cas9 Mutagenesis Causes Putative Deletion in *Schistosoma mansoni*

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Schistosoma mansoni is a flatworm parasite that causes human schistosomiasis which is first on the scale of devastating parasitic helminth diseases. Given the fact that lacking of suitable tools to effectively characterize schistosome gene products as potential drug and/or vaccine targets, we have developed CRISPR/Cas9 editing system by using electroporation delivery method to explore the functional genomics of *S. mansoni*.

To further improve modification efficiency of CRISPR/Cas9 editing, we transduced *S. mansoni* eggs, schistosomula and adult worms, respectively, with infectious lentiviral particles produced by transfection of HEK293T cells with a CRISPR-lentiviral vector. This vector contains a mCherry fluorescence marker and a guide RNA targeting *S. mansoni* acetylcholinesterase (*SmAChE)*. MCherry fluorescence was observed in transduced parasites, indicating the CRISPR components have entered into these worms. Significantly decreased AChE activity observed in *AChE*-edited parasites, reduced hatching ability of edited eggs and altered behaviour of miracidia hatched from these eggs strongly demonstrated the Cas9 cleavage disrupted *SmAChE*. Interestingly, large deletions were observed when genotyping individual adult worm by PCR assays. Next generation sequencing by using long-rang PCR products (15kb) has been undertaken to confirm the large deletion. Our results demonstrate the efficient applicability of CRISPR/Cas9 for functional study and control of this parasite.

(ID: 160)

Exploring *Ascaris* chemosensation and its importance in infection

Pradip Roy[1,2], Joy Liu[1], Peter Thurgood[3], Balu Balan[1,2], Samantha J Emery-Corbin[1], Verena Wimmer[1], Khashayar Khoshmanesh[3], Aaron R Jex[1,2]
[1]The Walter and Eliza Hall Institute of Medical Research, Parkville, Melbourne, Australia; [2]Faculty of Veterinary and Agriculture Science, The University of Melbourne, Melbourne, Australia; [3]School of Engineering, RMIT University, Melbourne, Victoria, Australia

Ascaris spp. infect ~700 million people worldwide and causes malnutrition and stunting. Current treatment is limited to a few drug classes; none offer long-term protection. Early in infection, *Ascaris* migrates through the host liver and lung. Recent studies suggest that this migration is guided by chemosensation. We propose that the chemosensory system of parasitic nematodes is an attractive but understudied therapeutic target. Here, we explore chemosensation in guiding larval *Ascaris* during infection. We show that newly hatched *Ascaris* larvae respond chemotactically to fresh liver homogenates and known chemotactic stimuli for skin-penetrating nematodes, including urocanic acid. We used comparative genomics, phylogenetics, sequence homology and 3D protein structural based modelling to manual curate and identify key players in the chemosensory pathways of *Ascaris suum*. We studied expression of these chemosensory genes in tissue specific transcriptomic and proteomic data, and found most are enriched in the head region. We also undertook high-resolution confocal fluorescent imaging of the chemosensory neurons of *A. suum* larvae, confirming their orthology with *C. elegans* and providing a detailed map for subsequent studies. We will be extending this work through observations of *Ascaris* in microfluidic behavioural mazes and transcriptomic and proteomic study of larval worms responding to chemotactic stimuli.

CP5: Contributed Papers 5

Time: Thursday, 24/June/2021: 2:30pm - 2:45pm
Session Chair: Sarah Preston, Federation University

(ID: 136)

Establishment of RNAi in *Sarcoptes scabiei* eggs to identify novel therapeutic targets

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Scabies is a parasitic skin disease caused by *Sarcoptes scabiei.* This worldwide problem has high morbidity and secondary bacterial infections cause life threatening sequelae. A female mite lays 2-3 eggs daily but current treatments lack ovicidal activity. Here we establish a method to introduce double-stranded RNA (dsRNA) and induce gene silencing to explore novel scabies ovicides.

Eggs were treated with sodium hypochlorite and fluorescent tagged dsRNA was used to determine the intake. A series of genes relevant in egg development were identified from recently established egg transcriptome/proteome. The target gene *S. scabiei* Deadpan is a single copy gene with predicted functions in embryo development. Eggs were incubated with 2.5 µg/µl of dsRNA encoding a fragment of *Ss*Deadpan or unrelated *E. coli* LacZ gene at 4^0C for 48h. Gene expression was quantified by qPCR and normalised with *Ss*EF1alpha gene expression. The results were analysed by student t-test. RNAi-treated eggs were tested at 37^0C for 3days for hatchability. Eggs immersed in *Ss*Deadpan dsRNA showed significant reduction ($p<0.05$) in gene expression (21913±7536 copies/µl) compared to LacZ negative control (105620±25190 copies/µl). In addition, 46.67±7.265% hatchability reduction was observed. The methods established here can be used to investigate the novel ovicidal targets in parasitic mites.

(ID: 141)

Parasite galectin inhibits mast cell degranulation

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Mast cell degranulation is a major mechanism preventing the establishment and survival of incoming nematode larvae and this has been clearly shown for *Teladorsagia circumcincta* in sheep. Galectins are a family of proteins that bind beta-galactosides and play important roles in a variety of cellular processes. Host galectin-3 plays a key role in mast cell degranulation and incoming nematode larvae produce large amounts of parasite galectin. We hypothesised that nematode galectin inhibits mast cell degranulation. Bioinformatic analyses have shown that nematode galectin has a similar structure to galectin-3 and the amino acids in the putative binding sites are identical. This is a remarkable example of convergent evolution. Nematode galectin both binds antibody and is bound by antibody. In vitro studies have shown that recombinant parasite galectin inhibits the degranulation of a rat mast cell line RBL-2H3. Together these results suggest that nematodes produce galectin to enhance their establishment and survival. This work was supported by grants from the National Science Center, POLAND No.2016/23/B/NZ6/03464 and La Trobe University.

(ID: 174)

The *Plasmodium falciparum* parasitophorous vacuole protein P113 interacts with the parasite protein export machinery and maintains normal vacuole architecture.

Hayley Bullen[1], Paul Sanders[1], Madeline Dans[1], Thorey Jonsdottir[1], Jo-Anne Chan[1], David Riglar[2], Catherine Palmer[3], Betty Kouskousis[1], Sarah Charnaud[4], Tony Triglia[4], Mikha Gabriela[1], Molly Parkyn Schneider[1], Tania de Koning-Ward[5], Jake Baum[2], James Beeson[1], Alan Cowman[4], Paul Gilson[1], Brendan Crabb[1]
[1]Burnet Institute, Australia; [2]Imperial College London; [3]Bio21; [4]Walter and Eliza Hall Institute; [5]Deakin University

The *Plasmodium* translocon of exported proteins (PTEX) is crucial to blood-stage growth and virulence of malaria parasites. This complex sits astride the parasitophorous vacuole membrane (PVM) and serves to export hundreds of effector proteins into the infected erythrocyte cytosol to ensure parasite survival and immune-avoidance. PTEX comprises 3 core components that are essential to its function, plus a number of additional accessory proteins that remain poorly characterised. Here, we report on P113, a new PTEX accessory protein that is released by invading parasites into the nascent PV that forms during erythrocyte invasion. This protein is plugged into the parasite plasma membrane via a GPI-anchor and appears to span the parasitophorous vacuole space where it interacts with both PVM bound PTEX and another related complex, the Exported Protein Interacting-Complex (EPIC), as well as numerous exported proteins. Although knockdown of P113 expression does not generate major defects in protein export or parasite growth, truncation or knockdown of P113 leads to significant morphological abnormalities of the PVM. These data suggest P113's binding to PTEX, EPIC and exported proteins also plays an architectural role in maintaining order within the PV space.

Symp6: Symposium6

Time: Thursday, 24/June/2021: 3:00pm - 3:30pm
Session Chair: Cibelly Goulart, University of Technology Sydney

(ID: 205)

Uncovering the lipid 'scavengome' in *Toxoplasma gondii* parasites

Serena Shunmugam[1], Sheena Dass[1], Laurence Berry[2], Christophe-Sebastien Arnold[1], Nicholas Katris[1], Samuel Duley[1], Fabien Pierrel[3], Marie-France Cesbron-Delauw[1], Yoshiki Yamaryo-Botte[1], Cyrille Botte[1]

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Apicomplexa are obligate intracellular parasites responsible for major human diseases. *Toxoplasma gondii* parasites, are unique as they can infected almost any nucleated eukaryotic cell from warm-blooded animals, and therefore face considerably varying host nutrient environments. Their intracellular survival relies on their metabolic adaption capacity towards nutrient availability. This is particularly true for phospholipid synthesis fueling membrane biogenesis. Parasite lipid-assembly follows an essential 'patchwork' combination of fatty acids (FAs), either synthesized *de novo* by the parasite or scavenged from their host. These parasites are governed by a fine balance between lipid synthesis and storage to efficiently propagate depending on host-nutrient availability. We have identified an essential phosphatidic acid phosphatase, *Tg*LIPIN, which is crucial in maintaining metabolic balance between lipid storage and active membrane biogenesis sustaining parasite development. Lipidomic analyses using our platform, shows that this protein serves as a central metabolic nexus. It is responsible for the diacylglycerol formation and regulates the phosphatidic acid levels, which is involved in the 'membrane biogenesis and energy storage' equilibrium. We developed fluxomic approaches to decipher the host-parasite lipid fluxes and unraveled the FA scavengome of the parasite. This work demonstrates that *Tg*LIPIN channels host-scavenged FAs to storage or membrane phospholipids and prevents lipotoxic parasite.

(ID: 217)

ANTIOXIDANT ENZYME AND CYTOKINE LEVEL RELATIONSHIPS DURING SEVERE AND UNCOMPLICATED MALARIA INFECTION IN URBAN GHANAIAN CHILDREN

Richard Asmah[2], Daniel Squire[1], Selorme Adukpo[5], Eric Kyei-Baafour[6], Ebenezer Aidoo[4], Patrick Ayeh-Kumi[3]

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Introduction: Malaria is an important infectious disease in tropical and subtropical regions. During malarial infection, both malaria parasites and the red blood cells come under oxidative stress. In this study we investigated superoxide dismutase (SOD) activity, parasitaemia levels and cytokines relationships in urban Ghanaian children with severe and uncomplicated malaria.

Methods: In this study 150 structured questionnaires were administered to study participants and blood samples taken to estimate malaria parasite density, haematological parameters and SOD activity. DNA comet assay was used to evaluate the extent of parasite DNA damage due to oxidative stress. T helper 1, Plasma $INF\gamma$, TNF_{α}, T helper 2, and IL-10 cytokine levels were measured.

Results: 150 participants; 54.67% males and 45.33% females were recruited. Participants positive for malaria were categorized as severe (n=79) **(**$56.75 \times 10^3 \pm 57.69$ /µl) or uncomplicated (n=26) ($5.87 \times 10^3 \pm 2.87$ /µl) ($p<0.0001$). Negative correlation was found between parasitaemia and SOD activity among severe malaria group ($p= 0.0428$). Difference in cytokine (IL-10) levels between control uncomplicated and complicated malaria groups was significant ($p<0.0001$) DNA comet assay revealed extent of damage on parasite DNA in participants.

Conclusion: This study demonstrated the essential roles SOD activity and cytokines play as anti-parasitic defense during malaria infection.

CP6: Contributed Papers 6

Time: Thursday, 24/June/2021: 3:30pm - 3:45pm
Session Chair: Cibelly Goulart, University of Technology Sydney

(ID: 115)

Comparison of the egg recovery rates and limit of detection for soil-transmitted helminths using the Kato-Katz thick smear, faecal flotation and quantitative real-time PCR in human stool.

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Soil-transmitted helminth (STH) infections predominately affect resource-poor communities and negatively impact on child and maternal health. Diagnostics play a critical role in guiding and informing existing STH control programs and the implementation and evaluation of intervention strategies. The diagnostic performance of the Kato-Katz (KK) thick smear technique, sodium nitrate ($NaNO_3$) faecal floatation (FF) and qPCR were calculated and expressed in eggs per gram (EPG), by experimentally seeding parasite-free human faeces with *Ascaris* spp., *Trichuris* spp. and *Necator americanus* eggs representing low, medium and high intensity infections. All diagnostic methods demonstrated strong direct correlation to the intensity of seeded EPG. KK and FF resulted in significant lower egg recovery rates compared to qPCR (p <0.05). qPCR demonstrated significantly (p <0.05) greater sensitivity with an ability to detect as little as 5 EPG for all three STH, compared to 50 EPG by KK and FF. These results indicate that the diagnostic performance of qPCR assays should be considered by control programs in the phase that aims to seek confirmation of transmission break and cessation of preventive chemotherapy in low-transmission settings, in line with the control targets of the WHO neglected tropical diseases 2030 Roadmap.

(ID: 132)

L672H mutation in the *P. falciparum* flavokinase confers resistance to roseoflavin and 8-aminoriboflavin

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We previously found that two riboflavin analogues, roseoflavin and 8-aminoriboflavin, inhibit malaria parasite proliferation by targeting riboflavin metabolism. To determine the mechanism of action of roseoflavin in *P. falciparum*, we generated roseoflavin-resistant parasites by culturing the parasites under continuous drug pressure for 27 weeks. The roseoflavin-resistant parasites were found to be six times more resistant to roseoflavin and 50 times more resistant to 8-aminoriboflavin. Cloned parasites were subjected to whole genome sequencing and a mutation, L672H, found in the flavokinase. To investigate this mutation, we generated two parasite lines episomally-expressing GFP-tagged versions of the wild type and mutant forms of flavokinase. The parasites expressing mutant *Pf*FK episomally had an increased roseoflavin IC_{50} (three-fold) compared to the parasites expressing the WT flavokinase, consistent with the mutation being responsible for the roseoflavin resistance phenotype. We found that PfFK-GFP localises to the parasite cytosol and immunopurified *Pf*FK-GFP phosphorylated riboflavin into flavin mononucleotide. L672H mutation caused a reduction in flavokinase binding affinity to roseoflavin and riboflavin by ~30 and 13 times, respectively. We also show that 8-aminoriboflavin is no longer a substrate to the mutant flavokinase. Our results show that the L672H flavokinase mutation in *P. falciparum* confers resistance to roseoflavin and 8-aminoriboflavin.

(ID: 164)

Geospatial analysis of pre-intervention prevalence of onchocerciasis in Ethiopia

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Onchocerciasis is a disease endemic in sub-Saharan Africa that is caused by the filarial nematode parasite Onchocerca volvulus. Due to the heterogenous prevalence of onchocerciasis, high prevalence endemic areas are often in proximity to low prevalence endemic areas, posing risk to the latter which are omitted from mass drug interventions as per the current treatment strategies. The nationwide elimination program for Ethiopia was launched in 2013 with the goal of interrupting transmission by 2020. However, because no prevalence mapping was done throughout the country pre-intervention, the effect of the interventions is difficult to quantify. Using pre-intervention nodule prevalence data from 914 endemic sites in Ethiopia collected from 2000 to 2012 as an indicator of history of infection due to the parasite, a Bayesian geostatistical map was created that incorporates environmental, climate, and socio-demographic factors.

Soil moisture, intensity of night lights, and the slope of the sites were found to be associated significantly with nodule prevalence. The prevalence of onchocerciasis was estimated to be higher in the southwestern and northwestern parts of the country. The map of modeled pre-intervention prevalence can serve as a baseline for assessing changes in onchocerciasis prevalence due to different interventions to meet the elimination goals.

ST2: Short talks: 3-minute presentations 3MT style day 2

Time: Thursday, 24/June/2021: 4:00pm - 5:15pm
Session Chair: Michelle Power, Macquarie University

Speed Talks! Each presenter has three-minutes to showcase their data. 3MT style presentations, one-slide and three minutes to spruik your research! Check out the abstract uploads for more information from the researcher.

(ID: 206)

Rapid *Schistosoma* DNA detection using a dipstick with LAMP assay

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Schistosomiasis is a disease of impoverished people in low-socio economic regions. The global disease burden remains high despite increased control and elimination efforts, in part due to inadequate diagnostics, including the high cost of DNA-based detection methods. The DNA dipstick is a simple, rapid and low-cost method for DNA extraction, and when combined with LAMP, may be an ideal tool for point-of-care diagnostics. This study aimed to optimize the dipstick in detecting *Schistosoma japonicum* in clinical samples. *S. japonicum* from different life cycles were isolated and purified from infected snails and livers of experimentally infected mice and homogenized in lysis buffer. The DNA dipstick was inserted into the lysed samples, washed to eliminate contaminants, and dipped into the amplification mix and incubated at 65°C for 60 mins. Similarly, cell-free DNA was also extracted from mice and naturally infected human urine samples using dipsticks. The DNA dipstick detected *S. japonicum* from infected snails, cracked eggs and adult worms as proof of concept. Low levels of cell-free DNA in urine from experimentally infected mice and naturally infected human samples were also detected. The DNA dipstick combined with LAMP, is a promising point-of-care testing method for detecting schistosomiasis infection in endemic regions.

(ID: 145)

The potential effects of host origin on attachment and engorgement of two parapatric ticks

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Understanding what limits geographical distributions of species is crucial to predicting distribution changes. Parapatric distributions are complex in that many mechanisms can be working together to maintain the boundary and limit distribution expansion of either species. One such interaction is between two ixodid tick species, *Amblyomma limbatum* and *Bothriocroton hydrosauri* and their main host *Tiliqua rugosa*. This system has been intensely researched since 1982. The southern tick species is limited by desiccation risk off host, but no compelling reasons for the northern tick not to survive further south have been found. Preliminary evidence suggest the lizards immune system maybe involved in the boundary maintenance. Using an experimental approach, we exposed tick larvae to *T. rugosa* from either side of the boundary and examined tick attachment and engorgement rates. Tick species had a significant influence on their attachment and there was a trend for *B. hydrosauri* to have a lower engorgement success when exposed to lizards from the other side of the boundary suggesting the distribution of *B. hydrosauri* may be limited by the immune response of *T. rugosa*, however this would not limit the distribution of *A. limbatum* which requires further investigation.

(ID: 170)

*Tg*MPODD and the quest for the missing membrane anchor of Succinate Dehydrogenase in *Toxoplasma gondii*

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Succinate dehydrogenase (SDH), or Complex II of the Electron Transport Chain (ETC), is a ubiquitous protein complex with a dual role in mitochondrial energy metabolism: it oxidises succinate to fumarate in the TCA cycle, and transfers the resulting electrons to Coenzyme Q in the ETC. In animals, yeast, and bacteria, SDH is highly conserved and comprises four subunits: SdhA and SdhB form the soluble, catalytic core of the complex, while SdhC and SdhD anchor the complex in the inner mitochondrial membrane. The apicomplexan parasite *Toxoplasma gondii,* which infects one-third of humans worldwide, expresses homologues of the catalytic subunits SdhA and SdhB, but no clear homologues of the membrane anchoring subunits, raising the question of what could be anchoring SDH in the membrane in these parasites. Here, we show that the small protein MPODD, previously shown to be essential for transmission of *Plasmodium berghei* into mosquitoes, is a membrane subunit of SDH in *T. gondii*. Knockdown of *Tg*MPODD causes *Tg*SdhA and *Tg*SdhB to dissociate from the membrane anchoring domain and abolishes SDH activity, decreasing parasite growth. Our findings propose a role for MPODD in SDH complex integrity and membrane integration, thus uncovering a unique feature of apicomplexan mitochondrial energy metabolism.

(ID: 193)

Ticks and tick-borne diseases of bovines in smallholder dairy farms

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Ticks and tick-borne diseases (TTBDs) are one of the major health and production constraints of large ruminants, particularly in those reared under resource-poor small-scale farming system like in Pakistan. To identify the gaps about important epidemiological aspects of TTBDs in a small-scale farming system, we appraised the literature from three databases on bovine

TTBDs in Pakistan. Our critical analyses of the selected 173 studies published between 1947 to 2021 showed that morphotaxonomy had been the most widely used method for the identification of ticks and tick-borne pathogens (TBPs) in Pakistan. The tick fauna includes at least 53 species, most of which belong to three genera, *Haemaphysalis*, *Hyalomma* and *Rhipicephalus*. The prevalence of ticks is higher in cattle (particularly exotic and crossbreeds), females, young animals and during summer season. Major TBPs include *Anaplasma*, *Babesia* and *Theileria* spp. and their prevalence is also higher in cattle than that in buffaloes. Data are scarce about risk factors, spatial temporal distribution, genetic diversity, vector potential, and the control of ticks and TBPs. Moreover, mathematical modelling has not been utilised to study the distribution patterns of TTBPs. Therefore, future research should address these knowledge gaps to supplement the limited control measures available for TTBDs.

(ID: 186)

Parasitism in the black-spotted croaker: analysis of species infection dynamics against environmental factors

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Marine parasitic organisms are more abundant and evolved than ever before meaning commercially important fish species such as the black-spotted croaker, represent crucial research objects for parasite studies in Australian waters. With parasites adapting and changing with the environment, it is with accelerated importance that parasite-host interactions and subsequent ecosystem impacts are understood. The black-spotted croaker houses several parasitic organisms and many of these have the potential to be impacted by environmental change both directly through developmental processes in a warming ocean, and indirectly through host health changes and migratory behaviour. External parasites of the black-spotted croaker such as monogeneans, are predisposed to many of these stressors and the study presented has identified these gill parasites in a hope to measure those species occurring against the corresponding ecological parameters of the surrounding environment. Through careful analysis of the parasite loads from different populations of the black spotted croaker, the effects of environmental instability on parasites are understood. By aiming to identify these parasites and provide some of the first reports of those infecting the black-spotted croaker, this study will demonstrate how parasitic organisms can be utilised in both host population and ecosystem level studies.

(ID: 190)

Thermal stability proteomics identifies protein targets for antimalarial compounds

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Thermal Stability Proteomics (TSP) is an emerging technique for identifying the protein targets of antimalarial compounds. TSP takes advantage of the thermal stabilisation that occurs when a protein is bound by a compound, allowing protein targets to be identified from a complex proteome, following a thermal challenge. Our TSP methodology takes advantage of a Data Independent Acquisition-Mass Spectrometry (DIA-MS) workflow combined with a comprehensive spectral library (over 3000 *P. falciparum* proteins), allowing us to perform reproducible, label free quantitative analysis of both high and low abundant parasite proteins more efficiently than traditional label-based proteomics methods.

We have successfully applied TSP-DIA-MS to current antimalarial compounds. We identified a significant stabilisation of dihydrofolate reductase-thymidylate synthase (known target) in the presence of pyrimethamine from a detected proteome of 1428 soluble proteins. This TSP-DIA-MS workflow was further validated with a known aminopeptidase inhibitor, which successfully stabilised its proposed targets, the M1 and M17 aminopeptidases, amongst a shortlist of proteins. Finally, TSP-DIA-MS was performed with novel aminobenzimidazoles, which have an unknown mechanism of action. We identified a shortlist of 11 potential protein targets, which warrant further investigation and highlight the potential of our new TSP workflow as a target identification method.

(ID: 142)

Plasmodium vivax malaria serological exposure markers: assessing the presence and implications of potential cross-reactivity with *P. knowlesi*

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New tools for malaria elimination are urgently needed. We have recently developed a panel of serological exposure markers that can inform on recent exposure to *Plasmodium vivax* parasites in the past 9-months. The objective of our current study was to assess cross-reactivity against a panel of *P. vivax* serological exposure markers in individuals with the genetically-related zoonotic parasite, *P. knowlesi.* We measured total IgG antibody responses against 21 *P. vivax* proteins in two cohorts of individuals with clinical *P. knowlesi* infections from Sabah, Malaysia. We observed cross-reactive antibodies against some of the *P. vivax* proteins assessed, with a clear relationship with the level of sequence identity between the *P. vivax* and *P. knowlesi* orthologs. There was a peak in cross-reactive antibodies at day 7 following *P. knowlesi* infection, with reduced magnitude by day 28 post-infection and complete absence of antibodies by one-year post-infection. As some *P. vivax* proteins had limited cross-reactivity, we will assess whether a redesigned panel of *P. vivax* serological markers that favours those with low cross-reactivity can be developed. Ideally this panel would still maintain high sensitivity and specificity for detecting recent *P. vivax* infections whilst not miss-classifying individuals with recent *P. knowlesi* infections.

(ID: 189)

Detection and characterization of *Coccidian* parasites in wild dogs and foxes from south-east Australia

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Parasites of the *Coccidian* genus pose a significant health risk to wild and domestic animal populations as well as humans worldwide. Australia is no exception where such parasites are the cause of health concerns and economic loss. This study aimed to determine the prevalence of *Coccidian* parasites in Australian wild dogs and foxes, by performing molecular analysis on 115 scat samples collected in south-east Australia. Using mitochondrial DNA analysis, host species were identified, and parasite identification was achieved through genetic analysis of 18S rRNA genes. We successfully identified the host species in 96% (n=110) of the samples, which were identified as either fox (n=50) or dog (n=60). *Coccidian* parasites were detected in a total of 41 samples. Parasite genus characterization was performed by PCR amplification, sequencing, and phylogenetic analysis of the *Neospora* Nc5 gene, the *Cystoisospora* and *Hammondia* ITS1 gene, and the *Sarcocystis* cox1 gene. *Neospora* spp., *Hammondia* spp., *Sarcocystis* spp. and *Cystoisospora* spp. were confidently identified in 1, 2, 15, and 17 samples, respectively. In addition, co-infection of *Neospora* spp. and *Sarcocystis* spp. was detected in one sample. Overall, this study indicates that wild dogs and foxes play an important role in the transmission of numerous *Coccidian* parasites in Australia.

(ID: 140)

β-triketones - A new prospective scabicide

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Scabies is a contagious skin disease caused by the obligate parasitic mite *Sarcoptes scabiei.* Scabies is linked to secondary bacterial infections with life-threatening sequelae and is a major problem in remote Australian Aboriginal communities. Available scabicides are suboptimal. We tested Manuka oil (MO) for its scabicidal activity. Six commercial MOs were tested *in-vitro.* MO fractionation, followed by gas chromatography and Spearman's Correlations identified the active compounds (β-triketones). The three most promising active compounds were synthesized and tested on mites and eggs at different concentrations and different time points. LC50 and LT50 values were determined using the Probit analysis. β-triketones were tested in combination to test for synergistic effects and analysed using Compusyn Software. The MO with the highest ovicidal (>95%) and miticidal (100%) activity resulted had 17 fractions and 28 compounds. The β-triketones flavesone, isoleptospermone and leptospermone had the highest acaricidal activity but did not act synergistically. Flavesone showed highest miticidal activity with LC50 of 57.81mM (95%CI 53.97-61.68) at 4h and leptospermone showed the highest ovicidal activity at day 3 with LC50 of 33.59mM (95%CI 29.23-38.04). Flavesone (150mM) showed lowest LT50 for mites and eggs, 1.34h (1.24-1.45) and 8.03h (6.30-9.70) respectively. Overall, β-triketones show potential for developing a novel scabicide.

(ID: 143)

Investigating the mode of action of the antimalarial drug proguanil

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With 3.2 billion people at risk of malaria and a global agenda focused on eradication there is a desperate need to discover new drugs with novel modes of action. It is also important that we protect current drugs by understanding their action. Proguanil is an antimalarial drug that is used in combination with atovaquone (as Malarone®) for malaria prevention and treatment. For decades, proguanil has been thought to lack potent intrinsic activity against malaria parasites, with its *in vivo* action attributed to atovaquone potentiation and metabolism to the dihydrofolate reductase inhibitor, cycloguanil. Our lab recently demonstrated that proguanil has potent, but slow action, activity an order of magnitude better than previously thought. To better understand this activity, we have selected *P. falciparum* parasites for *in vitro* resistance to proguanil, and a proguanil analogue that cannot cyclize to cycloguanil (tBuPG). Resistant lines have been cloned, whole genome sequenced, and data compared to the wildtype parasite genome of parent to identify a possible drug target and/or resistance mechanism. A mutation in a putative SNARE gene was identified in all three tBuPG-resistant clones, and studies are now underway to investigate the role of this mutation in proguanil action.

(ID: 166)

Descriptive Comparison of ELISAs for the Detection of *Toxoplasma gondii* Antibodies in Animals: A Systematic Review

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Toxoplasma gondii is the zoonotic parasite responsible for toxoplasmosis in warm-blooded vertebrates. This systematic review compares and evaluates the available knowledge on enzyme-linked immunosorbent assays (ELISAs), their components, and performance in detecting *T. gondii* antibodies in animals. Four databases were searched for published scientific studies on *T. gondii* and ELISA, and 57 articles were included. Overall, indirect (95%) and in-house (67%) ELISAs were the most used types

of test among the studies examined, but the 'ID Screen® Toxoplasmosis Indirect Multi-species' was common among commercially available tests. Varying diagnostic performance (sensitivity and specificity) and Kappa agreements were observed depending on the type of sample (serum, meat juice, milk), antigen (native, recombinant, chimeric) and antibody-binding reagents used. Combinations of recombinant and chimeric antigens resulted in better performance than native or single recombinant antigens. Protein A/G appeared to be useful in detecting IgG antibodies in a wide range of animal species due to its non-species-specific binding. One study reported cross-reactivity, with *Hammondia hammondi* and *Eimeria* spp. This is the first systematic review to descriptively compare ELISAs for the detection of *T. gondii* antibodies across different animal species.

(ID: 153)

Fast-tracking gastrointestinal nematode speciation in livestock

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Effective gastrointestinal nematode (GIN) management in livestock industries is becoming increasingly difficult due to the rise of anthelmintic resistance and changes in the temporal and geographical distribution of major GINs. Underpinning the response to these challenges is the need for a fast-tracked diagnostic speciation technique, making it easier for livestock producers to make informed GIN management decisions. The current 'gold-standard' approach for speciating GINs involves cultivating strongyle eggs into third-stage infective larvae (larval culture, ~10 days) followed by morphological differentiation. This technique is laborious and potentially inaccurate due to overlaps in the key morphological features used to distinguish genera. If made more accessible to livestock producers, advancements in both morphological and molecular diagnostic technology have the potential to significantly improve the productivity and profitability of farming enterprises. We will be presenting a diagnostic workflow capable of fast-tracking the speciation of complex GIN infections. Our approach incorporates an existing modern faecal egg count platform with next generation sequencing to explore the gastrointestinal 'nemabiome'.

(ID: 188)

Spatial variation in prevalence of hookworm infection in pet dogs in dog parks of GreaterBrisbane, Australia

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Dogs carry several zoonotic parasites and our earlier study in Greater Brisbane, indicated that perceptions of dog owners towards zoonotic canine parasites varies demographically. To further investigate and estimate the prevalence and geographical heterogeneity of hookworm infection in dogs, a parasitological survey was conducted in 2019 and 2020 in a total of 55 dog parks in the Brisbane city council. Faecal samples were collected from dogs visiting these parks and analysed for hookworm infections. We geocoded the dog park locations and quantified spatial autocorrelation in the observed prevalence of hookworm infection using a semivariogram. Using a generalised linear model with a random effect of dog park, we modelled the relationship between prevalence of hookworm in pet dogs and socio-environmental predictors. Our results suggest that dog park-specific prevalence of hookworm infection varied from 0% to 21% with a mean prevalence of 2.6%. We found significant spatial dependence in the observed prevalence of hookworm infection between dog parks within 4 km. Looking into the growing number of dog ownership in cities like Brisbane, these results are of public health importance not only for education and health promotion of local dog owners and veterinarians, but also for Brisbane city council dog park management.

(ID: 113)

The Development of a Novel Antimalarial Class with Antimalarials with Slow Acting Erythrocytic Stage Activity

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Malaria is one of the most significant parasitic diseases in human history with approximately half of the world's population at risk of infection.[1] Infected individuals are estimated to total 219 million annually with 435,000 succumbing to the disease in 2016.[2] Parasite resistance has developed against all available classes of antimalarials, including the current first-line treatment Artemisinin combination therapy (ACT).[3] Therefore, an urgent need has arisen towards the development of antimalarials with novel mechanisms of action.

In collaboration with Janssen Pharmaceuticals and Medicines for Malaria Venture, we have undertaken a high-throughput screen of a large drug-like library against the asexual blood stage of Plasmodium falciparum and identified a number of hit chemical series. One of these series is the focus of the present studies and is mediated by an unknown mechanism of action with an interesting delayed parasite killing profile. Medicinal chemistry techniques have been used to identify a tight SAR and have generated a potent nanomolar inhibitor. These optimised hits are now being used for further mechanistic studies towards the identification of novel P. falciparum cellular targets.

(ID: 147)

The exotic snake mite (*Ophionyssus natricis*), a neglected parasite of significant veterinary concern in Australia

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The snake mite, *Ophionyssus natricis* (Acari: Macronyssidae) is an ectoparasite of veterinary significance because infestations can cause abnormal shedding and anaemia in its hosts. This parasite has also been implicated in the transmission of pathogens, some of which are almost always fatal to the host. In Australia *O. natricis* is considered an introduced species in parts of coastal eastern and southern Australia and is thought to be absent in the wild. From our research and reviews of

previous records of this mite species based on published reports and the examination of museum specimens, we show that the snake mite has been collected on wild hosts at several localities in at least two states in Australia and it is therefore not restricted to reptiles in captivity. Herein we confirm sleepy lizards (*Tiliqua rugosa*) as competent hosts of this mite and also illustrate from our experience how easily this exotic pest can be introduced into new localities.

(ID: 135)

Investigating the antimicrobial effect of emerging scabicides on scabies associated pathogens

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With an estimated prevalence of 300 million cases worldwide, scabies is amongst the most common infectious skin disease worldwide. In tropical areas where prevalence is high there is an established link with severe secondary bacterial infections. Scabies mites have been shown to promote the growth of opportunistic pathogens. We aim to provide the fundamental knowledge required to deliver better treatment outcomes to patients, and to understand the role scabies mites play in severe secondary bacterial infections. This research used the broth microdilution method to investigate the antimicrobial effects of emerging scabicides on the most relevant pathogens associated with scabies infections. Minimum Inhibitory Concentration and the Minimum Bactericidal Concentration of these drugs were determined for 3 strains each of *Staphylococcus. aureus, Streptococcus. pyogenes and Acinetobacter. baumannii.* We found that Manuka Oil, and its Beta-Triketones exhibit antimicrobial activity on *S. aureus, S. pyogenes* and *A. baumannii.* The MIC for these pathogenic bacteria are >10 x lower than the effective concentration for scabies mites and eggs. The emerging head lice treatment Abametapir also exhibited antimicrobial activity against gram positive bacteria, however, had limited effectiveness on gram negative bacteria.

(ID: 138)

Abametapir – a potential new scabicide targeting metalloproteases in *S. scabiei* mites and eggs.

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Scabies is a highly contagious skin disease in humans caused by *Sarcoptes scabiei* var *hominis* mites. Therapeutics are the only option to control the disease. Prevailing drugs are neuro-inhibitors targeting single parasite proteins in motile stages. Hence, they have sub-optimal efficacies and require repeat treatments. Patient incompliance to repeat treatments and prolonged drug use have led to emerging parasite drug resistance. Abametapir is a FDA approved ovicidal lousicide with metal chelating properties capable of inhibiting multiple enzymes and pathways requiring metal ions as co-factors. We discovered good miticidal and exceptional ovicidal activity of abametapir against *S. scabiei in-vitro.* Our objective is to identify the molecular targets and validate Abametapir as a new scabicide with novel modes of action(s). Zymography studies using mite and egg extracts indicated metalloprotease activity inhibition in abametapir-treated gels. Higher metalloprotease activity observed in egg extract compared to mite extract could explain the drug's higher ovicidal activity over its miticidal activity. We will narrow down the targeted metalloprotease(s) by testing a series of metalloprotease substrates. Finding multiple enzymes/pathways being affected by abametapir would be an advantage over currently used single-target treatments, which are prone to drug resistance.

(ID: 161)

Ultrastructure and functions of nuclear microtubules in *Plasmodium falciparum* gametocytes

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Plasmodium falciparum is the most prevalent and fatal species among human malaria parasites. The parasite has a complex lifecycle in its human host, including asexual and sexual stages. The sexual-stage parasites (gametocytes) undergo a dramatic morphological change during their maturation. The shape-changing ability of gametocytes is regulated by their cytoskeletons, with microtubules playing a crucial role. We have identified an unusual microtubule-based structure in the nucleus of early-stage gametocytes that emanates from a microtubule organizing center (MTOC) associated with the nuclear membrane. In this project, we aim to study the structure and function of nuclear microtubules in *P. falciparum* gametocytes. To study the structure, we generated live-cell reporters probing nuclear microtubules, MTOC, the kinetochore, and the centromere in gametocytes and asexual blood stages. To obtain functional information, we knocked out the microtubule-associated proteins detecting the effects of their disruption on nuclear microtubule formation and gametocyte function. My work detects insights into an intriguing but overlooked aspect of *P. falciparum* gametocyte biology, and potentially provides new information about cell division.

(ID: 137)

Investigating the antiplasmodial activity and mode of action of the natural product alstonine

Jacinta Macdonald[1], Megan Arnold[1], Madeline Luth[2], Ronald Quinn[1], Elizabeth Winzeler[2], Tina Skinner-Adams[1], Katherine Andrews[1], Gillian Fisher[1]

[1]Griffith Institute for Drug Discovery, Australia; [2]University of California

Malaria causes significant morbidity and mortality, with 229 million cases and 409,000 deaths in 2019. Progress towards the goals of elimination and eradication are threatened by parasite drug-resistance. To combat drug-resistance, therapies that possess modes of action different to current antimalarial drugs are needed. Alstonine, a natural product compound, was recently identified to possess potent antiplasmodial activity against drug sensitive and resistant *P. falciparum* (72h IC_{50} 0.113 – 0.395 µM). This activity is also selective for parasites over human cells (>1500-fold selectivity index). To further understand the antiplasmodial activity of alstonine, we generated *P. falciparum* parasites 20-fold less sensitive to alstonine. We then

sequenced the genomes of three resistant sub-clones, comparing data to a wild type parental clone. These data identified a mutation and copy number variation in the gene encoding MPV17, a putative inner-mitochondrial membrane protein. Approaches to investigate the role of MPV17 in mediating alstonine-resistance will be discussed.

(ID: 209)

Quantifying appetite suppression in livestock during nematode infection

Fazel Almasi, Michael Stear

Agribio, Department of Animal, Plant and Soil Sciences, 5 Ring Road, La Trobe University, Bundoora, Victoria 3086, Australia

Loss of appetite is a major driver of reduced growth in deliberate nematode infection but the importance of inappetence in natural infections is unknown. In this study, accelerometer sensors (n=147) were attached for 26 days to 10-11-months-old Merino sheep grazing naturally infected pasture. Six categories of behaviour were identified: grazing, ruminating, walking, licking, walking and others. There was considerable variation among animals and among days. The best-fitting distribution for both males and females was the Box-Cox t distribution. The distribution of time spent grazing was symmetrical and unimodal in males, and quite similar to a normal distribution, but the distribution in females had a prominent left skew. Quantifying the variation in grazing behaviour is an essential step towards a detailed understanding of parasitic infection and a better understanding of variation in grazing behaviour will help the development of mechanistic models to improve animal health and productivity.

(ID: 207)

Exploring novel insights of the *Plasmodium vivax* sporozoite proteome

Caitlin Bourke[1,2], Samantha Emery-Corbin[1,2], Anthony Ruberto[3], Amélie Vantaux[4], Benoit Witkowski[4], Ivo Mueller[1,2], Aaron Jex[1,2]

[1]WEHI, Australia; [2]Department of Medical Biology, University of Melbourne, Australia; [3]Malaria: Parasites and Hosts, Institut Pasteur, France; [4]Institut Pasteur du Cambodge, Kingdom of Cambodia

Plasmodium vivax has both acute infections and a clinically silent dormant phase in hepatocytes. The mechanisms that drive this cell-fate decision between schizogony and dormancy in the liver is unknown. The sporozoite transitioning from invertebrate to human host is a particularly important transition as this precedes hepatocyte infection, where hypnozoites form. Translational repression has been shown to be essential as the sporozoite enters the human host and for active liver schizogony, but we hypothesise translational repression may help determine the sporozoite's active or dormant cell fate upon liver infection. Therefore, understanding what proteins are present or absent relative to the sporozoite's transcriptional profile is particularly important. To reduce mosquito contamination and improve proteome depth and coverage, we have explored sample purification methods, and compared offline and online fractionation methods, specifically high-field asymmetric waveform ion mobility spectrometry (FAIMS). To date, we have identified over 2000 *P. vivax* proteins with three-quarters of the peptides derived from *P. vivax*. This provides a critical resource and methodology as we explore the functional proteome of *P. vivax* sporozoites and the possible hypotheses of hypnozoite formation.

(ID: 126)

Prevalence and molecular characterization of cattle ticks in Burundi: First report on the presence of the invasive *Rhipicephalus microplus* tick

Lionel Nyabongo[1], David Odongo[1], Gad Milton[2], Eunice Machuka[3], Patrick Vudriko[4], Roger Pelle[3], Esther Kanduma[5]

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Tick vectors cause direct and indirect economic losses including exsanguination, transmission of animal pathogens and cost related to control of ticks and tick-borne diseases (TTBDs). Detailed information about tick species distribution and genetic diversity in Burundi is outdated and limited.

A cross-sectional study was conducted in 24 districts of Burundi. Identification and characterization of tick species was conducted using morphological keys and molecular tools (cox1 and 12S rRNA gene).

Six species of ticks were observed from all the studied regions. *R. appendiculatus* ticks were the most prevalent ticks (~45%). This study reported for the first time the presence of *R. microplus* in Burundi. Two cox1 haplotypes of *R. microplus* which clustered into the Clade A were observed. The overall proportion of *R. microplus* was 28.5% (138/483) and its predicted suitable habitat were the central highlands, suggesting an emergent threat for cattle farmers**.** *R. sanguineus* and *R. evertsi evertsi* ticks, the vectors of numerous zoonotic pathogens, were identified on cattle. These findings reveal a high genetic diversity and an overlapping distribution of tick species in Burundi. The design of TTBDs control strategies need to take into consideration the presence of the invasive *B. microplus* tick in Burundi.

(ID: 125)

Development of highly sensitive one step-PCR for improved detection of *B. bigemina* and *B. bovis*.

Martina Paoletta[1], Sofía de la Fournière[1], Eliana Guillemi[1], Néstor Sarmiento[2], Pablo Donati[3], Silvina Wilkowsky[1], Marisa Farber[1]

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Bovine babesiosis caused by *Babesia bigemina* and *B. bovis* is an economically relevant tick-borne disease distributed worldwide. Animals that recover from clinical disease are epidemiologically important since they remain persistently infected being a source of infection to others. Their minimum levels of parasitemias are a challenge for detection. The recommended

molecular diagnosis test for both species is a nested (nPCR) based on the amplification of the *rap-1* gene. To minimize costs and risks that nPCRs imply, we developed a single-step PCR for each species based on the multi-copy *ves-1α* gene (VESA PCRs). We achieved detection limits of $1x10^{-12}$% parasitemia for *B. bigemina* and $1x10^{-6}$% for *B. bovis* using reference strains, resulting in an improvement in sensitivity. When applying VESA PCRs in field samples we detected a significantly higher proportion of positive animals compared to the reference nPCRs. Concordance between both diagnostic schemes (Cohen's kappa coefficient) showed minimal to non-agreement since VESA PCRs have a significantly higher detection capacity. In conclusion, the high sensitivity of the assay, and the lower demand of time and reagents make the VESA PCR methods a valuable diagnostic tool for the molecular detection and epidemiological survey of both *Babesia* pathogens.

Symp7: Symposium7

Time: Friday, 25/June/2021: 12:00pm - 12:45pm
Session Chair: Deborah Holt, Charles Darwin University

(ID: 127)

A kinase that coordinates nuclear abscission in the malaria parasite *Plasmodium falciparum*.

Ben Liffner, Sabrina Absalon
Indiana University School of Medicine, Department of Pharmacology and Toxicology, United States of America

Apicomplexa, a phylum of parasitic unicellular eukaryotes, exhibits extraordinary diversity in their mechanisms of cellular division. *Plasmodium falciparum,* the deadliest cause of malaria in humans, undergoes alternative rounds of DNA replication and nuclear divisions followed by a single round of cytokinesis. This division strategy, known as schizogony, allows a single parasite to form approximately 30 daughter parasites every 48 hours. Despite the biological and therapeutic attractiveness of this division strategy, little is known about the proteins that coordinate this process. Here, we identify a protein we term Nuclear Envelope Assembly Protein interacting kinase (NEAPik) that was identified as an interacting partner of NEAP, a protein involved in nuclear envelope stability. Using super-resolution microscopy, we show that NEAPik has a dual localisation as it shows both a pericentromeric localisation and localises to the cleavage furrow of dividing nuclei. Inducible knockdown of NEAPik results in a severe growth defect, with NEAPik depleted parasites able to perform karyokinesis, but unable to undergo nuclear abscission, resulting in the formation of parasites with multiple conjoined nuclei. These findings begin to uncover molecular detail of the poorly explored biology of apicomplexan cell division and highlight a potential target for therapeutic development.

(ID: 155)

Apicoplast derived metabolites are essential for the biosynthesis of glycophosphatidylinositol anchors and egress of asexual stage *Plasmodium falciparum*.

Michaela Bulloch, Kit Kennedy, Julie Ralton, Long Huynh, Malcolm McConville, Stuart Ralph
University of Melbourne, Australia

The addition of glycophosphatidylinositol (GPI) anchors represents an important means by which proteins associate with biological membranes. During the asexual cycle, *Plasmodium falciparum* parasites anchor a selection of proteins to the surface of their daughter cells (merozoites) using GPI-anchors, and these proteins are thought to be required for both parasite egress and reinvasion. Notable among these is merozoite surface protein 1 (MSP1), which has an established function in destabilizing the host cell cytoskeleton, contributing to its rupture and the release of daughter parasites. The synthesis of GPIs is dependent on dolichol-phosphate to donate mannose residues, and dolichols themselves are believed to derive from isoprenoid precursors synthesised in the *Plasmodium* apicoplast. We found that treatment of *Plasmodium* parasites with apicoplast inhibitors decreases abundance of isoprenoid and GPI intermediates and untethers GPI-anchored proteins from their normal membrane association. This detachment results in the mis-localisation of surface GPI-anchored proteins to the parasitophorous vacuole. These GPI-deficient parasites experienced an egress defect, presumably due to the loss of surface-bound MSP1. Our data provides further evidence for the importance of GPI biosynthesis during the asexual cycle of *P. falciparum*, and suggests that GPI biosynthesis, and therefore egress, is dependent on isoprenoids synthesised in the apicoplast.

(ID: 219)

CRISPR gene knockout targeting *Ov*-GRN-1 in the carcinogenic liver fluke, *Opisthorchis viverrini*, reducing hamster pathogenesis

Michael Smout
JCU, Australia

Parasitic worms are large, invasive pathogens. The Thai liver fluke, *Opisthorchis viverrini,* induces such extensive immunopathology and protracted wound healing in chronic infections lasting decades that it causes cancer. With CRISPR gene editing techniques we have successfully knocked down the fluke's *Ov*-GRN-1 expression in the 60-day infection hamster model and show a range of reduced pathogenesis. Now we have further improved the CRISPR gene editing efficiency of *Ov*-GRN-1, the helminth wound healing growth factor. This presentation will explore this parasitic gene knockout with a carcinogenic hamster infection model that uses a sub-carcinogenic dimethylnitrosamine dose with 24 weeks of parasite infection. Gene expression has been successfully reduced by 78.5% and hamster liver pathogenesis will be detailed. Highlights include 79.1% reduced bile duct cell proliferation, and 87.7% reduction in p53 positive cells, both markers of pathogenesis. While we have previously built evidence for the pathogenic role of *Ov*-GRN-1, this is the first direct evidence of reduced carcinogenicity from parasites with reduced gene expression of *Ov*-GRN-1. Our model shows that efficient CRISPR gene editing of helminths is feasible and will be a powerful tool to explore parasite gene function across wide ranging species in the future.

CP7: Contributed Papers 7

Time: Friday, 25/June/2021: 12:45pm - 1:00pm
Session Chair: Deborah Holt, Charles Darwin University

(ID: 151)

Cross-predicting essential genes between two model eukaryotic species using machine learning

Tulio Campos, Pasi Korhonen, Neil Young
Department of Veterinary Biosciences, Melbourne Veterinary School, Faculty of Veterinary and Agricultural Sciences

Experimental studies of *Caenorhabditis elegans* and *Drosophila melanogaster* have contributed substantially to our understanding of molecular and cellular processes in metazoans at large. Since the publication of their genomes, functional genomic investigations have identified genes that are essential or non-essential for survival in each species. Recently, a range of features linked to gene essentiality have been inferred using a machine learning (ML)-based approach, allowing essentiality predictions within a species. Nevertheless, predictions between species are still elusive. Here, we undertake a comprehensive study using ML to discover and validate features of essential genes common to both *C. elegans* and *D. melanogaster*. We demonstrate that the cross-species prediction of gene essentiality is possible using a subset of features linked to nucleotide/protein sequences, protein orthology and subcellular localisation, single-cell RNA-seq, and histone methylation markers. Complementary analyses showed that essential genes are enriched for transcription and translation functions and are preferentially located away from heterochromatin regions of *C. elegans* and *D. melanogaster* chromosomes. The present work should enable the cross-prediction of essential genes between model and non-model metazoans.

(ID: 191)

Understanding antigen diversity and immune selection targets of leading *Plasmodium vivax* vaccine candidates and sero-surveillance markers

Paolo Bareng[1,2], Myo Naung[1,2,3,4], Somya Mehra[1,2], Alyssa Barry[1,2,3,4]
[1]Institute for Mental and Physical Health and Clinical Translation (IMPACT), School of Medicine, Deakin University, Geelong, Victoria, Australia; [2]Life Sciences Discipline, Burnet Institute, Melbourne, Victoria, Australia; [3]Division of Population Health and Immunity, Walter and Eliza Hall Institute of Medical Research, Parkville, Victoria, Australia; [4]Department of Medical Biology, University of Melbourne, Carlton, Victoria, Australia

One of the major gaps in *Plasmodium vivax (Pv)* research is the lack of information on the diversity of surface antigens, which could provide relevant details on vaccine development against *Pv*. Population genetics can not only assess transmission intensity but also provide insights in detecting genes under immune selection. We, therefore, aimed to determine the global distribution of antigen diversity and identify gene regions with signature of immune selection amongst leading *Pv* vaccine candidate antigens and sero-surveillance markers. Several signatures of diversity and balancing selection were measured based on published sequences from multiple geographic populations. Genetic relatedness of the sequences was visualized through haplotype network diagrams. Furthermore, sequences were mapped onto experimentally defined three-dimensional protein structures to analyze spatially derived nucleotide diversity and immune selection. Initial results showed low nucleotide and haplotype diversity in *P. vivax* antigen genes *rama, msp1*$_{19}$, and *csp*. In contrast, high diversity was observed in genes *rbp1a, rbp2b, dbp*RII, and *ama1*. Lastly, spatially-derived nucleotide diversity and Tajima's D were similar between different geographic populations suggesting that gene regions targeted by protective antibodies are potentially consistent across different populations. Information from this study will guide researchers in designing widely effective vaccines and serological tools against *Pv* parasites.

(ID: 184)

The identification of addiction to a human kinase inhibitor in *Plasmodium falciparum*

Tayla Williamson[1], Jack Adderley[1], Sarah Jackson[2], Chrsitian Doerig[1]
[1]Centre for Chronic Infectious and Inflammation Disease, Biomedical Sciences Cluster, School of Health and Biomedical Sciences, RMIT University, Bundoora VIC 3083, Australia; [2]Infection and Immunity Program, Biomedicine Discovery Institute and Department of Microbiology, Monash University, Clayton VIC 3800, Australia

Malaria parasites have become resistant to all current therapeutics, necessitating the development of novel treatment strategies. Host-Directed Therapy is a promising approach, as it deprives pathogens of the most direct pathway to resistance, namely the selection of genotypes encoding mutated targets under drug pressure. Previous studies have identified that *Plasmodium falciparum* relies on the activation of host erythrocyte protein kinases for its own proliferation and survival, in particular the mitogen-activated protein kinase kinase 1 (MAPKK1 or MEK1). Trametinib, a highly selective MEK1 inhibitor approved to treat melanoma, has shown inhibition of parasite proliferation *in vitro* with low nanomolar potency, consistent with the observation that MEK activity is required for parasite survival. Unexpectedly, we found that *P. falciparum* can rapidly gain resistance to Trametinib, showing a 100-fold increase in the IC_{50}. Fascinatingly, some of these parasites display not only resistance but also dependency to Trametinib, with optimal growth at a concentration of 200nM (10-fold above the parasites wildtype IC_{50}). We have now shown that the dependency phenotype is lost rapidly following Trametinib removal, raising interesting questions regarding the molecular basis for this phenotype. This work provides novel insights into the complexity of host-pathogen interactions between human erythrocytes and *P. falciparum*.

Symp8: Symposium8

Time: Friday, 25/June/2021: 1:45pm - 2:30pm
Session Chair: Clare Anstead, University of Melbourne

(ID: 216)

Development and use of 360-degree imaging and a virtual reality interface for veterinary education

Stuart Barber
Melbourne Veterinary School, Faculty of Veterinary and Agricultural Science, University of Melbourne, Australia

Most students in Australian veterinary schools come from non-farming backgrounds. Schools without preferential farming background selection processes report more than 80% of students come from urban backgrounds, similar to the overall Australian population demographic. This presents a challenge in early veterinary education to assist student understanding of the production systems and environment in which animal production and disease occurs. In 2011 we commenced working on building virtual properties for students to see what happens on an enterprise, both across the property at a particular time and also throughout the year. Over the past ten years hardware (cameras) and software have improved in ease of use, and have reduced cost and time required to develop outputs. We have developed 12 enterprises across Australasia as virtual farms that students are able to virtually visit on-line. This presentation will cover image collection, virtual farm design and integration into a learning management system for teaching and assessment. Virtual enterprises can add the ability for students to prepare for and reflect on visits to real properties maximising the benefit of these visits as well as providing options for online education where visits are not possible due to cost, biosecurity or a pandemic.

(ID: 112)

Con-FeS-ions of *Tg*ApiCox13, a novel iron-sulfur protein of the mitochondrial electron transport chain of *Toxoplasma gondii*

Jenni Hayward, Rachel Leonard, Giel van Dooren
Research School of Biology, Australian National University, Canberra, ACT, Australia

Toxoplasma gondii infects approximately a third of humans worldwide and causes the disease toxoplasmosis. The mitochondrial electron transport chain (ETC) is critical for *T. gondii* proliferation and is the target of anti-parasitic drugs. The ETC consists of several protein complexes that maintain mitochondrial membrane potential and generate energy. The ETC complexes of *T. gondii* differ considerably from human equivalents. *T. gondii* Complex IV is twice the mass and contains additional subunits not found in human Complex IV, including the 13 kDa protein *Tg*ApiCox13. Curiously, *Tg*ApiCox13 is homologous to a human iron-sulfur (Fe-S) cluster-containing protein called MiNT which is not part of Complex IV in humans. Here, we establish that *Tg*ApiCox13 is a critical component of *T. gondii* Complex IV, and is required for complex activity and stability. Furthermore, we demonstrate that the predicted Fe-S cluster binding sites of *Tg*ApiCox13 are necessary for ETC function. Fe-S clusters play crucial roles in electron transfer processes in ETC Complexes II and III, but have not been previously shown to occur in Complex IV. Our findings provide the first example of a Fe-S cluster protein in Complex IV of any organism, and highlight an important difference between the ETC of parasites and their hosts.

(ID: 114)

Schistosoma mansoni cercariae tegument-anchored proteins that facilitate host interaction and infection

Conor Fogarty[1], Tianfang Wang[1], Scott Cummins[1], Russell Wyeth[2], Donald McManus[3], Mary Duke[3]
[1]University of the Sunshine Coast, Australia; [2]St. Francis Xavier University; [3]QIMR Berghofer Medical Research Institute

Schistosoma mansoni is a widespread etiological agent of human schistosomiasis and threat to public health and socioeconomic wellbeing in developing nations. Due to shortcomings in praziquantel mass drug administration, alternative control approaches are being investigated. One such approach is the prevention of the free-swimming stage, cercariae, from penetrating mammalian host skin. Improvements in multi-omic technology have enabled increasingly detailed elucidation of underlying biological and molecular mechanisms of cercariae host infection. In this study a proteomic analysis of *S. mansoni* cercarial tegument-anchored proteins was performed. Protein identification involved annotation using transmembrane domain, signal peptide and protein domain analyses. The most significant finding was a pX2 purinoreceptor subunit. Because this protein has been characterised as sensitive to zinc and calcium, behaviour bioassays were conducted using zinc and calcium sulphate. Calcium sulphate did not produce any changes in cercariae behaviour in the short-term or long-term. In contrast, zinc sulphate produced both short-term excitation and long-term acceleration of cercariae tail separation. This suggests that zinc from mammalian skin may function as an excitation agent to *S. mansoni* cercariae. In summary, this study identified tegument-anchored proteins which may function as targets to interfere with *S. mansoni* cercarial infectivity.

CP8: Contributed Papers 8

Time: Friday, 25/June/2021: 2:30pm - 2:45pm
Session Chair: Clare Anstead, University of Melbourne

(ID: 213)

In vitro selection of *Giardia duodenalis* for Albendazole resistance identifies a β-tubulin mutation at amino acid E198K

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Benzimidazole-2-carbamate (BZ) compounds, including Albendazole (Alb), are widely used as anthelmintic, anti-fungal drug and are one of two limited drug classes to treat Giardiasis. In helminth and fungi, the mode of action (MOA) of BZ was showed to inhibit microtubule polymerization by binding to the tubulin dimer interface overlapping the colchicine binding site (CBS) of β-tubulin. Besides, point mutations at F167, E198 and F200 in β-tubulin are been proved. However, MOA and resistance mechanisms are presumed but not proven in *Giardia*, and no mutations in β-tubulin have been reported in association with Alb resistance (AlbR).

Hererin, we first found that our culture derived *Giardia* AlbR line is cross-resistant to other 13 BZ compounds and augments its resistance against 7 Alb analogues with increasing thiol substituents length by *in vitro* drug-susceptibility screening; then we revealed the Alb-β-tubulin interaction in *Giardia* partially overlaps the CBS and corresponds to residues associated with BZ-resistance in helminths and fungi. Lastly, a single nucleotide polymorphism in β-tubulin resulting in a mutation from glutamic acid to lysine at amino acid 198 (E198K) was identified in AlbR line by amplicon sequencing. This work provides new insight into *Giardia* AlbR and new avenue to clinical diagnosis and microtubule-inhibitor development.

(ID: 128)

The conduct of acaricide efficacy trials in Australia with highlight on the Australian Paralysis Tick (*Ixodes holocyclus*)

Florian Roeber
Invetus Pty Ltd, Australia

Data generated during acaricide efficacy trials, including dose confirmation and field studies, is essential for the registration of new ectoparasiticides in most developed countries. Specific guidelines for the conduct of such studies have been described by the W.A.A.V.P. and are being used by government regulators around the world. In Australia, the tick species *Rhipicephalus microplus*, *R. sanguineus*, *Haemaphysalis longicornis* and *Ixodes holocyclus* are of greatest veterinary significance. *Ixodes holocyclus* is of particular importance because it has very high pathogenic potential and every year ~10,000 domestic animals are presented to veterinarians with symptoms of tick toxicosis. This tick is exclusive to the Australian environment and has a specialized life cycle that involves native wildlife hosts which complicates the laboratory propagation of this species and currently no laboratory colony exists. For animal welfare reasons, and to reduce the incidence of tick toxicosis in untreated control animals during these trials, animals need to be 'immunized' with increasing numbers of ticks in the lead-up to such studies. Here we describe the conduct of specialized *I. holocyclus* efficacy trials at our Australian research facility. Furthermore, we discuss the challenges associated with the supply, storage and infestation procedure during *I. holocyclus* efficacy trials.

(ID: 100)

Parasites Online!

Lisa Jones[1], Sarah Preston[2], Coralie Boulet[3], Rina Fu[4], Michelle Power[5], Katherine Andrews[6], Shokoofeh Shamsi[7], Danny Wilson[8], Juan Miguel Balbin[8], Tina Skinner-Adams[6], Cameron Raw[9], Katja Fisher[10], Christina Spry[11]
[1]Australian Society for Parasitology; [2]Federation University; [3]Burnet Institute; [4]Edith Cowan University; [5]Macquarie University; [6]Griffith University; [7]Charles Sturt University; [8]University of Adelaide; [9]University of Melbourne; [10]QIMR Berghofer; [11]Australian National University

The Australian Society for Parasitology hosted "Parasites Online", 26 live events and one competition, on Facebook across National Science Week 15th – 23rd August 2020. Five of the events were AUSLAN interpreted and one was a Sensory Science show for special needs audiences. All events were broadcast live through the ASP Facebook page and scientists were available at the time to respond to any audience questions during the livestream or afterwards. Different delivery styles were used to cater to different audience types, all had an interactive component including; interactive workshops; hands-on science demonstrations; book readings; singing; dancing; quiz questions; playing augmented reality and other interactive games; watching experiments and then responding to science questions about the results; asking scientists questions live; creating artwork; and engaging in a science workshop that includes resources sent to the participants. This was the first time that the ASP has run such a large-scale live program of outreach events using Zoom and Facebook live. Eleven research groups delivered Parasites Online events during National Science Week 2020. An audience of 451 people watched the events live. The total minutes of videos viewed was 22507 with 12242 people having 3-sec views, 1743 engagements (comments/reactions) and 144 video shares.

Symp9: Symposium9

Time: Friday, 25/June/2021: 3:00pm - 3:30pm
Session Chair: Mike Gardner, Flinders University

(ID: 131)

Parasitic diseases in a climate crisis

Coralie Boulet
Burnet Institute, Australia

Since the Industrial Revolution, humans have emitted enough carbon dioxide that the atmospheric concentration is reaching a peak never experienced in 800,000 years. This increase of greenhouse gases leads to global warming; in less than 140 years, we have increased global average temperatures by 1.2°C. Although 196 countries have signed the Paris agreement, thus pledging to limit global warming “well below 2°C, preferably to 1.5°C”, only one country has policies in place compatible with a 1.5°C trajectory. Some models now predict that average warming over Australia could reach +7°C by the end of the century. In this context, what does this mean for parasitic diseases affecting humans? This talk will outline various factors impacting the prevalence and the morbidity of parasitic diseases worldwide. The first obvious factor is heat, influencing the distribution of vectors as well as human bodies’ capacity to function healthily. We will also explore the impact of increased extreme weather events, the likely consequences of increased poverty and conflicts, of food shortages, and of mass population movements. This presentation will investigate malaria, river blindness disease, helminth-infections and more. Note that this is not my original research, but rather a literature review.

(ID: 122)

From lumping to splitting and back again: on the evolution of species delineation philosophy in marine trematodes

Daniel Huston
CSIRO, Australia

Prior to widespread use of DNA sequencing, trematode taxonomists had little other than morphology for testing species boundaries. Host and geography have always been recognised as important, yet the prevailing pattern of the pre-molecular era was lumping of morphologically similar forms under single-species concepts, in many cases across great geographic range and unrelated hosts. The use of DNA sequencing greatly enhanced the ability of taxonomists to delineate morphologically similar forms into different species but also revealed an additional complicating phenomenon: cryptic species. The existence of genetically distinct, but morphologically indistinguishable species has gained widespread acceptance in trematode taxonomy and the number of cryptic species described has increased significantly over the last decade. However, it is possible that cryptic species designations are being applied too loosely as many are based on collections limited in geographic scope and in choice of molecular marker. Emerging data from several marine trematode lineages indicate that some species can occur across vast geographic range and that the intraspecific genetic variation found between populations of such species can easily be misinterpreted as interspecific variation, and in many cases likely has. This has major implications for understanding trematode biodiversity, and likely that of most other marine parasites.

CP9: Contributed Papers 9

Time: Friday, 25/June/2021: 3:30pm - 3:45pm
Session Chair: Mike Gardner, Flinders University

(ID: 169)

Decloaking the blackbox: Interpretable machine learning and parasites

Nicholas Fountain-Jones
University of Tasmania, Australia

I provide a guide to the latest advances in statistical machine learning to construct parasite exposure models and species distribution models that automatically incorporate complex nonlinear relationships with minimal statistical assumptions from data with missing d values. Our approach compares multiple machine learning algorithms in a unified environment to find the model with the best predictive performance and uses game theory to better interpret results. We apply this framework to African lion parasite data as well as to thermal tolerance data of kissing bugs (Reduviidae: Triatominae): the key vector for chagas disease (*Trypanosoma cruzi*).

Our modelling approach provided enhanced predictive performance compared to more traditional approaches, as well as new insights into parasite distributions and vector thermal limits. We were able to efficiently capture and visualize strong nonlinear patterns, as well as model complex interactions between variables in shaping exposure risk from CDV and feline parvovirus. For example, we found that lions were more likely to be exposed to CDV at a young age but only in low rainfall years.

When combined with our data calibration approach, our framework helped us to answer questions about pathogen exposure risk that are difficult to address with previous methods.

(ID: 146)

Super-resolved view of PfCERLI1, a rhoptry associated protein essential for *Plasmodium falciparum* merozoite invasion of erythrocytes

Sonja Frolich
The University of Adelaide, Australia

Invasion of human erythrocytes by *Plasmodium falciparum* merozoites involves the coordinated release of ligands from specialised organelles, the micronemes and rhoptries, which secrete parasite proteins onto host red blood cell (RBC) to prime attachment, mechanical entry and establishment of parasitophorous vacuole. Data to date suggests that prior to RBC entry, the two rhoptries fuse to the merozoite plasma membrane before neck contents can be released and the irreversible point of attachment to the RBC forms (the tight-junction). As invasion proceeds, fusion of the two rhoptries commences at the neck and continues to the bulb before the structure partially collapses to facilitate release of rhoptry bulb contents. Despite the importance of the protein network orchestrating the rapid multi-step, process of rhoptry secretion, the proteins involved are largely uncharacterised. Recently, we utilised knockdown studies, biochemical assays and quantitative super-resolution microscopy and identified an essential role for the conserved protein *P. falciparum* Cytosolically Exposed Rhoptry Leaflet Interacting protein 1 (PfCERLI1) in rhoptry function and merozoite invasion. While further studies are required to determine exactly how PfCERLI1 knockdown causes these changes in rhoptry function, use of semi-automated quantitative immunofluorescence microscopy highlights how this powerful tool can be used to study RBC invasion.

(ID: 103)

Shifts in genetic diversity of *Cryptosporidium* species in WA patients over the last decade: Four major outbreaks, three different stories.

Alireza Zahedi, Kamil Braima, Josephine Ng-Hublin, Una Ryan
Murdoch University, Australia

In Australia, data from the National Notifiable Diseases Surveillance System shows that cryptosporidiosis outbreaks occur every few years. To better understand the nature of cryptosporidiosis outbreaks in Western Australia, epidemiological and genomic data from three most recent cryptosporidiosis outbreaks were compared. The 2007 outbreak was the largest (n=608) compared with the outbreaks in 2011(n=449), 2017 (n=400) and 2020 (n=495). The 2007, 2011 and 2020 outbreaks appeared to have occurred predominantly in the metropolitan area, while highest number of cases in 2017 outbreak were observed in remote areas. In all outbreaks, the highest number of cryptosporidiosis notifications was observed in the 0-4 years age group and *C. hominis* was the most predominant species detected. Subtyping at the *gp60*locus identified subtype IbA10G2 in 46.3% and 89.5% of *C. hominis* isolates typed, respectively, in the 2007 and 2011 outbreaks, while in the 2017 and 2020 outbreaks, two emerging subtypes; IfA12G1R5 (52%) and IbA12G3 (92%) were the most dominant *C. hominis* subtype reported respectively. Until recently, subtype IfA12G1R5 and IbA12G3 were relatively rare subtypes, and have been previously identified only in a few sporadic cryptosporidiosis cases in WA but this is the first time they have emerged as outbreak subtype in Australia.

ST3: Short talks: 3-minute presentations 3MT style day 3

Time: Friday, 25/June/2021: 4:00pm - 5:15pm
Session Chair: Michelle Clark, The Walter and Eliza Hall Institute of Medical Research

Speed Talks! Each presenter has three-minutes to showcase their data. 3MT style presentations, one-slide and three minutes to spruik your research! Check out the abstract uploads for more information from the researcher.

(ID: 134)

Antibodies as Serological Markers of *Plasmodium vivax* Infections in Moderate Transmission Settings

Yanie Tayipto[1,2], Jason Rosado[3], Donicia Gamboa[4], Herbert Opi[5], James Beeson[5], Leanne Robinson[1,5], Ivo Mueller[1,2,3], Rhea Longley[1,2]

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Plasmodium vivax has a dormant stage in its human lifecycle, which is undetected using current diagnostic tools. Untreated individuals that are recently exposed to infection, become reservoirs of transmission. Our laboratory has developed an 8-antigen panel of serological markers that can detect *P. vivax* exposure within the prior 9 months in low endemic areas. However, the performance of this panel is poorer in moderate endemic areas, most likely because total IgG is longer-lived in higher transmission settings. In this study, we aimed to adapt our serological marker tool by identifying and applying a shorter-lived antibody biomarker. We first measured antibody kinetics (total IgG, IgG1, IgG3, IgM and C1q-binding antibodies) over 36 weeks following asymptomatic *P. vivax* infection in PNG children (n=31). IgG3 and C1q-fixing antibodies declined faster to background level, while total IgG, IgG1 and IgM were maintained over time. We then assessed IgG3 performance in classifying recent exposure in a cohort of Peruvian individuals (n=590). IgG3 was shown to be a poor marker of recent *P. vivax* infections in the Peruvian cohort. We are now further exploring factors that impact the acquisition and decay of IgG3 in moderate transmission settings, such as age and the level of past exposure.

(ID: 167)

Impact of *Trypanosoma cruzi* strain on the *in vitro* activity of compounds

Melissa Louise Sykes, Vicky Marie Avery
Discovery Biology, Griffith University, Australia

Chagas disease, caused by *Trypanosoma cruzi*, is endemic to 21 countries in the Americas and results in approximately 12, 000 deaths per year. Treatment of Chagas disease is restricted to the drugs benznidazole and nifurtimox, which show variable efficacy and cause adverse side effects. To identify compounds with improved safety and efficacy profiles, *T. cruzi* drug discovery campaigns frequently incorporate a diverse panel of *T. cruzi* strains to assess compound activity. To investigate if parasite strain influences the *in vitro* activity of compounds, we tested the sensitivity of a selection of compounds and drugs with known anti-*T. cruzi* activity against the Tulahuen strain, against an expanded panel of *T. cruzi* strains. We utilised the same host cell and multiplicity of infection for each strain to minimise the influence of experimental methodology on results. To determine if the method of analysis influenced results, analysis utilising the number of infected cells was compared to the number of parasites per well. Despite investigating diverse compound classes and methods of analysis, no significant differences in compound activity or efficacy were observed across strains. Hence, variation in laboratory adapted strains *in vitro* may not be essential in drug discovery, as has previously been suggested.

(ID: 162)

Determinants of parasite diversity and community structure in waterbirds

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Several studies have been conducted on the determinants of parasite species richness. Although host body size, host geographical range size, and host population density appear to be the significant determinants, further comparative tests are required. Such ecological and environmental factors are often intercorrelated and not independent of each other. Avian fauna often presents a uniqueness in ecological adaptation according to niche habitat, foraging technique and diet. In waterbirds, foraging techniques can be varied including shoreline mud pickers shallow water filter feeders, and deep-water divers. The environment and diet of these groups can influence the structure and diversity of parasite fauna within these groups. Here, a wide range of waterbird cadavers has been collected in cooperation with Western Australia Seabird Rescue, including grebes, terns, cormorants, gulls, gannets, darters, shearwaters, and black swans. Each bird was examined for ectoparasites and gastrointestinal parasites. The parasite data collected will be analysed and compared to each bird species ecological characteristics such as foraging techniques, habitat preference (freshwater, seawater, mixture), and diet (omnivore, herbivore, piscivore). This study will attempt to understand if ecological structures influence parasite community and will provide much needed data on parasite species richness and community structure within waterbirds of Perth Western Australia.

(ID: 154)

Investigating macrocyclic lactone resistance in *Dirofilaria immitis* from Australia

Rosemonde Power, Jan Šlapeta
The University of Sydney, Australia

Canine heartworm disease is caused by the mosquito-borne filarial nematode, *Dirofilaria immitis*. The main strategy for canine heartworm prevention involves the administration of macrocyclic lactone (ML) anthelmintics. However, lack of efficacy (LOE) reports for ML heartworm preventatives have occurred in the Mississippi Delta region of the USA since 2005. These LOE

reports indicate that heartworm populations in the USA have potentially developed ML resistance. With over 5 million dogs living in Australia and canine heartworm disease recently re-emerging in Queensland, an investigation into ML resistance in Australian heartworms is required. However, there are currently no genetic tools available to detect ML-resistant heartworms in Australia. By adopting existing approaches and comparing different techniques, this study will enquire into the existence of ML resistance in heartworms in an Australian context. The objective of this study is to select a simple tool that can serve the veterinary profession and easily screen for ML resistance in the Australian heartworm population. In this presentation, we will reveal the practicality of deploying the microfilaria suppression test, along with genetic testing using five molecular markers previously associated with ML resistance in heartworms from the USA.

(ID: 116)

Zoonotic soil-transmitted helminths in free-roaming dogs from Kiribati, Western Pacific

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Zoonoses caused by hookworms and *Strongyloides* spp. are broadly distributed in tropical and subtropical areas in settings featured by poor sanitation, and in socially marginalized groups. The island of Kiribati is one of the most geographically isolated countries in the world where the effects of poverty and climate change exert a huge toll on the ecology and health system of people and animals in the country. Despite the KIRIBATI–WHO Cooperation Strategy 2018–2022, to date, no information exists on the presence and diversity of zoonotic STHs in free-roaming dogs in Kiribati. In this study we investigated the occurrence of zoonotic STHs in free-roaming dogs (n= 198) using multiplex qPCRs as part of a dog health and population management programmes that aims to seek a sustainable locally driven solution to improving animal health and overpopulation problems. Overall, 96.46% of dogs were positive for at least one zoonotic STH, being 95.45% positive for *Ancylostoma caninum,* 26.26% for *A. ceylanicum,* 16.17% for *A. braziliense*, and 29.8% for *Strongyloides* spp. Here we demonstrate that dogs play a major role in the environmental contamination with zoonotic STHs, and potentially contribute to the disease burden in people from Kiribati.

(ID: 144)

The role of wild deer in the transmission of parasites to livestock in Australia

David Jenkins, Diane Barton

Charles Sturt University, Australia

Deer are exotic to Australia. Eighteen species were introduced in the 1800s, but only 6 have become established. Mainly due to a favourable climate, establishment of sambar and fallow deer in south-eastern Australia has been particularly successful, with their geographical range increasing annually. These deer species are susceptible to infection with a number of important parasite species that can also infect domestic livestock. Recent studies have shown that liver fluke (*Fasciola hepatica*) can be found commonly in wild fallow deer populations and also in sambar deer (*Rusa unicolour*). Lungworm (*Dictyocaulus spp*) has also been found commonly in fallow deer in some areas. These deer species can be found co-existing with domestic livestock in many grazing areas where they also share water sources. They may also be acting as parasite reservoirs and providing an important, constant source of infection for livestock.

(ID: 212)

Immune responses to strongyles in equines with pituitary *pars intermedia* dysfunction

Adelaina Horner[1], Nicholas Bamford[2], Michael Stear[3], David Piedrafita[1], Sarah Preston[1]

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Pituitary *pars intermedia* dysfunction (PPID) is the most commonly diagnosed endocrine dysfunction in equines. PPID results in the over-production of pro-opiomelanocortin (POMC) hormones such as adrenocorticotropin hormone (ACTH). An increase in circulatory hormones leads to clinical signs of PPID, including altered body shape, chronic inflammatory conditions and immunosuppression, which may cause increased helminth infections. Previous research confirmed PPID horses had significantly higher faecal egg counts than age matched control horses (McFarlane et al., 2010 & (Horner et al. unpublished, 2018). Research on causes of immunological dysfunction may result in the increased FEC in PPID horses is limited. This study aimed to compare differences PPID in immune responses to helminths and age matched controls (n=34). Plasma ACTH levels were measured by ELISA, faecal egg counts (FEC) for each horse was estimated with mini FLOTAC and leukocyte populations were quantified using flow cytometry. Spearman correlations indicated that horses with high ACTH had less lymphocytes (r_s= -0.38, p=0.01). Furthermore, horses with low FEC had higher B cells (r_s=-0.36, p=0.01) whereas $CD4^+$ lymphocytes were positively associated with FEC (r_s=0.53, p=0.001) and negatively correlated with B lymphocytes (r_s=-0.84, P=<0.000). To understand these relationships further sera and salivary antibody responses to helminths will be measured.

(ID: 181)

Membranes, monocytes, and malaria: *Plasmodium*-induced breakdown of phospholipid asymmetry leads to phagocytosis of infected erythrocytes

Merryn Fraser[1,2], Weidong Jing[1], Stefan Bröer[1], Florian Kurth[3,4], Leif-Erik Sander[3], Kai Matuschewski[2], Alexander G. Maier[1]

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Lipids are generally distributed asymmetrically in red blood cell (RBC) membranes, with phospholipids such as phosphatidylserine (PS) confined to the inner leaflet of the bilayer. The exposure of PS in the outer layer acts as an 'eat me' signal to phagocytes. In order to systematically analyse how the presence of intracellular *P. falciparum* affects host cells, we examined a series of interconnected molecular processes that influence and are influenced by this membrane asymmetry. We confirmed that membrane asymmetry is disrupted in parasitised RBCs, due to activation of lipid-scrambling proteins in the RBC

membrane. Furthermore, PS exposure in infected RBCs was higher when active regulation was disrupted with an ATP hydrolysis inhibitor, providing evidence that they expend energy to mitigate PS exposure. Infected cells were phagocytosed by human monocytes even without opsonisation, and without *Pf*EMP1, which binds to monocyte receptors. Phagocytosis was lower when exposed PS was shielded with the PS-binding protein Annexin V, confirming a direct role for recognition of this lipid. Together, these findings add to our understanding of the ways that *Plasmodium falciparum* parasites interfere with their host RBCs, and how parasite-induced modifications can contribute to immune cell clearance of infected RBCs, even without adaptive immune responses.

(ID: 199)

Interactions of pro-coagulatory *Sarcoptes scabiei* pseudo-cysteine proteases with human dermatopontin.

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Scabies is a common and highly contagious infectious skin disease in humans with potentially life-threatening sequelae. It is caused by the obligatory parasitic mite *Sarcoptes scabiei* var. *hominis*. Recently, a number of catalytically inactive cysteine-proteases (SMIPP-Cs), were shown to have significant effects on blood clotting. This indicates these proteins may play a role in micro-thrombi formation, which is commonly associated with scabies pathogenesis. When screening a human protein microarray SMIPP-Cs showed a strong binding affinity for the human extracellular matrix protein dermatopontin. In the skin, dermatopontin is thought to regulate collagen and fibrin fibril formation, thereby being directly involved in wound healing processes. An investigation into whether SMIPP-Cs and dermatopontin interact may be crucial for understanding the role of SMIPP-Cs in aiding parasitism in the host. We have shown that the SMIPP-Cs promote fibrin polymerisation by enhancing protofibril formation, and we propose that the interaction with Dermatopontin regulates this process. We will conduct functional blood clotting assays, as well as perform co-immunolocalisation assays and analyse the structure of fibrin clots through histology. We expect SMIPP-Cs and dermatopontin are involved in micro-thrombi formation in scabies patients. Experiments are underway and preliminary data will be presented during the presentation.

(ID: 156)

Development of a diagnostic index to identify nematode-resistant cattle

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La trobe University, Australia

Gastrointestinal nematodes pose a major threat to the health and wellbeing of cattle not only in Australia, but around the world. This problem is now worsening due to global warming, and the increasing development of drug resistance in parasite populations. In Victoria, individual cattle are now dying in situations where deaths previously did not occur. Anecdotal evidence suggests that new blood lines in Hereford and Angus breeds are more susceptible to this problem compared to other traditional populations. Through 4 markers; faecal egg counts, plasma pepsinogen concentrations, blood eosinophil counts and growth rates, we aim to compare host resistance to parasites of individual cattle on two large beef farms located in the Gippsland region, Southern Victoria. These farms were selected because of previous mortalities with brown stomach worm (*Ostertagi ostertagia).* This will be done via generalised linear mixed modelling and the creation of an index of parasite resistance that will combine and standardise these parameters. Eventually, we hope this index will allow farmers to selectively breed nematode-resistant cattle and also identify susceptible animals for treatment.

(ID: 133)

Field application of a novel multiplex qPCR assay reveals the occurrence of the zoonotic hookworm *Ancylostoma braziliense* in Nigerian dogs

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A number of gastrointestinal parasites have been reported from dogs in Nigeria, some of which have zoonotic potential. Of these, hookworms are the most prevalent, with both *Ancylostoma caninum* and *Uncinaria stenocephala* reported in the country. We subjected 203 hookworm microscopy-positive samples of the 885 individual faecal samples collected from dogs in Nigeria to a recently developed multiplex qPCR for the detection of canine hookworm species. The qPCR allowed the detection of *A. caninum* and *A. braziliense* in 81.3% (165/203, 95% CI 75.3-86.1) and 51.7% (105/203, 95% CI 44.9-58.5) of the microscopy-positive faecal samples, respectively and 35.4% (70/203, 95% CI 28.3-41.3) of mixed infections with both hookworm species.

The finding of *A. braziliense* is particularly worrisome given this is an agent of persistent cutaneous larva migrans, commonly referred to as “creeping eruptions” in humans. Although this parasite has been diagnosed in locals and in people travelling in Nigeria, this represent the first molecular identification of *A. braziliense* in its canine reservoir in the country. These results update the occurrence and distribution of hookworm species affecting dogs in Nigeria and validate the ability of a newly developed multiplex qPCR assay as a high-throughput tool for the surveillance of zoonotic hookworms, globally.

(ID: 171)

Immunomodulatory properties of *Schistosoma mansoni* egg-derived exosomes in food allergy

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Food allergy is considered the “second wave” of the allergy epidemic after asthma and allergic rhinitis. The primary forms of therapy for food allergies are avoidance of trigger allergens, and the use of epinephrine for anaphylaxis. With the prevalence of food allergies increasing rapidly in many countries, it is essential to develop new, safe therapeutics. Helminth infections induce modified Th2 immune responses and regulatory T cells and have been shown to confer protection against food allergens. In fact, it was previously demonstrated that *Schistosoma mansoni* infections protect mice against penicillin V-induced anaphylaxis. Due to the deposition of eggs in surrounding tissues, *S. mansoni* infections carry their own risks; however, *S. japonicum* eggs produce exosomes, which play essential roles in intercellular communication host immune response. There has been limited research into the therapeutic potential of helminth-derived exosomes *in vivo*, with most studies focusing on characterizing exosome contents. Therefore, this study aims to assess the safety and effectiveness of *S. mansoni* egg-derived exosomes as a potential therapeutic for tropomyosin allergy and will furthermore provide novel insights into the molecular mechanisms by which *S. mansoni* egg-derived exosomes modulate host immune response.

(ID: 163)

Four polyopisthocotyleans (Platyhelminthes: Monogenea) from carangid fishes in the Mediterranean, off the Algerian coasts

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Four polyopisthocotylean Monogenea were collected from the gill filaments of carangids from off the Algerian coast, southern Mediterranean. Specimens of *Gastrocotyle trachuri* van Beneden & Hesse, 1863 (Gastrocotylidae) and *Cemocotyle* cf. *trachuri* Dillon & Hargis, 1965 (Heteraxinidae) from the Mediterranean horse mackerel *Trachurus mediterraneus* (Steindachner), *Zeuxapta seriolae* (Meserve, 1938) (Heteraxinidae) from the greater amberjack *Seriola dumerili* (Risso) and *Pyragraphorus hollisae* Euzet & Ktari, 1970 (Pyragraphoridae) from the pompano *Trachinotus ovatus* (Linnaeus) are redescribed based on newly collected specimens. Their taxonomically important morphological features (male copulatory organ and clamp sclerites) are described and illustrated, and the morphometric variation between Mediterranean and oceanic specimens is highlighted. Careful examination of the specimens of *Cemocotyle* Sproston, 1946 from the Mediterranean revealed that they exhibited unusual features compared with *Cemocotyle trachuri* Dillon & Hargis, 1965 from the Pacific, mainly the absence of the terminal lappet, thus questioning previous records of this species in the Mediterranean. New geographical locality records are provided for *Z. seriolae* and *P. hollisae*. The presence of *C.* cf. *trachuri* and *Z. seriolae* in the Mediterranean is noteworthy as these monogeneans were initially described in the Pacific Ocean. This study extends the geographical range of *Z. seriolae* to the southern Mediterranean.

(ID: 179)

In vitro acaricidal activity of some plant extracts against *Rhipicephalus microplus*

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Odisha university of agriculture and technology, India

Around the world, the management of tick infestation relies mostly on use of acaricides, which are burdened with problems like high cost, residues and environment pollution, leading to a demand for searching of botanicals. In this study, acaricidal activity of leaves of *Azadirachta indica*, whole plant of *Argemone mexicana*, fruits of *Datura stramonium* and flowers of *Calotropis gigantea* on *Rhipicephalus microplus* were evaluated by Adult Immersion Test(AIT) and Larval Packet Test (LPT). As per result of AIT, ethanolic extracts of *A. indica, A. mexicana*, *D. stramonium* and *C.gigantea* showed significant mortality of 86%, 73.3%, 66.67% and 55.67% respectively at 100 mg/ml concentration . A significant percentage inhibition of oviposition (IO%) observed for the extracts were 92.58, 77. 06, 70.63 and 61.43 while the larval mortality recorded by LPT were 78.67%, 70.67%, 65% and 60.33% % respectively. From the regression equation, the LC_{50} values were found to be 29.21mg/ml, 46.77mg/ml, 61.66 mg/ml and 83.18 mg/ml respectively. Further studies are needed to identify the active ingredients as well as toxic effects present in the plant that caused the mortality of ticks and larva.

(ID: 158)

First molecular characterisation of the haemogregarine parasite *Hemolivia mariae* in the stump-tailed lizard tick (*Amblyomma albolimbatum*) in Western Australia

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Centre for Biosecurity and One Health, Murdoch University, Australia

Hemolivia mariae is a hemogregarine that parasitises erythrocytes of the Australian sleepy lizard, *Tiliqua rugosa.* Reptile ticks *Amblyomma limbatum* and *Bothriocroton hydrosauri* have been implicated in its transmission. In addition, oocytes proposed to be *Hemolivia* sp. have been identified within the gut epithelium of the stump-tailed lizard tick, *Amblyomma albolimbatum*, however molecular data confirming the species is lacking. Here we present for the first time, to the authors’ knowledge, molecular data supporting the presence of *H. mariae* within *Am. albolimbatum* in Western Australia (WA). Three hundred and six ticks, morphologically identified as *Am. albolimbatum*, were removed from 88 *T. rugosa* lizards at the Kanyana Wildlife Rehabilitation Centre, Perth, WA between 2013 to 2015. A subset of 45 ticks were subjected to genomic DNA extraction and screened for haemoparasites using a nested 18S rRNA assay and Sanger sequencing. Two (4.4%) samples generated a 782 bp product that had a 100% genetic identity to *H. mariae* (KF992721.1). The *H. mariae*-positive samples were an adult female and a male from different hosts. This finding is consistent with the previous report of *Hemolivia* within *Am. albolimbatum*. Further research is required to determine the prevalence of *H. mariae* within questing *Am. albolimbatum* ticks.

(ID: 108)

INTESTINAL PARASITES PRESENT IN THE MISQUITA INDIGENOUS ETHNIC, LIVING IN GRACIAS A DIOS, HONDURAS DURING THE YEAR 2019-2020.

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Objective: To determine the frequency of intestinal parasites present in the Misquita indigenous ethnic group, in Honduras.

Methods: 4132 fecal samples were collected from Miskito subjects of both sexes and indistinct age, who attended the Puerto Lempira Hospital, in the Municipality of Gracias a Dios, Honduras. All samples were examined macroscopically and microscopically using saline solution and Lugol's solution, by light microscopy.

Results: 83.45% (n: 3448) presented the presence of at least one parasite, being found more frequently in the female sex 55% (n: 1880) compared to the male sex 45% (n: 1568). Blastocystis spp was the most frequent parasite found in both groups (24%), followed by Ascaris lumbricoides (20%), Entamoeba coli (14%) and Trichuris trichiura (13%). In relation to the age of the patients, a correlation was observed with the presence of parasites and the different age groups (P <0.05), being those under 20 years of age the group with the highest incidence of infection with 52% (n: 1783).

Conclusion: The indigenous Misquita population has high frequencies of intestinal parasites, affecting all age groups, mainly those under 20 years of age. Intestinal protozoa and helminths continue to affect this population, so health interventions are recommended.

(ID: 109)

Intestinal parasitosis in patients admitted to the Juan Manuel Gálvez Hospital. Gracias Lempira, Honduras

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Introduction: intestinal parasites are a public health problem in Honduras, generating greater burdens and complications in the child population.
Objective: to estimate the prevalence of intestinal parasites in patients from different care rooms at the Juan Manuel Gálvez Hospital. Gracias Lempira, Honduras
Methods: stool samples from 2,164 patients from 8 different Hospital rooms were examined using optical microscopy, between the months of January 2019 to June 2020.
Results: 731 patients (33.8%) had at least one type of parasite in their digestive system, being Entamoeba coli 262 (35.8%), Blastocystis hominis 212 (29.0%) and Endolimax nana 104 (14.2%) the most identified. Regarding the wards, it was possible to identify a greater positivity in the Emergency room 339 (46.4%), followed by Outpatient Consultation and Pediatrics with 132 (18.1%) and 104 (14.22%) respectively.
Conclusions: It is identified that commensal amoebae are still very frequent among the study population, in addition to being present in patients with other infections or severe clinical conditions, which is why the importance of performing interventions to avoid greater complications in patients is highlighted. patients.

(ID: 105)

Global prevalence of hydatidosis in Equidae family, a systematic and meta-analysis review article

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Hydatidosis is a zoonotic parasite infection affecting mostly productive animals and humans. The current review was conducted to investigate the prevalence of hydatidosis in the Equidae family from January 2000 to February 2021 across the world. English engine databases were searched using keywords addressing the prevalence of hydatid cyst in Equine. The search process resulted in the inclusion of 17 out of 72 papers. A quality assessment was performed based on the Newcastle-Ottawa quality assessment scale. Based on the random-effects model meta-analysis, the pooled prevalence of hydatidosis in Equidae was 10.01% (95% CI=6.12–14.71). The sub-analysis results show a significant increase in the worldwide prevalence of hydatid cysts in the Equidae family population in the recent decade. Asia had the highest prevalence of hydatidosis among continents (14.5%). The highest prevalence of hydatid disease among countries was observed in Turkey (28.5%). The morphologic procedure was most commonly used for the diagnosis of hydatidosis. Hepatic cysts were most likely be formed in Equine with the rate of 98.2%. Additionally, horses have the highest prevalence of hydatid cyst among Equine. The current study highlights the importance of hydatidosis in Equine, which can help future planning research and evaluate the economic loss.

(ID: 106)

Evaluation of zoonotic platyhelminthe infections identified in slaughtered livestock in Iran, 2015-2019

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This study aims to evaluate the spatial frequency of cystic echinococcosis (CE), dicrocoeliasis, and fascioliasis in livestock slaughtered in Iran with calculation of economic losses. Abattoir data from 413 abattoirs representing all 31 Iranian provinces

were collected from the Iran Veterinary Organization during 2015-2019. The Local Moran's *I* statistic was performed to evaluate spatial autocorrelation of animals positive. Overall prevalence values for the study timeframe were as follows: sheep and goat fascioliasis 1.56% (95% CI: 1.56-1.56%), cattle fascioliasis 3.86% (95% CI: 3.85-3.88%), sheep and goat dicrocoeliasis 4.63% (95% CI: 4.62-4.63%), cattle dicrocoeliasis 3.08% (95% CI: 3.07-3.09%), sheep and goat CE 5.32% (95% CI: 5.32-5.33%), and cattle CE 7.26% (95% CI: 7.24-7.28%). Northwest Iran had the highest prevalence of CE and fascioliasis. High infection areas for *Dicrocoelium* spp. included the provinces of Zanjan, Gilan, Qazvin, and Tehran, which are located in northern Iran. Direct economic losses for sheep and goat fascioliasis, dicrocoeliasis, and CE for the study period were US$13,842,759, US$41,771,377, and US$22,801,054, respectively. Direct economic losses for cattle fascioliasis, dicrocoeliasis, and CE for the study period were US$1,989,200, US$1,668,986, and US$2,656,568, respectively. Our findings provide valuable data for future monitoring of these important parasitic diseases in Iranian livestock.

(ID: 107)

World-wide prevalence of *Anisakis* larvae in fish and its relationship to human allergic Anisakiasis: A systematic review

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A systematic spatio-temporal study was conducted to determine the prevalence of *Anisakis* spp. in fish from January 2000 to April 2019 firstly to explore the relationship between fish infection and cases of allergic Anisakiasis and secondly to use fish infection data to map potential allergic Anisakiasis hot spots. A systematic literature search for original English text articles was conducted through search engines, Web of Science, Scopus, PubMed, Science Direct, and Google Scholar. Out of 5222 articles, 245 were used for data extraction. A qualitative summary of the extracted data was performed using equal-interval method (ArcMap software) in order to compare the global distribution of *Anisakis* infected fish. Of the 151-identified fish hosts, five families were most commonly infected with Anisakidae. These included Trichiuridae (75.7%); Merlucciidae (68%); Lophiidae (66.7%); Zeidae (64.5%) and Gadidae (53.3%). The hot spot areas for allergic Anisakiasis were North Atlantic Ocean (confidence 99%) and East Asia, Canada and north of Norway (confidence interval 95%). The highest rate of allergic Anisakiasis was in Portugal and Norway with the prevalence rate of 14.73-22.50%. Allergologists should consider allergic Anisakiasis as a public health issue particularly in high-risk countries where high prevalence of fish infection has been demonstrated.

(ID: 210)

Australian Tick Microbiomes: What We've Learnt & Where to Next

Telleasha Greay

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In Australia, the study of microorganisms in ticks has increased in response to human patients reported to have locally acquired Lyme disease-like illness. The cause(s) of Lyme disease-like illness in people residing in Australia remains unclear as there is no definitive evidence that *Borrelia burgdorferi* s.l. species occur in Australian ticks and non-endemic ticks that vector *B. burgdorferi* s.l. have not been identified in Australia. Next-generation sequencing (NGS) studies on Australian ticks have revealed novel microbial agents that may be transmitted to animals and humans. However, their pathogenicity, transmissibility and roles in the tick microbiome are still unclear. This talk will discuss how NGS can be used to advance our understanding of tick-borne microbes, which is key to the development of tick-borne pathogen treatment and control strategies in the future.

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