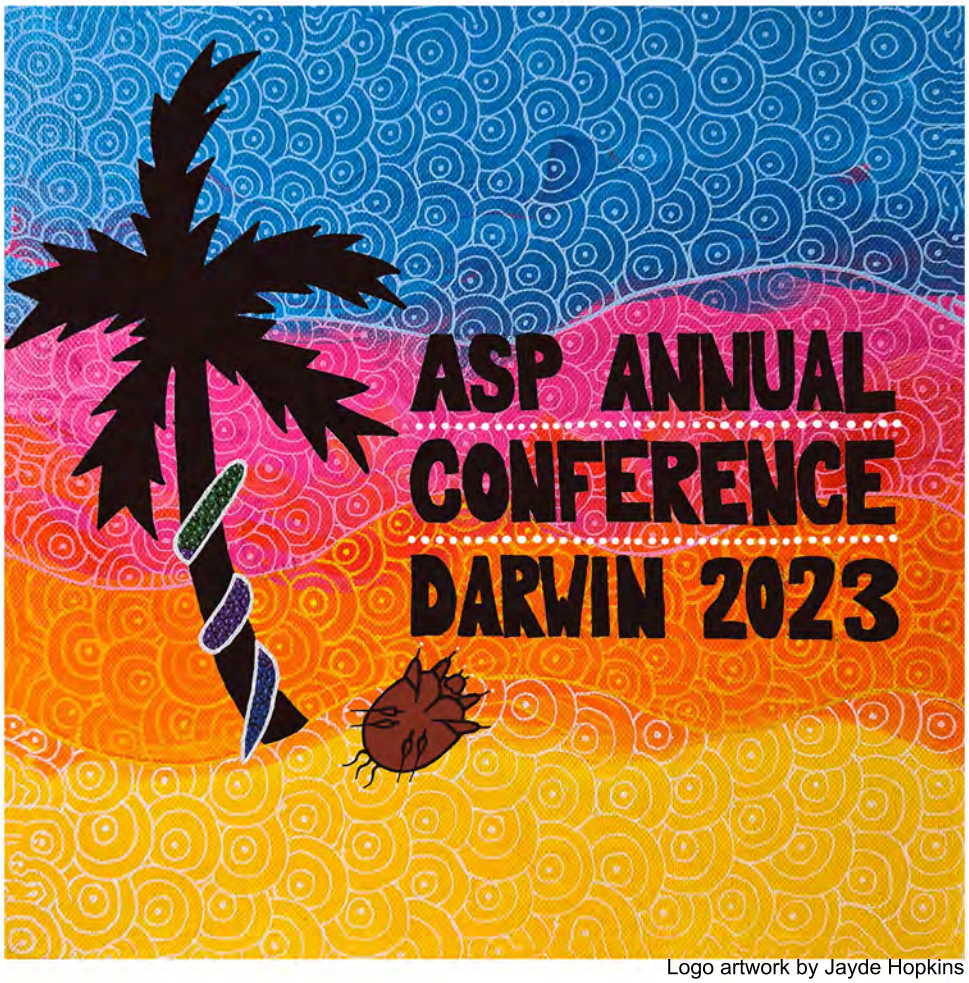

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Program and Abstracts
2023 Annual Conference of the Australian Society for Parasitology
September 5-8, DoubleTree by Hilton Hotel Esplanade Darwin

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2023 Annual Conference of the Australian Society for Parasitology Inc.

September 5-8, DoubleTree by Hilton Hotel Esplanade Darwin, NT, Australia

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2023 Annual Conference of the Australian Society for Parasitology Inc.

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Welcome from the ASP President

Dear Colleague,

On behalf of the ASP Council and the 2023 Conference Organising Committee, we extend a warm welcome to the 2023 ASP Annual Conference. The Conference, at the DoubleTree by Hilton Hotel Esplanade Darwin, will begin, with an evening Welcome Reception, on Tuesday 5 September, and culminate, with our Conference Dinner, on Friday 8th September.

We look forward to seeing you at the 2023 ASP Conference to discuss the latest research and state-of-the-art technologies in parasitology with an outstanding mix of quality international and Australian scientists in a beautiful location on the esplanade in Darwin, Northern Territory.

This year's conference has a strong One Health and Tropical Medicine theme with a One Health workshop sponsored by Elsevier, "A deep dive into One Health approaches and practices in parasitology", dedicated to the late Prof Don McManus. As part of this workshop, the ASP Disadvantaged Researcher Fund and the Australian Centre for International Agricultural Research (ACIAR) have sponsored four early-career academics to participate from Vietnam, Malaysia, Laos PDR and Ukraine. ASP Affiliate Strongyloides Australia will host a Stronglyoides workshop on the 'most neglected of neglected tropical diseases'.

The success of our conference is, as always, dependent on our supporters and we would like to thank sincerely the following organisations for their generous support; **Elsevier and the International Journal for Parasitology (IJP), IJP Drugs and Drug Resistance and IJP Parasites and Wildlife, Vetoquinol, Virbac, Elanco, New England Biolabs and Southern Cross Diagnostics** who are supporting this conference.

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

Professor Rebecca Traub
President, ASP

2023 Annual Conference of the Australian Society for Parasitology Inc.

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Program Overview

Date: Tuesday, 05/Sept/2023	
8:30am - 5:00pm ASP Council Meeting room	**2023 ASP ETM: ASP Council End Term Meeting 2023** Location: **ASP Council Meeting room**
2:00pm - 5:00pm	**Registration Desk is open**
7:00pm - 9:00pm Hilton Garden Inn Darwin	**Welcome: Welcome Reception sponsored by Vetoquinol** Location: **Hilton Garden Inn Darwin** This event will take place in the garden 😊
Date: Wednesday, 06/Sept/2023	
7:00am - 8:30am Workshop room 3	**ECRBreakfast: ASP 2024 Darwin ECR Breakfast Workshop** Location: **Workshop room 3** Session Chair: **Jill Chmielewski**, University of Adelaide The workshop theme is meet the editors & learn about the publishing process. Editors from parasitology related journals will be your mentors and give you an insight into how best to get your work published! The awesome mentors for this workshop are Dale Seaton, Elsevier; Brian Cooke, IJP; Andrew Thompson, IJP:PAW; Kevin Saliba, IJP:DDR; Malcolm Jones, UQ; Una Ryan, Murdoch; Christian Doerig, RMIT; Ala Tabor, UQ; Amanda Ash, Murdoch; Tomáš Scholz, Biology Centre of the Czech Academy of Sciences; Kate Miller, JCU and Sarah Preston, Federation Uni.
8:30am - 8:45am Plenary Room	**Welcome to Country by Youth Mill** Location: **Plenary Room** Session Chair: **Deborah Holt**, Charles Darwin University Welcome to Country presentation with one composition "A Culture Within" performance by Youth Mill
8:45am - 10:00am Plenary Room	**P1: One Health Plenary Lectures sponsored by Elsevier** Location: **Plenary Room** Session Chair: **Amanda Ash**, Murdoch University
10:00am - 10:30am Ballroom Foyer	**Morning Tea Break Wednesday** Location: **Ballroom Foyer**
10:30am - 11:00am Symposium room 2	**S1: Symposium 1 Livestock sponsored by Virbac** Location: **Symposium room 2** Session Chair: **Aleta Knowles**, Virbac
10:30am - 11:45am Symposium room 1	**CP1: Omics & Informatics 15 min talks** Location: **Symposium room 1** Session Chair: **Katja Fischer**, QIMR Berghofer MRI
10:30am - 12:00pm Workshop room 3	**W1: One Health Workshop sponsored by Elsevier** Location: **Workshop room 3** Session Chair: **Malcolm Jones**, University of Queensland
11:00am - 11:45am Symposium room 2	**CP2: Livestock 15 min talks sponsored by Virbac** Location: **Symposium room 2** Session Chair: **Aleta Knowles**, Virbac
11:45am - 12:00pm Symposium room 1	**CP1.1: Omics & Informatics 5 min talks** Location: **Symposium room 1** Session Chair: **Katja Fischer**, QIMR Berghofer MRI
11:45am - 12:00pm Symposium room 2	**CP2.1: Livestock 5 min talks sponsored by Virbac** Location: **Symposium room 2** Session Chair: **Aleta Knowles**, Virbac
12:00pm - 12:05pm Symposium room 1	**CP1.2: Omics & Informatics 3 min talks** Location: **Symposium room 1** Session Chair: **Katja Fischer**, QIMR Berghofer MRI
12:00pm - 1:00pm Ballroom Foyer	**Lunch Wednesday** Location: **Ballroom Foyer**
1:00pm - 1:30pm	

Symposium room 1	**S2: Symposium 2 Immunology & Pathogenesis** Location: **Symposium room 1** Session Chair: **Brendan McMorran**, Australian National University
1:00pm - 2:15pm	**CP3: Livestock 15 min talks sponsored by Virbac Australia**
Symposium room 2	Location: **Symposium room 2** Session Chair: **Aleta Knowles**, Virbac
1:00pm - 2:30pm	**W2: One Health Workshop sponsored by Elsevier**
Workshop room 3	Location: **Workshop room 3** Session Chair: **Darren Gray**, QIMR Berghofer Medical Research Institute
1:30pm - 2:00pm	**CP4: Immunology & Pathogenesis 15 min talks**
Symposium room 1	Location: **Symposium room 1** Session Chair: **Brendan McMorran**, Australian National University
2:00pm - 2:15pm	**CP4.1: Immunology & Pathogenesis 5 min talks**
Symposium room 1	Location: **Symposium room 1** Session Chair: **Brendan McMorran**, Australian National University
2:15pm - 2:30pm	**CP3.1: Livestock sponsored by Virbac 5 min talks**
Symposium room 2	Location: **Symposium room 2** Session Chair: **Aleta Knowles**, Virbac
2:15pm - 2:35pm	**CP4.2: Immunology & Pathogenesis 3 min talks**
Symposium room 1	Location: **Symposium room 1** Session Chair: **Brendan McMorran**, Australian National University
2:30pm - 3:00pm	**Afternoon Tea Break Wednesday**
Ballroom Foyer	Location: **Ballroom Foyer**
3:00pm - 3:15pm	**S3: Symposium 3 Aquatic**
Symposium room 2	Location: **Symposium room 2** Session Chair: **Diane Barton**, Charles Sturt University
3:00pm - 4:00pm	**CP5: Protozoan Biology 15 min talks**
Symposium room 1	Location: **Symposium room 1** Session Chair: **Paul Gilson**, Burnet Institute
3:00pm - 4:30pm	**W3: One Health Workshop sponsored by Elsevier**
Workshop room 3	Location: **Workshop room 3** Session Chair: **Rebecca Traub**, Australian Society for Parasitology
3:15pm - 4:30pm	**CP6: Aquatic 15 min talks**
Symposium room 2	Location: **Symposium room 2** Session Chair: **Diane Barton**, Charles Sturt University
4:00pm - 4:30pm	**CP5.1: Protozoan Biology 5 min talks**
Symposium room 1	Location: **Symposium room 1** Session Chair: **Paul Gilson**, Burnet Institute
4:30pm - 5:00pm	**Pre-Plenary Prosecco - Wednesday**
Ballroom Foyer	Location: **Ballroom Foyer**
5:00pm - 5:30pm	**President: 2023 ASP Presidential Address**
Plenary Room	Location: **Plenary Room** Session Chair: **Rebecca Traub**, Australian Society for Parasitology
5:30pm - 7:30pm	**AGM: 2023 Annual General Meeting ASP**
Plenary Room	Location: **Plenary Room** Session Chair: **Rebecca Traub**, Australian Society for Parasitology
7:30pm - 9:30pm	**Student social event: Student social event**
Date: Thursday, 07/Sept/2023	
8:30am - 9:15am	**BMM: 2023 Bancroft Mackerras Medal Award and Lecture**
Plenary Room	Location: **Plenary Room** Session Chair: **Rebecca Traub**, Australian Society for Parasitology
9:15am - 10:00am	**P2: IJP Plenary Lecturer**
Plenary Room	Location: **Plenary Room** Session Chair: **Rebecca Traub**, Australian Society for Parasitology
10:00am - 10:30am	**Morning Tea Break Thursday**
Ballroom Foyer	Location: **Ballroom Foyer**
10:30am - 11:00am	**S4: Symposium 4 Epidemiology & Diagnostics**
Symposium room 2	Location: **Symposium room 2** Session Chair: **Kamil Braima**, Menzies School of Health Research
10:30am - 11:30am	**CP7: Biodiversity & Wildlife 15 min talks**
Symposium room 1	Location: **Symposium room 1** Session Chair: **Michelle Power**, Macquarie University
10:30am - 12:00pm	

Workshop room 3	**W4: Bioinformatics Workshop** Location: **Workshop room 3** Session Chair: **Maree Widdicombe**, RMIT University Session Chair: **Jacob Westaway**, Menzies School of Health Research Session Chair: **Ashton Kelly**, University of Queensland
11:00am - 11:45am	**CP8: Epidemiology & Diagnostics 15 min talks**
Symposium room 2	Location: **Symposium room 2** Session Chair: **Kamil Braima**, Menzies School of Health Research
11:30am - 12:00pm	**CP7.1: Biodiversity & Wildlife 5 min talks**
Symposium room 1	Location: **Symposium room 1** Session Chair: **Michelle Power**, Macquarie University
11:45am - 12:00pm	**CP8.1: Epidemiology & Diagnostics 5 min talks**
Symposium room 2	Location: **Symposium room 2** Session Chair: **Kamil Braima**, Menzies School of Health Research
12:00pm - 1:00pm	**Lunch Thursday**
Ballroom Foyer	Location: **Ballroom Foyer**
1:00pm - 2:00pm	**CP9: Immunology & Pathogenesis 15 min talks**
Symposium room 1	Location: **Symposium room 1** Session Chair: **Steven Kho**, Menzies School of Health Research
1:00pm - 2:00pm	**S5: Symposium 5 Companion Animals sponsored by Vetoquinol**
Symposium room 2	Location: **Symposium room 2** Session Chair: **Clare Anstead**, University of Melbourne
1:00pm - 2:30pm	**W5: Bioinformatics Workshop**
Workshop room 3	Location: **Workshop room 3** Session Chair: **Maree Widdicombe**, RMIT University Session Chair: **Jacob Westaway**, Menzies School of Health Research Session Chair: **Ashton Kelly**, University of Queensland
2:00pm - 2:15pm	**CP9.1: Immunology & Pathogenesis 5 min talks**
Symposium room 1	Location: **Symposium room 1** Session Chair: **Steven Kho**, Menzies School of Health Research
2:00pm - 2:30pm	**CP10: Veterinary Parasitology sponsored by Vetoquinol 15 min talks**
Symposium room 2	Location: **Symposium room 2** Session Chair: **Clare Anstead**, University of Melbourne
2:15pm - 2:30pm	**CP9.2: Immunology & Pathogenesis 3 min talks**
Symposium room 1	Location: **Symposium room 1** Session Chair: **Steven Kho**, Menzies School of Health Research
2:30pm - 3:00pm	**Afternoon Tea Break Thursday**
Ballroom Foyer	Location: **Ballroom Foyer**
3:00pm - 3:30pm	**S6: Symposium 6 Education & Outreach**
Symposium room 1	Location: **Symposium room 1** Session Chair: **Sarah Preston**, Federation University Australia
3:00pm - 4:30pm	**W6: Bioinformatics Workshop**
Workshop room 3	Location: **Workshop room 3** Session Chair: **Maree Widdicombe**, RMIT University Session Chair: **Jacob Westaway**, Menzies School of Health Research Session Chair: **Ashton Kelly**, University of Queensland
3:30pm - 4:30pm	**CP11: Education & Outreach 15 min talks**
Symposium room 1	Location: **Symposium room 1** Session Chair: **Sarah Preston**, Federation University Australia
4:30pm - 5:00pm	**Pre-Plenary Prosecco - Thursday**
Ballroom Foyer	Location: **Ballroom Foyer**
5:00pm - 5:45pm	**P3: IJP:PAW Plenary Lecturer**
Plenary Room	Location: **Plenary Room** Session Chair: **Andrew Thompson**, Murdoch University
7:00pm - 8:30pm	**Outreach: Public Outreach event**
Date: Friday, 08/Sept/2023	
8:30am - 9:15am	**P4: Strongyloides Opening Plenary Lecture**
Plenary Room	Location: **Plenary Room** Session Chair: **Dr Jenni Judd**, Central Queensland University
9:15am - 10:00am	**P4.1: IJP:DDR Plenary Lecturer**
Plenary Room	Location: **Plenary Room** Session Chair: **Kevin Saliba**, Australian National University
10:00am - 10:30am	**Morning Tea Break Friday**
Ballroom Foyer	Location: **Ballroom Foyer**

10:30am - 11:00am	**S7: Drugs & Drug Resistance Symposium**
Symposium room 1	Location: **Symposium room 1** Session Chair: **Benedikt Ley**, Menzies School of Health Research
10:30am - 11:15am	**CP12: Zoonoses 15 min talks**
Symposium room 2	Location: **Symposium room 2** Session Chair: **Narelle Dybing**, Australian Pork Limited- National Feral Pig Action Plan
10:30am - 12:00pm	**W7: Strongyloides Workshop**
Workshop room 3	Location: **Workshop room 3** Session Chair: **Harsha Sheorey**, St Vincent`s Hospital, Melbourne
11:00am - 11:30am	**CP13: Drugs & Drug Resistance 15 min talks**
Symposium room 1	Location: **Symposium room 1** Session Chair: **Benedikt Ley**, Menzies School of Health Research
11:15am - 11:45am	**CP12.1: Zoonoses 5 min talks**
Symposium room 2	Location: **Symposium room 2** Session Chair: **Narelle Dybing**, Australian Pork Limited- National Feral Pig Action Plan
11:30am - 11:45am	**CP13.1: Drugs & Drug Resistance 5 min talks**
Symposium room 1	Location: **Symposium room 1** Session Chair: **Benedikt Ley**, Menzies School of Health Research
11:45am - 12:00pm	**CP13.2: Drugs & Drug Resistance 3 min talks**
Symposium room 1	Location: **Symposium room 1** Session Chair: **Benedikt Ley**, Menzies School of Health Research
11:45am - 12:00pm	**CP12.2: Zoonoses 3 min talks**
Symposium room 2	Location: **Symposium room 2** Session Chair: **Narelle Dybing**, Australian Pork Limited- National Feral Pig Action Plan
12:00pm - 1:00pm	**Lunch Friday**
Ballroom Foyer	Location: **Ballroom Foyer**
1:00pm - 1:30pm	**S8: Symposium 8 Companion Animals sponsored by Elanco**
Symposium room 2	Location: **Symposium room 2** Session Chair: **Liisa Ahlstrom**, Elanco Animal Health
1:00pm - 2:00pm	**CP14: Drugs & Drug Resistance 15 min talks**
Symposium room 1	Location: **Symposium room 1** Session Chair: **Brad Sleebs**, Walter and Eliza Hall Institute of Medical Research
1:00pm - 2:30pm	**W8: Strongyloides Workshop**
Workshop room 3	Location: **Workshop room 3** Session Chair: **Catherine Gordon**, QIMR Berghofer Medical Research Institute
1:30pm - 2:00pm	**CP15: Companion Animals sponsored by Elanco 15 min talks**
Symposium room 2	Location: **Symposium room 2** Session Chair: **Liisa Ahlstrom**, Elanco Animal Health
2:00pm - 2:15pm	**CP15.1: Companion Animals sponsored by Elanco 5 min talks**
Symposium room 2	Location: **Symposium room 2** Session Chair: **Liisa Ahlstrom**, Elanco Animal Health
2:00pm - 2:30pm	**CP14.1: Drugs & Drug Resistance 5 min talks**
Symposium room 1	Location: **Symposium room 1** Session Chair: **Brad Sleebs**, Walter and Eliza Hall Institute of Medical Research
2:15pm - 2:30pm	**CP15.2: Companion Animals sponsored by Elanco 3 min talks**
Symposium room 2	Location: **Symposium room 2** Session Chair: **Liisa Ahlstrom**, Elanco Animal Health
2:30pm - 3:00pm	**Afternoon Tea Break Friday**
Ballroom Foyer	Location: **Ballroom Foyer**
3:00pm - 3:30pm	**S9: Microscopy Symposium**
Symposium room 1	Location: **Symposium room 1** Session Chair: **Danny Wilson**, The University of Adelaide
3:00pm - 4:30pm	**W9: Strongyloides Workshop**
Workshop room 3	Location: **Workshop room 3** Session Chair: **Kirstin Ross**, Flinders University
3:30pm - 4:30pm	**CP16: Microscopy 15 min talks**
Symposium room 1	Location: **Symposium room 1** Session Chair: **Danny Wilson**, The University of Adelaide
4:30pm - 5:00pm	**Pre-Plenary Prosecco - Friday**
Ballroom Foyer	Location: **Ballroom Foyer**
5:00pm - 5:45pm	**P5: Strongyloides Closing Plenary Lecture**
Plenary Room	Location: **Plenary Room** Session Chair: **Wendy Page**, Strongyloides Australia "Strongyloides stercoralis, the smartest worm"

	Professor Zeno Bisoffi MD, PhD, DTM&H Scientific Director, IRCCS Ospedale Sacro Cuore Don Calabria, Italy
5:45pm - 6:00pm	**Award of Student Prizes**
Plenary Room	Location: **Plenary Room**
7:00pm - 10:00pm	**Dinner: Conference Dinner at Hanuman**
Hanuman Restaurant	Location: **Hanuman Restaurant**

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Presentations

P1: One Health Plenary Lectures sponsored by Elsevier

Time: Wednesday, 06/Sept/2023: 8:45am - 10:00am · *Location:* Plenary Room
Session Chair: Amanda Ash, Murdoch University

ID: 245 / P1: 1
Invited speaker abstract

Using novel epidemiological methods to support a Precision One Health approach for prevention, control and elimination of infectious diseases.

Colleen Lau
University of Queensland, Australia

Transmission of infectious diseases is strongly driven by sociodemographic, environmental, climatic, and ecological factors, many of which beyond the immediate control of individuals or small communities. Sustainable disease control will therefore require effective public health and environmental health management from higher levels. To maximise the cost-effectiveness and impact of interventions, efforts should ideally be specifically targeted towards the most important risk factors and drivers, and focused on the populations and geographic areas at highest risk. Following the principles of 'Precision Public Health', novel approaches to using data, technology, and analytics can improve our understanding of the complex transmission dynamics of infectious diseases, and optimise who, when, how, and where to target prevention and control strategies. Case studies of operational research on lymphatic filariasis and leptospirosis in the Pacific Islands will be used to illustrate these concepts. It's time to develop the science and practice of 'Precision One Health'.

ID: 255 / P1: 2
Invited speaker abstract

The Lawa Model: An Integrated Liver Fluke Control Program Using One Health Approach

Banchob Sripa[1,2,3]
[1]Tropical Disease Research Center; [2]WHO Collaborating Centre for Research and Control of Opisthorchiasis (Southeast Asian Liver Fluke Disease); [3]Department of Tropical Medicine, Faculty of Medicine, Khon Kaen University, Thailand.

Opisthorchis viverrini, a neglected foodborne trematodiasis, infects over 10 million individuals in the Lower Mekong River Basin, causing hepatobiliary diseases including cholangiocarcinoma. Northeast Thailand has the world's highest incidence of this fatal bile duct cancer due to *O. viverrini*'s endemicity. Despite previous control programs, infection rates remain high in certain areas due to the parasite's complex life cycle. To address this, an One Health approach was implemented in Lawa Lake, Khon Kaen province, an endemic region for over a decade. Infection rates decreased to less than 10% from the baseline estimate of 60% in surrounding villages. Improved knowledge and preventive practices were observed among residents. Prevalence of the intermediate host, Cyprinid fish species, dropped below 0.1% from a baseline survey maximum of 70%. The successful liver fluke control program, known as the "Lawa model," gained national recognition and is now integrated into Thailand's agenda against liver fluke and cholangiocarcinoma. The "Lawa model" is internationally recognized as one of the two successful helminth control programs showcased at the WHO/NZD4 meeting. Furthermore, the WHO Western Pacific Region's report recommends the One Health approach for controlling foodborne trematode infections, taeniasis, and cysticercosis, as demonstrated by the Lawa model.

CP1: Omics & Informatics 15 min talks

Time: Wednesday, 06/Sept/2023: 10:30am - 11:45am · *Location:* Symposium room 1
Session Chair: Katja Fischer, QIMR Berghofer MRI

ID: 131 / CP1: 1
Contributed abstract
Conference Topics: Genomics, Other, Bioinformatics
Keywords: Protein structure, non-model organisms, SNP-mapping, genotype-to-phenotype, 3D-visualisation

VIVID: a web application for variant interpretation and visualisation in multidimensional analyses

Swapnil Tichkule[1], Yoochan Myung[2], Myo T Naung[1], Brendan RE Ansell[1], Andrew J Guy[3], Namrata Srivastava[4], Somya Mehra[5], Simone M Cacciò[6], Ivo Mueller[1], Alyssa E Barry[7], Cock van Oosterhout[9], Bernard Pope[8], David B Ascher[2], Aaron R Jex[1]

[1]Walter and Eliza Hall Institute of Medical Research; [2]University of Queensland; [3]RMIT; [4]Monash University; [5]Burnet Institute; [6]Istituto Superiore di Sanità; [7]Deakin University; [8]University of Melbourne; [9]University of East Anglia

Large-scale studies in comparative genomics and population genetics generate vast amounts of DNA variant data. These studies aim to link genetic variants to observable traits or fitness. The field of parasitology has increasingly embraced such studies. However, the lack of automated tools and databases for non-model organisms hinders phenotypic association studies in parasites. Here, we present VIVID, a web application that integrates established algorithms, tools, and databases to associate genotypic information with phenotypic data in any organism. VIVID operates in three-dimensional (3D) space and enables mutation mapping, annotation, interaction and conservation score calculations, prediction of mutation effects, diversity, and selection analysis, as well as 3D visualization of genotypic information using Variant Call Format encoded on AlphaFold2 protein models.

The output of VIVID is designed to provide users with insights into the impact of mutations on protein structure and function, visualize protein evolution in 3D, and identify genomic regions under selection. This information assists in prioritizing targets for experimental validation. To demonstrate the utility of VIVID, we applied it to investigate the evolutionary genetics of *Plasmodium falciparum*, revealing geographic variation in the selection signature of potential targets for functional antibodies. VIVID is freely accessible at https://biosig.lab.uq.edu.au/vivid/.

ID: 175 / CP1: 2
Contributed abstract
Conference Topics: Veterinary Parasitology, Ectoparasites, Genomics, Bioinformatics
Keywords: Genomics, Ixodes holocyclus, Systems biology, Paralysis Toxin, Transcriptomics

The chromosome-scale assembly of the Australian Paralysis Tick, *Ixodes holocyclus,* provides insights into hematophagy, toxin biology, and developmental regulation.

Amrita Vijay[1], Thomas Karbanowicz[2], Quentin Gouil[1], Alexander Gofton[3], Balu Balan[1], Louise Baker[1], Stefano Gaiarsa[4], Ala Tabor[2], Nathan Lo[5], Jan Riemer[6], Fabrizia Stavru[7], Davide Sassera[8], Peter Czabotar[1], Tony Papenfuss[1], Aaron R Jex[1,9]

[1]Walter and Eliza Hall Institute, Department of Medical Biology, The University of Melbourne, Parkville, Victoria, Australia; [2]The University of Queensland, Queensland Alliance for Agriculture & Food Innovation, St Lucia, Queensland, Australia; [3]Zoonotic & Arboviral pathogens, Health & Biosecurity, CSIRO, Canberra, 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; [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; [9]Faculty of Veterinary and Agricultural Sciences, The University of Melbourne, Parkville, Victoria, Australia

Ixodes holocyclus, the Australian Eastern Paralysis tick, is an ectoparasite that impacts human and veterinary health. During blood feeding, the ticks inject fatal paralytic toxins. However, factors that drive toxin production, host specificity, and survival strategies are poorly characterized. Consequently, the current paralysis treatment relies on administering anti-serum after symptoms arise. To control *I. holocyclus*, molecular biology understanding is needed, but a lack of genomic, transcriptomic, and proteomic resources hinders this. In addition, their large size and repetitive sequence content impeded tick genomic research, including *I. holocyclus*.

We applied a hybrid genomics strategy that combined Oxford-Nanopore and Illumina sequencing with high-throughput chromosomal conformation capture sequencing to obtain results. We also used long- and short-read RNA sequencing to create a comprehensive *de novo* transcriptome. We produced a chromosomal-scale draft genome of 1.9GB. Our *de novo* transcriptome had 18,324 main transcript isoforms, which we used to predict accurate gene models and to identify alternative splice transcripts. This genomic data could provide insights into the tick's repertoire of immune evasion and host manipulation strategies. Identifying gene families involved in these processes could accelerate the development of efficient control measures, including novel tick-control strategies and therapeutic interventions against tick-induced paralysis.

ID: 173 / CP1: 3
Contributed abstract
Conference Topics: Proteomics, Cell Biology, Molecular Biology, Protozoa, Other, Bioinformatics
Keywords: Giardia duodenalis, RNA binding proteins, Post-transcriptional Regulation, CRISPR, RNA interactome capture, Encystation

The emergence of eukaryotic specific post-transcriptional regulatory networks: Insights from *Giardia duodenalis* RNA binding proteome

Balu Balan[1,3], Samantha J. Emery-Corbin[1,3], Jarrod Sandow[1,3], Ahmad Wardak[1,3], Amrita Vijay[1,3], Sachin Khurana[1,3], Jacob Munro[1,3], Swapnil Tichkule[1,3], Brendan Robert E. Ansell[1,3], Olivia Rissland[5], Staffan Svärd[4], Peter Czabotar[1,3], Andrew Webb[1,3], Aaron Jex[1,2]

[1]Walter and Eliza Hall Institute of Medical Research, Parkville, Victoria, Australia; [2]Faculty of Veterinary and Agricultural Science, University of Melbourne, Melbourne, Victoria, Australia; [3]Department of Medical Biology, University of Melbourne, Parkville, Victoria, Australia; [4]Department of Cell and Molecular Biology, Uppsala University, Uppsala, Sweden; [5]Department of Biochemistry & Molecular Genetics, Anschutz Medical Campus, University of Colorado, USA

RNA binding proteins (RBPs) are major post-transcriptional regulators (PTR). In higher eukaryotes RBPs control transcription, RNA transport, splicing and degradation, translation, and translational repression and are vital for cell fating, pluripotency, and differentiation. Surprisingly, the eukaryotic RBPome is fundamentally unchanged from yeast to humans, suggesting the emergence of novel RBPs in basal eukaryotes. Yet this is largely unstudied. Here, we characterised the RBPome of *G. duodenalis*, an early branching eukaryote, to understand eukaryotic PTR evolution.

We undertook *in silico* curation, RNA interactome capture (RIC), and high-resolution mass spectrometry to characterise *Giardia's* RBPome. We then explored the function of key RBPs, including the earliest known Pumilio homologs (PUF, PUM) and RNA helicases, DDX3X and EIF4A in *Giardia* using CRISPRi mediated knockdowns, RBP-crosslinking immunoprecipitation (CLiP), quantitative proteomics and *in vitro* protein expression. Despite *Giardia's* basal evolutionary origins and minimalistic regulatory systems, its RBPome has most novel functions found in higher eukaryotes, including the capacity to form membrane-less organelles, translationally repress complex mRNA networks, and use this to control its major life cycle changes and stress responses. *Giardia* provides the earliest eukaryotic record of many novel RBP families acquired by higher eukaryotes and highlights the central role these have played in eukaryotic evolution.

ID: 169 / **CP1: 4**
Contributed abstract
Conference Topics: Diagnostics, Molecular Biology
Keywords: schistosomiasis, CRISPR

Development of CRISPR-based technologies for schistosomiasis

Hong You[1], Skye MacGregor[1], Xiaofeng Du[1], Malcolm Jones[2]
[1]QIMR Berghofer Medical Research Institute, Brisbane, QLD 4006, Australia; [2]School of Veterinary Science, The University of Queensland, Gatton, QLD 4343, Australia

We exploited novel CRISPR-based technologies (CRISPR/Cas9, Cas12/13 and CRISPR interference/activation) for schistosome gene function studies to identify and characterise vaccine or drug targets of these parasites. To effectively improve genetic modification of the CRISPR/Cas9 editing system we established for schistosomes, we have successfully developed the first application of CRISPR interference (CRISPRi) in parasitic helminths for loss-of-function studies targeting a *Schistosoma mansoni* gene encoding fibroblast growth factor receptor A (SmFGFRA). The essential roles of SmFGFRA in maintaining schistosome stem cells and in the schistosome-host interplay were clearly demonstrated by using this novel CRISPRi approach. We developed new generation point-of-care diagnostics tools (based on CRISPR-Cas13 system) for the detection of *S. japonicum* and *S. mansoni* and achieved 93-100 % sensitivity and 100% specificity compared with gold-standard qPCR detection. The CRISPR/Cas13-based diagnostic tool was evaluated by using 150 faecal/serum samples collected from *Schistosoma*-infected mice, and 189 human faecal/serum samples obtained from an *S. japonicum*-endemic area of the Philippines and an *S. mansoni*-endemic area of Uganda. These findings confirm the potential and the utility of CRISPR-mediated technologies for functional genomics and diagnosis studies schistosomes, which could be readily extended to other helminths.

ID: 198 / **CP1: 5**
Contributed abstract
Conference Topics: Genomics, Protozoa, Bioinformatics
Keywords: Giardia, genomics, population genetics, evolutionary biology

Population genomics explores the role of sexual recombination in the early diverging eukaryote, *Giardia duodenalis*

Swapnil Tichkule, Aaron Jex
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Giardia duodenalis is an important and highly prevalent food and waterborne parasitic protist and a major cause of chronic, postinfectious gastrointestinal disorders. *Giardia* are also among the earliest-branching eukaryotes and have been proposed as a possible example of an ancient asexual eukaryote. Such lineages have been likened to an 'evolutionary scandal' in modern evolutionary genetic theories that eukaryotes require sex to maintain genetic diversity. Asexual eukaryotes ought to rapidly succumb to the accumulation of deleterious mutations they cannot remove through recombination. Over several decades, whether *Giardia* engages in sex has been a fascinating topic of research and has never been conclusively demonstrated. Using comprehensive population genomic analyses, we find compelling evidence for 'sex' (or parasexuality) in *Giardia* and identify a suite of putative virulence genes that may be evolving through a Red-Queen dynamic under immune selection. We also find that there likely is an exclusively asexual *G. duodenalis* lineage, ironically including the major laboratory reference strain adopted by the community. However, this lineage is not ancient and indeed shows signs of succumbing to its asexuality. Fittingly, this suggests *Giardia* is not the exception to, but rather proof of theories around the ubiquity and ancient origin of sex in eukaryotes.

CP1.1: Omics & Informatics 5 min talks

Time: Wednesday, 06/Sept/2023: 11:45am - 12:00pm · *Location:* Symposium room 1
Session Chair: Katja Fischer, QIMR Berghofer MRI

ID: 154 / **CP1.1: 1**
Contributed abstract
Conference Topics: Malaria, Bioinformatics
Keywords: technology, sequencing, parasite, selective sequencing, adaptive

Artificial Intelligence-based drug resistance screening of malaria parasites using 'Read Until'.

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Nanopore sequencing has been highly successful for sequencing a range of pathogens including malaria however is problematic when trying to obtain sufficient coverage of parasite DNA from clinical samples with significant human DNA contamination. Furthermore, enrichment amplification protocols are developed for library preparation for the MinION to sequence the desired selective target. Commonly, these methods require *a priori* knowledge to inform experimental design including design of target primers for selection. In any case, human DNA contamination remains a major issue that delays results, reduces data output, and increases cost. Thus, it is beneficial to improve the current Nanopore sequencing protocols to enable a simpler selective sequencing approach made possible through Adaptive Sampling 'Read Until'. We explored the use of Read Until to select for target alleles of known malaria drug resistant genes (*k13, mdr1, crt, dhfr, dhps)* to identify whether the method reduced costs, time and increased enrichment of samples improving malaria surveillance and possibly aid in identifying successful treatments for *P. falciparum.* Read Until proved to be a successful method for rapidly sequencing clinical samples although requires further development for low parasite density field samples and optimisation on *P. vivax* samples.

ID: 124 / CP1.1: 2
Contributed abstract
Conference Topics: Malaria, Immunology, Molecular Biology, Bioinformatics
Keywords: Malaria, Transcriptomics, Proteomics, Systems Biology

Characterisation of the molecular basis of immune heterogeneity between individuals

Ashton Kelly[2,1], Carla Proietti[2], Yide Wong[1], Helen McGuire[3], Barbara Fazekas de St Groth[3], James McCarthy[4,5], Denise Doolan[1,2]

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Human infection with *Plasmodium* spp parasites (and other pathogens) can lead to a range of clinical outcomes ranging from asymptomatic responses to mild disease to death. Although clinical immunity can be acquired by long-term natural exposure to *Plasmodium* parasites, malaria remains a global public health problem with an estimated 247 million infections and 619,000 malarial deaths in 2021, 80% of which were recorded in children under five. It is now well established that there is substantial variation in individual ability to control parasite multiplication rate and density between individuals. This has provided the foundation for unique insights into immune heterogeneity and the molecular and cellular basis underlying variation in individual capacity to control infection. Of particular interest, Natural Killer (NK) cells, an innate immune cell population, have been associated with varying levels of parasite control in heterogeneous responders. By applying comprehensive immunological and molecular approaches to well characterised samples from Controlled Human Malaria Infection studies, we are dissecting the molecular basis of inter-individual immune heterogeneity following *Plasmodium* infections, with a focus on NK cells. This work intends to identify specific molecular signatures associated with protection and define how baseline pre-infection repertoires of immune cells and molecules influence *Plasmodium* infection outcomes.

ID: 261 / CP1.1: 3
Contributed abstract
Conference Topics: Malaria, Apicomplexa Biology
Keywords: Plasmodium falciparum, malaria

Sequence elements within the PEXEL motif and its downstream region modulate PTEX dependent protein export in *Plasmodium falciparum*.

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For the malaria parasite *Plasmodium falciparum,* to replicate in red blood cells (RBCs), it exports hundreds of proteins across the encasing parasitophorous vacuole membrane (PVM) into the RBC. Most exported proteins possess a conserved Plasmodium Export Element (PEXEL) motif with the consensus RxLxE/D/Q, which acts as a proteolytic cleavage recognition site after the L residue. Cleavage releases the cargo so it can be putatively escorted by the HSP101 chaperone to the parasitophorous vacuole space surrounding the intraerythrocytic parasite. HSP101 and its cargo are then thought to assemble with the rest of a Plasmodium Translocon for Exported proteins (PTEX) complex, that then recognises the exported protein and translocates it into the RBC compartment. Here, we present evidence that supports a dual role for the PEXEL's conserved P2' position E/Q/D residue, firstly, for proteolytic cleavage, and secondly, for efficient PTEX mediated export across the PVM into the RBC. We also show that the downstream 'spacer' region separating the PEXEL motif from the folded functional region of the exported protein is important for export. The spacer must be of a sufficient length and permissive amino acid composition to engage the HSP101 unfoldase component of PTEX to be efficiently translocated into the RBC compartment.

CP1.2: Omics & Informatics 3 min talks

Time: Wednesday, 06/Sept/2023: 12:00pm - 12:05pm · *Location:* Symposium room 1
Session Chair: Katja Fischer, QIMR Berghofer MRI

ID: 265 / CP1.2: 1
Contributed abstract
Conference Topics: Immunology, Host-parasite interactions
Keywords: Schistosoma mansoni blood fluke

Winners vs. Losers - comparative transcriptomic analysis of *Schistosoma mansoni* mature and immature eggs from gut and liver

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Schistosoma mansoni blood fluke eggs cause chronic schistosomiasis symptoms. It is important to note, however, that only "loser" eggs trapped in host tissues, mainly the liver, cause these effects. "Winner" eggs attach to mesenteric vein endothelium, inducing granuloma growth that aids passage through the intestinal wall to the environment. "Loser" eggs carried by the bloodstream to non-specific tissues also develop but don't survive. Despite being a parasite life cycle dead end, studies focus on liver-trapped "losers" rather than gut-attached "winners," raising questions about egg gene expression's tissue influence. Our study isolated *S. mansoni* eggs from infected mice's liver and intestinal tissues, comparing mature and immature eggs' transcriptomic profiles and viability. Results show gene expression depends massively on tissue localization. While mitochondrial genes and VALs are significantly upregulated in intestinal eggs, primary egg immunomodulators IPSE/alpha-1, Omega-1, and most micro-exon genes (MEGs) are confined to liver eggs. We argue that fifferential expression of key molecules directly reflect egg environment. Up-regulated molecules in gut eggs likely aid external passage, while high immunomodulator expression in liver-trapped eggs may bait the immune system for intestinal egg benefit. This study underscores how egg location crucially impacts gene expression and biological function.

S1: Symposium 1 Livestock sponsored by Virbac

Time: Wednesday, 06/Sept/2023: 10:30am - 11:00am · *Location:* Symposium room 2
Session Chair: Aleta Knowles, Virbac

ID: 137 / S1: 1
Invited speaker abstract

An Australian vaccine and improved genome assemblies for *Tritrichomonas foetus*.

Ala Tabor
The University of Queensland, Australia

In North Australian extensively grazed beef herds, losses from confirmed pregnancy to weaning are typically in the order of 5-15% with the cost to industry estimated at $AUD60-100m/year. A recent abattoir survey undertaken across Northern Australia indicated that one in 10 culled bulls were infected with *Tritrichomonas foetus* diagnosed using qPCR. This prompted the development of an Australian vaccine for trichomoniasis. After generating pure cultures from two *T. foetus* positive bulls from Qld and NT, a preliminary vaccine pilot trial was conducted in six bulls using an established experimental bovine model of genital *T. foetus* infection. Bulls were vaccinated with two doses of inactivated whole cells of *T. foetus* one month apart (Qld isolate) and challenged with live *T. foetus* parasites (NT isolate). The preliminary trial demonstrated 67% efficacy in older mixed breed, cull bulls with 2 of the 6 vaccinated bulls remaining consistently positive after challenge. These two isolates were sequenced using Oxford Nanopore Technologies to yield genome lengths of 110 and 111.7 Mbp at 99.2% similarity with 194 and 226 contigs respectively. These genome assemblies have improved previous *T. foetus* and *Trichomonas vaginalis* genomes with 10 to 100-fold less contigs assembled. Future research will confirm Australian *T. foetus* genomic conservation and undertake larger vaccine trials towards product registration.

CP2: Livestock 15 min talks sponsored by Virbac

Time: Wednesday, 06/Sept/2023: 11:00am - 11:45am · *Location:* Symposium room 2
Session Chair: Aleta Knowles, Virbac

ID: 144 / CP2: 1
Contributed abstract
Conference Topics: Livestock Parasites, Genomics, Helminthology, Host-parasite interactions
Keywords: Ascaris, Chemosensation, Microfluidics

Chemosensation in *Ascaris* Infection

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Ascaris spp. infects ~750 million people globally, causing malnutrition and stunting. Current treatment strategies are curative but do not protect against reinfection. Control of ascariasis requires regular deworming by chemotherapeutics. Maintaining mass deworming programs is expensive and risks the emergence of drug resistance. Investigating the early stages of *Ascaris* infection may provide new prevention approaches. Recent studies suggest chemosensation may guide the migration of *Ascaris* larvae through the host's liver and lung during infection. Targeting these systems could provide opportunities to prevent *Ascaris* infection. However, current work on the *Ascaris* chemosensory system remains understudied. Using larval migration assays and microfluidic chambers, we show *Ascaris* larvae respond chemotactically to the host liver, displaying behaviours consistent with those described for *Caenorhabditis elegans*. We curated *Ascaris suum's* putative chemosensory genes *in silico*; these genes are transcriptionally enriched in head/amphidal tissues and up-regulated in freshly hatched larvae upon exposure to liver homogenates. Finally, we used confocal imaging to map the chemosensory neurons of *A. suum* larvae and confirmed their anatomical orthology with *C. elegans*. This will support future neuron-specific studies of *Ascaris* larvae. Further research will identify target-receptor interactions underlying this chemosensory behaviour and assess their potential to block chemotaxis and impede hepatopulmonary migration.

ID: 113 / CP2: 2
Contributed abstract
Conference Topics: Veterinary Parasitology, Ectoparasites, Immunology, Livestock Parasites, Host-parasite interactions
Keywords: Breech strike resistance, blowfly strike, Immunohistochemistry, Cytokine, Immune response

Breech-strike resistant and susceptible sheep: A comparative analysis

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Breech strike is commonly caused by the blowfly *Lucilia cuprina*; which lays eggs on sheep resulting in open wounds where maggots feed. Host responses in breech strike-resistant sheep (CSIRO, Armidale NSW) to non-selected sheep were compared following an implant challenge with *L. cuprina* eggs. Within 31 hours post-egg implantation skin biopsies from challenge and mock sites were collected. Histology and immunohistochemical analysis showed a large infiltration of leukocytes into the infected sites including a significant influx of CD4+, CD8+, γδ + T cells, T19+ cells, CD45RA+ cells and CD1+ cells compared to the mock sites. Using a milliplex ovine cytokine kit, significant increases ($P<0.05$) in IL-1α, IL-6, IL-8, IL-17a, and MIP-1a were observed in infected sites compared to mock sites, while there were no differences in IL-4 and IP-10 levels. IL-10, TNF-α, IFN-γ and IL-1β were not detected at any sites. While our analysis of both cellular and cytokine levels showed some significant differences between infected versus mock sites there were no significant changes between the breech strike resistant and non-selected sheep using the immunological parameters measured, suggesting that the measured innate immune response may not be important in conferring resistance to breech strike in these selected sheep.

ID: 134 / **CP2: 3**
Contributed abstract
Conference Topics: Veterinary Parasitology, Drugs, Livestock Parasites
Keywords: Anthelmintics, Goats, Resistance, Nematodes, Australia

Assessment of anthelmintic efficacy across meat goat farms in southern Queensland and northern New South Wales.Authors: K. T. Dawson[1], S. J. Meale[1], E. K. Doyle[2], B. Hine[3], A. M. Beasley[11]School of Agriculture and Food Science, The University of Queensland, Gatton, QLD, Australia[2]School of Environmental and Rural Science, The University of New England, Armidale, NSW, Australia[3]CSIRO Livestock Industries, Armidale, NSW

Kathryn Dawson[1], Anne Beasley[1], Sarah Meale[1], Emma Doyle[2], Brad Hine[3]
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Anthelmintic resistance (AR) in gastrointestinal nematodes (GIN) is a major constraint of goat producers worldwide, however, the extent of AR on Australian meat goat farms is unknown. The present study surveyed eleven meat goat farms from southern Queensland (n=5) and northern NSW (n=6) for resistance to a range of registered and 'off-label' anthelmintics using faecal egg count reduction (FECR) tests. On each farm, 150 goats shedding a minimum of 150 epg were randomly distributed into treatment groups (n=15) and administered treatment at 1.5x the recommended sheep dose based on body weight. Up to 10 anthelmintics were tested per property: abamectin, moxidectin, levamisole, fenbendazole, doramectin (pour-on), eprinomectin (pour on), monepantel + abamectin, derquantel + abamectin, abamectin + oxfendazole + levamisole, and finally abamectin + closantel + levamisole + albendazole. Resistance to single actives was more common across all properties than combination products. Results show emerging resistance to dual, triple, and quadruple combinations. Larval cultures from post treatment samples indicated that *Haemonchus contortus* and *Trichostrongylus colubriformis* were the predominant resistant genera. Correct use of anthelmintics and sustainable management practices are required to slow the development of AR.

CP2.1: Livestock 5 min talks sponsored by Virbac

Time: Wednesday, 06/Sept/2023: 11:45am - 12:00pm · *Location:* Symposium room 2
Session Chair: Aleta Knowles, Virbac

ID: 125 / **CP2.1: 1**
Contributed abstract
Conference Topics: Veterinary Parasitology, Vaccines, Immunology
Keywords: Genome, Pore-C, Tritrichomonas foetus, Vaccine

Journey into the Chromosomal Cosmos: Pore-C Exploration of *Tritrichomonas foetus* Genome and its Functional Implications

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Tritrichomonas foetus is a parasitic protozoan that causes a sexually transmitted disease in cattle, resulting in poor reproductive outcomes in infected cows. Vaccines have been limited to whole inactivated *T. foetus* relying on large scale protozoal culture (400L for 1000 doses). Reverse vaccinology offers an alternative approach to identify subunit candidates which has been hampered due to the lack of a comprehensive *T. foetus* genome.

Previously, an Australian *T. foetus* strain was sequenced using Oxford Nanopore Technologies (ONT) with an estimated genome size of 110 Mbp from 194 contigs at 67x coverage (unpublished). To improve the scaffolding of this draft assembly as well as to gain insights into the high-order 3D chromatin structure, this study will employ Pore-C, which is a method that utilizes ONT long read sequencing together with chromosome conformation capture (3C).

By using Pore-C, this study aims to provide insights into the genome organization of *T. foetus* and map the locations of interacting loci in the genome. This information could be used to identify genes that play a role in the parasite's biology, providing valuable information for further study and potential targets for vaccine development. An update on the progress will be presented and discussed.

ID: 192 / **CP2.1: 2**
Contributed abstract
Conference Topics: Apicomplexa Biology, Protozoa
Keywords: Coccidiosis, Eimeria, Global, Goat, Meta-analysis, Prevalence

Global Prevalence of *Eimeria* species in goats: A systematic review and meta-analysis

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Eimeria species are obligate intracellular protists that cause coccidiosis in various livestock animals including goats. This review aimed to appraise the literature on the prevalence of *Eimeria* spp. in goats, associated risk factors, and available methods used to identify *Eimeria* spp. Following the PRISMA guidelines for systematic reviews and meta-analysis, 261 articles were retrieved from five databases (PubMed, Web of Science, CAB Direct, Scopus and Google Scholar). The studies were conducted in 56 countries, spanning 6 continents, mainly from Asia (*n* = 133), Africa (*n* = 72) and Europe (*n* = 35). Forty-six percent of these studies (*n* = 122) identified *Eimeria* at the species level using the oocyst morphology, histopathology, and genetic characterisation of the small subunit of the nuclear ribosomal RNA (18S), mitochondrial cytochrome *c* oxidase 1, and the first internal transcribed spacer of the nuclear ribosomal DNA. Among the identified species, *Eimeria arloingi*, *E. ninakohlyakimovae,* and *E. caprina* were found to be the most prevalent. The findings of this study can serve as valuable

information for veterinarians, researchers, goat farmers, and policymakers to make informed decisions about the control of coccidiosis in goats.

ID: 239 / **CP2.1: 3**
Contributed abstract
Conference Topics: Veterinary Parasitology, Livestock Parasites
Keywords: Buffalo fly, cattle health

A comparison between visual scoring and a digital object counting platform to estimate buffalo fly counts on cattle.

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Buffalo fly (*Haematobia irritans exigua*) has a significant impact on cattle health, welfare, and production. Meat and Livestock Australia has recently ranked buffalo flies as the number one endemic disease for the Australian cattle industry. Accurate estimates of animal fly numbers are essential for evaluation of treatments, estimation of cattle breed susceptibility, and in the establishment of economic threshold levels for effective integrated pest management programs. Although essential, estimating fly numbers is difficult on a constantly mobile host. Estimation has been done with several different techniques including visual estimates, photographs, video, and infrared thermography. The current study uses digital images of buffalo fly infested cattle and compares a visual scoring method against an object counting digital platform. The two techniques were compared for consistency and agreement among 4 assessors. The results showed 99% consistency in fly counts within each assessor and 99% agreement in counts between assessors. This indicates that a digital counting platform can provide a useful and reliable count of buffalo fly numbers. A practical tool to assess buffalo fly infestation could be developed based on the methodology.

W1: One Health Workshop sponsored by Elsevier

Time: Wednesday, 06/Sept/2023: 10:30am - 12:00pm · *Location:* Workshop room 3
Session Chair: Malcolm Jones, University of Queensland

ID: 251 / **W1: 1**
Invited speaker abstract

10 years monitoring a *Taenia solium* 'hotspot' in Northern Laos.

Amanda Ash[1], Sarah Keatley[1], Breanna Knight[1], Kelly Taggart[1], Bounnaloth Insisengmay[2], Boualy Keokhamphavanh[2], Davina Boyd[1], Malavanh Chittavong[3]
[1]Murdoch University, Perth, Australia; [2]Ministry of Health Lao PDR; [3]National University of Lao PDR

Taenia solium is a zoonotic parasite transmitted between pigs and people and is a major cause of acquired epilepsy (neurocysticercosis) in endemic countries. In 2013 a village in northern Lao PDR was identified as a 'hotspot' for T. solium infections in the human population. In 2014 a human/pig therapeutic intervention was conducted aimed at eliminating T. solium from this same village. This intervention involved two Mass Drug Administrations (MDA) for village residents and treatment of village pigs with anti-cysticercosis TSOL18 vaccination and oxfendale. At the same time education material was delivered on food safety and hygiene practices. The dual impact of this anthelmintic regime on soil transmitted helminths within the community was also monitored and provided additional evidence for a multi-pronged approach targeting multiple parasitic infections.
The sustainability of this human/livestock intervention was monitored in 2015, 2019 and 2023 with the results identifying significant changes both positive and negative within the village.

ID: 247 / **W1: 2**
Invited speaker abstract

Diagnostics assays to inform One Health programs

Rebecca Traub
Parasitology Consultant, Newport, VIC, Australia

A plethora of established and emerging diagnostic assays ranging from conventional microscopy and serology to molecular-, proteomic- and artificial intelligence-based assays are becoming increasingly available to inform the epidemiology and monitor the success of One Health programs. The first step in selecting and implementing any diagnostic test, however, is to determine the assay's intended use. Diagnostic tests that map endemic foci of a zoonotic parasitic disease may not necessarily be appropriate for evaluating intervention efforts aimed at the complete elimination of the parasite in a low-transmission setting. Further considerations include the diagnostic test's performance parameters, cost, the availability of skilled technical personnel, the requirement of sample-to-result turn-around times, the scale of sampling, and the availability of sample types. These considerations will be discussed in relation to the choice of diagnostic assays, using examples.

ID: 250 / **W1: 3**
Invited speaker abstract

Economics for One Health interventions

Andrew Larkins
School of Medical, Molecular and Forensic Sciences, Murdoch University, Perth, Australia

Decision makers are frequently required to justify their investments as cost-effective and efficient. Economic analyses are used to support these decisions and can be key to attracting political and financial support to scale up successful projects. However, economic evaluations are often lacking in One Health research. Why are such evaluations missing and what is required to include economic evaluations as part of One Health interventions? This session will introduce the basics of disability-adjusted

life years, cost-effectiveness, and cost-benefit analyses whilst highlighting key considerations when collecting and analysing economic data for One Health.

S2: Symposium 2 Immunology & Pathogenesis

Time: Wednesday, 06/Sept/2023: 1:00pm - 1:30pm · *Location:* Symposium room 1
Session Chair: Brendan McMorran, Australian National University

ID: 246 / S2: 1
Invited speaker abstract

Molecular and Serological Studies of *Plasmodium* sp. in Indonesia during the Era of Malaria Elimination

Rintis Noviyanti[1,2]
[1]National Research and Innovation Agency (BRIN), Indonesia; [2]Exeins Health Initiative (EHI), Jakarta, Indonesia

Attempts to eliminate malaria by 2030 require massive and systematic efforts supported by high quality research in molecular and serological aspects to fight these tenacious parasites. As a malaria endemic region, Indonesia has a wide range of malaria transmission, with the highest transmission occurring in Papua, Eastern part of Indonesia. Five *Plasmodium* species infecting human are currently present in Indonesia. In areas where malaria control program has been successfully applied, positive cases have emerged due to human migration, undetectable form of hypnozoites, and zoonotic malaria.

The ability to perform molecular and serological diagnostics is critical to accurately identify the parasites to determine the most appropriate treatment for the infected individuals. High-resolution genotyping using next generation sequencing has improved our understanding on the effect of the intervention including anti-malarial drug treatments and vaccine, raising importance of developing this capacity in Indonesia. Studies on malaria genomics have been able to depict different population genetic structures of the two major malaria parasites: *P. falciparum* and *P. vivax.*

We have also validated serological markers to predict individuals with risk of relapses, thus more likely to harbor hypnozoites in their body. Using a panel of *P. vivax* antigens, our study has been able to identify people with recent *P. vivax* infection and those who will experience a relapse. PCR was used to confirm the serological results. The findings will help improve the strategy to target *P. vivax* infection particularly those with relapse potentials.

The research conducted by our group described above has been done with support from the government of Indonesia and our international partners. The outcomes will help in identification of appropriate molecular and serological diagnostic tools to be implemented in the targeted area. These will ultimately empower effective malaria control strategy in the country.

CP3: Livestock 15 min talks sponsored by Virbac Australia

Time: Wednesday, 06/Sept/2023: 1:00pm - 2:15pm · *Location:* Symposium room 2
Session Chair: Aleta Knowles, Virbac

ID: 104 / CP3: 1
Contributed abstract
Conference Topics: Drugs
Keywords: high throughput screening (HTS); drug discovery; target deconvolution; parasitic nematode; Haemonchus contortus

Discovery of novel anthelmintics and parasite-specific targets using a phenotypic-guided approach and thermal proteome profiling

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Parasitic nematodes (roundworms) cause destructive diseases and suffering in humans and other animals worldwide. Although the control of these worms relies on anthelmintic treatment, resistance to these drugs and treatment failures are common. As effective vaccines against parasitic nematodes are scant, there is a need for new interventions including anthelmintics with novel modes of action, in order to circumvent drug-resistant worms. In our drug discovery program, using a high-throughput whole-worm, phenotypic screening platform, we have identified and evaluated anthelmintic candidates that are now undergoing structure-activity relationship (SAR) studies and optimisation. We employ *Haemonchus contortus* (barber's pole worm) and *Caenorhabditis elegans* ('elegant worm') to test nematocidal activity and potency. Currently, we are studying the pharmacology of novel candidates via thermal proteome profiling, and inferring the targets of these candidates in *H. contortus*, *C. elegans* and other important parasitic nematodes. These candidates are also undergoing testing for efficacy and safety. The present "hit-to-target" pipeline should accelerate discovery efforts.

ID: 208 / CP3: 2
Contributed abstract
Conference Topics: Veterinary Parasitology, Livestock Parasites, Helminthology, Host-parasite interactions, Zoonoses
Keywords: 3D cell culture, liver fluke, invasion, cysteine proteases, zoonosis

A parasite's playground: Co-culture with HepG2 spheroids supports *Fasciola hepatica* growth and development *in vitro*

Aiste Vitkauskaite, Emma McDermott, Richard Lalor, Carolina De Marco Verissimo, Mahshid Hussein Dehkordi, Kerry Thompson, Howard Fearnhead, John Pius Dalton, Nichola Eliza Davies Calvani

The University of Galway, Ireland

Fasciola hepatica is a significant cause of animal and human morbidity worldwide. Part of the difficulty in developing new chemotherapeutics and vaccines for the control of Fasciolosis lies in our inability to culture and propagate juvenile worms *in vitro*. Several laboratories maintain *F. hepatica* short-term in simple media, but these lack biological relevance. Here we show that the infective stage of the parasite, the newly excysted juvenile (NEJ), exhibit significant growth and development when co-cultured with spheroids derived from HepG2 cells, a human non-tumorigenic liver cell line. We investigated parasite development using antibody probes against two major NEJ proteases, FhCL1 and FhCL3, and by scanning electron microscopy (SEM). Parasites co-cultured with HepG2 spheroids exhibit not only a rapid increase in size, but also extensive development of the gut caecum, musculature, and tegument. Parasites were observed regularly invading the spheroids, indicating the importance of tactile stimuli. There was also evidence of parasites 'grazing' on the cells of the spheroids. We propose that the methodology developed here mimic *in vivo* parasite host liver interactions, greatly improving our ability to investigate and understand *F. hepatica*-host biology with future prospects for the development of new parasite control methods, such as vaccines and anthelmintic drugs.

ID: 163 / CP3: 3
Contributed abstract
Conference Topics: Veterinary Parasitology, Diagnostics, Molecular Biology, Helminthology
Keywords: Helminth, miRNA, diagnostic biomarker, Fasciola hepatica

Assessing helminth microRNAs as potential biomarkers for the diagnosis of acute fasciolosis

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Management of parasitic infections on farms depends on early detection so control measures can be implemented without delay. Like most helminths, diagnosis of *Fasciola hepatica* infection relies on the detection of eggs in faeces or the quantification of circulating antibodies. Although specific, both methods lack sensitivity, only detecting infection after 3 weeks, at which point parasites have already entered the liver, causing the pathology leading to reduced bodyweight and loss in productivity.

In this study, we explored the diagnostic potential of miRNA expression during Fasciola infection. Using a longitudinal animal field trial, small RNA sequencing was performed on sera collected from sheep from day 0 to 14 weeks after infection (n= 6). This provided a panel of four sheep and two parasite miRNAs that were differentially expressed throughout infection. The expression of these markers was validated by RT-qPCR in sheep sera from a second trial with a larger cohort of infected sheep, and compared to age-matched uninfected sheep (n=5-11). This analysis revealed the differential expression of miRNAs as the sheep aged, independently of infection, and uncovered the presence of miRNA sequence variants (isomiRs). From this analysis we identified fhe-miR-124-5p as a potential diagnostic marker of pre-hepatic infection by *Fasciola hepatica*.

ID: 117 / CP3: 4
Contributed abstract
Conference Topics: Veterinary Parasitology, Drugs, Proteomics, Livestock Parasites, Helminthology
Keywords: Anthelmintics, parasitic nematodes, drug discovery, phenotypic screen, small molecules

Identification and structure-activity relationship investigation of a new anthelmintic chemotype

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Parasitic roundworms (nematodes) cause infections and diseases (nematodiases) in humans and animals and have a major adverse socioeconomic impact worldwide. Human helminth infections disproportionately affect poverty-stricken communities, and global agricultural losses attributed to nematodiases are estimated at tens of billions of dollars. The excessive use of anthelmintic compounds to treat livestock animals has led to widespread resistance to these drugs, such that there is a need for new anthelmintic chemotypes with distinctive mechanisms of action.

To discover such chemotypes, we screened the Medicines for Malaria Venture (MMV) *Pandemic Response Box* of compounds against two model nematode organisms, the free-living *Caenorhabditis* and its relative *Haemonchus contortus*. This screen, conducted using an established phenotypic platform, identified compound ABX464, which significantly inhibited motility and the development of *C. elegans* and/or *H. contortus* stages in the low micromolar range. This presentation will focus on our efforts to define the structure-activity relationship of ABX464 as a nematicide and to unravel its mechanism of action.

ID: 114 / CP3: 5
Contributed abstract
Conference Topics: Veterinary Parasitology, Drugs, Ectoparasites, Livestock Parasites, Molecular Biology
Keywords: RNA interference, Blowfly, sheep, Insecticide resistance, dsRNA

Screening for new drug targets against *Lucilia cuprina*, the Australian sheep blowfly, using RNAi

Sugandhika Welikadage[1], Shilpa Kapoor[1], Ting Yang Ying[2], Laura Wines[2], Jean-Pierre Scheerlinck[1], Clare Anstead[1], Trent Perry[2], Simon Baxter[2], Vern Bowles[1]

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Development of resistance to insecticidal products available for controlling flystrike necessitates the need to find new targets in *Lucilia cuprina*. Changes in gene expression were compared between larvae collected from fly-struck sheep and control populations reared on an artificial diet, with the aim of identifying specific proteins essential for parasitism and potential drug

targets. Using transcriptomic and proteomic data, we identified a group of genes and their corresponding proteins that were upregulated during the earliest events of flystrike. Eighty candidates were further filtered using selection criteria that included lethality and phenotypic data from the model organism *Drosophila melanogaster*. Six protein-coding genes were selected for evaluation using RNA interference (RNAi), which involves treatments of double-stranded RNA (dsRNA) to silence the selected genes in *Lucilia cuprina* larvae. Two approaches for delivering dsRNA, include embryo microinjection, or soaking embryos in solution. Phenotypic observations together with quantitative-PCR will be used to assess the efficacy of gene silencing and the function of these specific gene targets

CP3.1: Livestock sponsored by Virbac 5 min talks

Time: Wednesday, 06/Sept/2023: 2:15pm - 2:30pm · *Location:* Symposium room 2
Session Chair: Aleta Knowles, Virbac

ID: 188 / CP3.1: 1
Contributed abstract
Conference Topics: Genomics, Helminthology, Bioinformatics
Keywords: Parasitic nematode, Haemonchus contortus, protease and protease inhibitor, proteome, bioinformatic workflow

Genome-wide analysis of *Haemonchus contortus* proteases and protease inhibitors using an advanced informatic workflow, and its implications

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Here, we constructed and assessed the first sequence- and structure-based informatic workflow to identify, classify and annotate proteases and protease inhibitors of *Haemonchus contortus* – a highly pathogenic parasitic nematode. This workflow performed markedly better than conventional, sequence-based classification and annotation alone, and allowed the first genome-wide characterisation of protease and protease inhibitor genes and gene products in this worm. In total, we identified 790 genes encoding 860 proteases and protease inhibitors representing 83 gene families. The proteins inferred included 280 metallo-, 145 cysteine, 142 serine, 121 aspartic and 81 'mixed' proteases as well as 91 protease inhibitors, all of which had marked physicochemical diversity and inferred involvements in > 400 biological processes or pathways. Detailed study revealed a remarkable expansion of some protease or inhibitor gene families, which are likely linked to parasitism (e.g., host-parasite interactions, immunomodulation and blood-feeding) and exhibit stage- or sex-specific transcription profiles. This investigation lays a foundation for conducting comprehensive explorations of proteases and protease inhibitors in *H. contortus* and related nematodes, and might facilitate the discovery of novel drug or vaccine targets.

ID: 219 / CP3.1: 2
Contributed abstract
Conference Topics: Veterinary Parasitology, Apicomplexa Biology, Livestock Parasites
Keywords: Toxoplasma gondii, small ruminants

Risk Factors Associated with Increased Toxoplasma gondii Seroprevalence in South Australian Sheep

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Toxoplasma gondii has substantial impact to small ruminants, with reproductive failure a possible outcome of exposure. This study aimed to assess *T. gondii* prevalence within the South Australian sheep population and investigate on-farm risk factors to exposure via a cross-sectional survey. 1445 individual animals were serologically screened for *T. gondii*-specific antibodies. A risk-analysis questionnaire was conducted for each property. Seroprevalence was 37%, with a flock level seroprevalence of 100%. Seroprevalence was found to be higher in sheep on Kangaroo Island (46.6%) compared to the South Australian mainland (31.3%), however this difference was not statistically significant (P=0.125). A highly significant association was observed between *T. gondii* seroprevalence and age, with seroprevalence increasing from 30.2% in one year old sheep, to 69.7% in sheep older than six years (P=0.001). An individual animal exposed to a surface water source was found to be more than ten times as likely to be exposed to *T. gondii*, than an animal sourcing only reticulated mains water (odds ratio:10.68; 95% CI 1.30 to 87.88). Mitigation strategies should be further developed and targeted at reducing contact between oocysts and water sources and reducing interaction between livestock and contaminated water.

ID: 180 / CP3.1: 3
Contributed abstract
Conference Topics: Veterinary Parasitology, Ectoparasites, Livestock Parasites, Invasive Species
Keywords: Haemaphysalis longicornis, microbiome, endosymbionts, bush tick

Microbiome of the bush tick (*Haemaphysalis longicornis*): the current state of the play

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Haemaphysalis longicornis, a three-host tick, is an important vector of numerous bacterial, protozoal, and viral pathogens, and widely distributed in Australia, eastern Asia, New Zealand, and the USA. We systematically reviewed the literature on the microbiome of *H. longicornis* using PRISMA guidelines. Our inclusion criteria identified 240 studies from four databases (Web of Science, PubMed, Scopus and CAB Direct). Most studies focused on identifying "pathogen" components of the tick microbiome, including bacteria (*Anaplasma*, *Borrelia*, *Bartonella*, *Coxiella*, *Ehrlichia*, *Francisella* and *Rickettsia*), viruses (Dabie bandavirus, Heartland bandavirus, Powassan virus and Nairobi sheep disease virus) and protists (*Babesia*, *Hepatozoon*, *Theileria* and *Toxoplasma*). Additionally, endosymbionts such as *Arsenophonus*-like, *Coxiella*-like and *Rickettsia*-like were also

detected in ticks. Our findings suggest that the microbiome of *H. longicornis* plays a significant role in tick's life cycle and its capability to transmit several microorganisms to humans and animals. Future investigations should encompass the "non-pathogen" microbiome components of *H. longicornis* to understand their role in tick biology and the transmission of pathogens to develop sustainable strategies for controlling ticks and tick-borne diseases.

CP4: Immunology & Pathogenesis 15 min talks

Time: Wednesday, 06/Sept/2023: 1:30pm - 2:00pm · *Location:* Symposium room 1
Session Chair: Brendan McMorran, Australian National University

ID: 120 / CP4: 1
Contributed abstract
Conference Topics: Proteomics, Host-parasite interactions, Protozoa
Keywords: Trichomonas vaginalis, microbiome, extracellular vesicles

Lessons from a parasite and commensals: bacterial extracellular vesicles modulate the pathogenicity of *Trichomonas vaginalis* mirroring protozoan-bacterial interactions

Anastasiia Artuyants[1], Jiwon Hong[2], Priscila Dauros-Singorenko[2], Anthony Phillips[2], Augusto Simoes-Barbosa[1]
[1]School of Biological Sciences, University of Auckland, New Zealand and; [2]Surgical and Translational Research Centre, University of Auckland, New Zealand

Trichomonas vaginalis causes trichomoniasis, the most prevalent non-viral sexually transmitted infection globally. Our research, alongside others, has revealed the significant impact of human vaginal bacterial commensals on *T. vaginalis* pathogenesis. The vaginal microbiome consists of a limited number of culturable bacterial species, that have been well categorized into eubiosis or dysbiosis. Trichomoniasis is accompanied by a dysbiotic vaginal microbiome. Our study demonstrates that two key bacterial species, *Lactobacillus gasseri* in eubiosis and *Gardnerella vaginalis* in dysbiosis, release extracellular vesicles (EVs) with distinct protein content. Using SWATH-MS proteomics, we identified species-specific protein cargoes linked to their ecological roles in the vaginal biome. *G. vaginalis* EVs contained elevated levels of cytotoxic factors, while *L. gasseri* EVs carry host-protective proteins. Importantly, we found that these bacterial EVs selectively alter the responses of the protozoan parasite and human ectocervical cells, either protecting against or exacerbating pathogenicity, and mimicking previous observations for the bacterial species that produce these vesicles. These findings highlight the central role that EVs from commensal bacteria of a particular microbiome play in mediating host-parasite interactions, providing new insights into parasitic disease pathogenesis and potential novel treatments.

ID: 126 / CP4: 2
Contributed abstract
Conference Topics: Drugs, Biochemistry, Helminthology, Host-parasite interactions
Keywords: wound healing, liver fluke, granulin, peptide, therapeutics

Saving diabetic feet from chronic wounds: developing a wound healing peptide inspired by the *Opisthorchis viverrini* fluke granulin growth factor.

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Parasitic worms are large, invasive pathogens. Liver flukes, such as *Opisthorchis viverrini,* evolved strategies to promote wound repair in infected hosts likely to combat the pathogenesis they induce. These powerful repair mechanisms can be hijacked for advanced wound healing treatments and may be useful weapons against chronic non-healing wounds, a growing problem for diabetics, smokers, and the elderly. These devastating wounds cost the world $50 billion annually to treat and result in devastating consequences with ~10% patients requiring amputations (~1 million annually). One worm protein with therapeutic potential is the potent wound healing granulin growth factor. Inspired by granulin, we have developed an easily and cheaply produced peptide as a wound healing treatment candidate. Initially we improved on the native sequence by removing prolines that induce "structural kinks" and doubled both healing and production yields. The peptide significantly stimulated human fibroblast proliferation and keratinocyte cell line migration over a surprisingly wide 0.1-100 nM range. Human *ex-vivo* skin healing shows significant 35% healing stimulation and pig healing is improved 26%. We plan to develop this unique peptide product as a treatment to help heal the millions of patients worldwide in the war against diabetes and other chronic non-healing wounds.

CP4.1: Immunology & Pathogenesis 5 min talks

Time: Wednesday, 06/Sept/2023: 2:00pm - 2:15pm · *Location:* Symposium room 1
Session Chair: Brendan McMorran, Australian National University

ID: 100 / CP4.1: 1
Contributed abstract
Conference Topics: Malaria, Apicomplexa Biology, Molecular Biology
Keywords: Malaria, quantitative imaging, invasion

The essential cytosolically exposed rhoptry leaflet interacting proteins and their role in RBC entry.

Benjamin Liffner[1], Miguel Balbin[1], Sonja Frölich[1], Gerald J. Shami[2], Ghizal Siddiqui[3], Jan Strauss[4], Boyin Liu[2], Arne Alder[4,5], Jan Stephan Wichers[4,5], Stuart Ralph[2], Darren J. Creek[3], Leann Tilley[2], Matthew Dixon[2,6], Tim Gilberger[4,5], Danny Wilson[1,7]

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Malaria merozoite invasion is a complex process that requires coordinated secretion of ligands from invasion organelles such as the rhoptries. We recently characterised two proteins, the cytosolically exposed rhoptry leaflet Interacting proteins (PfCERLI) 1 and 2, and their role in rhoptry secretion. Comparison of *Pfcerli* phylogeny across published apicomplexan genomes suggests that *Pfcerli2* most likely arose from a duplication of the ancestral gene *Pfcerli1*, with divergence of their sequence suggesting they have undergone sub-functionalisation. Using semi-quantitative super-resolution microscopy, both PfCERLI1 and 2 were found to localise to the rhoptry bulb of merozoites. Failure to knock-out the proteins indicates that they have an important role in blood stage parasite growth. Knock-down of PfCERLI proteins led to inhibition of merozoite invasion either before (PfCERLI1) or around (PfCERLI2) tight-junction formation. These phenotypes were associated with changes in rhoptry antigen distribution and in the dimensions of the rhoptry as quantitated using fluorescence and electron microscopy respectively. Collectively, these data implicate PfCERLI1 and 2 as proteins essential for correct rhoptry formation and function, and also demonstrate the utility of super-resolution imaging to explore the function of proteins required for malaria parasite invasion of the host RBC.

ID: 146 / **CP4.1: 2**
Contributed abstract
Conference Topics: Malaria, Vaccines, Immunology
Keywords: Malaria, Vaccines, Immunology, RTS, S, Protection

Defining the fine specificity of antibody responses to polymorphic epitopes of the lead malaria vaccine antigen *Plasmodium falciparum* circumsporozoite protein.

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RTS,S is the only malaria vaccine recommended for at-risk children; however, it confers only modest protection against disease. RTS,S is based on the *Plasmodium falciparum* circumsporozoite protein (*Pf*CSP) of the lab-adapted 3D7 strain.The vaccine construct comprises a truncated form of the central repeat region including only 19 NANP repeats (excluding the minor NVDP repeat) and the C-terminal region of *Pf*CSP. The central repeat region is disordered forming epitopes that vary by the number of NANP/NVDP. The C-terminal region is highly polymorphic, whereby the 3D7 RTS,S strain represents <10% of circulating African parasite isolates. We hypothesise that RTS,S-induced immune responses will be impacted by polymorphisms in *Pf*CSP.

We defined the specificity of RTS,S-induced antibodies to peptides (n=21) representing variable central repeat and polymorphic C-terminal *Pf*CSP epitopes. We evaluated children from an RTS,S phase IIb clinical trial (n=735) in Mozambique and demonstrated that antibody binding increased with the number of NANP repeats in a sequence; however, short NANP sequences may better represent protective *Pf*CSP epitopes. Furthermore, antibody binding was reduced to non-3D7 *Pf*CSP prevalent in African parasites, which may contribute to suboptimal vaccine efficacy. Our findings reveal how polymorphisms in *Pf*CSP impact RTS,S-induced immunity and protection in malaria endemic populations.

ID: 222 / **CP4.1: 3**
Contributed abstract
Conference Topics: Malaria, Apicomplexa Biology
Keywords: Plasmodium knowlesi, Plasmodium falciparum, P. vivax, malaria

Differential importance of malaria MSP5 and MSP4 between *Plasmodium knowlesi* and *Plasmodium falciparum* during invasion of human erythrocytes

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During human infection, asexual *Plasmodium* spp. malaria parasites undergo cycles of replication within erythrocytes where they cause disease. Merozoites are the form which invade erythrocytes, but little is known regarding merozoite cell-entry biology, particularly for *P. vivax* which has yet to be *in vitro* culture adapted. Merozoite surface proteins (MSPs) are proposed to play a role in attachment of merozoites to erythrocytes and have long been considered as potential vaccine targets. Here, I applied targeted gene editing which revealed the zoonotic *P. knowlesi* (a model species for *P. vivax*) MSP5 is refractory to gene deletion, but it could be functionally replaced by *P. vivax* MSP5. Conditional knock-down of *Pv*MSP5 protein expression revealed that this protein is essential for *P. knowlesi* blood stage parasite growth. Live cell microscopy revealed a severe cell-entry defect with *Pv*MSP5 knock-down prior to formation of the tight-junction. Conversely, deletion of MSP5 from *P. falciparum* had no phenotype, whereas conditional knock-down of *Pf*MSP4 was detrimental to blood stage parasite replication, confirming it is essential for this species. This study emphasises *P. vivax* MSP5s potential as a vaccine candidate and highlights the importance of characterising vaccine candidates individually for the two most prominent human malarias.

CP4.2: Immunology & Pathogenesis 3 min talks

Time: Wednesday, 06/Sept/2023: 2:15pm - 2:35pm · *Location:* Symposium room 1
Session Chair: Brendan McMorran, Australian National University

ID: 181 / CP4.2: 1
Contributed abstract
Conference Topics: Drugs, Proteomics, Cell Biology, Biochemistry, Immunology, Molecular Biology, Host-parasite interactions
Keywords: N.americanus, T2D, Therapeutic, secretome, excretory/secretory proteins

Necator americanus recombinant proteins as novel type 2 diabetes therapeutics

Connor McHugh, Suchandan Sikder, Kim Miles, Maxine Smith, Darren Pickering, Yide Wong, Roland Ruscher, Paul Giacomin, Alex Loukas
James Cook University

The prevalence of Diabetes is at pandemic levels, affecting 1 in 10 adults globally. The rapid rise of type 2 diabetes (T2D) has coincided with a lack of effective treatments and preventative therapeutics. According to epidemiology and de-worming studies, helminth infections share an inverse relationship with T2D. Experimental human infection with the hookworm *Necator americanus* has demonstrated improved insulin sensitivity in pre-diabetic individuals (Preprint, DOI: 10.1101/2023.03.16.23287372). *N.americanus* regulates their host immune response via the active release of excretory/secretory proteins (ESP) into the host tissues, which promotes a T helper type 2 (TH2) immune response. This project aims to identify bioactive recombinant ESP that have potential therapeutic value for T2D and other inflammatory diseases. The *N.americanus* secreted proteome was recombinantly produced in mammalian cells and then screened in a range of *in vitro* and *in vivo* assays to identify proteins that induce potentially therapeutic TH2 responses. Candidate proteins are currently undergoing *in vivo* assessment in a mouse model of diet induced T2D. Ultimately, this project aims to identify one or more *N. americanus* protein/s that protect against the onset of T2D and underpin future clinical development and testing of an entirely safe and novel biologic.

ID: 172 / CP4.2: 2
Contributed abstract
Conference Topics: Veterinary Parasitology, Vaccines, Immunology, Livestock Parasites, Helminthology, Host-parasite interactions, One Health
Keywords: mRNA vaccine, Schistosomiasis, Triose phosphate isomerase, Insulin receptors, Immunology

Development of mRNA-based transmission blocking vaccines against zoonotic schistosomiasis

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Schistosomiasis is the second most devastating tropical disease, affecting over 200 million people annually. In Asia, about 120,000 people die from *Schistosoma japonicum* infections, where water buffalo account for 75% of egg transmission. A mathematical model of schistosome transmission predicts that schistosome vaccines, capable of reducing faecal egg output by 45% in water buffalo, in conjunction with PZQ treatment, will lead almost to the point of elimination within 10 years.

In this PhD project, we will generate mRNA vaccines targeting two key genes encoding critical proteins for parasite survival, a triose phosphate isomerase and a surface-linked insulin receptor. The molecules act in metabolism of adult *S. japonicum*, by regulating glucose uptake. We will test the vaccine efficacy and immunological response in murine model immunised with the single or multivalent mRNA vaccines. If successful in fully/partially protecting mice against challenge infection, the vaccines will be translated to test efficacy in the natural infections of the caribou reservoir host. It is anticipated that the targets will be the basis of efficacious transmission-blocking mRNA vaccines. On field deployment, these One Health vaccines will result in a substantial flow-on reduction in human schistosomiasis with clear positive public health outcomes.

ID: 241 / CP4.2: 3
Contributed abstract
Conference Topics: Immunology, Helminthology
Keywords: Inflammatory bowel diseases, Hookworms

A potential helminth-derived therapeutic for early life inflammatory bowel disease

Maxine Smith, Kim Miles, Connor McHugh, Paul Giacomin, Alex Loukas, Roland Ruscher
Australian Institute of Tropical Health and Medicine, James Cook University, Cairns, QLD.

Inflammatory bowel diseases (IBD), including ulcerative colitis and Crohn's disease, are chronic inflammatory disorders that affect millions worldwide and currently has no cure. Pediatric IBD often presents as a more aggressive disease than IBD in adults, contributing to 25% of the overall cases. These heterogeneous diseases are prevalent in westernised countries, where the widespread use of antibiotics and excessive sanitation have reduced exposure to many beneficial organisms. Research has indicated that external stimuli from essential co-evolutionary commensal organisms may play a vital role in regulating the immune system. These organisms include the microbiota, and the less well-appreciated macrobiota such as gastrointestinal hookworms. Hookworms, secrete a plethora of bioactive molecules with immunomodulatory properties, some of which have anti-inflammatory capacities. We expressed individual hookworm-derived proteins to identify potential therapeutic properties during chronic inflammatory conditions. One recombinant protein effectively reduced disease severity and alleviated inflammation induced by experimental colitis in mice prior to sexual maturity. We now seek to understand the mechanism of action of the hookworm-derived protein by investigating its binding partners, its effect on intestinal barrier integrity and other intestinal immune processes. Ultimately, we aim to identify a novel and safe therapeutic to alleviate chronic inflammatory responses during pediatric IBD.

ID: 141 / CP4.2: 4
Contributed abstract
Conference Topics: Veterinary Parasitology, Helminthology, Host-parasite interactions
Keywords: Exosomes, Schistosoma mansoni, Enzymes, miRNA

Exosomes like Vesicles of *Schistosoma mansoni* and Their Role in Host Adaption and Pathogenicity

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Exosomes have an important role in intercellular communication in vertebrates and invertebrates. In the case of parasites, these vesicles serve as a medium of transmission for invading secondary areas of infection. Helminthes such as Schistosoma mansoni during infection also secretes exosomes like vesicles which play an important role in host-parasite adaption and development of Schistosome pathogenicity in the host. Exosomes perform a variety of functions either by attaching to receptors or fusing with host cells. These vesicles are enriched with proteins, enzymes, and microRNA (miRNA). When the schistosome moves in small vessels it exerts pressure on vessels inducing a clot activation mechanism so it releases glycolytic enzymes through exosomes which bind to mammalian plasminogen in addition to that these exosomes also consists of ATP-diphosphohydrolase 1 which prevents platelet aggregation thus preventing clot formation these glycolytic enzymes also affects the immune system of host thus facilitating schistosome development in host. These exosomes also consist of a homologue of leucine aminopeptidase which modulates the host immune response toward schistosomal eggs. miRNA secreted in exosomes has anti-inflammatory activities by binding with different inflammatory cells such as macrophages and these exosomes also modulates gene expression of host specie especially those related to host immunity.

ID: 106 / CP4.2: 5
Contributed abstract
Conference Topics: Drugs, Immunology
Keywords: nanoparticles, schistosomiasis, Garcinia mangostana

Green synthetized silver nanoparticles using *Garcinia mangostana* peel extract reduce the schistosomiasis-induced hepatic injury in mice

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Schistosomiasis is a widely spread infection that induce hepatic inflammatory and fibrotic cellular response. The most used anthelmintic drug (Praziquantel, PZQ) cannot reverse the induced hepatic injury especially in the advanced stages of Schistosoma mansoni infection. Therefore, using plant-based therapy is a good strategy to develop an innovative anti-schistosomal drug. In this study, silver nanoparticles (GS-AgNPs) were synthetized using Garcinia mangostana peel extract (GMPE) and their anti-schistosomal activity was investigated in mice. The results showed that the GS-AgNPs and GMPE treatments could reduce the hepatic injury in the infected mice expressed by lowering the ova count and the granuloma size in the hepatic tissues. Also, α-SMA gene expression and the protein level of the TGF-β1 were restored in the treated mice showing the anti-fibrotic effect of both GS-AgNPs and GMPE. Moreover, GS-AgNPs and GMPE reversed the Schistosomiasis-induced changes in the levels of oxidative stress markers and showed their anti-oxidant capacity. Inflammatory markers (IL-1β, IL-6, TNF-α, CXCL1 and MCP-1) and apoptotic markers (Bax, Bcl-2 and caspase-3) investigation revealed the anti-inflammatory and anti-apoptotic effects of both Gs-AgNPs and GMPE. These findings concluded the anti-oxidant and anti-inflammatory activities suggest the promising use of Gs-AgNPs and GMPE as an anti-schistosomal adjuvant or complementary therapy.

ID: 264 / CP4.2: 6
Contributed abstract
Conference Topics: Malaria, Apicomplexa Biology
Keywords: structural phylogeny, malaria

Structural Phylogeny Of Plasmodium Kinases

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Despite the use of sequence-based alignment, the kinome of *P. falciparum* still contains many orphan kinases, whose functions are unknown. What if the parasite evolved homoplastic protein structure and therefore function, but through a different evolutionary pathway? We propose a method for understanding the structural relationships between proteins, specifically protein kinases, by using structural phylogeny. The method employs state-of-the-art protein folding tools, Meta AI's ESMFold, ESM-2 and DeepMind's Alphafold, to predict the structures of all human and P. falciparum kinases. We then use structure comparison algorithms, TM-Align and FATCAT, to generate a distance matrix that can be used to construct a tree showing the structural and implied functional similarity of the studied kinases. The proposed method is validated by comparing predicted structures to known crystal-structures, which enables the assessment of the models accuracy. Newly hypothesised 'functional assignments' may prove important in the case of host-parasite biology, as parasites are evolutionarily distant to their human hosts, however they do interact with (perhaps obligately) the kinase networks of their hosts. The interactions of host and parasite proteins are vital to developing host directed therapy, and structural phylogeny may be able to develop important hypotheses of similarity and interaction.

W2: One Health Workshop sponsored by Elsevier

Time: Wednesday, 06/Sept/2023: 1:00 - 2:30pm · *Location:* Workshop room 3
Session Chair: Darren Gray, QIMR Berghofer Medical Research Institute

CP5: Protozoan Biology 15 min talks

Time: Wednesday, 06/Sept/2023: 3:00pm - 4:00pm · *Location:* Symposium room 1
Session Chair: Paul Gilson, Burnet Institute

ID: 130 / CP5: 1
Contributed abstract
Conference Topics: Epidemiology, Genomics, Protozoa, Zoonoses, One Health, Bioinformatics
Keywords: Cryptosporidium parvum; whole genome sequencing; gene flow; recombination; population admixture; evolution

Recent genetic exchanges and admixture shape the genome and population structure of the zoonotic pathogen*Cryptosporidium parvum*

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Cryptosporidium parvum is a widely distributed pathogen that causes diarrheal disease in both humans and ruminants. The parasite undergoes an obligatory sexual phase in its life cycle, allowing for genetic exchanges between previously isolated lineages. In this study, we examined 32 whole genome sequences obtained from *C. parvum* isolates found in humans and ruminants across Europe, Egypt, and China. Our analysis revealed three well-supported clusters comprising a mixture of isolates from different host species, geographic locations, and subtypes. We also observed recombination between ruminant and human isolates, with the resulting recombinant regions being passed on to other human subtypes through gene flow and population admixture. Multiple recent genetic exchanges were identified, with notable enrichment of putative virulence genes within these exchanges, leading to increased diversity at the nucleotide level. Our findings suggest that increased globalization and close interactions between humans and animals may have facilitated genetic exchanges between previously isolated *C. parvum* lineages, leading to spillover and spillback events. We further discuss the potential implications of these exchanges on the coevolutionary dynamics between the parasite and its hosts, particularly in the context of the Red Queen's arms race.

ID: 214 / CP5: 2
Contributed abstract
Conference Topics: Malaria
Keywords: Nanopore sequencing, epitranscriptome, Plasmodium falciparum

mRNA base modifications in the malaria parasite *Plasmodium falciparum* impact transcript stability and translational efficiency

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RNA can be chemically modified at a gene-specific level, and this modification has been central to the success of RNA vaccines against COVID-19. Despite the importance of these modifications the role of the most abundant RNA modifications remains unclear. We used Nanopore sequencing to interrogate the epitranscriptome of *Plasmodium falciparum*. *Plasmodium* has a small transcriptome with only 3000 genes expressed in any one life stage, making it ideally suited for whole transcriptome analyses. We mapped transcriptomes with individual Nanopore flow cells, interrogate the prevalence and position of RNA modifications. *Plasmodium* transcripts are the most adenosine rich in any known eukaryote, and we find the modification N6-Methyladenosine (m6A) is particularly abundant in *Plasmodium* mRNA. We perturbed the writing and reading of this epitranscriptome code by inducibly knocking down the methyltransferase that lays down m6A in mRNA and the reader proteins that detect and decode m6A containing transcripts. These perturbations impact mRNA and protein abundance, pointing to nuanced roles for m6A in RNA stability and translational efficiency. The contextual importance of m6A sites remains enigmatic, and we are investigating the impact of methylation position and density within transcripts to better understand how m6A can be effectively exploited as a biotechnology tool.

ID: 143 / CP5: 3
Contributed abstract
Conference Topics: Cell Biology, Apicomplexa Biology, Biochemistry, Protozoa
Keywords: Toxoplasma gondii, Electron Transport Chain (ETC), Mitochondrial dehydrogenases, Malate metabolism

Investigating the role of mitochondrial dehydrogenases in *Toxoplasma gondii*

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Toxoplasma gondii is an apicomplexan parasite that causes severe disease in immunocompromised individuals, newborns, and livestock. This widespread parasite is dependent on its mitochondrial Electron Transport Chain (ETC) for proliferation and survival. Electrons enter the ETC via multiple dehydrogenases that localise to the inner mitochondrial membrane, several of which have been identified as potential drug targets in *T. gondii* despite their lack of in-depth characterisation. Using a combination of forward and reverse genetics as well as physiological and metabolomic analyses, we investigated the role of key mitochondrial dehydrogenases in the parasite. We discovered that whilst most of these dehydrogenases are not essential

for the survival of *T. gondii* during *in vitro* culture, several are important for optimal parasite proliferation and mitochondrial oxygen consumption. Furthermore, we found that two dehydrogenases which mediate malate oxidation are members of a synthetically lethal pair. We are currently investigating the essential metabolic processes that require malate oxidation in the parasite. Overall, our findings demonstrate that there are flexible and redundant entry routes for feeding the ETC in *T. gondii*, and that mitochondrial dehydrogenases play a range of critical roles in parasite metabolism.

ID: 156 / **CP5: 4**
Contributed abstract
Conference Topics: Malaria, Molecular Biology, Protozoa
Keywords: Malaria, Plasmodium, falciparum, knowlesi, co-infection

The dynamics of parasite growth in *P. falciparum* and *P. knowlesi* co-cultures.

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In Malaysia, incidence of *Plasmodium knowlesi* has increased alongside the elimination of *P. falciparum* and *P. vivax*. Whether the decrease in *P. falciparum* and/or *P. vivax* has contributed directly to the increase of *P. knowlesi* is unknown. We utilised co-culture to investigate the *in vitro* interaction between *P. knowlesi* and *P. falciparum,* and determined parasitaemia by digital PCR (dPCR) with primer and probes specific for the 18S gene of each species. Co-cultures and monocultures were maintained under standard conditions for 6 days, with daily sampling for PCR. In the co-culture, *P. knowlesi* and *P. falciparum* were seeded at 234 copies/µL and 412 copies/µL, respectively; in the monocultures, *P. knowlesi* was seeded at 473 copies/µL and *P. falciparum* at 950 copies/µL. By day 6, *P. knowlesi* parasitaemia had increased 22-fold (10,305 copies/µL) in the monoculture, but only 12-fold (2820 copies/µL) in the co-culture. In contrast, the *P. falciparum* parasitaemia increased 12-fold in both the mono (11,903/µL) and co-culture (4991/µL). These preliminary results suggest that in co-infections, *P. falciparum* may exhibit an inhibitory effect on *P. knowlesi*, raising the possibility that the elimination of *P. falciparum* may have directly contributed to the increase in cases of *P. knowlesi* in Malaysia.

CP5.1: Protozoan Biology 5 min talks

Time: Wednesday, 06/Sept/2023: 4:00pm - 4:30pm · *Location:* Symposium room 1
Session Chair: Paul Gilson, Burnet Institute

ID: 132 / **CP5.1: 1**
Contributed abstract
Conference Topics: Malaria, Biochemistry, Molecular Biology, Bioinformatics
Keywords: PfFNT, lactate, proton-transfer, molecular dynamics, malaria

The malaria parasite lactate/H^+ symporter PfFNT: transporter or channel?

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The malaria parasite *Plasmodium falciparum* relies on anaerobic glycolysis for energy production in the intraerythrocytic phase of its lifecycle. Parasites depend on their formate-nitrite transporter (PfFNT) to extrude lactate and protons, major by-products of anaerobic glycolysis, from their cytosol to prevent lethal cytosolic pH and cell volume disruptions. Cryo-EM structures of PfFNT reveal a structure similar to bacterial formate-nitrite transporters that are known to function as channels: proteins with a continuous pathway for substrate passage. However, previous studies suggest PfFNT functions as a transporter.

Each PfFNT subunit contains a transport cavity with a critical histidine residue (His230) bordered by hydrophobic constrictions on each side. Using extensive molecular dynamics simulations of all possible His230 and substrate protonation states, we show substrate binding only occurs between lactate and positively charged His230. With additional simulations and quantum mechanics calculations, we show His230 favourably protonates lactate to lactic acid, allowing the substrate to be released from the cavity. Subsequently, we propose a proton-transfer mechanism for PfFNT transport that requires no significant protein conformational changes. As lactate does not have a continuous pathway entirely through the protein, we suggest the requirement for proton-transfer allows PfFNT to be defined as a transporter rather than a channel.

ID: 165 / **CP5.1: 2**
Contributed abstract
Conference Topics: Malaria, Cell Biology, Apicomplexa Biology, Molecular Biology
Keywords: Mitochondria, Apicoplast, inheritance, Plasmodium

Investigating organellar inheritance of the apicoplast and mitochondrion in *Plasmodium berghei*

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Plasmodium parasites harbour a single mitochondrion and a single relic plastid (apicoplast) throughout the entirety of their complex life cycle. Both organelles are essential to parasite growth and are pursued as valid drug targets. Whilst both organelles are believed to be maternally inherited during sexual reproduction, the precise mechanisms underpinning their inheritance remains unknown. To investigate organellar inheritance in a sex-specific manner, we have developed single sex *P. berghei* lines with fluorescently tagged apicoplasts and mitochondria. Using live-cell microscopy, we show that the mitochondrion and apicoplast are absent from newly formed male microgametes through exclusion and degradation mechanisms executed during exflagellation. In turn, live-cell microscopy reveals the presence of an elongated, perinuclear positioned apicoplast and an expanded mesh-like mitochondrial network that cradles the nucleus in activated female gametocytes. To explore whether the organellar genome is degraded prior to elimination, we used ddPCR analysis to show there is a decrease in the copy number of the apicoplast and mitochondrial genomes in male gametocytes compared to

females. Overall, this work will help to better inform future therapeutic strategies targeting these organelles and will improve our understanding of how organelle encoded resistance mutations are transmitted and how this might impact malaria treatment.

ID: 204 / **CP5.1: 3**
Contributed abstract
Conference Topics: Malaria, Apicomplexa Biology, Molecular Biology, Protozoa, Microscopy, Bioinformatics
Keywords: Plasmodium, Protists, m6A, RNA, epitranscriptomics

The Effect of N^6-methyladenosine (m^6A) Enrichment on mRNA Export and Stability in the Intraerythrocytic Development Cycle of *Plasmodium falciparum*.

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Department of Biochemistry and Pharmacology, Bio21 Molecular Science and Biotechnology Institute, The University of Melbourne, Parkville, Australia

Plasmodium falciparum has a complex lifecycle which requires the parasite to adapt to many environments. These and other parasite processes are orchestrated by dynamic regulation of gene expression as revealed by the cascading pattern of mRNA abundance in the intraerythrocytic development cycle (IDC). In addition to regulating transcription, the parasite modifies the stability of mRNA as a post-transcriptional mechanism of regulating the expression of genes in the IDC. The processes that affect the stability of mRNA in *P. falciparum* are poorly understood.

Post-transcriptional (epitranscriptional) modification of adenosine in mRNA to N^6-methyladenosine (m^6A) has been shown to be essential in the IDC. m^6A enrichment of mRNA is conserved in all eukaryotic organisms and is known to affect splicing, nuclear export, stability, and translational efficiency.

In this study we aim to test the effect of m^6A enrichment on mRNA export and stability in the IDC of *P. falciparum*. We used RNA-FISH to observe spatial distribution of total mRNA. Direct RNA sequencing data was used to predict m^6A enriched mRNA. The abundance of these transcripts after the inhibition of transcription was used to measure the stability of each transcript. Our findings have implications for other parasitic protists like *Toxoplasma gondii* and *Trypanosoma* spp.

ID: 123 / **CP5.1: 4**
Contributed abstract
Conference Topics: Apicomplexa Biology
Keywords: Cryptosporidium, in vitro, three-dimensional intestinal model

Comparison of *in vitro* growth characteristics of *Cryptosporidium hominis* (IdA15G1) and *Cryptosporidium parvum* (Iowa-IIaA17G2R1 and IIaA18G3R1)

Samantha Gunasekera[1], Benjamin Thierry[2], Brendon King[3], Paul Monis[3], Jillian M. Carr[4], Abha Chopra[5], Mark Watson[5], Mark O'Dea[6], Una Ryan[1]
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Parasites of the *Cryptosporidium* genus are a major cause of childhood diarrhoeal disease and mortality, with Sub-Saharan Africa and Asia being disproportionately affected by the global disease burden attributed to cryptosporidiosis. Currently, no vaccines and inadequate therapeutic options are available for the treatment and prevention of *Cryptosporidium* infection. Research into *Cryptosporidium* has fallen behind other enteric pathogens of similar epidemiological importance due to a lack of reproducible *in vitro* culturing systems that can support the life cycle of *Cryptosporidium* to completion.

In recent years, the increasing accessibility of sophisticated bioengineered intestinal models and organoid-based culturing systems has driven massive advances in our ability to support *Cryptosporidium* throughout its life cycle. The present study describes a streamlined microfluidic device that is able to support the complete life cycle of *Cryptosporidium hominis* and *Cryptosporidium parvum*. This study reports a comparison of the *in vitro* growth characteristics of both species of *Cryptosporidium* under static and dynamic culturing conditions using quantitative PCR, immunofluorescence assays, scanning electron microscopy, and transcriptomics.

ID: 237 / **CP5.1: 5**
Contributed abstract
Conference Topics: Malaria, Apicomplexa Biology, Biochemistry, Molecular Biology, Protozoa, Microscopy
Keywords: nuclear protein transporter, Toxoplasma, peptide inhibitors

Role of the auto-inhibitory domain of a nuclear protein transporter in *Toxoplasma gondii* biology

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Nuclear transporter proteins, like importin α (Impα), transport cargoes to the nucleus by recognizing the nuclear localization signals (NLSs). It is a key control site for transporting proteins in crucial processes like replication and transcription. The cargo binding and release are regulated by the N-terminal domain of Impα, which is auto-inhibitory and competes with the cargo-binding sites. Auto-inhibition can thus regulate the type of NLSs being recognized and the release inside the nucleus and was demonstrated to be essential in Saccharomyces *cerevisiae.* Our lab work with Impα proteins of apicomplexan parasites *Plasmodium falciparum and Toxoplasma gondii* show a lack of and low levels of auto-inhibition, respectively. What role does a weak auto-inhibitory Impα play in the nuclear transport pathway of apicomplexans? To answer this, the mutants of TgImpα with varied levels of auto-inhibition were expressed in *Toxoplasma*, and the implications on the growth rate will be presented. Does a weak auto-inhibition also affect NLSs binding/release? Our study with overexpression of strong NLSs shows an effect on the

viability of *Toxoplasma*, which we can overcome by an additional Impα copy. This work sheds light on understanding the nuclear transport mechanism of apicomplexans and gives insights into therapeutics by using peptide inhibitors against this pathogen.

ID: 238 / CP5.1: 6
Contributed abstract
Conference Topics: Cell Biology, Apicomplexa Biology, Molecular Biology, Protozoa, Microscopy
Keywords: apicomplexan parasites, malaria, toxoplasma

Apicoplast proteins consist of trafficking signals throughout the protein and work in unison with N-terminal signal sequences to determine their final destination and their traffciking pathway

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[1]Indian Institute of Technology Bombay; [2]Ismar Healthcare, Lier, Belgium; [3]Cactus Communications; [4]Indian Institute of Technology Bombay

The apicoplast, a secondary endosymbiont, is present in most apicomplexan parasites, including *Toxoplasma gondii* and *Plasmodium* species. Apicoplast proteins are trafficked from the Endoplasmic Reticulum (ER) to the apicoplast by two pathways in *T.gondii*. Proteins exclusively localizing to the apicoplast (e.g. *Tg*ACP) follow a Golgi-independent pathway, while proteins dually targeted to the apicoplast and the mitochondrion (*Tg*TPx1/2, *Tg*SOD2, *Tg*ACN) follow a Golgi-dependent pathway. Previously we showed that *Tg*TPx1/2 has an N-terminal signal sequence for dual targeting of this protein to both organelles. We asked whether this signal sequence can replicate dual targeting when fused with other reporter proteins and showed that depending on the reporter protein, the signal sequence of *Tg*TPx1/2 targeted the protein to the apicoplast or the mitochondrion with varied efficiency. Next, we asked whether the signal sequences of dually localized proteins are sufficient to direct any protein via a Golgi-dependent route to the apicoplast. We generated several chimeric constructs by swapping the N-terminus and the coding sequences of dually localized proteins with exclusive apicoplast proteins. We show for the first time, that apicoplast proteins contain trafficking signals throughout the protein sequence, and chimeras with different N-terminal signal sequences can change their trafficking pathway to the apicoplast.

S3: Symposium 3 Aquatic

Time: Wednesday, 06/Sept/2023: 3:00pm - 3:15pm · *Location:* Symposium room 2
Session Chair: Diane Barton, Charles Sturt University

ID: 244 / S3: 1
Invited speaker abstract

Parasites as biological tags – used with multiple lines of evidence to identify stocks in sharks – with new species described

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The small-bodied sharks, *Carcharhinus coatesi* and *Rhizoprionodon acutus,* are bycatch of fisheries across northern Australia and Papua New Guinea. There is currently no information on the spatial structure of populations of these sharks to guide their conservation and management. We employed a combination of techniques (genetics, vertebral chemistry, and parasite taxonomy) to assess stock structure across three regions in northern Australia. Parasite taxa assemblages of *C. coatesi* were significantly different between regions. Additionally, parasites have differences between assemblages of adults and juvenile *C. coatesi* from regions sampled in the Gulf of Carpentaria. For *R. acutus*, the sample of sharks infected with parasites was small, with no significant differences in parasite taxa assemblages among the regions sampled. Parasites as biological tags have had little application to elasmobranch stock structure studies, but this study demonstrates they have promise in determining stocks. Examining the parasite fauna of these two sharks resulted in the description of two new parasitic copepods, *Tripaphylus squidwardi* and *Tripaphylus dippenaarae*. Parasites display high host specificity and there are many species still to be described. The applications of studying their taxonomic assemblages is not yet fully realised and will be foundational to using parasites as biological tags in sharks.

CP6: Aquatic 15 min talks

Time: Wednesday, 06/Sept/2023: 3:15pm - 4:30pm · *Location:* Symposium room 2
Session Chair: Diane Barton, Charles Sturt University

ID: 152 / CP6: 1
Contributed abstract
Conference Topics: Diagnostics, Molecular Biology, Fish parasitology, Aquaculture
Keywords: Diagnostics, Molecular Biology, Aquaculture, Fish Parasitology

Detection of *Cardicola forsteri* and *C. orientalis* in Southern Bluefin Tuna samples using recombinase polymerase amplification coupled with lateral flow assay (RPA-LF)

Cecilia Power, Melissa Carabott, Luke Norbury, Barbara Nowak, Nathan Bott
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Aporocotylid blood flukes *Cardicola forsteri* and *C. orientalis* are considered one of the most significant health concerns for Southern Bluefin Tuna (SBT) *Thunnus maccoyii* ranched in Australia. The development of rapid diagnostics to detect *Cardicola*

spp. in SBT is an important step forward in improving the biosecurity response of the industry. Recombinase polymerase amplification (RPA) is an isothermal technique which operates at constant low temperature (25-42˚C), and when coupled with a lateral flow (LF) strip, makes an ideal diagnostic tool for rapid, specific and sensitive identification of pathogens in field applications. RPA-LF assays were designed and validated for detection of *C. forsteri* and *C. orientalis*. For each assay, no cross-species amplification was seen and detection as low as 30-50 genome copy equivalents was achieved. Reactions can be completed in 10 minutes. Similar specificity and sensitivity were demonstrated for SBT samples when compared to qPCR analysis, and use of equipment-free incubation using body heat outside of laboratory settings was demonstrated. By developing rapid, ready-to-use diagnostics, the SBT industry can identify risks relating to blood flukes far quicker than is currently available and enable analysis to be undertaken on-site.

ID: 196 / CP6: 2
Contributed abstract
Conference Topics: Veterinary Parasitology, Helminthology, Fish parasitology, Aquaculture
Keywords: Extended ranching, Southern Bluefin Tuna, Cardicola, aquaculture, blood fluke

Epizootiology of *Cardicola* spp. (Trematoda: Aporocotylidae) infection in Southern Bluefin Tuna during extended ranching

Maree Widdicombe[1], Melissa Carabott[1], Paul A. Ramsland[1], Barbara F. Nowak[2], Cecilia Power[1], Daryl Evans[1], Nathan J. Bott[1]
[1]RMIT; [2]University of Tasmania

The aim of this study was to determine the effects of extended tuna ranching beyond the typical harvest on both fish condition and infection with blood fluke parasites (*Cardicola* spp.) in a single company from Port Lincoln, South Australia. Samples of SBT gills were collected up to seven months post-harvest in 2021. Infection severity was quantified using qPCR to calculate copy numbers of *C. forsteri* and *C. orientalis* ITS-2 DNA. *C. forsteri* adult prevalence and intensity peaked 15 weeks post-harvest, and the intensity significantly declined after this timepoint. By 7 weeks post-harvest *C. forsteri* (ITS-2) reached 100% prevalence in SBT gills and remained at 100% for the remainder of the sampling period, however a significant negative correlation was observed between ranching duration and *C. forsteri* (ITS-2) intensity. *C. orientalis* (ITS-2) prevalence peaked 15 weeks post-harvest, when a significant negative correlation was observed between ranching duration and *C. orientalis* (ITS-2) intensity. *C. orientalis* prevalence was higher than at harvest and 12.8% greater than the average prevalence of all the companies at harvest in the previous 5 years. The results of this investigation showed that time in extended ranching was negatively correlated with *C. forsteri* (ITS-2) and *C. orientalis* (ITS-2) infection intensity.

ID: 185 / CP6: 3
Contributed abstract
Conference Topics: Host-parasite interactions, Fish parasitology, Aquaculture, Bioinformatics
Keywords: Aporocotylidae, Aquaculture, Immune, Transcriptome

Transcriptome analysis of farmed Southern Bluefin Tuna infected with *Cardicola forsteri* (Trematoda: Aporocotylidae)

Maree Widdicombe[1], Oliver White[2], Bronwyn Campbell[1], Melissa Carabott[1], Cecilia Power[1], Paul Ramsland[1], Barbara Nowak[3], Cinzia Cantacessi[2], Nathan Bott[1]
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Southern Bluefin Tuna (SBT), *Thunnus maccoyii,* are economically important fish and South Australia's largest finfish aquaculture product. The biggest threats to ranched SBT health are from *Cardicola forsteri* and *C. orientalis* (Trematoda: Aporocotylidae). This study aimed to understand how the more prevalent of these species, *C. forsteri*, alters the SBT immune system. The anterior kidney and gills of SBT were collected during the commercial harvest from a single company. *C. forsteri* infection was determined through heart flushes and quantitative polymerase chain reaction (qPCR). SBT were considered uninfected if negative in both diagnostics. Total RNA was extracted from each sample and the mRNA was sequenced to identify transcriptomic differences in infected and uninfected SBT in both the anterior kidney and gills. The average uniquely mapped reads to the SBT genome from all samples was 84.6%. This research is important to understanding the host-parasite interactions that may help identify new treatment targets to improve the overall health of farmed SBT.

ID: 193 / CP6: 4
Contributed abstract
Conference Topics: Helminthology, Fish parasitology, Aquaculture
Keywords: Glycobiology, Protein structure, Aquaculture, Cardicola, Southern Bluefin Tuna

Modelling protein structures of *Cardicola forsteri*, a blood fluke of southern bluefin tuna

Jemma Hudson[1], Nathan Bott[1], Paul Ramsland[1], Barbara Nowak[2], Lachlan Coff[3]
[1]RMIT; [2]University of Tasmania; [3]CSIRO

Parasitic diseases provide one of the main constraints on aquaculture, an industry that is continually increasing with the rise in global demand for sustainable protein sources. In Australia, Southern Bluefin Tuna (*Thunnus maccoyii)* are ranched in near-shore cages in Port Lincoln, South Australia. The blood fluke, *Cardicola forsteri,* is the most prominent species impacting this industry, and is responsible for obstruction of blood vessels in the gills leading to branchitis and mortalities. Recently, the glycome and genome of *C. forsteri* have been reported. This research aims to further the understanding of glycosylation of *C. forsteri* by modelling the glycosyltransferases. These enzymes are responsible for catalysing gylcosidic linkages of various acceptor molecules involved in a range of key biological processes. The artificial intelligence system Alphafold2 will be used to generate predicted protein structures for 47 putative glycosyltransferases, and the three dimensional structure will be matched to previously modelled proteins to identify function. Visualising the structure of the proteins will aid in the recognition of binding sites and thus the potential identification of drug targets. This research will increase the general understanding of protein function in platyhelminth species.

ID: 160 / **CP6: 5**
Contributed abstract
Conference Topics: Helminthology, Fish parasitology
Keywords: Trematoda, Cryptogonimidae, Taxonomy, Biogeography

An enigmatic snapper parasite (Trematoda: Cryptogonimidae) in thick-lipped wrasses may suggest regional host diet shift.

Helen Armstrong[1], Storm Martin[1], Alan Lymbery[1,2], Scott Cutmore[3]
[1]School of Environmental and Conservation Sciences, Murdoch University, Western Australia; [2]Centre for Sustainable Aquatic Ecosystems, Harry Butler Institute, Murdoch University, Western Australia; [3]Biodiversity and Geosciences, Queensland Museum, Queensland

The Cryptogonimidae are a group within the Trematoda that have a three host life-cycle: snail, fish, fish. The previously known final fish hosts of cryptogonimids have been larger reef associated fish such as snapper (Lutjanids), likely due to the intermediate stage relying on its host fish being eaten by a larger fish.

During a field expedition to Ningaloo Reef, I discovered a cryptogonimid infection in the thick-lipped wrasses, *Hemigymnus fasciata* and *H. melapterus*. Most wrasses (*Labridae*) do not prey substantially on fishes and so are atypical hosts for cryptogonimids and this worm is apparently absent in Queensland where these fishes have been well-examined.

I will target multiple single marker regions, mostly ITS2, 28S and 18S rDNA, and cox1 mtDNA to identify the worm species and gut contents analysis to identify the host fish diet, I aim to provide taxonomic descriptions of these cryptogonimids and identify the diet changes of these fishes in Ningaloo Reef compared with those from the Great Barrier Reef. This study would be the first biogeographic comparison of cryptogonimids from Australia.

W3: One Health Workshop sponsored by Elsevier

Time: Wednesday, 06/Sept/2023: 3:00 - 4:30pm · *Location:* Workshop room 3
Session Chair: Rebecca Traub, Australian Society for Parasitology

President: 2023 ASP Presidential Address

Time: Wednesday, 06/Sept/2023: 5:00pm - 5:30pm · *Location:* Plenary Room
Session Chair: Rebecca Traub, Australian Society for Parasitology

ID: 249 / **President: 1**
Invited speaker abstract

Academia and protecting your mental health.

Rebecca Traub
Australian Society for Parasitology, Australia

Increased competitiveness for grants, pressure to publish or perish, increased university corporatisation, managerialism, and micromanagement, coupled with a decrease in continuing academic appointments, are some of the stressors faced by academics within the current university environment. According to several studies, on average, 1 in 3 academics experience mental health problems such as stress, burnout, anxiety, and depression, with the covid-19 pandemic leading to an exacerbation of such issues, especially for those with primary carer responsibilities. From an individual perspective, balancing life with a career means that faculty are able to set realistic expectations of their workload and are also able to advocate for a culture of declining additional responsibilities and opportunities in favour of clear boundaries that make time for themselves and their family. However, it is insufficient just to discuss healthy work-life balance on an individual level. Senior leaders, therefore, play a key role in creating a mentally healthy university and must ensure that work design and organisational culture drive positive mental health outcomes. Recent data from the UK shows a clear business case for supporting a sector-wide mental health plan for staff, with organisation-wide culture change and awareness-raising providing a six-time return on investment.

BMM: 2023 Bancroft Mackerras Medal Award and Lecture

Time: Thursday, 07/Sept/2023: 8:30am - 9:15am Location: Plenary Room, Grand Ballroom, Doubletree Hilton Esplanade
Session Chair: Rebecca Traub, Australian Society for Parasitology

P2: IJP Plenary Lecturer

Time: Thursday, 07/Sept/2023: 9:15am - 10:00am Location: Plenary Room
Session Chair: Rebecca Traub, Australian Society for Parasitology

Zoonotic malaria: a OneHealth approach to surveillance

Matt Grigg
Menzies School of Health Research, NT

The emergence of zoonotic transmission of the monkey parasite *Plasmodium knowlesi* threatens national malaria elimination goals across Southeast Asia. Novel integrated One Health approaches to surveillance of humans, parasites, mosquito vectors and monkey hosts are required to understand factors involved in transmission and design appropriate public health control measures.

CP7: Biodiversity & Wildlife 15 min talks

Time: Thursday, 07/Sept/2023: 10:30am - 11:30am · *Location:* Symposium room 1
Session Chair: Michelle Power, Macquarie University

ID: 205 / CP7: 1
Contributed abstract
Conference Topics: Wildlife parasitology, Epidemiology
Keywords: wombat, disease ecology, sarcoptic mange, environmental transmission

Host, environment, and anthropogenic factors drive landscapedynamics of an environmentally transmitted pathogen:Sarcoptic mange in the bare-nosedwombat

Elise Ringwaldt[1], Barry Brook[1], Jessie Buettel[1], Calum Cunningham[1,2], Carley Fuller[1], Riana Gardiner[3], Rowena Hamer[1], Menna Jones[1], Alynn Martin[4], Scott Carver[1]
[1]School of Natural Sciences, Biological Science, University of Tasmania, Hobart, Tasmania, Australia; [2]School of Environmental and Forest Sciences, University of Washington, Seattle, Washington, USA; [3]School of Science, Engineering and Technology, University of Sunshine Coast, Sippy Downs, Queensland, Australia; [4]Caesar Kleberg Wildlife Research Institute, Texas A&M University—Kingsville, Kingsville, Texas, USA

Sarcoptic mange disease is caused by the mite *Sarcoptes scabiei* and is responsible for animal welfare issues and local population declines in bare-nosed wombats (*Vombatus ursinus*) across south-eastern Australia. However, the factors influencing the distribution and prevalence of this wildlife pathogen at a landscape level are unknown. Here, I used passive surveillance (camera trap images) of sarcoptic mange in bare-nosed wombats across Tasmania to identify landscape factors associate with pathogen severity and population outbreaks. Using Species Distribution Modelling in conjunction with fine scale environmental and landscape variables, I found high host suitability, low annual rainfall, and highly modified environments such as agriculture, increase mange disease risk for bare-nosed wombats. The areas identified as highly suitable for the pathogen may be more likely for sporadic epizootic episodes, causing devastating population declines such as what was seen in Narawntapu National Park. The projected mange disease risk assessment has management implications across mainland Tasmania. This study is the largest spatial assessment of sarcoptic mange in a host to date, and advances understanding of the landscape epidemiology of environmentally transmitted sarcoptic mange. Broadly, understanding the host-pathogen interaction within the environment is an essential foundation for future south-eastern Australia wide studies in bare-nosed wombats.

ID: 211 / CP7: 2
Contributed abstract
Conference Topics: Wildlife parasitology, Biodiversity
Keywords: Nematoda, Cloacinidae, marsupial, biodiversity

The nematode family Cloacinidae (Strongyloidea), parasites of Australasian kangaroos, wallabies and wombats: from morphology and ecology to molecules

Tana Sukee, Ian Beveridge, Abdul Jabbar
Melbourne Veterinary School, Faculty of Science, The University of Melbourne, Werribee, Victoria, Australia, 3030

Strongyloid nematodes (Nematoda: Strongyloidea) are highly prevalent parasites of the gastrointestinal tracts of Australasian macropodoid (kangaroos, wallabies, rat-kangaroos, and potoroos) and vombatoid (wombats) marsupials. The cloacinid nematodes are endemic and considered as one of the most diverse groups of endoparasites found in mammalian hosts. This review evaluated the current understanding of morphology, biology, ecology and recent developments in the molecular phylogeny of cloacinid nematodes. In a 125-year period, 349 species of strongyloid nematodes have been described from Australasian marsupials, all of which belong to the family Cloacinidae. Previous studies have documented the diversity, explored community structures and key drivers of speciation of these nematodes. More recently, the integration of nuclear ribosomal DNA and mitochondrial protein datasets has shed new insights on the phylogenetic origins of the Cloacinidae. There are, however, opportunities for future studies to address remaining ecological and phylogenetic knowledge gaps with expanded sampling of underrepresented hosts and geographic regions as well as more widespread use of molecular tools.

ID: 224 / **CP7: 3**
Contributed abstract
Conference Topics: Biodiversity, Other
Keywords: taxonomy, systematics of Australian biodiversity

Australian Biological Resources Study: celebrating 50 years of support for parasite taxonomy.

Haylee Crawford-Weaver, Jaever Santos
Australian Biological Resources Study, Department of Climate Change, Energy, the Environment and Water. Canberra, Australia.

The Australian Biological Resources Study (ABRS) was established in 1973 to provide research grant funding and support for taxonomy. ABRS has awarded over $89 million (unadjusted dollar value) for research on taxonomy and systematics of Australian biodiversity since its inception. Parasite taxonomists have been highly successful in attracting research funding. with approximately 3% of the total grant budget awarded to parasite taxonomy projects. Given that taxonomy in general is woefully under-funded as a biological science research discipline, this funding has been integral to increasing our understanding of Australian parasite biodiversity. I will take you on a short journey through the benefits that this research funding for parasite taxonomy has had on the sector, and the impacts that come from increasing our knowledge of parasite biodiversity. I will also provide a snapshot of the contribution of the small but highly industrious band of parasite taxonomists who lead the research.

ID: 112 / **CP7: 4**
Contributed abstract
Conference Topics: Veterinary Parasitology, Fish parasitology, Aquaculture
Keywords: snail, digenea, parasites, aquaculture

Parasite Fauna of Freshwater Snails in the Murrumbidgee Catchment Area, Australia

Nidhish Francis[1], Alice Banfield[1], Diane Barton[1], Matthew McLellan[2], Shokoofeh Shamsi[1]
[1]School of Agricultural, Environmental and Veterinary Sciences, Charles Sturt University, Wagga Wagga, 2678, Australia; [2]Fisheries and Aquaculture Management, NSW Department of Primary Industries, Narrandera Fisheries Centre, Narrandera, NSW, 2700, Australia

Freshwater snails play an important role as intermediate hosts in the life cycles of many parasites, particularly for digenetic trematodes. Although many studies have identified various adult parasites from snails, studies investigating the larval stages are very limited. The current study was conducted to determine the infection of freshwater snails with parasites using morphological and molecular analyses, within the Murrumbidgee catchment area, an area of widespread intensive aquaculture in Australia. A total of 163 freshwater snails, belonging to four species: *Isidorella hainesii, Physella acuta, Glyptophysa novaehollandica* and *Bullastra lesson,* were examined for infection with parasites. Morphologically, the parasites were grouped into three digenean morphotypes. Sequences obtained from (the internal transcribed spacers (ITS) of nuclear ribosomal DNA, small subunit (18S) ribosomal DNA and large subunit (28S) ribosomal DNA) suggested the parasites collected from these snails belonged to five different species. The ITS, 18S and 28S sequences from one parasite had 100% homology to *Choancotyle hobbsi*. Two other potentially zoonotic digeneans namely *Clinostomum sp.* and *Echinostoma sp.* were also identified. These results provide crucial information to the lifecycle and distribution of several parasites in freshwater snails. Future studies with a larger sample size and longer duration are warranted.

CP7.1: Biodiversity & Wildlife 5 min talks

Time: Thursday, 07/Sept/2023: 11:30am - 12:00pm · *Location:* Symposium room 1
Session Chair: Michelle Power, Macquarie University

ID: 101 / **CP7.1: 1**
Contributed abstract
Conference Topics: Biodiversity, Protozoa, Other, Microscopy
Keywords: Protozoa, freshwater, amoebae, testates, survey

Freshwater testate amoebae from three Australian drainage divisions

Peter O'Donoghue
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Heterotrophic amoebae are vital in aquatic ecosystems as consumers (predators) and producers (nutrients). Testate amoebae have external shells of secreted or gathered materials (proteinaceous, siliceous, calcareous, agglutinate) used for protection, refuge, camouflage and dispersal. A survey was conducted at 150 sites in the Murray-Darling (R4), Northeast (R1) and Northwest (R8) drainage divisions of Australia and testate amoebae were identified by scanning electron microscopy. A total of 120 species belonging to 27 genera were detected (8 cercozoan, 1 retarian and 18 amoebozoa genera). Two genera were commonly detected (>90% prevalence): *Difflugia* and *Centropyxis*. Six genera were frequently detected (27-67% prevalence): *Chlamydophrys, Euglypha, Cochliopodium, Microchlamys, Arcella* and *Lesquereusia*. The remaining 19 genera were detected sporadically (<17% prevalence): *Pseudodifflugia, Assulina, Cyphoderia, Trinema, Sphenoderia, Gromia, Diplophrys, Gocevia, Paragocevia, Phryganella, Cryptodifflugia, Cyclopyxis, Plagiopyxis, Cucurbitella, Lagenodifflugia, Pontigulasia, Quadrulella* and *Nebela*. While water quality parameters (especially salinity, turbidity, nitrogen and phorphorus) demonstrated considerable variability (increasing downstream), none were found to correlate with the distribution of testacea. [Grants from the Australian Biological Resources Study (ABRS) are gratefully ackowledged].

ID: 218 / **CP7.1: 2**
Contributed abstract
Conference Topics: Ectoparasites
Keywords: Amblyomma cajennense, ticks in Australasia

The first cryptic genus of a tick (Ixodida) for a lineage of ticks from North Queensland and Papua Guinea?

Stephen Barker, S Kelava

Department of Parasitology, School of Chemistry and Molecular Biosciences, The University of Queensland, Brisbane, Qld, 4072, Australia.

The possibility of cryptic species is often spoken about in the tick literature but so far there is apparently only one case of cryptic species of ticks being described: the six species of the *Amblyomma cajennense* species complex in North America. This is testament to the diagnostic power of the morphology of ticks. There are, however, many cases of cryptic species in other groups of animals. So, the discovery of a cryptic species of ticks is remarkable: even more remarkable perhaps would be the possible discovery of a cryptic genus of ticks which we will present in our talk concerning a lineage of *Amblyomma*-like ticks with eyes. Of the 125 species of ticks in Australasia about 97 are endemic to Australasia: we will give an overview of these ticks and thus discuss where the newly discovered lineage sits in the of ticks of Australasia.

ID: 110 / CP7.1: 3
Contributed abstract
Conference Topics: Wildlife parasitology, Biodiversity, Invasive Species, Ecology, Fish parasitology, Aquaculture
Keywords: Larval, Murray-Darling Basin, infection dynamics

Larval freshwater fish and parasites in Australia

Diane Barton[1,2], Jason Thiem[3], Shokoofeh Shamsi[1,2]

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Freshwater fish in Australia are known to have a diverse, yet largely undescribed, parasite fauna. However, little is known about the dynamics of these parasitic infections, including at what size fish start to become infected and by which particular parasites. This study is examining larval and juvenile fish from waterways within the Murray Darling Basin to determine levels of infection in these groups of fish. Fish have been collected as part of annual surveys of waterways to monitor river health. The fish species to be examined include native fish (Murray cod, golden perch, Australian smelt and gudgeons) as well as introduced species (carp). Parasites will be collected and identified to determine which species are infecting larval and juvenile fish and whether these are native or introduced species of parasites. Potential impact of these parasites on the health and survival of larval and juvenile fish will also be determined. This study will provide the first detailed examination of the parasites of larval and juvenile freshwater fish in Australia.

ID: 220 / CP7.1: 4
Contributed abstract
Conference Topics: Veterinary Parasitology, Wildlife parasitology, Apicomplexa Biology
Keywords: Toxoplasma gondii, feral house mice

Serology is not a reliable method for detecting *Toxoplasma gondii* exposure in feral house mice

Ryan O'Handley[1], L Lignereux[1], WH Tong[2], S Tan[2], A Vyas[2]

[1]School of Animal and Veterinary Sciences, University of Adelaide, Roseworthy Campus, SA 5371; [2]School of Biological Sciences, Nanyang Technological University, Singapore

The single-celled parasite *Toxoplasma gondii* uses the mouse as an intermediate host to reach its definitive host, the cat, where it can accomplish its sexual reproduction and produce oocysts, which will contaminate the environment. In this study, we captured 103
feral house mice (Mus musculus) on Kangaroo Island, Australia and measured
the level of exposure to *T. gondii* serologically with the Modified Agglutination Test and
conjointly with a *T. gondii* B1 gene PCR. We included stringent quality control
steps in the molecular analysis to reduce the risk of false positive and false negative results.
Our results demonstrate a low seroprevalence of 0.97%, in mice (95%CI [-0.36; 0.58]) despite the detection of *T. gondii* genetic material in 51.46% (95%CI [41.93, 60.88]) in brain tissue of mice. Neither sex nor body weight had an effect on the PCR outcome. We postulate that both the transmission route, horizontal or vertical, and natural selection processes could lead to this discordance which has been observed elsewhere in wild mice but question the biological mechanisms allowing the chronic infection of wild mice. Our findings indicate that serological studies should not be used to measure the level of exposure to *T. gondii* in feral house mice.

ID: 202 / CP7.1: 5
Contributed abstract
Conference Topics: Wildlife parasitology, Epidemiology, Ectoparasites, Immunology, Livestock Parasites, Molecular Biology, Invasive Species, Helminthology, Ecology, Host-parasite interactions, Protozoa, Zoonoses, One Health, Other, Strongyloides, Microscopy
Keywords: Ducks, Australian wildlife, helminths, Riverina, haemosporidians

Parasites of Australian native ducks and how they influence measures of stress

Maddy Ray, Nidhish Francis, Melanie Massaro, Shokoofeh Shamsi

School of Agricultural, Environmental and Veterinary Sciences, Charles Sturt University, Locked Bag 588, Wagga Wagga, NSW 2678, Australia.

Birds play a significant role in the spread of diseases as they can migrate great distances in short periods of time. Waterbirds are of particular interest to parasitology as they are exposed to greater diversities of parasites due to using both aquatic and terrestrial environments. Moreover, during years of drought, waterbirds aggregate in large numbers in wetlands, which can further accelerate intra- and inter-specific parasite transmission. It is already known that ducks carry a variety of diseases that are zoonotic and in other countries zoonotic parasites have been recognised. In Australia, the knowledge of parasite species

infecting waterbird populations is lacking with one of the last major pieces of work being published over forty years ago. Furthermore, there have been only a few studies that have examined how infection with haemosporidian parasites influences overall body condition and haematological indices of stress in birds. By conducting necropsies, helminth parasites can be identified and illustrated. While sampling independent measures of stress (i.e., hemoglobulin levels, presence of haematoza) can be used to determine whether parasite infection affects stress indicators. Initial results have indicated differences in the number of populations of helminths infecting native duck species.

ID: 176 / CP7.1: 6
Contributed abstract
Conference Topics: Wildlife parasitology, Invasive Species, Protozoa
Keywords: Writing, dissection, extractions

Sarcocystis in deer in south-eastern Australia

Keira Brown, Shokoofeh Shamsi, David Jenkins, Diane Barton
School of Agricultural, Environmental, and Veterinary Sciences, Charles Sturt University, Wagga Wagga, NSW 2678, Australia

In 2020, a deer shot in Taree, NSW was found to have cysts of what was believed to be *Sarcocystis* in its rump muscles (D. Barton, pers. comm.). Unfortunately, these tissues were not kept for confirmation but have sparked further research. This project aims to assess the prevalence of a protozoan parasite, *Sarcocystis*, in deer populations in south-eastern Australia. This will be achieved through the dissection and collection of the heart, diaphragm, and oesophagus as these organs have been identified as common locations of *Sarcocystis* spp. in deer (López et al., 2003). There are limited data regarding *Sarcocystis* infections in deer around the world including Australia. Out of this, two have been conducted in Australia and have not found evidence of *Sarcocystis* in deer (Huaman et al., 2021; Munday et al., 1978). Due to the lack of data regarding *Sarcocystis* in deer the organs; lungs, liver, and kidney will also be processed as potential sites of infection. If found, the parasites' DNA will be extracted, and species will be determined. Furthermore, detailed information including the location and species of the host will also be recorded for more in-depth analysis.

S4: Symposium 4 Epidemiology & Diagnostics

Time: Thursday, 07/Sept/2023: 10:30am - 11:00am · *Location:* Symposium room 2
Session Chair: Kamil Braima, Menzies School of Health Research

ID: 259 / S4: 1
Invited speaker abstract

Molecular surveillance of *Plasmodium vivax*: new developments in the vivax Genomic Epidemiology Network

Sarah Auburn
on behalf of vivaxGEN

Plasmodium vivax is the dominant cause of malaria in the Asia-Pacific and Americas, highlighting a critical need for novel surveillance strategies to improve the detection and treatment of the reservoirs of infection. The vivax Genomic Epidemiology Network (vivaxGEN) is a partnership including researchers, policy makers and other key stakeholders from >16 vivax-endemic countries with a shared interest in leveraging genetic information to accelerate *P. vivax* elimination. In this talk, I will discuss new developments from vivaxGEN that are improving our understanding of the genetic relatedness within and between infections, and how this can inform parasite lineages and transmission. Using genomic data from a clinical trial of anti-hypnozoite regimens, we demonstrate the utility of identity-by-descent (IBD) measures to inform on the probable cause of recurrences (relapse, recrudescence or re-infection). We have also developed a novel microhaplotype (multi-SNP) marker panel for targeted genotyping of *P. vivax* that accurately captures genome wide IBD information, enabling characterization of recurrent infections and of spatio-temporal trends in parasite transmission at high density. Our research highlights the great potential of genetic epidemiology to inform on *P. vivax* transmission and adaptation to inform the analysis and interpretation of clinical trials and novel intervention strategies.

CP8: Epidemiology & Diagnostics 15 min talks

Time: Thursday, 07/Sept/2023: 11:00am - 11:45am · *Location:* Symposium room 2
Session Chair: Kamil Braima, Menzies School of Health Research

ID: 213 / CP8: 1
Contributed abstract
Conference Topics: Diagnostics, Molecular Biology, Protozoa
Keywords: Leishmania, Viannia, diagnostic PCR

Clinical samples of leishmania; outgrows diagnostics, and their applications

Andrea Paun[1], Gary Fahle[2], Elise O'Connell[3], Michael E. Grigg[1]
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Current PCR-based diagnostics for cutaneous leishmaniasis can have difficulty discriminating between *Leishmania* species within the *Viannia* complex. A correct diagnosis is critical to inform on the treatment regimen for cutaneous leishmaniasis. We evaluated whether the genomic *ITS2* gene sufficiently differentiates between the species within the *Viannia* complex and whether it is a more sensitive locus than the mitochondrial *7SL* gene currently utilized at the NIH Clinical Center for diagnostic screening (Stevenson, 2010). Our *ITS2* assay had a log-fold greater sensitivity by qPCR. It also bracketed SNPs that

discriminate between *L. braziliensis, L. panamensis* and *L. guyanensis* by DNA sequencing, allowing for appropriate treatment choice to avoid mucocutaneous disease. Further, *Leishmania* parasites are not uniformly distributed throughout a cutaneous lesion, a characteristic that contributes to a lack of sensitivity with the molecular tests to detect sufficient parasite DNA for a definitive diagnosis. By improving the efficiency of parasite outgrows from lesion punch biopsies using a novel combination of antibiotics (piperacillin and cefotaxime) to inhibit bacterial contamination, we provide an additional test to confirm diagnosis and to facilitate research.

ID: 197 / **CP8: 2**
Contributed abstract
Conference Topics: Diagnostics, Helminthology
Keywords: filariasis, human, antigen, diagnostics, Asia-Pacific

Evaluation of a New Rapid Circulating Antigen Test for Lymphatic Filariasis

Patricia M Graves[1], Jessica Scott[1], Antin Widi[1], Alvaro Berg Soto[1], Maxine Whittaker[1], Jonathan D King[2], Derek Lee[3], Colleen L Lau[4], Kimberly Y Won[5]
[1]College of Public Health, Medical and Veterinary Sciences, James Cook University, Cairns and Townsville, Queensland, Australia; [2]Department of Control of Neglected Tropical Diseases, WHO, Geneva, Switzerland; [3]SD Biosensor, Republic of Korea; [4]School of Public Health, The University of Queensland, Brisbane, Queensland, Australia; [5]Division of Parasitic Diseases and Malaria, CDC, Atlanta GA, USA

Accurate and user-friendly rapid antigen detection tests are needed to assess prevalence of *Wuchereria bancrofti* in the Global Programme to Eliminate Lymphatic Filariasis (LF). We compared performance of a new Standard Q Filariasis Antigen test (QFAT) against the Bioline Filariasis Test Strip (FTS) for use in the Asia-Pacific region, using a panel of 372 serum and plasma samples from Samoa, American Samoa and Myanmar with known antigen and/or microfilaria (Mf) status, and 46 Australian negative controls. Under laboratory conditions, the proportion of invalid tests (no flow, no control line) was similar for both tests (0.5-0.7%). Discordance between blind readers was more common with FTS than QFAT (3.0% vs 1.3%). QFAT identified LF antigen in serum and both heparin and EDTA plasma, with the proportion testing positive consistently higher with QFAT (44.8%) than FTS (41.3%). Concordance between the two tests was 93.5% (kappa 0.8681, N=417 with valid results on both tests). QFAT positively identified all Mf-positive samples, whereas FTS missed 3 of 66 Mf-positives. Relative costs are yet unknown. A disadvantage of QFAT was need for an additional buffer step. Advantages of QFAT include ease-of-use, smaller sample (10-20 uL vs 75 uL), clearer control line, and higher sensitivity for Mf-positive samples.

ID: 153 / **CP8: 3**
Contributed abstract
Conference Topics: Malaria, Epidemiology, Genomics
Keywords: drug resistance, genomics, identity-by-decent, plasmodium falciparum

Genetic epidemiology of malaria improves the understanding of population structure and drug resistance in Cambodia to inform appropriate treatments.

Kirsty McCann[1,2], Zuleima Pava[2], Benoit Witkowski[3], Amelie Vantaux[3], Leanne Robinson[2,4], Ivo Mueller[4], Alyssa Barry[1,2]
[1]Centre for Innovation in Infectious Disease and Immunology Research (CIIDIR), The Institute for Mental and Physical Health and Clinical Translation (IMPACT) and School of Medicine, Faculty of Health, Deakin University, HERB Building B, Geelong, VIC 3220; [2]Life Sciences Discipline, Burnet Institute, 85 Commercial Road, Melbourne VIC 3000; [3]Institut Pasteur Cambodia, Phnom Penh, CAMBODIA; [4]Population Health and Immunity Division, Walter and Eliza Hall Institute, Parkville, Victoria, AUSTRALIA

Genomic analysis of remaining *Plasmodium falciparum* infections throughout Cambodia will improve our understanding on persisting pockets of high malaria risk, asymptomatic infections and the emergence and spread of multi-drug resistance. We sequenced the whole genome of 29 *P. falciparum* isolates collected from patients with clinical malaria residing in the Kaev Seima District in the Mondulkiri Province, Cambodia. A parasite DNA enrichment step was used to optimise sequencing and remove human contamination. We obtained 200 Gbases Illumina NovaSeq output including ~645,323,683 bp *P. falciparum* mapped reads. We then used a GATK/variant calling best practices analysis pipeline to identify high-quality genotypes and investigated *P. falciparum* population structure in Mondulkiri Province compared with 1) MalariaGen Pf3kv5 collected data of neighbouring countries, 2) structure between Cambodian provinces and 3) within Mondulkiri Province. We filtered the dataset to identify genotype calls for known drug resistant genes including *crt, mdr1, dhfr, dhps* and *kelch*13. We identified variants associated with resistance to multiple antimalarials within these Mondulkiri isolates with high levels of IBD driving the observed population structure. Most Mondulkiri isolate genomes contained molecular markers associated with resistance against multiple antimalarial treatments. Genomics can inform patterns of antimalarial resistance and population structure to determine appropriate malarial treatments.

CP8.1: Epidemiology & Diagnostics 5 min talks

Time: Thursday, 07/Sept/2023: 11:45am - 12:00pm · *Location:* Symposium room 2
Session Chair: Kamil Braima, Menzies School of Health Research

ID: 151 / **CP8.1: 1**
Contributed abstract
Conference Topics: Epidemiology, Zoonoses, One Health, Strongyloides
Keywords: Soil-transmitted helminths, STH, Strongyloides stercoralis, Mathematical modelling

A MATHEMATICAL MODEL FOR CONTROLLING *STRONGYLOIDES STERCORALIS* INFECTION

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Soil-transmitted helminths (STHs) cause neglected tropical diseases that significantly affect humans and animals, worldwide. *Strongyloides stercoralis* is one such STH that affects over 600 million people living in endemic areas (World Health Organization [WHO], 2023). The life cycle of *S. stercoralis* has complexities that distinguish it from other STHs, with parthenogenesis and auto-infection enabling the persistence of infection in the host for decades. Humans and dogs are hosts for *S. stercoralis*, making infection and disease control challenging. Therefore, understanding the determinants of parasite transmission, the potential role of each host in transmitting the *S. stercoralis* pathogen, and the impact of treating hosts, on infection control is essential. This research aims to find an effective way to control *S. stercoralis* infection using mathematical modelling techniques. The study involves identifying the determinants of infection transmission in the host population, including the parasite life cycle and the contribution of human and canine hosts to the environmental reservoir. The peculiar life cycle and infection dynamics of *S. stercoralis* have been adapted using the compartmental model.

ID: 183 / **CP8.1: 2**
Contributed abstract
Conference Topics: Epidemiology, Genomics, Bioinformatics
Keywords: onchocerciasis, genomics, microfilariae, epidemiology, mass drug administration

What can DNA tell us about parasite biology? Inferences about *Onchocerca volvulus* reproduction and worm burden for assessing progress towards elimination

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Onchocerciasis, or River blindness, is characterized by severe skin, ocular, and neurological pathology. It is caused by the filarial nematode parasite *Onchocerca volvulus*. The primary strategy for elimination is mass drug administration with ivermectin (MDAi), a drug that reduces transmission by killing microfilariae in the skin and reducing adult female fertility. Over the course of a decade, MDAi should reduce the number of reproducing female worms. In some regions, transmission persists despite MDAi. We apply whole-genome sequencing to microfilariae to infer the number of reproductively active worms per person. We found that despite similar microfilaraemia, both the prevalence and average adult female worm burden was higher in Maridi County, South Sudan than in the bordering Ituri Province, Democratic Republic of the Congo (minimum 36 vs 13 worms/person). Analysis of nuclear diversity indicates that female worms mate with multiple males, and diversity on the sex chromosomes can be used to estimate the minimum number of males per person. Our results suggest that genetic tools to track changes in the number of reproductively active worms may be more useful than counts of microfilaraemia alone when evaluating whether MDA is effectively reducing worm burden and for comparing the efficacy of alternative treatment strategies.

ID: 102 / **CP8.1: 3**
Contributed abstract
Conference Topics: Diagnostics
Keywords: Crohn's disease, Inflammatory Bowel Disease, Intestinal parasite infections, and Ulcerative colitis, Mekelle, Ethiopia

Prevalence of Intestinal Parasites and associated risk factors among Inflammatory Bowel Disease suspected patients in Tigray Regional State, Northern Ethiopia.

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Intestinal parasite infections are important public health concerns globally. Besides, some Intestinal parasite infections aggravate symptoms, have a clinical similarity, and considered differential diagnosis with Inflammatory Bowel Disease. Hence, the prevalence of intestinal parasites and associated risk factors among Inflammatory Bowel Disease suspected patients were determined. A cross-sectional study was conducted among 297 Inflammatory Bowel Disease suspected patients from February 01, 2019 to July 30, 2020 attending in Ayder Comprehensive Specialized Hospital, Mekelle, Tigray region, Ethiopia. Descriptive statistics, Bivariate and multivariate logistic regressions were used. Hence, the p-value less than 0.05 were considered as statistically significant. Of these, 54.9% were males. The overall prevalence of intestinal parasites was 127 (42.76%). Entamoeba histolytica/dispar 76 (25.58%), and Giaardia lamblia 32 (10.77%) were the most predominantly identified parasites. Participants with untrimmed fingernail (AOR =2.4 95% CI =1.3-4.3, p =0.002), eating unwashed vegetables (AOR=2.3, 95%, CI: 1.2-4.3, p =0.011), and family size of greater than five (AOR=1.7, 95% CI= 1.029-2.881, p = 0.039) were found to be independent predictors of intestinal parasites. Therefore, health care providers should screen and treat Inflammatory Bowel Disease suspected patients for intestinal parasites in order to ensure good diagnosis, and treatment.

CP9: Immunology & Pathogenesis 15 min talks

Time: Thursday, 07/Sept/2023: 1:00pm - 2:00pm · *Location:* Symposium room 1
Session Chair: Steven Kho, Menzies School of Health Research

ID: 116 / CP9: 1
Contributed abstract
Conference Topics: Malaria, Vaccines
Keywords: Plasmodium falciparum, invasion, merozoites, vaccines, monoclonal antibodies, reticulocyte-binding protein homolog 5.

The Dual Action of Human Antibodies Specific to *Plasmodium falciparum* PfRH5 and PfCyRPA: Blocking Invasion and Inactivating Extracellular Merozoites.

Paul Gilson[1,4], Greta Weiss[1], Robert Ragotte[2], Doris Quinkert[2,3], Amelia Lias[2,3], Madeline Dans[1], Coralie Boulet[1], Oliver Looker[1], Olivia Ventura[1], Barnabas Williams[2,3], Simon Draper[2,3], Brendan Crabb[1,4]
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The *Plasmodium falciparum* reticulocyte-binding protein homolog 5 (PfRH5) is the current leading blood-stage malaria vaccine candidate. PfRH5 functions as part of the pentameric PCRCR complex which are essential for infection of human red blood cells (RBCs). To trigger RBC invasion, PfRH5 engages with RBC protein basigin in a step termed the RH5-basigin binding stage. Although we know how antibodies specific for PfRH5 can block invasion, much less is known about how antibodies recognizing other members of the PCRCR complex can inhibit invasion. We therefore performed live cell imaging using monoclonal antibodies (mAbs) which bind PfRH5 and PfCyRPA and showed that parasite invasion is blocked by individual mAbs, and the degree of inhibition is enhanced when combining a mAb specific for PfRH5 with one binding PfCyRPA. We also identified a secondary action of certain mAbs on extracellular parasites that had not yet invaded where the mAbs appeared to inactivate the parasites by triggering a developmental pathway normally only seen after successful invasion. These two protective mechanisms, prevention of invasion and inactivation of extracellular parasites, indicate a possible route to the development of more effective vaccines.

ID: 168 / CP9: 2
Contributed abstract
Conference Topics: Malaria, Drugs, Biochemistry
Keywords: Plasmodium, host defence protein, anti-plasmodial peptide, peptide-drug conjugate

Development and characterisation of anti-plasmodial peptides derived from a human host defence protein.

Brendan McMorran[1], Dianne Xu[1], Isabella Palombi[2,3], Bruce Munro[1], Caitlin Gare[2,3], Karoline White[1], Huma Sohail[1], Andrew White[2,3], David Craik[4,5], Lara Malins[2,3], Nicole Lawrence[4,5]
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Platelets produce an anti-plasmodial molecule called platelet factor 4 (PF4) which in previous work inspired the development of peptide-based molecules that possess specific and potent activity distinct from other antimalarial drugs. This activity is attributed to a paired amphipathic alpha helical domain of PF4, which was synthesised into a cyclised alpha-hairpin peptide called PDIP (PF4 Derived Internalization Peptide). Here, using a combination of cell biology and biochemical methods, we investigated how PDIP recapitulates the PF4 parent protein's potency and selectivity for Plasmodium. PDIP was selectively internalised into infected red cells and accumulated within the parasite cytosol after only a few minutes, and the treatment resulted in lysis of the digestive vacuole (DV). It also retained its cyclic structure despite the parasite's reducing environment. The speed and extent of peptide accumulation depended on the proportion of negatively charged phosphatidylserine lipid in the outer membrane of the host cell, and the kinetics of peptide uptake and subsequent DV lysis were directly observed using live imaging techniques. Residue substitutions and modifications of the peptide allowed identification of important structural constraints underlying these activities, and development of peptide-drug conjugates enabled other molecules with anti-plasmodial activity to be specifically targeted to the parasite.

ID: 128 / CP9: 3
Contributed abstract
Conference Topics: Ectoparasites, Molecular Biology, Host-parasite interactions
Keywords: Scabies, Microbiota, Microbiome, secondary-bacterial infections

A shift in the host skin microbiota towards opportunistic pathogens during scabies infestation.

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Scabies is a contagious skin infection caused by the obligate parasitic mite *Sarcoptes scabiei* causing significant global morbidity, with an estimated incidence of 300 million cases. Prevalence is high in tropical regions, where a link with secondary bacterial infections has been established through epidemiological studies. Scabies mites create an ideal microenvironment for opportunistic pathogens, particularly, *Staphylococcus aureus* and *Streptococcus pyogenes*. These pathogens can cause

serious sequelae. Despite this, there is limited molecular evidence demonstrating how the scabies infestation modulates the host's skin microbiota. We aim to provide quantified details about the microbial changes due to scabies infection to better understand the role scabies mites play in severe secondary bacterial infections and to inform improved treatment strategies.

In a multi-national collaboration we collected skin scrapings from scabies infected patients in India, France and Australia. Microbial DNA was extracted from 751 samples, and 16s full-length rRNA and ITS long-read amplicon PacBio sequencing was performed. We have analysed the data to determine the microbial profiles present during scabies infection in 1-3 lesions and uninfected control sites of 134 patients. Preliminary data demonstrates an increase in opportunistic pathogenic bacteria in scabies lesions.

ID: 206 / **CP9: 4**
Contributed abstract
Conference Topics: Malaria, Vaccines, Biochemistry, Molecular Biology
Keywords: malaria, vaccines, invasion, nanobodies, plasmodium falciparum

The molecular definition of potent *Plasmodium falciparum* invasion inhibitory epitopes on PTRAMP-CSS

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Plasmodium falciparum invasion of human erythrocytes is a complex multi-step process that can be targeted with therapeutics to reduce global malaria burden. The leading blood-stage vaccine candidate PfRh5 has a significant role during invasion by forming a pentameric complex with PfCyRPA, PfRipr and the disulphide-linked heterodimer PfPTRAMP-CSS. This complex has been called PCRCR and it binds to the receptor basigin on human erythrocytes. PCRCR is essential for invasion, and neutralising biologics to all members have been identified. Recently described nanobodies to PfPTRAMP and PfCSS showed moderate growth inhibition in comparison to antibodies developed against PfRh5, PfRipr and PfCyRPA. Further development of these blood-stage immunogens is required to induce a more potent immune response. Through antigen optimisation we have extended this campaign by screening a larger nanobody library specific to the PfPTRAMP-CSS heterodimer to determine more relevant inhibitory epitopes. We have identified four potent inhibitory nanobodies against PfPTRAMP-CSS and have elucidated the molecular structure of these novel neutralising and non-neutralising epitopes using X-ray crystallography. Through understanding the molecular definition of potent inhibitory epitopes on PfPTRAMP-CSS, a rational basis is provided for the structure-guided development of a next-generation malaria vaccine.

CP9.1: Immunology & Pathogenesis 5 min talks

Time: Thursday, 07/Sept/2023: 2:00pm - 2:15pm · *Location:* Symposium room 1
Session Chair: Steven Kho, Menzies School of Health Research

ID: 217 / **CP9.1: 1**
Contributed abstract
Conference Topics: Malaria, Vaccines, Apicomplexa Biology
Keywords: Plasmodium vivax, apical membrane antigen-1, antigen diversity, Immune evasion, vaccine development

Defining antigenic diversity and immune escape polymorphisms within *Plasmodium vivax* apical membrane antigen-1 (AMA-1)

Alison Paolo Bareng[1,2], Myo Naung[1,3], Zahra Razook[1,2], Alicia Arnott[3], Jessica Brewster[3], Enmoore Lin[4], Moses Laman[4], Ivo Mueller[3], Alyssa Barry[1,2]
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There are currently no available vaccines against *Plasmodium vivax* (Pv). However, several antigens have been studied as potential vaccine candidates; among these is AMA-1. AMA-1 is a micronemal protein essential in the parasite invasion of host cells, therefore it is a promising blood-stage vaccine target. Understanding AMA-1 antigen diversity and identifying polymorphisms that influence host immunity are critical in formulating a broadly-effective vaccine against Pv infection. In this study, we investigated the genetic diversity of *ama-1* gene by analysing global data; and using sequenced samples from a longitudinal cohort in Papua New Guinea (PNG), we examined polymorphisms that are potentially associated with parasite immune evasion. Traditional diversity measures showed extremely high *ama-1* genetic variability. In addition, balancing selection hotspots were observed in domains I and II, consistent in different populations. Interestingly, strong evidence of balancing selection was observed in the N-terminal distinct to PNG sequences. Lastly, polymorphic positions that may be associated to either host immunity or host-parasite interaction were determined and found to be located in regions with signatures of balancing selection. Overall, this study provides essential information for the rational selection of alleles to be included in the development of *ama-1* based vaccine against Pv.

ID: 209 / **CP9.1: 2**
Contributed abstract
Conference Topics: Malaria, Drugs, Proteomics, Molecular Biology, Host-parasite interactions
Keywords: Plasmodium falciparum, B-Raf kinase, Host-directed therapy, Anti-malarial treatments, Malaria

The role of the human kinase B-Raf in *Plasmodium falciparum* blood-stage infection.

Adedoyin Akinware, Jack Adderley, Christian Doerig
School of Health and Biomedical Sciences, RMIT University, Bundoora VIC 3083, Australia.

Malaria, a disease caused by the infection of parasites from the genus *Plasmodium*, remains a primary global health concern. Traditional anti-malarial medications target parasite-encoded enzymes or processes. The selection of mutations under drug pressure highlights the need for alternative treatments. Recent studies show that several host erythrocyte signalling kinases

are required for parasite survival, suggesting that Host-Directed Therapy can be implemented. This approach is refractory to direct resistance pathways since the target proteins are not under the parasite's genetic control. Possible targets for this approach include host cell B-Raf, c-MET, and MEK kinases. We have shown that inhibitors of these kinases impair parasite proliferation and survival. More specifically, SB-590885, PLX8394, and Dabrafenib, which all inhibit B-Raf activation through unique mechanisms, have antimalarial properties. As expected, resistance to SB-590885 and Dabrafenib has not been observed in drug-selection experiments. However, parasites with reduced susceptibility to PLX8394, as indicated by a 2x shift in IC50 value, have been isolated. We now investigate the role of host cell B-Raf in *Plasmodium falciparum* blood-stage infection and the mechanism of PLX8394-resistance. This will shed light on host-parasite interaction at the molecular level and provide insights for the development of host-directed therapy for malaria treatment.

ID: 228 / CP9.1: 3
Contributed abstract
Conference Topics: Malaria, Apicomplexa Biology
Keywords: Plasmodium falciparum, malaria

Characterising growth inhibitory activity of i-bodies targeting Plasmodium falciparum AMA1.

Keng Heng Lai[1], Dimuthu Angage[2], Jill Chmielewski[1], Robin Anders[2], Mick Foley[2], Danny Wilson[1]
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Nearly half of the world's population is at risk of malaria caused by Plasmodium spp. parasites, with P. vivax and P. falciparum being the major causes of disease. Antigens on the surface of the malaria merozoite, such as apical membrane antigen 1 (AMA1), have long been targeted as vaccine candidates. Here, we characterised the potency, species specificity and activity against merozoite surface protein knock-out line for i-bodies raised against AMA1. We show that the most potent i-body, WD34, was inhibitory against the AMA1 allele it was originally panned against (3D7), but also had potent activity against different Plasmodium falciparum isolates that express variant AMA1 alleles and against P. knowlesi. The inhibitory activity of WD34 was superior to that of well-known AMA1 targeting monoclonal antibodies and was potentiated further in parasites that lacked MSP2. Addition of a human FC region to the WD34 i-body increased the size of this single domain antibody and increased potency compared to WD34 alone in MSP2 knock-out parasites, indicating that the size of AMA1 antibodies is important for increased potency when MSP2 is absent. These findings help characterise i-bodies targeting AMA1 and their broad activity against malaria parasites.

CP9.2: Immunology & Pathogenesis 3 min talks

Time: Thursday, 07/Sept/2023: 2:15pm - 2:30pm · *Location:* Symposium room 1
Session Chair: Steven Kho, Menzies School of Health Research

ID: 150 / CP9.2: 1
Contributed abstract
Conference Topics: Malaria, Host-parasite interactions
Keywords: malaria, protein kinase, kinomics, host-directed therapy HDT, host-pathogen interactions

Host erythrocyte and reticulocyte cell signalling during infection with *Plasmodium* spp.

Mohammad Jamiu Shuaib, Christian Doerig, Jack Adderley
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Intracellular pathogens, such as *Plasmodium* parasites, modulate their host phosphorylation signalling pathways for survival and proliferation during infection. However, signalling information is complex and challenging to comprehend holistically. In this project, we implemented an antibody microarray approach to evaluate the signalling environment during *Plasmodium knowlesi* infection of human reticulocytes. This allowed us to measure the difference in kinase expression and phosphorylation levels between the infected and uninfected samples. A comprehensive analysis identified the top 10 signals (in terms of fold-change from the uninfected control) with consistent patterns across two biological replicates and specific parasite exposure times. Specifically, UBS (Upstream Binding Factor), RSK (Ribosomal s6 Kinase), and MEK exhibited consistent activation at12-hour post-infection time. HGK, TrkB, and c-Jun N-terminal kinases (JNKs) were also prominently activated in the 24-hour time post-infection. Many of these top signals (such as UBS and RSK) correspond to signalling elements implicated in haematopoiesis. Additional analysis will be done to identify other top-consistent signals prior to validation through biochemical and pharmacological methods.

ID: 147 / CP9.2: 2
Contributed abstract
Conference Topics: Malaria, Vaccines, Immunology, Molecular Biology
Keywords: Malaria, Merozoite, Vaccine, Antibody, MSP

Characterising functional antibodies to *P. falciparum* merozoite surface protein domains and epitopes to inform next-generation vaccine design.

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P. falciparum expresses numerous proteins on merozoites that could be targets of vaccines. However, well-defined correlates of protection are lacking, complicating candidate selection for vaccine development. Recent studies have shown that antibodies with specific functional activities can target merozoites effectively and are associated with protection. Merozoite surface proteins (MSPs) are responsible for erythrocyte attachment and invasion. Many are abundant on the surface, making

them attractive vaccine targets. However, how to elicit functional antibodies targeting specific domains and epitopes is not well understood. Here we used an abundant surface protein, MSP2, as a proof-of-concept to identify regions that are strongly targeted by functional antibodies to inform vaccine design. Serum samples from Kenyan donors were tested against peptides corresponding to regions of MSP2. We found that the cohort displayed high IgG titres against each peptide. Fc-receptor binding and complement fixation assays, which quantify specific protective functions, are being used to further define targets of functional antibodies. Our results will demonstrate that certain regions within MSP2 are highly targeted by functional antibodies. Incorporating these regions in a vaccine may afford better protection against malaria. The fine-tuning of protective epitopes can also be applied to other MSPs to design an effective multi-antigen vaccine.

ID: 161 / **CP9.2: 3**
Contributed abstract
Conference Topics: Malaria, Vaccines, Immunology, Host-parasite interactions
Keywords: antibody-mediated, adaptive immunity, immunology, vaccines, vivax

Identifying merozoite surface proteins as targets of protective functional antibody responses against *Plasmodium falciparum* and *P. vivax*

Kaitlin Pekin[1,2], D. Herbert Opi[1,3,4], Liriye Kurtovic[1,3], Gaoqian Feng[1,5], Jill Chmielewski[2], Isabelle Henshall[2], Daisy Mantila[6], Benishar Kombut[6], Maria Ome-Kaius[5], Moses Laman[6], Ivo Mueller[7], Leanne Robinson[1,7,8], Danny Wilson[2], James Beeson[1,3,4,9]

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Reduction in the burden of malaria has stalled in recent years highlighting the need for efficacious vaccines against both *Plasmodium falciparum* and *P. vivax* to support malaria elimination. Despite one *P. falciparum* vaccine recently being approved for use, vaccine efficacy is modest, and there are no *P. vivax* vaccines available, with limited candidates under development. A better understanding of the targets and mechanisms of action of protective antibodies is needed to develop highly efficacious *P. falciparum* and *P. vivax* vaccines.

We are investigating merozoite surface proteins (MSP) as major targets of protective functional antibody responses to *P. falciparum* and *P. vivax.* Including their ability to activate the complement system and inhibit merozoite invasion and replication within red blood cells, and to engage Fcγ-receptors to promote opsonic phagocytosis and antibody dependent cellular cytotoxicity. *P. falciparum* cell culture has been well established, whereas long-term *P. vivax* culture has been challenging. To overcome this, we are evaluating antibodies against transgenic lines of closely related *P. knowlesi* expressing homologous and *P. vivax* MSPs and short-term culture of *ex vivo* clinical *P. vivax* field isolates.

Our work will gain insight into functional antibody immunity to *P. falciparum* and *P. vivax* and inform future vaccine development.

ID: 194 / **CP9.2: 4**
Contributed abstract
Conference Topics: Malaria, Apicomplexa Biology, Host-parasite interactions
Keywords: Plasmodium, Iron deficiency, malaria

Host iron environment impact in P. falciparum infection

Rafael Oliveira[1], Frank P Mockenhaupt[2], Brendan J. McMorran[1]

[1]Australian National University; [2]Charité – Universitätsmedizin Berlin Institute of Tropical Medicine and International Health

Plasmodium infection and host iron metabolism share an axis of complex interactions. Clinical findings have shown that on one hand iron deficiency protects against the risk of malaria while on the other hand, iron supplementation raises this risk. We developed an *in vitro* model using cultured *P. falciparum* parasites and red blood cells exposed to different iron environments to studyhow the parasite replication and transmission are affected. Our results demonstrated that in an iron-deficient environment, parasite growth rate is was reduced. In contrast, the transition and timing of parasite intraerythrocytic development was not impaired.[BM1] Moreover, iron supplementation conditions do contribute to a significant increase of parasite growth. Overall, the study indicates that this *in-vitro* model represents a suitable approach to study iron deficiency interactions on malaria infection. Additionally, in vitro experiments using our model to study parasite iron requirements are concordant with what is observed with other *in-vitro* studies using human donors, with iron deficiency anaemia. Future steps will explore the impact of the iron environment on transmission stages of Plasmodiumand changes in transcriptional programs that mark the parasite's adaption to changing iron conditions.

ID: 158 / **CP9.2: 5**
Contributed abstract
Conference Topics: Ectoparasites
Keywords: scabies, itch, Sarcoptes scabiei, Immunohistology

Immunohistological localisation of pruritogenic mediators in scabies itch

Deepani D. Fernando, Katja Fischer

Department of Infection and Inflammation, QIMR Berghofer Medical Research Institute, Brisbane, Australia

Scabies is one of the most common skin diseases worldwide that is caused by the parasitic mite *Sarcoptes scabiei* and is highly contagious. Unbearable itch is the cardinal symptom of scabies that manifests 4-6 weeks following primary infection. Scratching in response to itching facilities the entrance of pathogenic bacteria that often leads to life-threatening sequelae. The mechanisms underlying the scabies itch are poorly understood, hence scabies itch targeted therapies are missing.

Due to the non-responsiveness to anti-histamines, a histamine-independent pathway is proposed for scabies itch. We aimed to investigate expression of non-histaminergic itch mediators; PAR-2, thymic stromal lymphopoietin, neuron-signalling ion channels (TRPV1 and TRPA1), mast cell tryptase, histamine and IL-31 over a course of scabies infection in a pig model.

Skin biopsies from three scabies infected pigs were collected pre-infection and 2, 4, 8, 12 and 20 weeks post-infection. Anti-tryptase IgG and cy-3 labelled secondary antibodies were used to localise tryptase$^+$ mast cells. Aperio FL slide scanner and QuPath software were used to image and quantify the typtase$^+$ mast cells. We observed reduced typtase$^+$ mast cell counts in the early infection and an increase thereafter.

Expression profiles of proposed itch mediators will assist in identifying contributing factors for scabies itch.

S5: Symposium 5 Companion Animals sponsored by Vetoquinol

Time: Thursday, 07/Sept/2023: 1:00pm - 2:00pm · *Location:* Symposium room 2
Session Chair: Clare Anstead, University of Melbourne

ID: 243 / S5: 1
Invited speaker abstract

From HTS to an innovative animal health product: the bispyrazole tigolaner in Felpreva® spot-on for cats

Norbert Mencke[1], Katrin Blazejak[1], Michael Maue[2], Ulrich Ebbinghaus-Kintscher[2], Klaus Raming[2], Andreas Turberg[3]
[1]Vetoquinol S.A. Global Medical Marketing Parasitology, Paris France; [2]Bayer AG, Crop Science Division, Monheim Germany; [3]retired from Elanco Animal Health, Monheim Germany

Background:
Innovation, thus the search for new molecules and the successful development into a medicine, is the driving force in the animal industry. It is the aim of this presentation to share some insights into the laborious, costly and year-long R&D activities. The way from High Throughput Screening (HTS) in discovery research, through development, leading to an innovative animal health ectoparasiticide will be presented. From first *in-vitro* hits to a highly active and selective class of allosteric modulators of GABA-gated channel finally leading to the identification of Tigolaner as the lead development candidate.

Methods:
The activities in discovery chemistry, *in-vitro* and *in-vivo* research, followed by the development towards a veterinary medicinal ectoparasiticide will be presented.

Results:
Tigolaner strongly modulates a broad variety of insect GABA-gated channels, whereas mammalian GABA-gated channels are significantly less affected resulting in a favorable toxicity and safety profile. Tigolaner holds insecticidal and acaricidal properties, thus was developed as an ectoparasiticide in veterinary medicine. The pharmacokinetic properties of tigolaner offering the 13-week long-lasting efficacy against ectoparasites (fleas and ticks) in cats. Tigolaner in the product Felpreva® has received marketing authorization by the EMA in Europe in November 2021 and is marketed by Vetoquinol S.A. Paris, France. Tigolaner has been invented by a team of Bayer CropScience and Bayer Animal Health researchers.

Conclusion:
The joint team approach allowed a very comprehensive Structure-Activity-Relationship optimization looking for Crop Protection and Animal Health activity at the same time. The result, Felpreva®, the first endectocide spot on for cats to treat both internal and external parasites, including tapeworms, in addition to providing 3-months ongoing protection against fleas and ticks.

ID: 242 / S5: 2
Contributed abstract
Conference Topics: Veterinary Parasitology, Drugs
Keywords: paralysis tick, Ixodes holocyclus

Efficacy and safety of Felpreva®, a spot-on formulation for cats containing Emodepside, Praziquantel and Tigolaner against experimental infestation with the Australian paralysis tick (*Ixodes holocyclus*)

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The Australian paralysis tick *Ixodes holocyclus* continues to be a serious threat to companion animals. To investigate the therapeutic and long-term persistent efficacy of Felpreva® (2.04% w/v emodepside, 8.14% w/v praziquantel and 9.79% w/v tigolaner) against experimental infestation with *I. holocyclus* in cats, two studies were undertaken. Fifty cats were included in the studies on study Day -17. Cats were treated once on Day 0. Group 1 cats were treated with the placebo formulation and Group 2 cats were treated with Felpreva®. Cats were infested on Days -14 (tick carrying capacity test), 0, 28, 56, 70, 84 and 91 (weeks 4, 8, 10, 12 and 13). Ticks were counted on cats 24, 48 and 72 hours post-treatment and infestation, except during the tick carrying capacity test when they were counted approximately 72 hours post-infestation only. Significant differences in ToL tick counts at ~24, ~48 and ~72 hours post infestation were observed between the treatment and control group. Differences were significant ($p<0.05$ to <0.001) in all instances. Treatment efficacies of 98.1 – 100% were observed ~72 hours post infestation through to 13 weeks (94 days) post-treatment. Felpreva® provides effective treatment and control against induced infestation with paralysis ticks for 13 weeks.

ID: 257 / S5: 3
Invited speaker abstract

Aleurostrongylus abstrusus infection in cats – a clinical perspective

Rachel Korman
Cat Specialist Services, Australia

The presentation of cats with *Aleurostrongylus abstrusus* infection varies from severe respiratory disease to subclinical infections. In this clinically focused based lecture we will discuss case presentations, diagnostic techniques and treatment.

CP10: Veterinary Parasitology sponsored by Vetoquinol 15 min talks

Time: Thursday, 07/Sept/2023: 2:00pm - 2:30pm · *Location:* Symposium room 2
Session Chair: Clare Anstead, University of Melbourne

ID: 139 / CP10: 1
Contributed abstract
Conference Topics: Veterinary Parasitology, Helminthology, Bioinformatics
Keywords: Dirofilaria immitis, whole-genome sequencing, genetic diversity, drug resistance, Australia

Defining the genetic diversity of the canine heartworm *Dirofilaria immitis* in Australia

Rosemonde Power[1], Stephen Doyle[2], Jan Šlapeta[1]
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The canine heartworm *Dirofilaria immitis* is a filarial parasitic nematode that causes canine heartworm disease in dogs. Now that drug-resistant isolates have been confirmed in the United States, researchers have identified genetic markers associated with resistance. Although a handful of these markers have been characterised in Australian *D. immitis*, the remaining parts of the genome remain unknown to us and the population structure of this parasite in Australia remains poorly understood. The aim of this study was to define the genetic diversity of *D. immitis* across Australia and generate local representative genomes of this parasite which can be rapidly interrogated for any markers associated with drug resistance. To do so, we conducted whole-genome sequencing on 31 adult *D. immitis* obtained from dogs and foxes in various coastal regions in Queensland and New South Wales. This sequencing data was mapped against a recent reference genome, and levels of within and between population diversity were subsequently evaluated. Lastly, we determined whether any of the US-identified markers were present in our *D. immitis* samples from Australia. In this presentation, we will reveal the results of our whole-genome sequencing analysis.

ID: 162 / CP10: 2
Contributed abstract
Conference Topics: Veterinary Parasitology, Helminthology
Keywords: Horse strongyles, Anthelmintic resistance, Macrocyclic lactones, DNA metabarcoding, Australia

Status of anthelmintic resistance in cyathostomins in Australian horses

Ghazanfar Abbas[1], Anne Beasley[2], Abdul Ghafar[1], Emma McConnell[3], Jenni Bauquier[1], Edwina J.A. Wilkes[4], Charles El-Hage[1], Peter Carrigan[5], Lucy Cudmore[5], John Hurley[6], Elysia Ling[1], Charles G. Gauci[1], Ian Beveridge[1], Martin K. Nielsen[7], Kristopher J. Hughes[8], Caroline Jacobson[3], Abdul Jabbar[1]
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This study aimed to investigate anthelmintic resistance in cyathostomins of Australian horses using conventional and molecular techniques. Seventy-four faecal egg count reduction tests were conducted for eight anthelmintics across Australia. The modified McMaster technique was used to perform faecal egg counts, and percentage fecal egg count reduction (%FECR) was calculated using the Bayesian hierarchical model. DNA-metabarcoding was used to determine cyathostomin species composition pre- and post-treatment. The highest efficacy was observed for combinations of macrocyclic lactones with pyrantel (>97% FECR) in 15 trials. Resistance was observed against ivermectin (2/15 trials; FECR range: 82-92%; LCL range: 80-89.5%), abamectin (2/4; 73-92%; 65-88%), moxidectin (3/14; 88.6-91%; 84-89%), and oxfendazole (6/6 trials; FECR range: 0-56%; 0-31%), whereas oxfendazole-pyrantel combination was found effective in 3/18 trials. Shortened egg reappearance periods (4-6 weeks) were observed in 31 trials where resistance was not detected 2-weeks post-treatment. *Cylicocyclus nassatus*, *Cylicostephanus longibursatus* and *Coronocyclus coronatus* were the most prevalent species at 2-weeks-post-treatment, whereas *Cylicocyclus nassatus, Cylicostephanus longibursatus* and *Cyathostomum catinatum* were dominant among first appearing species at 3-weeks and beyond. These findings highlight the prevalence of anthelmintic resistance in Australian horses and emphasise the need for awareness about this problem and routine monitoring of anthelmintic efficacy on horse farms.

S6: Symposium 6 Education & Outreach

Time: Thursday, 07/Sept/2023: 3:00pm - 3:30pm · *Location:* Symposium room 1
Session Chair: Sarah Preston, Federation University Australia

ID: 253 / S6: 1
Invited speaker abstract

Appreciated Parasites and Talented Parasitologists

Alexander G. Maier
Research School of Biology, Australian National University, 134 Linnaeus Way, Canberra, ACT 2601, Australia

Engaging students in hands-on experiments and reflections (also known as experiential learning) is an effective way to teach new skills and knowledge. But how can this be done in a field like parasitology? How can we “experience” parasites in a personal way when we normally try everything not to be exposed to these pathogens? How can we make parasites, the “Masters of Stealth”, obvious and observable to the students? And how can the parasites’ complexity and enormous diversity across the phylogenetic tree be reflected in a few handfuls of lectures?

In this talk I will present different active forms of learning that are student-focused, multi-disciplinary and immersive. Aligning the course content with the talents and aspirations of the learner allows for an easier access to the exciting world of parasites and results in sustained retention of biological concepts and principles.

CP11: Education & Outreach 15 min talks

Time: Thursday, 07/Sept/2023: 3:30pm - 4:30pm · *Location:* Symposium room 1
Session Chair: Sarah Preston, Federation University Australia

ID: 216 / CP11: 1
Contributed abstract
Conference Topics: Helminthology, One Health
Keywords: Soil-transmitted helminths, Opisthorchis viverrini

Acceptability and impact of a cartoon-based helminth education package among schoolchildren in the Lower Mekong Basin

Suji O'Connor
Australian National University

Soil-transmitted helminths and *Opisthorchis viverrini* are a major public health concern in the Lower Mekong Basin;[1] associated with anaemia, malnutrition, stunting,[2-5] and in cases of chronic Opisthorchiasis, cholangiocarcinoma, cancer of the bile duct.[6] The primary control strategy for helminth infections is mass drug administration but this does not prevent reinfection. As such, additional health promotion measures are needed. Children are an important group for helminth intervention, with several studies reporting high incidence of helminthiases among preschool- and school-aged children in affected areas.[7-10]

A cluster-randomised controlled trial will be conducted to investigate the acceptability of the ‘Magic Glasses Lower Mekong’ and its impact on knowledge, attitudes and practices surrounding helminthiases among schoolchildren in Cambodia, Thailand and Lao PDR. The Magic Glasses is a school-based educational cartoon with demonstrated success in China[11] and the Philippines.[12] This study will provide evidence of the acceptability of Magic Glasses, an important indicator of sustained intervention success[13] and be the first Magic Glasses intervention to target *Opisthorchis viverrini*, and multiple countries.

I will present on the measures developed to assess the acceptability of Magic Glasses Lower Mekong, including an acceptability questionnaire adapted from Sekhon’s Theoretical Framework of Acceptability[13,14] and qualitative tools developed for the trial.

ID: 231 / CP11: 2
Contributed abstract
Conference Topics: Education/Outreach
Keywords: Work integrated learning

Work integrated learning partnerships – a case example for development of zoonotic health resources

Michelle Power[1], Jessica Hoopes[2], Bonny Cumming[2], John Hunter[3]
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Work integrated learning (WIL) in higher education enables students to undertake learning towards their degree in a real-world work context. The most authentic WIL experience for students involves partnerships with industry. This presentation will showcase a WIL partnership between AMRRIC (Animal Management in Rural and Remote Indigenous Communities) and Macquarie University Bachelor of Medical Sciences students. Students were asked to help develop fact sheets and infographics to explain the potential impacts of zoonotic diseases on the health of people and animals living in rural and remote Aboriginal and Torres Strait Islander communities. Students learnt about AMRRICs activities and strategic direction from AMRRIC staff and were guided in the types of zoonoses of significance for AMRRIC, Aboriginal and Torres Strait Islander communities and pets in communities. Students also learned about the One Health approach in the context of improving human health through companion animal health and management. Additionally, students undertook cultural training and engaged with First Nations health professionals to learn about effective, safe, and appropriate ways for health communication to First Nations Peoples. The WIL partnership resulted in tangible outcomes for AMMRIC, the students, and the communities with several high-quality fact sheets and infographics now available on the AMRRIC website.

ID: 210 / **CP11: 3**
Contributed abstract
Conference Topics: Veterinary Parasitology, Education/Outreach
Keywords: Veterinary Parasitology, education, online learning, teaching innovation

Teaching veterinary parasitology in a digital world

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To enter the work force, veterinary students require strong clinical knowledge in addition to practical problem-solving skills in order to apply this knowledge in the field. Treatment and control of parasites are integral components of veterinary practice. To successfully treat and manage parasitic diseases, veterinarians must take a multidisciplinary approach, including understanding the parasite, the host's response to infestation, relevant diagnostic tests and pharmacological treatments, animal management, epidemiology, and effective clinical communication. Therefore, it is important to teach veterinary students how to incorporate these many fields of study, and parasitology teaching activities are good examples of how technology can help students achieve this. Our aim is to demonstrate how adaptive learning can assist students integrate information from many disciplines to tackle real-world parasitological problems at their own pace, in an online environment.

ID: 199 / **CP11: 4**
Contributed abstract
Conference Topics: Malaria, Veterinary Parasitology, Ectoparasites, Apicomplexa Biology, Helminthology, Education/Outreach, Host-parasite interactions, One Health
Keywords: Outreach, STEAM, STEM, science education, disability, inclusive

ASP's Crafty Parasites: bringing the love of Malaria and Hookworms through a multi-media STEAM resource into the classroom and community.

Rina Wong (Fu)[1], Paul Giacomin[2], Lisa Jones[3], Sarah Preston[4], Michelle Power[5], Kate Miller[2], Rebecca Traub[3], Alex Loukas[2]
[1]Edith Cowan University; [2]James Cook University; [3]Australian Society for Parasitology; [4]Federation University; [5]Macquarie University

The ASP Crafty Parasites series is a multi-media resource that combines the love of pesky parasites with fun, interactive activities. The STEAM approach integrates learning of scientific knowledge with applications through creativity, technology and the arts. Produced by Rina Fu, the videos are embedded with authentic research footage, stop animation, original song, novel craft activities with step-by-step pictorial instructions, puzzles, teachers notes and curriculum links. These offer a rich and adaptive 'ready-to-go' resource for time-poor teachers and science presenters. In 2022-2023, Crafty Parasites: Malaria was implemented for participants aged 5 to 83 years old, including primary school age children, teens, retired seniors and people living with disabilities (n = >180). A novel aspect is the trial of this multi-media resource to empower pre-service teachers to engage students in post-workshop learning through the use of technology to create a stop-animation using their hand-crafted pipe-cleaner models of parasites (at various life cycle stages). Students have the opportunity to write their malaria story, script, narrate and build their backdrop using our pre-designed, printable erythrocytes and blood vessels.

In development is the second episode, Crafty Parasites: Hookworm. Filmed in tropical Cairns in Australia, this project is star-studded with world class parasitologists and their progeny.

P3: IJP:PAW Plenary Lecturer

Time: Thursday, 07/Sept/2023: 5:00pm - 5:45pm · *Location:* Plenary Room
Session Chair: Andrew Thompson, Murdoch University

ID: 256 / **P3: 1**
Invited speaker abstract

Parasites of wildlife: Gaps and challenges in the molecular era

Tomáš Scholz
Institute of Parasitology, Biology Centre of the Czech Academy of Sciences, České Budějovice, Czech Republic

Molecular and "-omic" methods have opened up unprecedented opportunities for biological research, including all areas of parasitology. However, there are two sides to every coin, and too one-sided a focus on new approaches can lead to major gaps as "old-fashioned" topics are neglected, including faunal surveys of parasites in wildlife. In recent decades, much emphasis has been placed on studying the interactions between parasites and their hosts at the molecular level. While this is useful, this ignores the fact that parasitology is primarily an ecological discipline. In this talk, I briefly review selected areas of parasitological research and highlight the achievements and problems of current research, which focuses heavily on molecular and "-omic" methods. These areas include taxonomy and biodiversity studies, classification and evolution of parasites, parasitological surveys and screening, life cycles, and ecology of parasites. It is recommended to combine both "classical" and modern methods (molecular and "-omic" approaches) without neglecting the complexity of parasite interactions with their hosts and the environment, which is even more urgent in today's rapidly changing world. The younger generation should be more involved in field investigations and multidisciplinary assessment of parasites to understand the complexity of parasitology.

P4: Strongyloides Opening Plenary Lecture

Time: Friday, 08/Sept/2023: 8:30am - 9:15am · *Location:* Plenary Room
Session Chair: Dr Jenni Judd, Central Queensland University

ID: 263 / P4: 1
Invited speaker abstract

Working together to close the gap on Strongyloidiasis in remote Indigenous communities.

Wendy Page
Strongyloides Australia, Australia

Background: Chronic strongyloidiasis is managed as a preventable chronic infectious disease in primary health care services, where early diagnosis, treatment and follow-up can prevent life-threatening clinical complications and decrease transmission in endemic communities. The aim was to evaluate the effectiveness of the primary healthcare intervention in decreasing the hyperendemic rates of strongyloidiasis in four remote Indigenous communities.

Method: A prospective, longitudinal, before-and-after intervention integrated serological testing for chronic strongyloidiasis into the preventive adult health assessment in four Aboriginal health services in endemically infected communities. A strongyloides report developed for the patient information record system extracted data on coverage and prevalence for current adult residents at half- yearly intervals from 2012 to 2016. A post-study strongyloides report extracted data to assess sustainability and effectiveness of the intervention in endemic communities where reinfection can occur.

Results: The strongyloides report from four communities in December 2020 showed 84% (2390/2843) of current adult population were tested at least once, 44% (1056/2390) of those tested were positive at least once, and prevalence reduced to 9.7% (232/2390) positive on their last test. Of positive cases who had a follow-up serology test, 85% (824/967) declined to negative.

Conclusions. Health services in endemically infected communities have a key role in strongyloidiasis prevention and control programs.

P4.1: IJP:DDR Plenary Lecturer

Time: Friday, 08/Sept/2023: 9:15am - 10:00am · *Location:* Plenary Room
Session Chair: Kevin Saliba, Australian National University

ID: 260 / P4.1: 1
Invited speaker abstract

Leveraging chemogenetics for antimalarial drug discovery and target identification

Jacquin Niles
Massachusetts Institute of Technology, United States of America

Antimalarial drugs are critical for malaria treatment and eradication efforts. However, resistance to clinically approved drugs is rapidly spreading, and the pipeline of new antimalarial drugs is relatively limited. Phenotypic screens are valuable for discovering promising lead compounds, but target identification is a separate, time-consuming process. To overcome this bottleneck in lead compound discovery and optimization, we are combining genetic engineering, synthetic biology and chemical screening approaches to rapidly identify functional interactions between compounds and their molecular targets. In this way, we simultaneously obtain evidence of a compound's antimalarial activity and likely mode of action. We illustrate the potential to scale this target-based screening approach, and to integrate it with increasingly higher throughput screening activities towards improving the efficiency with which new and promising antimalarial compounds can be identified.

S7: Drugs & Drug Resistance Symposium

Time: Friday, 08/Sept/2023: 10:30am - 11:00am · *Location:* Symposium room 1
Session Chair: Benedikt Ley, Menzies School of Health Research

ID: 254 / S7: 1
Invited speaker abstract

Towards the elimination of vivax malaria

Kamala Thriemer
Menzies School of Health Research, Australia

Plasmodium vivax malaria is becoming the predominant cause of malaria in many regions, accounting for 4-7 million annual cases in 49 endemic countries in Asia, Oceania, the Horn of Africa, and the Americas. Vivax malaria is associated with significant morbidity and mortality, and there is increasing recognition of the public health importance related to *P. vivax* control and elimination. The control and elimination of P. vivax is particularly challenging because of the parasite's ability to form dormant liver stages (hypnozoites) that can reactivate weeks or months following an acute infection (relapse). Relapses are associated with a febrile illness and a cumulative risk of direct and indirect morbidity and mortality and are an important source of onward transmission of the parasite. Widespread access to safe and effective radical cure (the treatment of blood and liver forms) is critical for the elimination of *P. vivax*. However current radical cure treatment policies are suboptimal and there is a need to optimise treatment regimens.

CP13: Drugs & Drug Resistance 15 min talks

Time: Friday, 08/Sept/2023: 11:00am - 11:30am · *Location:* Symposium room 1
Session Chair: Benedikt Ley, Menzies School of Health Research

ID: 212 / CP13: 1
Contributed abstract
Conference Topics: Malaria, Drugs, Livestock Parasites
Keywords: Malaria, toxoplasmosis, microbial metabolites.

Screening a library of natural microbial metabolites against the apicomplexan parasites *Plasmodium falciparum* and *Toxoplasma gondii*

Maria Gancheva[1], Ernest Lacey[2], Stephen Page[3], Ryan O'Handley[4], Danny Wilson[1]
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Malaria, caused by mosquito-transmitted *Plasmodium* spp. parasites, results in over 200 million cases and over 500,000 deaths each year. The related apicomplexan parasite *Toxoplasma gondii* infects 30-50% of the world's population and causes 190,000 cases of congenital toxoplasmosis every year, as well as causing a large economic impact on the livestock industry. Parasite resistance to our best antimalarial drugs is spreading whilst toxoplasma drugs have questionable efficacy and safety, highlighting the urgent need to develop new safe and effective drugs with novel mechanisms of action. We screened the BioAustralis Discovery Plates, a unique library of 812 natural microbial metabolites and semi-synthetic derivatives. One third of compounds inhibited *Plasmodium falciparum* growth whilst 19 per cent of compounds inhibited *T. gondii* growth by more than 80 per cent at 2 µg/mL. These compounds belonged to 69 and 46 different chemical classes for *P. falciparum* and *T. gondii* respectively. Compounds resulting in a delayed-death phenotype in *P. falciparum* were also detected. Compounds with low EC_{50}s were identified, and stage specificity and cell toxicity against a human cell line were analysed. This library of natural microbial metabolites presents potent compounds that may possess novel mechanisms of action for further investigation.

ID: 103 / CP13: 2
Contributed abstract
Conference Topics: Malaria, Drugs, Cell Biology, Apicomplexa Biology, Molecular Biology, Protozoa, Microscopy
Keywords: Malaria, invasion, drugs, phospholipase, lipids

MMV687794 impairs blood-stage *Plasmodium falciparum* invasion by perturbing lysophospholipids

Dawson Ling[1,2], Madeline G Dans[3], Greta E Weiss[1], Zahra Razook[4,5], Somya Mehra[4], Christopher A MacRaild[6], Darren J Creek[6], Alyssa E Barry[4,5], Brendan S Crabb[1,2], Hayley E Bullen[1,2], Paul R Gilson[1,2]
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Responsible for parasite proliferation and symptomatic malaria, parasite invasion of erythrocytes represents an attractive novel drug target. Our group discovered a compound that specifically blocked invasion from schizonts, MMV687794. Genomic analysis on MMV687794-resistant parasites unveiled mutations in an alpha/beta hydrolase enzyme containing a lysophospholipase (LysoPL) motif we termed ABH-83. To validate ABH-83 as the drug target, these mutations were engineered into wild-type parasites using CRISPR/Cas9, which recapitulated the MMV687794-resistant phenotype. An epitope tag and a GlmS riboswitch were also introduced into these parasites, enabling closer examination of the role/s of ABH-83. By conducting a time-course western blot series on the transgenic parasites, the LysoPL ABH-83 is most highly expressed in schizonts, concordant with a role in invasion. ABH-83 has also been visualised by microscopy at the rhoptry surface, organelles which secrete important invasion-related proteins during erythrocyte invasion. Using a western blot-based assay, reduced ABH-83 expression led to decrease rhoptry protein (Rh5) processing. Lipidomics data indicate MMV687794-treated schizonts have elevated lysophospholipids, an effect less pronounced in parasites with mutant ABH-83. Overall, these results suggest that ABH-83 is involved in rhoptry lipid metabolism vital for its functioning/morphology and, subsequently, efficient merozoite invasion of erythrocytes. Further lipidomic investigations aim to examine this.

CP13.1: Drugs & Drug Resistance 5 min talks

Time: Friday, 08/Sept/2023: 11:30am - 11:45am · *Location:* Symposium room 1
Session Chair: Benedikt Ley, Menzies School of Health Research

ID: 122 / CP13.1: 1
Contributed abstract
Conference Topics: Drugs, Proteomics, Protozoa
Keywords: drug discovery, target identification, Giardia, kinase, drug target, proteomics

Target Deconvolution in *Giardia duodenalis* Using a Kinase Inhibitor

Alex Lam[1,3], Samantha Emery-Corbin[1,3], Louise Baker[1], Guillaume Lessene[1], Subash Adhikari[1], Jumana Yousef[1], Aaron Jex[1,2,3]

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Giardia duodenalis, a gastrointestinal parasite, causes 200 million infections annually, primarily affecting children in lower socioeconomic groups. Chemotherapeutic options are limited to toxic nitroheterocyclics like metronidazole, with up to 20% of cases showing drug resistance. A safer and novel alternative is urgently required for treating giardiasis.

The *Giardia* kinome is an attractive druggable space, as the NEK (Never-in-Mitosis-A related kinases) family of kinases are expanded in this genus' otherwise reduced kinome (198/278 of annotated kinases). We performed an *in vitro* screen of a published kinase inhibitor library, identifying a compound series that kills *Giardia* at sub-micromolar concentrations. Further, we have undertaken drug-target identification using the Proteome Integral Solubility Alteration (PISA) assay with MS-based identification; we shortlisted 63 proteins demonstrating dose-dependent thermal-(de)stabilisation resulting from drug binding. Four from this shortlist were classified as kinases, the likely putative targets of our compound. Further, *in silico* binding predictions of our lead compound with the four kinases identified in PISA produced comparable ligand-protein intermolecular interactions to those described in the literature. Together, this has allowed us to identify credible candidate targets for the compound in *Giardia*, which we will now explore through target-based assays and additional compound chemistries.

ID: 129 / CP13.1: 2
Contributed abstract
Conference Topics: Veterinary Parasitology, Drugs, Diagnostics, Livestock Parasites, Molecular Biology, Helminthology
Keywords: levamisole, benzimidazole, nemabiome, ruminants, surveillance

A mixed amplicon metabarcoding and sequencing approach for surveillance of drug resistance to levamisole and benzimidazole in *Haemonchus* spp.

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Anthelmintic resistant parasitic nematodes present a significant threat to sustainable livestock production worldwide. The ability to detect the emergence of anthelmintic resistance at an early stage, and therefore determine which drugs remain most effective, is crucial for minimising production losses. We developed a mixed deep amplicon sequencing approach to determine the frequency of the levamisole (LEV) resistant single nucleotide polymorphism (SNP) within *arc*-8 exon 4 (S168T) in *Haemonchus* spp., coupled with benzimidazole (BZ) resistance SNPs (*β-tubulin* isotype-1) and ITS-2 nemabiome. This constitutes the first multi-drug and multi-species molecular diagnostic developed for helminths of veterinary importance. Of the Australian field isolates we tested, S168T was detected in the majority of *Haemonchus* spp. populations, but rarely at a frequency greater than 16%; an arbitrary threshold we set based on whole genome sequencing of LEV resistant *H. contortus* GWBII. Overall, BZ resistance was far more prevalent in *Haemonchus* spp., confirming that LEV is still an important anthelmintic class for small ruminants in New South Wales. The mixed amplicon metabarcoding approach described herein, paves the way towards the use of large scale sequencing as a surveillance technology in the field, the results of which can be translated into evidence-based recommendations for the livestock sector.

ID: 135 / CP13.1: 3
Contributed abstract
Conference Topics: Malaria, Drugs, Biochemistry, Molecular Biology, Bioinformatics
Keywords: PfCRT, Malaria, Drug resistance, Molecular dynamics

How the world lost one of its most effective anti-malarials to mutations in a Malarial multi-drug resistance protein: a molecular post-mortem

John Tanner, Ben Corry
Research school of Biology, Australian Na=onal University, Canberra, ACT, 2601

The eradication of Malaria is faltering due to the development of drug resistance. Of the six WHO recommended antimalarial combination therapies, five consist of a partner drug whose susceptibility can be modulated by mutations in the P. falciparum Chloroquine resistance transporter (PfCRT). Mutations in PfCRT were responsible for the evolution of resistance to the once powerful and effective drug, Chloroquine; evolving the ability to transport it away from its target.

Interestingly, not all of the mutations arising in Chloroquine resistant malaria strains increase PfCRT's ability to transport the drug. This suggests that some of the mutations may have been required to rescue PfCRT's natural function as a peptide transporter, yielding an evolutionary compromise in function.

To investigate the molecular basis for the evolution of Chloroquine resistance and its functional consequences, we have performed molecular dynamics simulations of Chloroquine susceptible and resistant isoforms of PfCRT with Chloroquine and a series of peptide substrates. These demonstrate the accessibility of the binding cavity, the likely binding sites, and the access routes of each substrate. The simulations suggest plausible roles for a number of mutations in substrate access and binding, aiding in understanding the evolutionary history of PfCRT, a fulcrum point of antimalarial resistance.

CP13.2: Drugs & Drug Resistance 3 min talks

Time: Friday, 08/Sept/2023: 11:45am - 12:00pm · *Location:* Symposium room 1
Session Chair: Benedikt Ley, Menzies School of Health Research

ID: 111 / CP13.2: 1
Contributed abstract
Conference Topics: Malaria
Keywords: Malaria, vitamin, drug, FAD synthetase, riboflavin

Characterising flavin adenine dinucleotide synthetase of the human malaria parasite *Plasmodium falciparum* as a potential drug target

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Despite relentless efforts in combating malaria, current treatment methods continue to become less effective due to drug resistance. New treatment options are therefore vital.

During the asexual blood stage of its lifecycle, *Plasmodium falciparum* extracts from the host essential nutrients such as riboflavin (vitamin B_2) to sustain its growth and proliferation. Flavin adenine dinucleotide synthetase (FADS) is an enzyme involved in the conversion of riboflavin to FAD, a redox-active coenzyme essential for the activity of several important enzymes. Inhibiting FADS to arrest the production of FAD is an attractive antiplasmodial strategy. However, its utility for antiplasmodial purposes remains to be determined.

To characterise *Pf*FADS we initially tried to express the protein heterologously in *E. coli*, but the expressed protein was insoluble. We therefore attempted to express *Pf*FADS using the *E. coli* cell-free expression system. We found that *Pf*FADS was expressed in a soluble and functional form, but in quantities too small for characterisation. Experiments to express *Pf*FADS in the wheat-germ and *Leishmania tarentolae* cell-free expression systems in the hope of increasing the yield are underway and will be presented. We also aim to overexpress *Pf*FADS within the parasites and determine whether this influences the activity of recently-described antiplasmodial riboflavin analogues.

ID: 174 / CP13.2: 2
Contributed abstract
Conference Topics: Malaria, Drugs, Host-parasite interactions
Keywords: Malaria, Host-interactions, Kinase inhibitors, resistance

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

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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, inhibits parasite proliferation in vitro with low nanomolar potency, consistent with the observation that MEK activity is required for parasite survival. Unexpectedly, *P. falciparum* can rapidly gain resistance to trametinib, showing a 100-fold increase in the IC50, suggesting a parasite-encoded off-target. Fascinatingly, some of these resistant parasites display an absolute dependency to trametinib and are unable to grow in the absence of this drug. We are now investigating the genetic and molecular basis for this unexpected phenotype. This work provides novel insights into the complexity of host-pathogen interactions between human erythrocytes and P. falciparum.

ID: 187 / CP13.2: 3
Contributed abstract
Conference Topics: Malaria, Apicomplexa Biology, Microscopy
Keywords: artemisinin, resistance, cytostome, dynamin, membrane, fission

Zooming in on the *Plasmodium* dynamins

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Artemisinin is the world's primary defence against malaria, a deadly parasitic disease that kills over half a million people annually. Of particular concern has been the recent increase in artemisinin resistance. Due to its short half-life, this drug is commonly given in combination with a longer-acting partner. This means that a rise in artemisinin resistance also allows the malaria parasite time to develop resistance against its partner drug. We are exploring the fundamental cell biology behind this all-important artemisinin resistance mechanism in *Plasmodium falciparum* – by far the deadliest species of malaria. In particular, we will determine the involvement of the three *Plasmodium* dynamins in this process. Very little is currently known about the resistance mechanism, except that it is likely associated with the way in which *P. falciparum* parasites feed on their human red blood cell hosts. It is unknown how engulfed host material travels from the cytostomal 'mouth' to the parasite's

digestive compartment, or how the cytostomal machinery itself operates. The dynamin proteins have not been comprehensively characterised in *Plasmodium* before, and since their canonical role in eukaryotes as membrane 'pinchases' suggest they likely play a role in parasite feeding, our study could help tease apart artemisinin resistance.

ID: 182 / CP13.2: 4
Contributed abstract
Conference Topics: Malaria, Drugs
Keywords: Novel antimalarials, drug resistance, mechanism of action, azithromycin analogues

Azithromycin analogues with quick-killing activity exhibit a multi-factorial mechanism of action against multidrug resistant and sensitive blood-stage malaria parasites

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Malaria is a mosquito-borne disease caused by *Plasmodium* spp. parasites. In 2021, malaria was responsible for approximately 247 million cases and 619 thousand deaths worldwide. While antimalarials have contributed significantly to the decline in global mortality, drug resistance is a looming threat. Azithromycin is a safe and long-acting antibiotic that can be chemically modified to improve its quick-killing activity against early blood-stage parasites. We tested the antimalarial activity of one partially characterised and four novel azithromycin analogues against *Plasmodium* parasites. All analogues rapidly killed drug sensitive and resistant parasites within one blood stage lifecycle at low nanomolar IC50s ranging between 6-400 nM. Our lead compound has been observed to maintain potency throughout blood-stage development and further demonstrated activity against both mature and immature gametocytes. Two of our compounds possess chloroquinoline moieties, and therefore, may function like the former frontline antimalarial, chloroquine, targeting the parasite's digestion of host haemoglobin. However, as chloroquine is not known to block mature gametocytes, these results highlight the potential for a multi-factorial mechanism of quick-killing. With the rise in drug resistance, it has become a major priority for new drugs to have novel mechanisms of action that do not exhibit cross-resistance to existing antimalarials.

ID: 166 / CP13.2: 5
Contributed abstract
Conference Topics: Drugs, Proteomics, Apicomplexa Biology
Keywords: Malaria, antimalarial drugs, drug-target identification, drug-mechanism of action, TPP, MS-CETSA, SPP, Thermal Proteome Profiling, Solvent Proteome Profiling

Functional Proteomics approaches for drug-target identification and drug-mechanisms of action profiling in *Plasmodium falciparum.*

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Target identification for antimalarial drugs has historically represented a major challenge, resulting in only fragmentary understanding of the mechanism of action (MoA) of many among clinically used and candidate antimalarial compounds. The lack of a well-characterised drug-target space prevents prioritization of compounds with novel MoA for development, structure-activity optimization studies, as well as the rational design of synergistic drug combination therapies that are safe for the patient and effective surveillance of drug-resistance emergence in the field. Consequently, versatile and comprehensive methods to identify antimalarial drug targets are urgently needed.

To address this, we developed a comprehensive workflow relying on powerful functional proteomics technologies: Thermal Proteome Profiling (TPP) and Solvent Proteome Profiling (SPP) to identify drug-targets and to characterise drug MoA in *Plasmodium falciparum.* TPP and SPP identify drug-targets on the whole proteome scale based on differential stability of drug-bound proteins, but rely on different biophysical concepts: susceptibility to temperature or organic solvent induced denaturation, respectively. Through monitoring of proteome stability dynamics in live drug-treated cells, TPP offers further insights into downstream molecular events of drug MoA, including protein interactions with intracellular ligands, nucleic acids and other proteins. We evaluated methods' performance with a set of structurally diverse antimalarial compounds.

CP12: Zoonoses 15 min talks

Time: Friday, 08/Sept/2023: 10:30am - 11:15am · *Location:* Symposium room 2
Session Chair: Narelle Dybing, Australian Pork Limited- National Feral Pig Action Plan

ID: 229 / CP12: 1
Contributed abstract
Conference Topics: Wildlife parasitology, Apicomplexa Biology, One Health
Keywords: brushtail possum, Cryptosporidium

Animal personality and personality-mediated urban space use drives pathogen carriage of common brushtail possums

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Multi-host pathogens are a threat to human and animal health. Understanding which factors influence multi-host pathogen occurrence in urban adapted wildlife is important. Host personality may influence pathogen carriage because individuals with different personalities perceive and react differently to similar environments. We studied free-ranging common brushtail possum (*Trichosurus vulpecula*), and their pathogen, Genus *Cryptosporidium,* to test whether pathogen carriage differ as a function of their personality via urban space use. We predicted that pro-active individuals (exploratory, bold, active) would have a greater likelihood of carrying *Cryptosporidium*; as would possums on the urban fringe, whose home range encompassed proportionally more urban habitat. We studied n = 123 possums in Sydney, Australia, quantified personality, characterised *Cryptosporidium* species and determined urban space use using GPS tracking data. We detected *Cryptosporidium parvum* (a pathogen found in humans and animals, possibly a reverse zoonosis) in possums. The probability of possums carrying *Cryptosporidium* was greater in proactive individuals and those with a higher proportion of their home range in urban habitat. Such individuals may be super pathogen carriers and disproportionately affect disease dynamics within and among species. Understanding, pathogen carriers have predictable traits provides the basis for targeted disease management important in a One Health framework.

ID: 234 / CP12: 2
Contributed abstract
Conference Topics: Helminthology
Keywords: cure rate of hookworm infection

Breaking Transmission: A Transdisciplinary One Health Approach to Improve Hookworm Control

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Hookworm disease is a major global public health concern, despite targeted control programs of at-risk populations. The success of these programs has been hindered by the rapid re-infection rates linked to persistent reservoirs and the low sensitivity of conventional coprodiagnostic techniques employed.

In study 1, we revealed a substantial difference in cure rate of hookworm infection(s) following albendazole treatment using the standard faecal floatation (81.5%) and mqPCR (46.4%) assays, and provide the first data on the efficacy of this drug against the zoonotic hookworm *Ancylostoma ceylanicum*. In study 2, we identified infections with *Trichostrongylus* spp. of livestock origin and spurious passage of *Melodoygine* eggs in people living in remote communities. In study 3, we developed a novel multi-hosts (dog and human) transmission model of *A. ceylanicum* and showed that One Health interventions—targeting both dogs and humans—could suppress prevalence in humans to ≤ 1% by the end of 2030, even with only modest coverage (25–50%) of the animal reservoir. We provide evidence that a transdisciplinary One Health approach could be highly effective against zoonotic hookworms in endemic regions of Southeast Asia and beyond and will be essential for sustained elimination and reaching the WHO 2030 goals.

ID: 201 / CP12: 3
Contributed abstract
Conference Topics: Diagnostics, Helminthology, Other
Keywords: Parasite control; medical parasitology; public health

Validation of risk mapping tools for Soil Transmitted Helminths in Lao PDR.

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Soil Transmitted Helminths (STHs) are estimated to infect 1.5 billion people worldwide, with poor communities tropical and subtropical areas overly represented. The recent WHO 2030 roadmap for Neglected Tropical Disease has set the goal for STHs to be eliminated as a public health problem in 96% of endemic countries by 2030. One critical element identified to achieve this target is the need for comprehensive surveillance and mapping systems which would enable governments to target limited resources to highly endemic regions.

Combining available prevalence data of STHs within Lao PDR with freely available household census data, risk maps were created identifying high risk areas for STHs. The accuracy of this risk mapping technique was then validated through biological testing for STHs. In total ~2000 human faecal samples were collected from 14 villages within the northern province of Luang Prabang of Lao PDR. The intensity and prevalence of STHs within these communities was ascertained through microscopy techniques, and results compared to the risk maps.

Preliminary data indicates that the risk mapping strategies employed may help inform and strategically guide national intervention strategies for the control of STHs within Lao PDR.

CP12.1: Zoonoses 5 min talks

Time: Friday, 08/Sept/2023: 11:15am - 11:45am · *Location:* Symposium room 2
Session Chair: Narelle Dybing, Australian Pork Limited- National Feral Pig Action Plan

ID: 215 / CP12.1: 1
Contributed abstract
Conference Topics: Helminthology, One Health
Keywords: S. stercoralis, A. ceylanicum, schoolchildren, Philippines

Prevalence, burden, determinants and spatial distribution of Strongyloides stercoralis and Ancylostoma ceylanicum in schoolchildren in Laguna, province, the Philippines

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S. stercoralis and A. ceylanicum (a hookworm species) are parasitic intestinal nematodes that belong to the group of soil-transmitted helminths (STH), causing infections and morbidities to humans. S. stercoralis is one of the most overlooked of the neglected tropical diseases (NTDs), largely because its larvae, when present in the human feaces, are not readily detected by the coprological methods used to screen for helminth eggs. Very few studies have been conducted to estimate the burden of S. stercoralis in the Philippines. Recently, A. ceylanicum has emerged as an important zoonotic species of hookworm in Southeast Asia, however information on this parasite is also limited in the Philippines. Using the stored samples from “The Magic Glasses Philippines” cluster randomised controlled trial, epidemiological, molecular and geospatial approaches were conducted to determine the prevalence, associated risk factors, spatial distribution and morbidity outcomes of S. stercoralis and A. ceylanicum infections among schoolchildren in Laguna province, the Philippines. Here we detail results from this study to provide epidemiological context to the less commonly reported S. stercoralis and A. ceylanicum in the Philippines to identify their importance and the need for effective control program in the country.

ID: 235 / CP12.1: 2
Contributed abstract
Conference Topics: Helminthology, One Health
Keywords: zoonotic capillarid nematode

Detection of *Calodium hepaticum* spurious infection in humans in Angola

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Calodium hepaticum (syn. *Capillaria hepatica*) is a zoonotic capillarid nematode that parasitises the liver of murid rodents (primary definitive hosts) and mammals, including humans. There are two types of *C. hepaticum* manifestations in humans: hepatic capillariasis and spurious infections. Spurious infections occur when humans ingest uncooked rodent livers containing unembryonated eggs. These eggs are mechanically shed in faeces, where they embryonate to the infective stage in the environment. Hepatic capillariasis represents true infection and occurs through ingesting food, water or soil contaminated with the parasite's embryonated eggs. A cross-sectional study of soil-transmitted helminths of schoolchildren in three provinces in Angola identified 39 faecal samples that were positive for *Trichuris* eggs by Kato Katz but negative by qPCR. Re-examining selected samples revealed bipolar plugged asymmetrical capillarid eggs. Subsequent PCR and sequencing identified these as spurious *C. hepaticum* infections. In humans, the deposition of eggs in the liver parenchyma causes granuloma formation and necrosis. Trapped eggs of *C. hepaticum* cannot be passed in faeces, making their diagnosis in humans challenging. This first report of *C. hepaticum* eggs in human faeces in Angola highlights the necessity for local health authorities to be vigilant about this aetiological differential for hepatic dysfunction in humans.

ID: 232 / CP12.1: 3
Contributed abstract
Conference Topics: Apicomplexa Biology, Zoonoses
Keywords: brushtail possums, cryptosporidium

Into the wild: integration of human-derived *Cryptosporidium* species in urban possums

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Spillover of zoonotic pathogens from wildlife to humans is a growing threat to global health. In contrast, reverse transmission (zooanthroponosis), whereby parasites move from humans into wildlife species remains largely unexplored. Globally, increasing urbanisation and habitat loss are driving wildlife species into urban areas, creating a conduit for microbial traffic between humans, domestic animals and wildlife. In Australia, possum species are well established in urban areas and share the environment with people, domestic pets, other urban-adapted wildlife and their parasites. Screening of urban brushtail possums (*Trichosuris vulpecula*; n =123) for *Cryptosporidium* resulted in the detection of in 23 samples (18%). A single *C. parvum* strain appears to be circulating in brushtail possums as indicated by minimal diversity in the glycoprotein 60 gene, a highly variable surface antigen commonly used for source tracking. *Cryptosporidium fayeri*, the marsupial adapted species, has

mainly been reported in brushtail possums. The detection of *C. parvum,* a species that is common in domestic animals and contributes to ~50% of human cryptosporidiosis cases, in brushtail possums adds to the growing number of Australian wildlife where human-associated *Cryptosporidium* species have been detected. These findings exemplify the necessity of a One Health framework for investigating infectious disease.

ID: 177 / CP12.1: 4
Contributed abstract
Conference Topics: Veterinary Parasitology, Zoonoses, One Health
Keywords: cyclophylidean cestode, dogs, dingos, dog hybrids, cats

Spirometra erinacei/S. erinaceieuropaei: occurrence in wild carnivores in south-eastern Australia and northern Western Australia

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Spirometra erinaceiuropei is a cyclophylidean cestode and like its life cycle is complicated. Definitive hosts are cats (feral and domestic), wild dogs (dingos and dingo/domestic dog hybrids) and domestic dogs. The definitive host contains one or more tapeworms attaining a maximum size of about 75 cm. There are two main intermediate hosts, the first being aquatic copepods containing the first intermediate (procercoid) stage of the parasite, the second being tadpoles/frogs containing the second (pleurocercoid) lifecycle stage. Paratenic hosts such as feral pigs and tiger snakes may also be part of the lifecycle. Both lifecycle stages are zoonotic. Transmission occurs through a prey/predator interaction where definitive hosts consume tadpoles or frogs or drink water containing infected copepods. This tapeworm occurs commonly in wild carnivores in Australia. We will present infection data from feral cats and wild dogs collected from locations in south-eastern Australia and wild dogs from northern Western Australia. We will also present scanning EM pictures showing the contrast between the means of attachment to the intestinal wall between taeniid cestode species and *S. erinaceieuropaei.* Although *S. erinaceid* infection is treatable using praziquantel the dose needs to be about five times higher than for treating other cestode species.

ID: 236 / CP12.1: 5
Contributed abstract
Conference Topics: Apicomplexa Biology
Keywords: Leishmania

A Nanopore sequencing-based tool to explore the genetic diversity of *Leishmania* species in animals, humans, and sand flies in endemic areas

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Leishmaniases caused by protozoa of the *Leishmania* genus are endemic to tropical and subtropical regions and cause significant diseases in animals and humans. The epidemiology of *Leishmania* depends on ecological interactions between parasites, animals reservoir and vectors. In the Mediterranean area, *Phlebotomus* sandflies and dogs play a crucial role in maintaining the lifecycle of *Leishmania infantum*. However, several other species of *Leishmania* have been documented in the region and are considered endemic, albeit some poorly researched. Similarly, in South America, a variety of *Leishmania* species exert an important public health toll, including in the Amazon, where ideal ecological conditions for the vectors and mammalian reservoirs support the maintenance of these protozoa. Understanding of *Leishmania* epidemiology in the New and Old Worlds has been hindered by the inability of traditional molecular techniques to capture the full diversity of parasite species. Conversely, nanopore-sequencing based metabarcoding assays can provide excellent taxonomic resolution and have demonstrated utility in the simultaneous detection of vector-borne pathogens in mammal and reservoir hosts. Here, we present the initial results of the development of a portable metabarcoding assay using nanopore-sequencing to elucidate the diversity of *Leishmania* species infecting animals and vectors in endemic areas of Israel and Brazil.

ID: 195 / CP12.1: 6
Contributed abstract
Conference Topics: Veterinary Parasitology, Wildlife parasitology, Ectoparasites, Molecular Biology, Other, Bioinformatics
Keywords: Ticks, Zoonotic, Viruses, Metatranscriptome, Sydney

Discovery of a novel orthomyxovirus in *Ixodes tasmani* ticks

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UNSW

Ticks play a crucial role as vectors of zoonotic diseases, posing significant risks to humans and animals. While bacterial pathogens in ticks have been extensively studied, the understanding of tick-associated viruses is less understood. This study aimed to explore the viral diversity in *Ixodes tasmani* ticks, a common species with a wide host range including humans, domestic animals, and marsupials.

Tick samples were collected from cats, dogs, and possums in northern Sydney. Morphological analysis and 16S sequencing were conducted to identify tick species. Metatranscriptomics analysis using NovaSeq 6000 sequencing unveiled novel viral sequences, including an orthomyxovirus: Sydney tick quaranjavirus. This orthomyxovirus showed close genetic affinity with Granville quaranjavirus, from South America. Viruses from taxa such as *Reoviridae*, *Rhabdoviridae, Adenoviridae, Retroviridae,* and *Iridoviridae* were also detected.

The detection of Sydney tick quaranjavirus in *I. tasmani* ticks has implications for tick-borne diseases in Australia. These ticks can parasitise humans and domestic animals and host a quaranjavirus with highly zoonotic viral relatives, like influenza. The known host and geographical range of quaranjaviruses has been expanded. Further research in this field is essential to identify and mitigate the health risks associated with tick bites and enhance preparedness against emerging tick-borne infections worldwide.

CP12.2: Zoonoses 3 min talks

Time: Friday, 08/Sept/2023: 11:45am - 12:00pm · *Location:* Symposium room 2
Session Chair: Narelle Dybing, Australian Pork Limited- National Feral Pig Action Plan

ID: 127 / CP12.2: 1
Contributed abstract
Conference Topics: Veterinary Parasitology, Wildlife parasitology, Host-parasite interactions
Keywords: Angiostrongylus cantonensis, rat lungworm, larval emergence, aquatic snail, Bullastra lessoni

Rat lungworm (*Angiostrongylus cantonensis*) active larval emergence from deceased bubble pond snails (*Bullastra lessoni*) into water

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Angiostrongylus cantonensis (the rat lungworm) is a zoonotic parasite of non-permissive accidental (dogs, humans, horses, marsupials, birds) hosts. The 3rd stage larvae (L3s) in the intermediate host (molluscs) act as the source of infection for accidental hosts through ingestion. Larvae can spontaneously emerge from dead gastropods (slugs and snails) in water, which are experimentally infective to rats. We sought to identify the time when infective *A. cantonensis* larvae can autonomously leave dead/dying experimentally infected *Bullastra lessoni* snails. The proportion of *A. cantonensis* larvae that emerge from crushed and submerged *B. lessoni* is higher in snails 62 days post-infection (DPI) (30.3%). The total larval burden of snails increases at 91 DPI, indicating that emerged larvae subsequently get recycled by the population. There appears to be a window of opportunity between 1 and 3 months for infective larvae to autonomously escape dead snails. From a human and veterinary medicine viewpoint, the mode of infection needs to be considered; whether that be through ingestion of an infected gastropod, or via drinking water contaminated with escaped larvae.

ID: 119 / CP12.2: 2
Contributed abstract
Conference Topics: Epidemiology, Helminthology, Zoonoses
Keywords: Lao PDR, Neglected topical diseases, Neurocysticercosis, Taenia solium, zoonoses.

Risk mapping for Taenia solium: The case of Lao PDR

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Introduction and Objectives
Taenia solium is the most significant global food-borne parasite and the leading cause of preventable epilepsy in low and middle-income countries. The objective of this study was to identify high-risk areas in Lao PDR without the demanding resource requirements of national prevalence surveys that are often hampered by the nature of current diagnostic tools.
Methods
Census data were analysed using multicriteria decision analysis. Village risk scores were calculated using linear combination of weighted risk factors. District risk scores were calculated as the mean village score for a given district. One-at-a-time sensitivity analysis summarised variance across all scenarios. Results will be compared against available biological data.
Results
24% of villages and 14% of districts were classified as high risk, with high-risk locations present across the country. Two main areas of high risk and low variability were revealed. The first in northern Laos is consistent with current knowledge. The second in the south-east has not been investigated. Validation of results using biological data is ongoing.
Conclusion
Multicriteria decision analysis can rapidly produce sub-national risk maps. The application of census data allows for increased coverage and versatility compared to WHO's current risk mapping template that relies heavily on disease occurrence.

ID: 138 / CP12.2: 3
Contributed abstract
Conference Topics: Veterinary Parasitology, Wildlife parasitology, Ectoparasites, Diagnostics, Biodiversity, Zoonoses
Keywords: Mosquito-borne parasites, Urbanisation, seasonal variation

Adapting to big city life: Using mosquito biodiversity to monitor parasite and virus abundance in urban and peri-urban areas.

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Mosquitoes form complex communities which vary over time and space, particularly from seasonal and anthropogenic changes. Urban land change can affect Mosquito-borne diseases (MBD) by altering local mosquito biodiversity. Such changes can favour the proliferation of aggressive and disease-transmitting mosquito species. In addition, land change can facilitate the zoonotic and enzootic transmission of MBD by increasing the proximity between competent vectors and susceptible hosts. Understanding local mosquito population dynamics will help identify underlying risks from competent MBD transmitters within the area.

This study will monitor the biodiversity of mosquito species and the prevalence of mosquito-borne parasites and viruses across ten urban and peri-urban locations around Perth's metropolitan area. To compare shifts in mosquito population diversity and

disease prevalence across time, traps have been set to represent both the four seasons and the six Noongar seasons. Mosquitoes, being hematophagous, will be utilised as a non-invasive surveillance tool to detect MBD. The prevalence of MBD has been determined using viral NGS and PCRs specific to mosquito-borne parasites, such as Dirofilaria, Plasmodium, and Haemoproteus. These results can provide insight into local disease risks to humans, domestic animals, and wildlife, and potential disease vectors, which may aid future mosquito control programs.

ID: 105 / **CP12.2: 4**
Contributed abstract
Conference Topics: Molecular Biology, Host-parasite interactions
Keywords: Blastocystis, gut-brain axis, microbiome, parasitology, neurotransmitter

Blastocystis: a parasite with mind-altering implications

Steven Santino Leonardi, Kevin Shyong Wei Tan

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Blastocystis is a genus of highly unusual parasitic eukaryotes prevalent across the world. These organisms colonize the lower intestine and infect a wide variety of hosts, including mammals, birds, and reptiles. The pathogenic potential of *Blastocystis* is controversial, with reports of both positive and negative health outcomes in infected patients and mouse models. Infection with *Blastocystis* is most commonly associated with Irritable Bowel Syndrome (IBS), in particular perturbations to intestinal inflammation and permeability.

In 2017, a suite of horizontally-acquired prokaryote genes was identified within the *Blastocystis* genome. We set out to characterize one of these genes: the enzyme tryptophanase, which converts tryptophan to indole. In 2021, we published a paper demonstrating that *Blastocystis* tryptophanase is structurally unique and preferentially performs its' reverse reaction – the synthesis of tryptophan from indole.

Our current work explores the implications of this across both *in vitro* and *in vivo* settings. Tryptophan produced in the gut is trafficked throughout the human body to produce a wide array of downstream products, including the neurotransmitter serotonin and the neuromodulator precursor kynurenine. We show evidence that *Blastocystis*' ability to produce tryptophan can lead to perturbation of a variety of downstream pathways, including the action of these small molecules.

ID: 252 / **CP12.2: 5**
Contributed abstract
Conference Topics: Ecology
Keywords: water mite parasites

Are there more parasites in tropics? Latitudinal variation of water mite infection in damselflies

Shatabdi Paul

Macquarie University, Australia

Parasites are a strong evolutionary force on their host and there is some evidence suggesting that parasites are more abundant in the tropics. Here we test this idea by comparing the prevalence and intensity of water mite parasites (*Arrenurus*) on *Ischnura heterosticta* damselflies (Odonata) across an extensive latitudinal gradient along the east coast of Australia from far north Queensland (16°S) to south-eastern New South Wales (34°S). The ectothermic behavior of damselflies and their life history components are known to be affected by climate as well as water mite parasites, presenting as a good system to study host-parasite interactions. We sampled 45 different populations between tropical Cairns (Queensland) and temperate Wollongong (New South Wales) collecting over 1100 individuals. In support of our prediction, we found a higher prevalence and intensity of parasitism in tropical (48%) populations compared to sub-tropical (12%) and temperate (0.5%) regions. The outstanding individual was a female from tropical Cairns infected by over 28 water mites. Preliminary climatic analysis suggests that both temperature and rainfall are strong predictors of parasite infection. We are currently using molecular tools to determine the species identity of the mites and to quantify the fitness costs (condition, fecundity) and mating behaviour associated with parasite infection.

W7: Strongyloides Workshop

Time: Friday, 08/Sept/2023: 10:30am - 12:00pm · *Location:* Workshop room 3
Session Chair: Harsha Sheorey, St Vincent`s Hospital, Melbourne

ID: 190 / W7: 1
Invited speaker abstract

Diagnosis of Human Strongyloidiasis

Rogan Lee, Taran Finemore, Matthew Watts
NSW Health Pathology, AU

Strongyloidiasis is now a recognised neglected tropical disease. The infection is hard to diagnose and we are slowly making inroads into improving the detection of this parasite. The idenfication of this parasite in humans will be discussed.

ID: 200 / W7: 2
Invited speaker abstract

Wormatology and dermatology

Rhiannon Russell, Ian McCrossin, Dana Slape
Justice Health, AU

Dermatologists are involved in the identification and management of the cutaneous stigmata of strongyloidiasis. Further to this summary of urban, rural and remote case-based examples of the protean clinical manifestations; the controversies relating to systemic classical immunosupression, systemic steroids, and the question of Dupilumab will be explored.

ID: 230 / W7: 3
Invited speaker abstract

Strongyloides hyperinfection: a preventable complication of immunosuppression.

Robert Stolz[1], Mark R Dowling[2], Belinda B Lin[3], Kylie Mason[3], Stephen Muhi[3]
[1]Victorian Infectious Diseases Service,; [2]Royal Melbourne Hospital; [3]Peter MacCallum Cancer Centre

A 70-year-old man of non-English speaking background migrated from Vietnam to Melbourne, Australia in 2007. In 2019 he was diagnosed with stage IV Epstein-Barr virus-positive plasmablastic lymphoma and commenced on first line chemotherapy including prednisolone. 12 days after his third cycle of chemotherapy, he developed septic shock with non-bloody diarrhoea. Faecal microscopy revealed multiple parasites consistent with filariform *Strongyloides stercoralis.* He was successfully treated with a 14 day course of oral ivermectin and made a full recovery. *Strongyloides* hyperinfection in immunosuppressed patients is a highly morbid, yet preventable disease that should be suspected in patients from endemic regions. Clinicians should remain vigilant with screening prior to commencement of immunosuppression and prompt empirical antibacterial and antiparasitic therapy in those suspected to have hyperinfection.

ID: 179 / W7: 4
Invited speaker abstract

Case Report: severe disseminated Strongyloidiasis in an immunocompromised host complicated by ivermectin toxicity

Lauren McShane[1], Harsha Sheorey[2], Kumar Visvanathan[2]
[1]Royal Darwin Hospital, AU; [2]St Vincent's Hospital Melbourne

A case report of a 54 year old female from Ethiopia on immunosuppression for pemphigus vulgaris who developed disseminated Strongyloidiasis during the first wave of the COVID19 pandemic in Melbourne, Australia despite having negative Strongyloides serology on screening. She was commenced prednisolone 50mg and mycophenolate mofetil 1g BD two months prior to presenting with pancolitis and respiratory failure. During the clinical course of her disseminated strongyloidiasis she had many complications, including a severe disseminated Klebsiella infection, ileus requiring subcutaneous ivermectin formulation, biopsy proven CMV disease, eosinophilic meningitis, encephalopathy with slow neurological recovery and most interestingly features of ivermectin toxicity associated with a loss of function ABCB1 drug efflux pump mutation. Despite supportive therapy, our patient remained encephalopathic with features of ivermectin toxicity 6 weeks post cessation of ivermectin. St Vincent's Hospital, Melbourne was the first to trial an intralipid infusion in a patient with ivermectin toxicity and ABCB1 mutation with some objective neurological improvement, prior to her passing three weeks later due to likely complications of her tracheostomy. Discussion will highlight the utility of testing for the ABCB1 mutation or ivermectin therapeutic drug monitoring if there is suspicion for ivermectin toxicity.

CP14: Drugs & Drug Resistance 15 min talks

Time: Friday, 08/Sept/2023: 1:00pm - 2:00pm · *Location:* Symposium room 1
Session Chair: Brad Sleebs, Walter and Eliza Hall Institute of Medical Research

ID: 133 / CP14: 1
Contributed abstract
Conference Topics: Malaria, Drugs
Keywords: Malaria, Drugs, Proteomics, Metabolomics

Confirming the target of a multistage M1 alanyl aminopeptidase inhibitor in *P. falciparum* using proteomics and metabolomics

Carlo Giannangelo[1], Ghizal Siddiqui[1], Matthew P. Challis[1], Rebecca Edgar[2,3], Christopher A. MacRaild[1], Natalie A. Counihan[2,3], Tess R. Malcolm[4], Chaille T. Webb[4], Nyssa Drinkwater[4], Natalie B. Vinh[5], Tania de Koning-Ward[2,3], Peter J. Scammells[5], Sheena McGowan[4], Darren J. Creek[1]

[1]Drug Delivery, Disposition and Dynamics, Monash Institute of Pharmaceutical Sciences, Monash University, Parkville, Australia; [2]School of Medicine, Deakin University, Geelong, Australia; [3]The Institute for Mental and Physical Health and Clinical Translation, Deakin University, Geelong, Australia; [4]Monash Biomedicine Discovery Institute and Department of Microbiology, Monash University, Clayton, Australia; [5]Medicinal Chemistry, Monash Institute of Pharmaceutical Sciences, Monash University, Parkville, Australia

Current treatments for malaria are threatened by drug resistance, and new antimalarial candidates that act on novel pathways are required. We previously discovered *Plasmodium falciparum* M1 (*Pf*A-M1) and M17 (*Pf*A-M17) metalloaminopeptidase inhibitors with excellent antimalarial activity, and no significant host-cell toxicity. Biochemical assays with purified enzymes identified three sub-series of compounds that were selective for either *Pf*A-M1 or *Pf*A-M17, or were dual inhibitors of both enzymes.

The M1-selective inhibitor, MIPS-2673, demonstrated multistage activity and potency against a panel of drug resistant *P. falciparum* strains. Analysis by thermal stability and limited proteolysis proteomics – which use mass spectrometry to detect thermal or proteolytic stabilisation of proteins in a parasite lysate due to ligand binding – identified *Pf*A-M1 as the sole target of MIPS-2673 from ~2,000 detected proteins. Furthermore, our limited proteolysis approach could estimate the binding site of MIPS-2673 on *Pf*A-M1 within ~5 Å of that determined by X-ray crystallography. Untargeted metabolomics revealed significant accumulation of short peptides in MIPS-2673-treated parasites, also consistent with *Pf*A-M1 inhibition.

Our unbiased omics-based target deconvolution strategies confirmed the novel *Pf*A-M1 inhibitor, MIPS-2673, was on-target, and validated *Pf*A-M1 as a target for multistage antimalarials. These methods may also help uncover targets of other promising antimalarial candidates.

ID: 191 / CP14: 2
Contributed abstract
Conference Topics: Malaria
Keywords: Malaria, Control

Can we target the mosquito stages of *Plasmodium* with 'drugs' to reduce transmission?

Sarah Farrell[1], Anton Cozijnsen[1], Vanessa Mollard[1], Papireddy Kancharla[2], Rozalia A. Dodean[2], Jane Kelly[2], Christopher D. Goodman[1], Geoffrey I. McFadden[1]

[1]The University of Melbourne, Victoria 3010 Australia; [2]Portland State University, Portland, Oregon, 97201 United States

A decade-long decline in malaria cases has plateaued, primarily due to parasite drug resistance and mosquito resistance to insecticides used in bed nets. Here, we explore an innovative control strategy using anti-malarial compounds to target *Plasmodium* during the mosquito stages. This strategy has the potential to reduce the risk of drug resistance emerging due to the relatively small population of parasites within the mosquito. We screened a range of parasiticidal compounds by feeding them to mosquitoes at different timepoints. Different compounds were able to target specific stages of *Plasmodium berghei* development in the mosquito. Atovaquone-treated mosquitoes hosted fewer oocysts and sporozoites, consistent with atovaquone blocking crucial mitochondrial electron transport in insect stages of the parasite. Borrelidin, a tRNA synthetase inhibitor, was able to reduce sporozoite numbers. Azithromycin, an antibiotic targeting apicoplast protein synthesis, significantly lowered sporozoite infectivity in mice. Finally, a novel drug targeting the electron transport chain, T111, reduced sporozoite numbers of the human malaria parasite *Plasmodium falciparum*. Targeting mosquito staged parasites via baits or surfaces opens the option of using potent parasiticidal compounds that failed to meet the exacting standards required of human antimalarial drugs and would therefore improve malaria control for minimal cost.

ID: 142 / CP14: 3
Contributed abstract
Conference Topics: Malaria, Drugs
Keywords: antimalarial, Plasmepsin V, drug development, protein export, peptidomimetics

Chemical-genetics using substrate peptidomimetics defines their on-target activity for the essential malaria aspartyl protease, plasmepsin V

Wenyin Su, Madeline Dans, William Nguyen, Alan Cowman, Brad Sleebs

Walter and Eliza Hall Institute of Medical Research, 1G Royal Parade, Parkville, VIC 3052, Australia

The prevalence of resistance of malaria parasites against drugs in the field leads to a need for novel antimalarial discovery and development. Plasmepsin V is an aspartyl protease which is essential for the export of proteins from the parasite to the host erythrocyte during the asexual stage of parasite, making it an ideal target for novel antimalarial development. Peptidomimetics that mimic the substrate of plasmpesin V have been designed and shown to elicit parasite death via blocking protein export. While the peptidomimetics have been used to validate plasmepsin V as a bone fide antimalarial target, disparities between biochemical and parasite activity have questioned their on-target activity.

Here, we generated a parasite line with reduced sensitivity to the peptidomimetics. A single nucleotide polymorphism (SNP) located in the plasmepsin V gene was identified through whole genome sequencing. Reverse genetics and biochemical assays using immunoprecipitated plasmepsin V were used to validate the resistance-causing SNP. This data was supported by methods such as cellular thermal shift assays that showed target engagement with plasmepsin V in parasites. This data supports the previous evidence that the peptidomimetics kill the malaria parasite by targeting plasmepsin V and further establishes plasmepsin V as a promising antimalarial drug target.

ID: 223 / **CP14: 4**
Contributed abstract
Conference Topics: Malaria, Drugs, Apicomplexa Biology
Keywords: doxycycline, malaria, Plasmodium falciparum

Doxycycline inhibits both apicoplast and mitochondrial translation in the malaria parasite *Plasmodium falciparum*

Michaela Bulloch[1], Emily Crisafulli[1], Jenni Hayward[2], Stuart Ralph[1]
[1]1. University of Melbourne, Department of Biochemistry and Pharmacology, Bio21 Molecular Science and Biotechnology Institute; [2]Australian National University, Division of Biomedical Science and Biochemistry

Doxycycline is a tetracycline-class antibiotic used for malarial prophylaxis and as a partner drug. Doxycycline's antimalarial mechanism of action has widely been accepted, though not demonstrated, as a translation inhibitor specifically blocking the prokaryotic 70S ribosomes of the *Plasmodium* apicoplast. At low concentrations (<5 µM) doxycycline exhibits a delayed death phenotype, typical of inhibitors of apicoplast housekeeping processes. At higher concentrations (≥10 µM) doxycycline has rapid schizonticidal activity via an unknown and apicoplast-independent mechanism. In other eukaryotes, and plausibly in *Plasmodium*, doxycycline inhibits mitochondrial 70S ribosomes.

To measure changes in protein abundance we used a mass spectrometry approach to assess the steady state protein levels and protein turnover using isotope-labelled amino acids. We directly detected apicoplast encoded proteins for the first time and showed that these proteins decrease following treatment with doxycycline and the proposed apicoplast translation inhibitor clindamycin. Mitochondrial encoded proteins are required for complex formation in the electron transport chain. Perturbations to oxidative phosphorylation were detected in both *Plasmodium* and the related parasite *Toxoplasma gondii* following high doxycycline treatments. Our data demonstrates the mechanism of action of apicoplast translation inhibitors for the first time and reveal doxycycline as the first described mitochondrial translation inhibitor of *Plasmodium*.

CP14.1: Drugs & Drug Resistance 5 min talks

Time: Friday, 08/Sept/2023: 2:00pm - 2:30pm · *Location:* Symposium room 1
Session Chair: Brad Sleebs, Walter and Eliza Hall Institute of Medical Research

ID: 118 / **CP14.1: 1**
Contributed abstract
Conference Topics: Malaria, Drugs, Cell Biology, Apicomplexa Biology, Molecular Biology
Keywords: Artemisinin resistance, PTEX, protein export

Is the protein export machine PTEX involved in artemisinin resistance in *Plasmodium falciparum*?

E Ploeger[1], T Jonsdottir[1], H Bullen[1], G Siddiqui[2], D Creek[2], T de Koning-Ward[3], B Crabb[1], P Gilson[1]
[1]Malaria Virulence and Drug Discovery Group, Burnet Institute, Melbourne, VIC, Australia; [2]Drug Delivery Disposition and Dynamics, Monash Institute of Pharmaceutical Sciences, Monash University, Parkville, VIC, Australia; [3]School of Medicine and Institute for Mental and Physical Health and Clinical Translation, Deakin University, Waurn Ponds, VIC, Australia

Drug resistance in *Plasmodium falciparum* is emerging to nearly all antimalarials including the most frequently used antimalarial, artemisinin. Artemisinin is activated into its toxic form by heme-iron in the food vacuole of the parasite. Heme is a by-product from the digestion of haemoglobin (Hb) and as it is harmful to parasites, it is detoxified into hemozoin crystals. Resistance to artemisinin has been linked to a delay in the uptake of Hb from the RBC cytosol in young parasites which reduces the activation of artemisinin. Hb digestion has also been recently linked to the parasite's PTEX machine, that exports parasite proteins into the cytosol of the infected RBC. Knockdown of PTEX appears to cause a build-up of undigested Hb in the parasite as PTEX may play a role in delivering proteases to the food vacuole via the parasite surface. We are now investigating if expression of one or more of the components of PTEX might be reduced in artemisinin resistant clinical isolates by immunoblot and immunofluorescence microscopy analysis. We will also conditionally knockdown PTEX subunits to determine if this confers resistance to artemisinin using ring survival assays. Improvements in understanding artemisinin resistance will inform new approaches to overcome it.

ID: 140 / **CP14.1: 2**
Contributed abstract
Conference Topics: Malaria, Drugs, Biochemistry, Molecular Biology
Keywords: PfTPK; Oxythiamine; Thiamine

A single point mutation in the *Plasmodium falciparum* thiamine pyrophosphokinase is likely responsible for oxythiamine resistance.

Imam Fathoni[1], Terence Ho[2], Alex Chan[2], Finian Leeper[2], Kevin Saliba[1]
[1]Research School of Biology, The Australian National University, Canberra, ACT, Australia; [2]Yusuf Hamied Department of Chemistry, The University of Cambridge, Cambridge, UK.

Oxythiamine, an antiplasmodial thiamine (vitamin B_1) analogue, is converted by the *Plasmodium falciparum* thiamine pyrophosphokinase (*Pf*TPK) into the antimetabolite oxythiamine pyrophosphate (OxPP) and goes on to inactivate at least two thiamine pyrophosphate (TPP)-dependent enzymes (Chan *et al*., 2013). In an attempt to investigate the oxythiamine mechanism of action in more detail, we used *in vitro* evolution to generate parasites resistant to oxythiamine by 8-10 fold (a process that took four weeks). Whole-genome sequence analysis identified an alanine to valine single-point mutation in *Pf*TPK

at position 284. Oxythiamine-resistant parasites accumulated 4-5 times less [^{3}H]thiamine than wild-type parasites, consistent with mutated *Pf*TPK having a reduced capacity to metabolise thiamine. This observation is supported by homology modelling of the position of the mutated residue using the *Mus musculus* TPK crystal structure, showing that the mutation is close to ATP/AMP binding sites, potentially reducing *Pf*TPK activity. To investigate whether the mutated gene is responsible for the resistance, parasites overexpressing a GFP-tagged version of the mutated TPK transfected into wild-type parasites and wild-type TPK transfected into oxythiamine-resistant parasites were successfully generated. These parasites, and their immunoprecipitated GFP-tagged *Pf*TPK, will be used to probe further the role of the mutation in oxythiamine resistance.

ID: 148 / **CP14.1: 3**
Contributed abstract
Conference Topics: Malaria, Proteomics, Cell Biology, Protozoa, Bioinformatics
Keywords: P. falciparum, novel anti-malarial, 2-aminobenzimidazoles, mechanism of action, nuclear fractionation-coupled proteomics

Exploring the Potential of *Plasmodium falciparum* Exportin-1 as a Target for 2- Aminobenzimidazoles through Nuclear Fractionation Coupled Proteomics

Yunyang {Eileen} Zhou, Ghizal Siddiqui, Matthew Challis, Darren Creek

Monash Institute of Pharmaceutical Sciences, Drug delivery, disposition and dynamics, Global Health Therapeutic Program Area, Monash University, Parkville, VIC 3052

The rapid emergence of artemisinin resistance highlights the urgent imperative for new antimalarials. A novel drug class 2-aminobenzimidazoles (ABIs) have exhibited remarkable potency against the erythrocytic stage of *Plasmodium falciparum*. Preliminary studies have identified *P. falciparum* exportin-1 (*Pf*XPO1), involved in nucleocytoplasmic export, as a potential ABI target. Notably, an ABI-resistant strain R1 revealed a H1061N point mutation within *Pf*XPO1. To validate *Pf*XPO1 as an ABI target, we developed a nuclear fractionation-coupled proteomics approach, probing nucleocytoplasmic transport between trophozoite stage parasites of the ABI-resistant line R1 and parent line DD2.

Analysis of nuclear fractions identified 85 significantly different proteins between R1 and the parent line DD2, whereas 69 proteins showed significant disparity in cytosolic fractions. Gene ontology analysis revealed perturbed proteins involved in DNA transcription, gene expression process, cellular oxidant detoxification, and localization to cellular compartments such as RNA polymerase II. Notably, some perturbed proteins contained nuclear export signal (NES) binding regions for export through *Pf*XPO1.

These findings support the role of *Pf*XPO1 in the nucleocytoplasmic transport of transcription-associated proteins. Further investigations aim to elucidate the mechanism of ABI resistance induced by H1061N mutation, by comparing nuclear and cytoplasmic proteome changes in R1 and DD2 parasite lines upon ABI treatment.

ID: 108 / **CP14.1: 4**
Contributed abstract
Conference Topics: Malaria, Drugs
Keywords: Malaria, Plasmodium, antimalarial, PfATP4

Development and characterisation of a novel antimalarial chemotype that targets PfATP4

Brad Sleebs[1,2], Madeline Dans[1,2], Trent Ashton[1,2], Alan Cowman[1,2], Stephen Brand[3], Paul Jackson[4]

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Malaria is a devastating disease caused by the Plasmodium parasite. Due to the threat of emerging drug resistance, the current arsenal of clinically used artemisinin combination therapies and drug candidates undergoing clinical assessment may not be sufficient in eliminating the disease. Thus, novel chemotypes that target multiple stages of the parasite lifecycle are required to continually populate the antimalarial clinical portfolio.
To contribute to the global effort to treat and eliminate malaria we have performed a high throughput screen of the Janssen Jumpstarter library of 80,000 drug-like small molecules against the asexual stage of *P. falciparum* parasite. Several hit classes with unique scaffolds were identified and shown to exhibit sub-micromolar EC_{50} values against asexual *P. falciparum* and did not display cytotoxicity towards human cell lines highlighting their attractiveness as starting points for antimalarial development.

This presentation will focus on the optimisation and characterisation of the multistage antimalarial activity of one unique hit scaffold. We established that the molecular target of the novel scaffold is PfATP4 using forward genetic studies, phenotypic models, and drug resistant clinical strains. We show the optimised scaffold cleared parasitaemia in transmission and asexual mouse models demonstrating its potential in a curative or a population control antimalarial therapy.

ID: 155 / **CP14.1: 5**
Contributed abstract
Conference Topics: Malaria, Drugs, Apicomplexa Biology, Molecular Biology
Keywords: Malaria, Plasmodium falciparum, Drug development, Lipid transfer protein, Blood stage

Stopping malaria parasites before they StART: aryl-acetamide compound MMV006833 inhibits lipid transfer and ring development [Part 1]

Coralie Boulet[1], Madeline Dans[1,2], Gabby Watson[2], William Nguyen[2], Somya Mehra[1,3], Zahra Razook[1,3], Kitsanapong Reaksudsan[2], Cindy Evelyn[2], Niall D Geoghegan[2], Michael J Mlodzianoski[2], Dean Goodman[4], Geoffrey I McFadden[4], Alyssa Barry[1,3], Brendan S Crabb[1], Tania F de-Koning-Ward[3], Kelly L Rogers[2], Alan F Cowman[2], Wai-Hong Tham[2], Brad E Sleebs[2], Christiaan van Ooij[4], Paul R Gilson[1]

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Efforts to eradicate malaria have stalled partly due to parasites developing resistance to many antimalarials. Therefore, new drugs with novel modes of action are urgently needed. Our laboratory recently identified an aryl-acetamide compound called MMV006833 (MMV833), that stops parasites from growing inside red blood cells soon after the parasites had invaded these cells.

Plasmodium falciparum parasites resistant to MMV833 were generated and their genomes sequenced. Two mutations were identified in StART domain phospholipid transferase protein (PF3D7_0104200, called StART): N309K and N330K. These mutations were engineered into wild-type drug-sensitive parasites and reproduced resistance to MMV833. Further, knocking down StART expression sensitised the parasites to MMV833, and recombinant StART protein has been shown to bind to MMV833. Overall, the data confirm that StART is the biological target of MMV833.

Little is known about the StART protein, and our work has yielded valuable insights into its role: when and where it is expressed, and how different regions of the protein may function.

Overall, this indicates that StART is a novel and promising drug target and a second presentation about this protein will further discuss the development of potent MMV833 analogues and the impact of these analogues on different stages of *Plasmodium* parasite lifecycle.

ID: 240 / CP14.1: 6
Contributed abstract
Conference Topics: Veterinary Parasitology, Drugs, Helminthology
Keywords: Pyrantel resistance, canine hookworms, Southeast Queensland

Pyrantel resistance in canine hookworms in Southeast Queensland, Australia

Swaid Abdullah[1], A Dale[1], G Xu[1], S R Kopp[1], M K Jones[1], A C Kotze[2]
[1]The University of Queensland, School of Veterinary Science, Gatton 4343, QLD, Australia; [2]CSIRO Agriculture and Food, Queensland Bioscience Precinct, St. Lucia, Brisbane, QLD 4067, Australia

Hookworms are the most common intestinal nematode parasites of dogs in Australia. The control of these parasites relies mostly on regular deworming with anthelmintics, with pyrantel-based dewormers being a relatively low cost and readily available option for dog owners. Pyrantel resistance in canine hookworms in Australia was first reported in 2007, however pyrantel-based dewormers are still used against hookworm infection in dogs across Australia. The present study was conducted to evaluate the efficacy of pyrantel against hookworms infecting dogs housed in a shelter facility in Southeast Queensland which receives rescued or surrendered animals from greyhound rescue centres and dog shelters across this region. A total of 10 dogs were examined using the faecal egg count reduction test (FECRT). There was no reduction in FEC in any of the dogs following pyrantel treatment, with drug efficacies ranging from -0.9 % to -283.3 %. Given that these dogs originated from various sites across Southeast Queensland, the present study suggests that pyrantel resistance is widespread in this region, and hence this anthelmintic may not be a useful option for treatment of hookworm infections in dogs.

S8: Symposium 8 Companion Animals sponsored by Elanco

Time: Friday, 08/Sept/2023: 1:00pm - 1:30pm · *Location:* Symposium room 2
Session Chair: Liisa Ahlstrom, Elanco Animal Health

ID: 262 / S8: 1
Invited speaker abstract

Monthly deworming in pet dogs – truths and fallacies

Rebecca Traub
Industry Consultant; Director, Tropical Council for Companion Animal Parasites, Newport, Victoria, Australia.

The Tropical Council for Companion Animal Parasites (TroCCAP) strongly recommends monthly deworming as part of an integrated approach to negating the risks gastrointestinal helminths pose to the health of pet dogs (and cats) and the public. Common questions surrounding this recommendation include whether monthly deworming is overkill and whether deworming of pets promotes anthelmintic resistance. Sometimes, a canine patient is found positive for tapeworm or hookworm eggs despite being monthly dewormed, and poor anthelmintic efficacy or, even worse, anthelmintic resistance is commonly blamed for this outcome. The truths and common fallacies surrounding monthly deworming in pet dogs will be revealed using the example of a 12-month longitudinal field-efficacy study comparing monthly administration of topical 10% imidacloprid / 2.5% moxidectin (Advocate for Dogs, Elanco) with monthly administration of subcutaneous off-label ivermectin at 200 µg/ kg for the treatment and prevention of intestinal helminths in pet and working dogs in Cambodia.

CP15: Companion Animals sponsored by Elanco 15 min talks

Time: Friday, 08/Sept/2023: 1:30pm - 2:00pm · *Location:* Symposium room 2
Session Chair: Liisa Ahlstrom, Elanco Animal Health

ID: 107 / CP15: 1
Contributed abstract
Conference Topics: Veterinary Parasitology, Diagnostics
Keywords: Metabarcoding, Vector-Borne Pathogens, Next-Generation Sequencing, Canines, Nanopore

Metabarcoding using nanopore sequencing for the holistic characterisation of vector-borne bacterial, apicomplexan and filarial worm pathogen communities in dogs and other animals

Lucas Huggins, Vito Colella, Ushani Atapattu, Anson Koehler, Rebecca Traub
Faculty of Science, Veterinary Preclinical Sciences Building, University of Melbourne, Parkville, Victoria 3052, Australia

Globally dogs are afflicted by diverse blood- and vector-borne pathogens (VBPs), of which many cause severe disease and are fatal. Diagnosis of VBP infections can be challenging due to intermittent parasitaemia, frequent coinfections and the wide range of emerging, and novel VBP species encounterable. Hence, there is an urgent need for diagnostics that are both sensitive and capable of detecting all VBP from a group of interest simultaneously. We demonstrate how a nanopore sequencing-based metabarcoding approach conducted on Oxford Nanopore Technologies' (ONT) MinION device can accurately characterise all bacterial, apicomplexan and filarial worm VBPs from canine blood through near full-length sequencing of the 16S rRNA, 18S rRNA and COI genes, respectively. We detected a diverse range of canine VBPs including *Anaplasma platys*, *Babesia gibsoni*, *Babesia vogeli, Bartonella clarridgeiae*, *Brugia malayi*, *Dirofilaria* sp. Hong Kong genotype, *Ehrlichia canis*, *Hepatozoon canis*, *Mycoplasma haemocanis* and a novel species of haemotropic mycoplasma. Our nanopore-based protocols performed as well as both qPCR and Illumina sequencing and outperformed microscopy-based diagnostics for the detection of VBP. Utilising MinION's ability to sequence long-reads provides an excellent diagnostic tool through which entire blood-borne pathogen communities can be characterised to a species-level in a way previously unachievable using short-read technologies.

ID: 203 / **CP15: 2**
Contributed abstract
Conference Topics: Veterinary Parasitology
Keywords: Canine, Ancylostoma caninum, resistance, anthelmintics

Evidence of combination treatment failure in an Australian *Ancylostoma caninum* isolate

Sarah George, Kathleen Vanhoff, Rebecca Obereigner
E-Mail: sarah.george@elancoah.com

Reports of anthelmintic resistance in companion animal nematodes are becoming more frequent. Fecal diagnostics are not considered a reliable indicator of efficacy, however in practice this may be the only option. Increasing frequency of hookworm infection in a colony of research dogs was investigated. Study 1 was a randomized repeat FECRT of naturally infected 3–4-month-old puppies, to determine both mixed stage and adult infection efficacy of three commercial anthelmintics administered as per label. Study 2 utilized experimental infection, with expelled worm counts and FEC post-treatment as the efficacy endpoint. The FECRT trial identified milbemycin oxime as the only effective (>90%) treatment against mixed stage natural infection, whilst combination treatments demonstrated <49% efficacy. Efficacy against adult natural infection was 100% (milbemycin oxime) and 60.4% (fenbendazole/pyrantel/praziquantel). In study 2 oxibendazole/praziquantel was ineffective with no adult nematodes recovered, whilst nematodes were successfully recovered following milbemycin oxime treatment. These findings demonstrate initial evidence of potential multiple resistance to benzimidazole and pyrantel in an Australian *A. caninum* isolate. Implications for kennel, community and companion animal management, alongside One Health considerations are likely to evolve should resistance spread. Additionally, a potential non-terminal model for resistance investigation and anthelmintic efficacy studies in canines is indicated.

CP15.1: Companion Animals sponsored by Elanco 5 min talks

Time: Friday, 08/Sept/2023: 2:00pm - 2:15pm · *Location:* Symposium room 2
Session Chair: Liisa Ahlstrom, Elanco Animal Health

ID: 136 / **CP15.1: 1**
Contributed abstract
Conference Topics: Veterinary Parasitology, Helminthology, Protozoa, Zoonoses, Microscopy
Keywords: companion dogs, Western Australia, helminths, protozoa

Peas, Corn and Parasites!: The prevalence of gastrointestinal parasites in puppies and adult dogs in Western Australia

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Australia has one of the highest pet ownership rates in the world, with 6 million dogs residing in intimate contact with owners nationwide, providing physiological and psychological benefits. Gastrointestinal (GI) parasites are a common health concern, causing chronic or recurrent infections in canines, and many can be zoonotic. Few studies have been conducted monitoring the overall prevalence of GI parasites, including protozoa, in healthy dogs in the Western Australian metropolitan community, with previous studies completed in 1999 and 2008.

Faecal samples were collected from healthy six-week old puppies in kennel environments and healthy juvenile and adult dogs in public dog exercise areas and analysed via coproscopy. The total parasite prevalence within puppies was 50.9%; with *Ancylostoma* spp., *Toxocara* spp., *Cystoisospora* spp. and *Giardia* spp. detected. 18.7% of juvenile and adult dogs had a gastrointestinal parasite: however only protozoans; *Cystoisospora* spp. and *Giardia* spp. were observed. In adult dogs , age was found to be a significant determinant of infectivity, with older dogs more likely to be infected with *Giardia.* Although helminth prevalence has declined since previous studies, the prevalence of *Giardia* has persisted. Ancylostoma, Toxocara and Giardia are considered zoonotic and are therefore a public health concern.

ID: 207 / **CP15.1: 2**
Contributed abstract
Conference Topics: Veterinary Parasitology, Immunology, Livestock Parasites, Host-parasite interactions
Keywords: IgG(T), cyathostomin, immune function, horse

Serum IgG(T) and cytokine responses to cyathostomin egg shedding in equines with and without pituitary *pars intermedia* dysfunction

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Pituitary *pars intermedia* dysfunction (PPID) affects approximately 20% of aged equines. The over-production of pituitary peptide hormones in PPID can lead to immunosuppression and susceptibility to cyathostomin infections. However, pathways influencing immunological dysfunction and susceptibility to cyathostomin infection are uncertain. This study measured serum antigen specific IgG(T) and cytokine levels during natural cyathostomin infection in horses with PPID (n=10) and age-matched controls (n=27). Horses were classified according to clinical signs and plasma ACTH concentration. Mini-FLOTAC estimated cyathostomin infection at day-0, before Ivermectin treatment (200mg/kg BW), and post-treatment (day-14, 28, 70, 77 and 84). In Autumn (day-0) and Winter (day-70) IgG(T) and cytokines were measured by ELISA and multiplex-ELISA. Generalised linear mixed models determined that PPID horses had higher average FECs throughout the study (2651 ±2374 EPG vs 1218 ±1425 EPG, $p<0.0001$). In Autumn, when PPID ACTH was significantly increased ($p<0.0001$), FEC and specific IgG(T) was positively correlated for control horses only ($r_s=0.4$, $p=0.04$). Cytokines were below detectable levels in majority of the horses. Together, data suggests higher FECs in PPID horses are unmatched by antigen specific IgG(T) responses. Elevated ACTH levels in PPID horses may be responsible for immune dysregulation, leading to higher cyathostomin infection, however, further investigations are required.

ID: 164 / **CP15.1: 3**
Contributed abstract
Conference Topics: Veterinary Parasitology, Wildlife parasitology, Epidemiology, Diagnostics, Protozoa, Zoonoses, One Health
Keywords: Toxoplasmosis, Seroprevalence, Felines, Modified agglutination test (MAT)

Australian cats in remote and rural regions display high levels of seroprevalence to *Toxoplasma gondii*

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Toxoplasma gondii is a globally distributed zoonotic protist capable of infecting all warm-blooded animals. In Australia, cats (*Felis catus*) are the only definitive host capable of spreading toxoplasmosis via infected oocysts with their faeces. Therefore, investigating the epidemiology of *T. gondii* in cats is essential to understand the potential risks of *Toxoplasma* infection in animals and humans. Cat serum samples (*n* = 552) from four states representing different proximities to humans, age groups and sex composition were screened for *T. gondii* antibodies using an in-house modified agglutination test (MAT). The overall seroprevalence for *T. gondii* in cats was 40.4% (223/552), with the highest in Tasmania (74.8%; 101/135). Male cats had higher seroprevalence (45.8%; 121/264) than females (37.9%; 100/264). A seroprevalence of 50.9% (174/342) in adult animals indicated more exposure to *T. gondii* compared to sub-adults (30%; 33/110) and juveniles (16.7%; 14/84). Stray cats had higher seroprevalence (41%; 187/456) for *T. gondii* compared to feral cats (33.3%; 30/90). Findings of this study indicate that high seroprevalence of *T. gondii* in Australian cats may translate to significant health impacts for wildlife species, livestock and the public.

CP15.2: Companion Animals sponsored by Elanco 3 min talks

Time: Friday, 08/Sept/2023: 2:15pm - 2:30pm · *Location:* Symposium room 2
Session Chair: Liisa Ahlstrom, Elanco Animal Health

ID: 115 / **CP15.2: 1**
Contributed abstract
Conference Topics: Veterinary Parasitology, Epidemiology, Zoonoses, One Health
Keywords: B. malayi, D. repens, Mosquito, Canine, Onchocercidae

Dogs are reservoir hosts of the zoonotic *Dirofilaria* sp. 'hongkongensis' and *Brugia* sp. Sri Lanka genotypes in Sri Lanka

Ushani Atapattu, Anson V. Koehler, Lucas G. Huggins, Anke Wiethoelter, Rebecca J. Traub, Vito Colella
Melbourne Veterinary School, Faculty of Science, University of Melbourne

The arthropod-borne filarioids *Dirofilaria repens*, *Brugia malayi*, *Brugia ceylonensis*, and *Acanthocheilonema reconditum* are known to be endemic in Sri Lankan dogs. However, limited information on the prevalence, diversity, and predictors of these infections in Sri Lankan dogs resulted in suboptimal control and prevention of these potentially zoonotic parasites. To address this, whole blood and metadata were collected and analysed from 423 pet dogs across three geo-climatic zones within Sri Lanka. Blood was screened using the Modified Knott's Test (MKT) and PCR, followed by Sanger sequencing. Multivariable logistic regression was used to assess predictors for canine filarial infections. Two genotypes, *Dirofilaria* sp. 'hongkongensis'(*Dirofilaria* sp. HK) and *Brugia* sp. Sri Lanka genotypes were identified in Sri Lankan dogs. The overall prevalence of filarial infection in pet dogs was 36.9% (95% CI 32.3 - 41.7%) with *Dirofilaria* sp. HK is the most prevalent. Increasing age ($p<0.001$) and residing in the low-country wet zone ($p<0.001$) were associated with filarial infections in dogs. The absence of pathognomonic signs in infected dogs indicates that dogs could act as reservoirs for these potentially zoonotic pathogens. Prevention and control measures for these canine filarial infections are highly advocated to safeguard both canine and human health.

ID: 121 / CP15.2: 2
Contributed abstract
Conference Topics: Veterinary Parasitology, Drugs, Diagnostics, Helminthology, Bioinformatics
Keywords: hookworms, ITS-2, nemabiome, tubulin, resistance

Unambiguous identification of Ancylostoma caninum and Uncinaria stenocephala in Australian and New Zealand dogs from faecal samples

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[1]Sydney School of Veterinary Science, Faculty of Science, The University of Sydney, New South Wales 2006, Australia; [2]School of Veterinary Science, Massey University, Palmerston North 4410, New Zealand; [3]The University of Sydney Institute for Infectious Diseases, New South Wales 2006, Australia

Hookworms (Ancylostomatidae) are well-known parasites in dogs due to their health impacts and zoonotic potential. While faecal analysis is the traditional method for detection, improvements in husbandry and deworming have decreased their prevalence in urban owned dogs. Drug resistance in Ancylostoma caninum is becoming a discussion point in small animal practices across the region. This study aimed to identify hookworm species present in Australian and New Zealand dogs using molecular techniques. The ITS-2 and isotype-1 β-tubulin assays were used to identify and quantify hookworm species. Results showed absence of coinfection in Australian samples from Greater Sydney region belonging either to A. caninum or Uncinaria stenocephala, while New Zealand samples were a mixture of A. caninum and U. stenocephala. The amplified isotype-1 β-tubulin sequences exhibited susceptibility to benzimidazole drugs. Rare mutations were identified in A. caninum and U. stenocephala sequences, representing a small percentage of reads. This study highlights the importance of molecular techniques in accurately identifying and quantifying hookworm species in dog populations.

ID: 184 / CP15.2: 3
Contributed abstract
Conference Topics: Veterinary Parasitology, Immunology, Host-parasite interactions
Keywords: Pituitary Pars Intermedia Dysfunction (PPID), Peripheral Blood Mononuclear Cells (PBMC), Immunology, RNA sequencing

Investigating Peripheral Blood Mononuclear Cell (PBMC) function of horses with Pituitary *Pars Intermedia* Dysfunction (PPID)

Rebecca Farnell, Sarah Preston, Leni Horner, David Piedrafita
Institute of Innovation Science & Sustainability. Federation University, PO Box 633, Ballarat, VIC, 3353

Pituitary *Pars Intermedia* Dysfunction (PPID) is a chronic, slow progressing endocrinopathy affecting 20-25% of geriatric horses. Oxidative degeneration of the dopaminergic neurons in the hypothalamus leads to the absence of dopaminergic inhibition of the pars intermedia. Hyperplasia of this tissue leads to the overproduction of hormones, producing several complications. Horses with PPID display multiple symptoms including hypertrichosis, lethargy, weight loss and increased susceptibility to infections including gastrointestinal worms. The immune mechanisms underlying the increased susceptibility is largely unknown. Reduced circulating eosinophils has been implicated but little differences in serum cytokines and antibodies have been observed.

This research will investigate the reduced immune response in PPID horses by testing the function of Peripheral Blood Mononuclear Cells (PBMC). PMBC isolated from PPID (n=5) and aged-matched control (non-PPID, n=5) horses will be stimulated with lipopolysaccharide, Concanavalin A, and extract from nematodes at varying concentrations for 24-48 h. Following stimulation, cell proliferation rates will be measured using MTT assay (24h and 48h) and RNA will be sequenced to determine if any differences exist between PPID and non-PPID horses (24h). Changes in RNA sequences relating to cytokine production following cell stimulation will be verified by measuring protein using ELISA.

ID: 149 / CP15.2: 4
Contributed abstract
Conference Topics: Veterinary Parasitology, Genomics, Zoonoses, One Health, Strongyloides
Keywords: Zoonoses, Hookworms, Strongyloides, One Health, Genomics

Whole genome sequencing to elucidate the zoonotic transmission of *Strongyloides stercoralis* and *Ancylostoma ceylanicum* between dogs and school-aged children living in the same communities.

Patsy A. Zendejas-Heredia[1], Shannon M. Hedtke[2], Virak Khieu[3], Martin Walker[4,5], Warwick N. Grant[3], Rebecca J. Traub[1], Vito Colella[1]
[1]Faculty of Science, The University of Melbourne, Melbourne, Australia; [2]Department of Environment and Genetics, La Trobe University, Melbourne, Australia; [3]National Center for Parasitology, Entomology and Malaria Control, Ministry of Health, Cambodia.; [4]Department of Pathobiology and Population Sciences, Royal Veterinary College, University of London, UK.; [5]London Centre for Neglected Tropical Disease Research, Department of Infectious Disease Epidemiology, Imperial College London, London, UK

Strongyloides stercoralis and *Ancylostoma ceylanicum* are parasitic soil-transmitted helminths that impact on the health of humans and dogs in the tropics. The ability of these parasites to transmit between humans and dogs living in closed proximity via contaminated environments is a significant concern. Despite this, there is a lack of understanding about the extent to which these parasitic nematodes are transmitted between humans and community dogs. To quantify the zoonotic potential and transmission of *S. stercoralis* and *A. ceylanicum*, we isolated single eggs of *A. ceylanicum* from faecal samples of 14 children and 25 dogs and single larvae of *S. stercoralis* from 20 children and 35 dogs living in the same communities in Cambodia. Whole genome sequencing was performed to analyse the genetic variation within and among parasites, the intra- and interspecies transmission and dispersal between communities of these parasites with the ultimate goal of identifying genetic markers associated with specific human/animal host species. This information will help elucidate the risk of transmission from domestic animals to humans and inform the parameterisation of multi-host transmission dynamics models. These findings will be essential to the development of effective elimination strategies for these zoonotic parasites of major public health and socio-economic importance.

ID: 221 / **CP15.2: 5**
Contributed abstract
Conference Topics: Veterinary Parasitology, Livestock Parasites, Helminthology
Keywords: anthelmintic, faecal egg count, horse

A decade of targeted selective equine parasite control: The drugs and the horses are still working!

Ryan O'Handley, A Hines
School of Animal and Veterinary Sciences, University of Adelaide, Roseworthy Campus, SA 5371

A targeted selective program has been used to control parasites in the veterinary teaching horse herd at the University of Adelaide since 2012. Faecal egg counts are conducted on each horse approximately quarterly, and horses with egg counts over 200 epg are treated with ivermectin. Faecal egg count reduction tests have been performed every 2-3 years in the herd and larval cultures have been performed annually. This program has resulted in a 10-fold reduction in anthelmintic use compared to scheduled treatments and no resistance to ivermectin has developed during this time. No horses have demonstrated any clinical signs related to parasitism, and larval cultures indicate only small strongyles to be present in the herd. This program has also revealed that Individual horses have predictable faecal egg counts and can be easily grouped in to low, moderate, and high shedding categories. Most interesting is in 10% of horses, not a single strongylid egg has ever been detected despite all horses sharing the same paddock. These results demonstrate a targeted selective approach to parasite control is highly effective in horses and prevents the development of anthelmintic resistance. It also demonstrates a likely genetic component to faecal egg counts in horses.

W8: Strongyloides Workshop

Time: Friday, 08/Sept/2023: 1:00pm - 2:30pm · *Location:* Workshop room 3
Session Chair: Catherine Gordon, QIMR Berghofer Medical Research Institute

ID: 225 / **W8: 1**
Invited speaker abstract

A community connector and communicator about Strongyloides as part of community co-designed holistic and sustainable health programs

John Morgan
Miwatj Aboriginal Health Corporation (retired)

I have been a Board Member for Miwatj Health Aboriginal Corporation for 23 years and former Chair for 12 years with various other roles including Aboriginal Health Worker and Environmental Health Officer, developing a role as a Community Connector. Miwatj Health services 10 communities and 10,000 people including people in 26 Yolŋu, 8 Anindilyakwa (Groote Eylandt and Biggenden Island) and 4 Nunggubuyu/Wubuy (Numbulwar) language groups. We foster an open community centred relationship of trust, respecting Dhuwa/Yirritja moieties, skin and kinship relationships through our own Community Contolled Health Services.

When I was training, one of my colleagues, a senior Aboriginal Health Worker, died from an infection with Strongyloides. I attended the Strongyloides Workshop at Nhulunbuy in 2001, and I want to celebrate the work of Dr Wendy Page. The contribution of knowledge by the elders should have similar status to that of the other investigators.

We want to eradicate Strongyloides as part of an integrated health system that is also integrated with economic well-being. I would love to see enviromental health officers working together with the other health workers in a way that is co-shared and co-designed. We want this work published to benefit all who are living with Strongyloides infections.

ID: 171 / **W8: 2**
Invited speaker abstract

A new rapid test for the detection of *Strongyloides stercoralis* infection

Rahmah Noordin, Anizah Rahumatullah, Nickel Beatrice, Dora Buonfrate, Emelia Osman, Suhada Anuar, Norashikin Samsudin, Zeehaida Mohamed, Paiboon Sithithaworn
Universiti Kebangsaan Malaysia, MY

A point-of-care (POC) lateral flow cassette test that uses recombinant NIE antigen and specific IgG4 detection has been developed. The initial laboratory study using defined positive and negative serum samples showed a sensitivity of 97% and a specificity of 95%. Subsequently, it was evaluated in laboratory and field studies in several countries. They included comparisons with parasitological methods, commercial ELISAs, and real-time PCR. The samples were from patients (immunocompetent and immunocompromised), endemic area residents with and without other infections, and healthy individuals. A summary of the results will be discussed. Overall, the rapid test shows good diagnostic performance and is promising to fill the gap in the current need for a rapid strongyloidiasis test.

ID: 157 / **W8: 3**
Invited speaker abstract

Clinical Performance of Real-Time Polymerase Chain Reaction for Strongyloides stercoralis Compared with Serology in a Nonendemic Setting

Christopher Swan[1,3], Thuy Phan[1,2], Genevieve McKew[1,2]
[1]NSW Health Pathology, Department of Microbiology and Infectious Diseases, Concord Repatriation and General Hospital, Hospital Rd, Concord NSW 2139; [2]Concord Clinical School, Faculty of Medicine and Health, The University of Sydney; [3]School of Molecular and Biosciences, The University of Sydney

Strongyloides stercoralis is a nematode endemic to subtropical and tropical regions that may cause asymptomatic carriage, peripheral eosinophilia, cutaneous, gastrointestinal, and pulmonary disease, or hyperinfection syndrome. Conventional diagnostic methods for strongyloidiasis include faeces microscopy and culture, with low sensitivity in chronic infection due to the low helminth burden, and serology, which may be prone to false-negative or false-positive results.

We evaluated a laboratory-developed real-time polymerase chain reaction (RT-PCR) assay, detecting the 18S SSU ribosomal RNA gene, compared with conventional diagnostic methods, using serology (ELISA) as the comparator standard, in nonendemic setting. Stool specimens underwent microscopy and RT-PCR. Agar plate culture (APC), Harada-Mori culture (HMC), and ELISA were performed in conjunction with 141, 135, and 177 of the specimens, respectively. RT-PCR yielded 13 positive and 730 negative results, with inhibition in seven specimens.

ELISA yielded 53 positive, 18 equivocal, and 106 negative results. Compared with ELISA, RT-PCR, microscopy, APC, and HMC exhibited sensitivities of 38%, 6%, 3%, and 0%, respectively, and specificities of 100%. Given the low sensitivities commensurate with testing a population with remote infection and thus low parasite burden, we recommend a combination of serological and molecular diagnostic testing to achieve the best balance of sensitivity and specificity.

ID: 233 / **W8: 4**
Invited speaker abstract

Strongyloides stercoralis and environmental health hardware

Kirstin Ross
Flinders University, Australia

In Australia, strongyloidiasis primarily affects returned travellers, Vietnam veterans and refugees or asylum seekers, and First Nations people. Non-overseas acquired cases are seen almost exclusively in Australian First Nations remote communities. Australian First Nations communities have one of the highest rates of strongyloidiasis in the world. Our work has shown that strongyloidiasis is a disease of poverty. Acknowledging this is important – we need to shift the lens to socioeconomic factors, particularly environmental health hardware such as working toilets and sewerage systems, showers and laundries, and effective wastewater and rubbish removal. The rates of strongyloidiasis in First Nations communities is a result of decades of inadequate, poorly constructed and/or poorly maintained housing, and poor environmental health hardware. The solution lies in adequate funding, resulting in well designed and maintained housing and appropriate hardware. Governments need to allow First Nations communities themselves to take the lead role in funding allocation, and design, construction and maintenance of their housing and hardware. This will ensure housing and hardware fulfils cultural and physical needs and desires, and protects health. Improving housing and hardware will also improve other health outcomes.

W9: Strongyloides Workshop

Time: Friday, 08/Sept/2023: 3:00pm - 4:30pm · *Location:* Workshop room 3
Session Chair: Kirstin Ross, Flinders University

ID: 159 / **W9: 1**
Invited speaker abstract

Strongyloides stercoralis in Australia: a mapping project using pathology laboratory data

Jennifer Shield, Sabine Braat, Beverley-Ann Biggs
Strongyloides Australia

Strongyloides stercoralis are parasitic roundworms that cause a persistent infection. They multiply out of control on immunosuppression, causing a frequently fatal hyperinfection. In Australia, *Strongyloides* infections are acquired either locally or overseas.

Major diagnostic pathology laboratories that carried out serological tests for *Strongyloides* contributed deidentified results of *Strongyloides* serology tests from 2012 to 2016 inclusive.

We mapped the number of people positive per 100,000 of population, https://public.tableau.com/app/profile/jennifer.shield/viz/StrongyloidesstercoralisinAustraliabyregion2012-2016/Strongyloidesbyregion as well as the number positive in each suburb of residence https://public.tableau.com/app/profile/jennifer.shield/viz/StrongyloidesstercoralisinAustraliabylocality2012-2016/Story1

The number of people positive/100,000 of population was outstandingly highest in the Northern Territory (489/100,000). The highest seropositivity was in regions across Northern Australia, north-west South Australia and north-east New South Wales where many Aboriginal and Torres Strait Islander people live in remote communities.

The percentage positive increased with age from a relatively low percentage in 0-5 year olds. Children were under-represented in the data except in Tasmania.

The data strongly suggest that Aboriginal and Torres Strait Islanders bear the major burden of strongyloidiasis. This study underestimates the number of people who were infected because one laboratory declined to contribute data. If strongyloidiasis were notifiable nationally, we would have more comprehensive up-to-date data on which to base control strategies.

ID: 170 / **W9: 2**
Invited speaker abstract

Is *Strongyloides stercoralis* a zoonosis from dogs?

Richard Bradbury
Federation University, Berwick, VIC, 3806, Australia

Strongyloidiasis remains a major veterinary and public health challenge globally. This chronic and potentially life-long disease has fatal outcomes in immunosuppressed people and dogs. Currently, the role of companion animals in the transmission cycle of human strongyloidiasis remains enigmatic. While zoonotic transmission to humans from companion animals has been proposed, it is not been confirmed. Cross-infection experiments between dogs and people during the 20th century suggest that *S. stercoralis* has varying capacity for cross-species transmission based on geographical origin. Recent genotyping studies of *Strongyloides* from dogs, cats, non-human primates, and people indicate that *S. stercoralis* is a species complex containing at least two taxa. One taxon has been demonstrated to infect cats, dogs and humans while the second appears specific to dogs (provisionally named "*S. canis*"). Despite recent advances in *Strongyloides* genotyping, sufficiently discriminatory tools to prove transmission from one host to another have not yet been developed. It remains unclear if dogs act as a zoonotic reservoir for human infection, or vice versa, or if this occurs only in some regions of the world and not in others. These questions must be answered before effective control strategies for strongyloidiasis can be instituted.

ID: 226 / **W9: 3**
Invited speaker abstract

Is One Health the way forward in preventing and controlling Strongyloidiasis?

Jenni Judd
Professorial Fellow, Graduate Research School, Research Division, Central Queensland University, Bundaberg

Strongyloides Australia Inc is an incorporated multidisciplinary professional association to address the prevention and control of Strongyloidiasis. This presentation will overview who we are, a little about our history, our aims, and why One Health might be a way to prevent and control Strongyloidiasis. My presentation will also outline why Health promotion is a crucial driver in preventing Strongyloides from an individual, community and population perspective.

This paper will highlight why a systems approach might be helpful, the building blocks of health systems and health outcomes, and how One Health might help us to address Strongyloides in endemic Aboriginal communities. One of the roles of this group is to advocate for mandatory reporting of the incidence and impact of this Neglected Tropical disease. We can provide some evidence and strategies for reducing the morbidity and mortality of this disease in affected communities.

ID: 178 / **W9: 4**
Invited speaker abstract

A Systems/One Health Approach to Eliminating Strongyloidiasis in Australia

Darren Gray
QIMR Berghofer Medical Research Institute

Strongyloidiasis is caused by parasitic nematodes (roundworms) of the genus *Strongyloides* and is considered to be one of the most neglected of the neglected tropical diseases (NTDs). There are two main *Strongyloides* species that cause human infection; *S. stercoralis* and *S. fuelleborni*. In Australia, *S. stercoralis* is the infecting species that disproportionately affects remote Indigenous communities, with the prevalence ranging from 10-60%. The lifecycle and transmission is complex with both a parasitic cycle and a free-living cycle. This is further complicated by autoinfection and the possibility of zoonotic transmission– recent genetic evidence suggests the possibility of a dog reservoir. These factors coupled with less than ideal diagnostics and treatment options (Ivermectin and Albendazole) where there is evidence of treatment failures, the spectre of emerging resistance and their inability to prevent reinfection, all have implications for control and elimination efforts.

It is our ***central thesis*** that strongyloidiasis is a zoonotic neglected tropical disease of public health importance in Australia and that an integrated interdisciplinary "Systems/One Health" approach is required for its elimination.

S9: Microscopy Symposium

Time: Friday, 08/Sept/2023: 3:00pm - 3:30pm · *Location:* Symposium room 1
Session Chair: Danny Wilson, The University of Adelaide

ID: 258 / **S9: 1**
Invited speaker abstract

Parasites through the looking glass-secrets revealed by advanced microscopy techniques

Joanne Lee[1], Daryl Webb[1], Angus Rae[1], Zala Gluhic[2], Frank Brink[1], Chung-Han Tsai[1], Christian Schmitz-Linneweber[2], Giel van Dooren[3], Alex Maier[3], Melanie Rug[1]
[1]Centre for Advanced Microscopy, The Australian National University, ACT 2601; [2]Molecular Genetics Group, Humboldt-University of Berlin, Institute of Biology, 10115 Berlin; [3]Research School of Biology, The Australian National University, Acton ACT 2601

We have been intrigued by microscopy images since van Leeuwenhoek demonstrated the power of identifying intricate details of parasites (and many other cells and organisms) with a simple magnifying lense held in front of the observer's eye in the 17th century. The last decade has seen an enormous jump in resolution revolution with developments in the optical as well as electron microscopy space. Multiple Nobel prizes have been bestowed on researchers for having ventured into areas of overcoming the diffraction limit of light (Betzig, Hell and Moerner) and imaging single biomolecules with the help of cryo-electron microscopy (Dubochet, Frank and Henderson).

We will present a journey through imaging parasites with various microscopy techniques, allowing us an insight into the life of parasites from 2D to 4D.

CP16: Microscopy 15 min talks

Time: Friday, 08/Sept/2023: 3:30pm - 4:30pm · *Location:* Symposium room 1
Session Chair: Danny Wilson, The University of Adelaide

ID: 189 / CP16: 1
Contributed abstract
Conference Topics: Cell Biology, Microscopy
Keywords: Transmission, Cyst, Dientamoeba fragilis, Electron Microscopy

Observations on the transmission of *Dientamoeba fragilis*: Ambiguity of the life cycle and the cyst stage.

Luke Hall[1], Nicole Vella[2], Damien Stark[3], John Ellis[1]
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The life cycle and mode of transmission of *Dientamoeba fragilis* is not well understood. Historically, transmission was believed to occur through *Enterobius vermicularis* ova or directly via trophozoites in stool. Recently evidence for fecal–oral transmission of cysts has emerged. In order to establish an infection, *D. fragilis* is required to remain viable when exposed to the stomach acid of the new host. Consequently, we investigated the ability of cultured trophozoites to withstand extremes of pH. We provide evidence that trophozoites of *D. fragilis* are vulnerable to highly acidic conditions showing the need to further investigate transmission by other methods such as a cyst stage or *Enterobius vermicularis*ova. This also includes the possibility that dientamoebiasis is a zoonosis. We also investigated further the ultrastructure of *D. fragilis* cysts obtained from mice and rats by transmission electron microscopy. These studies of cysts showed a clear cyst wall surrounding an encysted parasite. The cyst wall was double layered with an outer fibrillar layer and an inner layer enclosing the parasite. Hydrogenosomes and nuclei were present in the cysts. Basal bodies were identifiable. This study therefore provides additional novel details and knowledge of the ultrastructure of the cyst stage of *D. fragilis*.

ID: 109 / CP16: 2
Contributed abstract
Conference Topics: Veterinary Parasitology, Ectoparasites, Other, Microscopy
Keywords: Embryogenesis, Scabies eggs, First reference atlas, Time-lapse microscopy, Microgrid device

Embryonic development and hatching process of *Sarcoptes scabiei*: First temporal reference atlas of morphological development and larval movements

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Scabies is a contagious skin disease in humans caused by the parasitic mite *Sarcoptes scabiei* var. *hominis*. *S. scabiei* has four distinct life stages - eggs, larvae, nymphs and adults. The eggs are the only "amplification stage" in its life cycle, hence targeting this stage is essential to disrupt parasite propagation. There is no vaccine, and commonly used ivermectin/permethrin are ineffective on eggs, thus, require repeat treatments. Understanding the embryogenesis is crucial to identify potential targets and develop efficient ovicidal drugs. As there is very limited knowledge about mite embryology, and even less about *S. scabiei* embryogenesis, we investigated the egg development of *S. scabiei*. We developed a medium throughput microgrid device, to perform and observe *in vitro* assays. Time-lapse images of 40 individual freshly-laid eggs were taken over a period of 72 hours. We identified six embryonic stages and 42 accompanying dynamic events in *S. scabiei*, referring to embryogenesis of other arthropods. Our first temporal reference atlas of *S. scabiei* embryogenesis provides a basis to expand the knowledge on *S. scabiei* embryogenesis and for molecular studies. The microgrid device and time-lapse technique can be adapted for use in drug screening studies in *S. scabiei* and other microscopic parasitic mites.

ID: 227 / CP16: 3
Contributed abstract
Conference Topics: Malaria, Apicomplexa Biology, Microscopy
Keywords: ultrastructural expansion microscopy. malaria

Investigating development of malaria parasites through the mosquito

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Malaria parasites have complicated lifecycles involving both human and mosquito hosts. In ~8 days, a single parasite can form an oocyst in the mosquito midgut produces thousands of daughter sporozoites. These sporozoites then egress from the oocyst and undergo a complex series of translocation and invasion events to reach the mosquito salivary gland. Sporozoite formation and salivary gland invasion are both important and interesting processes but are poorly understood. The small size of these parasites, and the difficulty of imaging them in their anatomical context, has made it challenging to interrogate their cell biology. To better understand sporozoite development and salivary gland invasion *in situ*, we used ultrastructural expansion microscopy (U-ExM), a method that enlarges the sample ~4.5x. We performed U-ExM on whole mosquito midguts and salivary glands, allowing us to visualise sporozoites in 3D from whole tissue architecture to parasite ultrastructure. In this study, we define when and where sporozoites establish their apical polarity and how they undergo biogenesis of organelles involved in host cell

invasion. These findings begin to uncover the fascinating cell biology of the least well understood stages of the parasite lifecycle and pave the way to development of treatments or prevention strategies targeting these stages.

ID: 145 / **CP16: 4**
Contributed abstract
Conference Topics: Malaria, Drugs, Cell Biology, Apicomplexa Biology, Molecular Biology, Microscopy
Keywords: antimalarial, drug development, target identification, START protein

Stopping Malaria Parasites Before They StART: Aryl-acetamide Compound MMV006833 Inhibits Lipid Transfer and Ring Development (Part 2)

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There is an urgent need for novel antimalarials to combat current drug resistance by the malaria parasite, *Plasmodium falciparum*. Through resistance studies, we recently identified a parasite StART domain phospholipid transferase protein (START) as the putative target of MMV006833 (MMV833). To further investigate this chemical series, we conducted structure activity relationship studies and significantly improved the potency of the compound >30-fold with new analogues. These analogues were found to be resistant to the MMV833-resistant lines, indicating selectivity against the START protein was maintained. This was confirmed through isothermal titration calorimetry studies which measured the binding of the inhibitors to recombinant START protein with nanomolar affinity.

We next turned to lattice light shield microscopy to further investigate the phenotype of these compounds. Filming invading merozoites allowed us to determine that these compounds prevented the lipid-dependent establishment of the parasite parasitophorous vacuole membrane (PVM), indicating that the START protein may be crucial for transferring lipids to the developing PVM. Currently we are evaluating these compounds against other stages of the parasite's lifecycle and assessing the rate of kill against the parasite. Overall, this study will further the antimalarial development of this series and evaluate the druggable nature of the novel START protein.

P5: Strongyloides Closing Plenary Lecture

Time: Friday, 08/Sept/2023: 5:00pm - 5:45pm · *Location:* Plenary Room
Session Chair: Wendy Page, Strongyloides Australia

ID: 266 / **P5: 1**
Invited speaker abstract

Strongyloides stercoralis, the smartest worm

Zeno Bisoffi
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Attributing terms such as "smartest" to parasites is unscientific, and this title is more of a joke. Parasites have developed different strategies to survive and reproduce in their hosts, and these strategies are adaptations to their specific ecological niches rather than indicators of "intelligence". But if intelligence were a quality by which we could qualify worms, *Strongyloides stercoralis* would have to be considered the most ingenious worm of all. Others have very complex cycles involving intermediate hosts, or vector insects, or whatever. But often the most ingenious inventions are quite simple. In my presentation, a bit light, as befits a closing lecture after a pre-Plenary Prosecco, I will start from afar, from the pioneering research of Silvio Pampiglione and Maria Luisa Ricciardi, who discovered that another *Strongyloides*, *S. fuelleborni*, can infect humans, not only from infected monkeys, but also from another infected human.

I will pay tribute to the ingenious and simple "strategy" that has allowed *S. stercoralis* to survive in an advanced European country like Italy, when other geohelminthes have been extinct for decades. I will report on some clinical cases, or rather memorable patients, and finally I will mention how, eventually, guidelines on the control of strongyloidiasis are about to be officially issued by the WHO.

2023 Annual Conference of the Australian Society for Parasitology Inc.

September 5-8, DoubleTree by Hilton Hotel Esplanade Darwin, NT, Australia

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Bowles, Vern	113, 114	CP2 (Wed, 2023/9/6 11:00-11:45; Symposium room 2), CP3 (Wed, 2023/9/6 13:00-14:15; Symposium room 2)
Boxshall, G.	244	S3 (Wed, 2023/9/6 15:00-15:15; Symposium room 2)
Boyd, Davina	251	W1 (Wed, 2023/9/6 10:30-12:00; Workshop room 3)
Bradbury, Richard	170	W9 (Fri, 2023/9/8 15:00-16:30; Workshop room 3)
Brewster, Jessica	217	CP9.1 (Thu, 2023/9/7 14:00-14:15; Symposium room 1)
Brink, Frank	258	S9 (Fri, 2023/9/8 15:00-15:30; Symposium room 1)
Brook, Barry	205	CP7 (Thu, 2023/9/7 10:30-11:30; Symposium room 1)
Brown, Keira	176	CP7.1 (Thu, 2023/9/7 11:30-12:00; Symposium room 1)
Buettel, Jessie	205	CP7 (Thu, 2023/9/7 10:30-11:30; Symposium room 1)
Bulloch, Michaela	223	CP14 (Fri, 2023/9/8 13:00-14:00; Symposium room 1)
Bury, C	219	CP3.1 (Wed, 2023/9/6 14:15-14:30; Symposium room 2)

Cadavid Restrepo, Angela	215	CP12.1 (Fri, 2023/9/8 11:15-11:45; Symposium room 2)
Calvani, Nichola Eliza Davies	208	CP3 (Wed, 2023/9/6 13:00-14:15; Symposium room 2)
Carabott, Melissa	196	CP6 (Wed, 2023/9/6 15:15-16:30; Symposium room 2)
Caraguel, C	219	CP3.1 (Wed, 2023/9/6 14:15-14:30; Symposium room 2)
Carver, Scott	205	CP7 (Thu, 2023/9/7 10:30-11:30; Symposium room 1)
Cavallaro, Antonino	125	CP2.1 (Wed, 2023/9/6 11:45-12:00; Symposium room 2)
Chittavong, Malavanh	251	W1 (Wed, 2023/9/6 10:30-12:00; Workshop room 3)
Chittavong, Malavanh	201	CP12 (Fri, 2023/9/8 10:30-11:15; Symposium room 2)
Chmielewski, Jill	222	CP4.1 (Wed, 2023/9/6 14:00-14:15; Symposium room 1)
Chmielewski, Jill	228	CP9.1 (Thu, 2023/9/7 14:00-14:15; Symposium room 1)
Chmielewski, Jill	161	CP9.2 (Thu, 2023/9/7 14:15-14:30; Symposium room 1)
Chosidow, Olivier	128	CP9 (Thu, 2023/9/7 13:00-14:00; Symposium room 1)
Chowdhury, Sumaiya	163	CP3 (Wed, 2023/9/6 13:00-14:15; Symposium room 2)
Clemens, Archie	215	CP12.1 (Fri, 2023/9/8 11:15-11:45; Symposium room 2)
Colella, V	234	CP12 (Fri, 2023/9/8 10:30-11:15; Symposium room 2)
Colella, V	235	CP12.1 (Fri, 2023/9/8 11:15-11:45; Symposium room 2)
Colella, V	236	CP12.1 (Fri, 2023/9/8 11:15-11:45; Symposium room 2)
Colella, Vito	151, 107, 115, 149	CP8.1 (Thu, 2023/9/7 11:45-12:00; Symposium room 2), CP15 (Fri, 2023/9/8 13:30-14:00; Symposium room 2), CP15.2 (Fri, 2023/9/8 14:15-14:30; Symposium room 2), CP15.2 (Fri, 2023/9/8 14:15-14:30; Symposium room 2)
Collier, Sophie	165	CP5.1 (Wed, 2023/9/6 16:00-16:30; Symposium room 1)
Corry, Ben	132	CP5.1 (Wed, 2023/9/6 16:00-16:30; Symposium room 1)
Crabb, B	118	CP14.1 (Fri, 2023/9/8 14:00-14:30; Symposium room 1)
Crabb, Brendan	261, 116, 145	CP1.1 (Wed, 2023/9/6 11:45-12:00; Symposium room 1), CP9 (Thu, 2023/9/7 13:00-14:00; Symposium room 1), CP16 (Fri, 2023/9/8 15:30-16:30; Symposium room 1)
Crabb, Brendan S	103, 155	CP13 (Fri, 2023/9/8 11:00-11:30; Symposium room 1), CP14.1 (Fri, 2023/9/8 14:00-14:30; Symposium room 1)
Crawford-Weaver, Haylee	224	CP7 (Thu, 2023/9/7 10:30-11:30; Symposium room 1)
Creek, Darren J.	100	CP4.1 (Wed, 2023/9/6 14:00-14:15; Symposium room 1)
Crisafulli, Emily	223	CP14 (Fri, 2023/9/8 13:00-14:00; Symposium room 1)
Crook, D.A.	244	S3 (Wed, 2023/9/6 15:00-15:15; Symposium room 2)
Cumming, Bonny	231	CP11 (Thu, 2023/9/7 15:30-16:30; Symposium room 1)
Cunningham, Calum	205	CP7 (Thu, 2023/9/7 10:30-11:30; Symposium room 1)
Dale, A	240	CP14.1 (Fri, 2023/9/8 14:00-14:30; Symposium room 1)

Dans, Madeline	116, 142, 108, 155, 145	CP9 (Thu, 2023/9/7 13:00-14:00; Symposium room 1), CP14 (Fri, 2023/9/8 13:00-14:00; Symposium room 1), CP14.1 (Fri, 2023/9/8 14:00-14:30; Symposium room 1), CP14.1 (Fri, 2023/9/8 14:00-14:30; Symposium room 1), CP16 (Fri, 2023/9/8 15:30-16:30; Symposium room 1)
Dans, Madeline G	103	CP13 (Fri, 2023/9/8 11:00-11:30; Symposium room 1)
Darben, Troy	128	CP9 (Thu, 2023/9/7 13:00-14:00; Symposium room 1)
Dawson, Kathryn	134	CP2 (Wed, 2023/9/6 11:00-11:45; Symposium room 2)
de Koning-Ward, Tania F.	261	CP1.1 (Wed, 2023/9/6 11:45-12:00; Symposium room 1)
Dixon, Matthew	100	CP4.1 (Wed, 2023/9/6 14:00-14:15; Symposium room 1)
Doerig, Christian	264	CP4.2 (Wed, 2023/9/6 14:15-14:35; Symposium room 1)
Doerig, Christian	209, 150, 174	CP9.1 (Thu, 2023/9/7 14:00-14:15; Symposium room 1), CP9.2 (Thu, 2023/9/7 14:15-14:30; Symposium room 1), CP13.2 (Fri, 2023/9/8 11:45-12:00; Symposium room 1)
Doolan, Denise	124	CP1.1 (Wed, 2023/9/6 11:45-12:00; Symposium room 1)
Dowling, Mark R	230	W7 (Fri, 2023/9/8 10:30-12:00; Workshop room 3)
Dvořák, J.	265	CP1.2 (Wed, 2023/9/6 12:00-12:05; Symposium room 1)
Dziekan, Jerzy	166	CP13.2 (Fri, 2023/9/8 11:45-12:00; Symposium room 1)
Ebbinghaus-Kintscher, Ulrich	243	S5 (Thu, 2023/9/7 13:00-14:00; Symposium room 2)
Farnell, Rebecca	184	CP15.2 (Fri, 2023/9/8 14:15-14:30; Symposium room 2)
Farrell, Sarah	191	CP14 (Fri, 2023/9/8 13:00-14:00; Symposium room 1)
Fathoni, Imam	140	CP14.1 (Fri, 2023/9/8 14:00-14:30; Symposium room 1)
Fazekas de St Groth, Barbara	124	CP1.1 (Wed, 2023/9/6 11:45-12:00; Symposium room 1)
Feez, A M	239	CP2.1 (Wed, 2023/9/6 11:45-12:00; Symposium room 2)
Fernando, Asela Lakvin	204	CP5.1 (Wed, 2023/9/6 16:00-16:30; Symposium room 1)
Fernando, Deepani D.	128	CP9 (Thu, 2023/9/7 13:00-14:00; Symposium room 1)
Fernando, Deepani D.	158, 109	CP9.2 (Thu, 2023/9/7 14:15-14:30; Symposium room 1), CP16 (Fri, 2023/9/8 15:30-16:30; Symposium room 1)
Fischer, Katja	128	CP9 (Thu, 2023/9/7 13:00-14:00; Symposium room 1)
Fischer, Katja	158, 109	CP9.2 (Thu, 2023/9/7 14:15-14:30; Symposium room 1), CP16 (Fri, 2023/9/8 15:30-16:30; Symposium room 1)
Foley, Mick	228	CP9.1 (Thu, 2023/9/7 14:00-14:15; Symposium room 1)
Francis, Emily	129	CP13.1 (Fri, 2023/9/8 11:30-11:45; Symposium room 1)
Francis, Nidhish	112, 202	CP7 (Thu, 2023/9/7 10:30-11:30; Symposium room 1), CP7.1 (Thu, 2023/9/7 11:30-12:00; Symposium room 1)
Frölich, Sonja	100	CP4.1 (Wed, 2023/9/6 14:00-14:15; Symposium room 1)
Fuller, Carley	205	CP7 (Thu, 2023/9/7 10:30-11:30; Symposium room 1)

Gabriela, Mikha	261	CP1.1 (Wed, 2023/9/6 11:45-12:00; Symposium room 1)
Gancheva, Maria	212, 182	CP13 (Fri, 2023/9/8 11:00-11:30; Symposium room 1), CP13.2 (Fri, 2023/9/8 11:45-12:00; Symposium room 1)
Gardiner, Riana	205	CP7 (Thu, 2023/9/7 10:30-11:30; Symposium room 1)
Gasser, R	234	CP12 (Fri, 2023/9/8 10:30-11:15; Symposium room 2)
Gasser, R	236	CP12.1 (Fri, 2023/9/8 11:15-11:45; Symposium room 2)
George, Sarah	203	CP15 (Fri, 2023/9/8 13:30-14:00; Symposium room 2)
Ghafar, Abdul	192, 180, 162	CP2.1 (Wed, 2023/9/6 11:45-12:00; Symposium room 2), CP3.1 (Wed, 2023/9/6 14:15-14:30; Symposium room 2), CP10 (Thu, 2023/9/7 14:00-14:30; Symposium room 2)
Giacomin, Paul	241	CP4.2 (Wed, 2023/9/6 14:15-14:35; Symposium room 1)
Giannangelo, Carlo	133	CP14 (Fri, 2023/9/8 13:00-14:00; Symposium room 1)
Gilberger, Tim	100	CP4.1 (Wed, 2023/9/6 14:00-14:15; Symposium room 1)
Gilson, P	118	CP14.1 (Fri, 2023/9/8 14:00-14:30; Symposium room 1)
Gilson, Paul	116, 145	CP9 (Thu, 2023/9/7 13:00-14:00; Symposium room 1), CP16 (Fri, 2023/9/8 15:30-16:30; Symposium room 1)
Gilson, Paul R	103, 155	CP13 (Fri, 2023/9/8 11:00-11:30; Symposium room 1), CP14.1 (Fri, 2023/9/8 14:00-14:30; Symposium room 1)
Gilson, Paul R.	261	CP1.1 (Wed, 2023/9/6 11:45-12:00; Symposium room 1)
Glennon, Elizabeth	227	CP16 (Fri, 2023/9/8 15:30-16:30; Symposium room 1)
Gluhic, Zala	258	S9 (Fri, 2023/9/8 15:00-15:30; Symposium room 1)
Goodwin-Gower, Jeremy	156	CP5 (Wed, 2023/9/6 15:00-16:00; Symposium room 1)
Gordon, Catherine	215	CP12.1 (Fri, 2023/9/8 11:15-11:45; Symposium room 2)
Gordon, Iain	229	CP12 (Fri, 2023/9/8 10:30-11:15; Symposium room 2)
Gordon, Iain	232	CP12.1 (Fri, 2023/9/8 11:15-11:45; Symposium room 2)
Graves, Patricia M	197	CP8 (Thu, 2023/9/7 11:00-11:45; Symposium room 2)
Gray, Darren	178	W9 (Fri, 2023/9/8 15:00-16:30; Workshop room 3)
Gray, Darren J	215	CP12.1 (Fri, 2023/9/8 11:15-11:45; Symposium room 2)
Gregory, Kasimir	132	CP5.1 (Wed, 2023/9/6 16:00-16:30; Symposium room 1)
Gunasekera, Samantha	123	CP5.1 (Wed, 2023/9/6 16:00-16:30; Symposium room 1)
Hall, Luke	189	CP16 (Fri, 2023/9/8 15:30-16:30; Symposium room 1)
Hamer, Rowena	205	CP7 (Thu, 2023/9/7 10:30-11:30; Symposium room 1)
Hayward, Jenni	223	CP14 (Fri, 2023/9/8 13:00-14:00; Symposium room 1)
Hedtke, Shannon M	183	CP8.1 (Thu, 2023/9/7 11:45-12:00; Symposium room 2)
Hedtke, Shannon M.	149	CP15.2 (Fri, 2023/9/8 14:15-14:30; Symposium room 2)
Henshall, Isabelle G.	222	CP4.1 (Wed, 2023/9/6 14:00-14:15; Symposium room 1)

Herath, Anushika	232	CP12.1 (Fri, 2023/9/8 11:15-11:45; Symposium room 2)
Herath, Anushika P.H.M.	229	CP12 (Fri, 2023/9/8 10:30-11:15; Symposium room 2)
Hii, SF	235	CP12.1 (Fri, 2023/9/8 11:15-11:45; Symposium room 2)
Hilton, Elaine	227	CP16 (Fri, 2023/9/8 15:30-16:30; Symposium room 1)
Hines, A	221	CP15.2 (Fri, 2023/9/8 14:15-14:30; Symposium room 2)
Ho, Timothy	147	CP9.2 (Thu, 2023/9/7 14:15-14:30; Symposium room 1)
Hoopes, Jessica	231	CP11 (Thu, 2023/9/7 15:30-16:30; Symposium room 1)
Horner, Leni	207, 184	CP15.1 (Fri, 2023/9/8 14:00-14:15; Symposium room 2), CP15.2 (Fri, 2023/9/8 14:15-14:30; Symposium room 2)
Hudson, Jemma	193	CP6 (Wed, 2023/9/6 15:15-16:30; Symposium room 2)
Huggins, L	236	CP12.1 (Fri, 2023/9/8 11:15-11:45; Symposium room 2)
Huggins, Lucas	107	CP15 (Fri, 2023/9/8 13:30-14:00; Symposium room 2)
Huggins, Lucas G.	115	CP15.2 (Fri, 2023/9/8 14:15-14:30; Symposium room 2)
Hunter, John	231	CP11 (Thu, 2023/9/7 15:30-16:30; Symposium room 1)
Hysa, Alessia	146	CP4.1 (Wed, 2023/9/6 14:00-14:15; Symposium room 1)
Inobaya, Marianette	215	CP12.1 (Fri, 2023/9/8 11:15-11:45; Symposium room 2)
Insisengmay, Bounnaloth	251	W1 (Wed, 2023/9/6 10:30-12:00; Workshop room 3)
Jedličková, L.	265	CP1.2 (Wed, 2023/9/6 12:00-12:05; Symposium room 1)
Jenkins, David	176, 177	CP7.1 (Thu, 2023/9/7 11:30-12:00; Symposium room 1), CP12.1 (Fri, 2023/9/8 11:15-11:45; Symposium room 2)
Jex, Aaron	173, 198, 122	CP1 (Wed, 2023/9/6 10:30-11:45; Symposium room 1), CP1 (Wed, 2023/9/6 10:30-11:45; Symposium room 1), CP13.1 (Fri, 2023/9/8 11:30-11:45; Symposium room 1)
Jex, Aaron R	131, 175, 144, 130	CP1 (Wed, 2023/9/6 10:30-11:45; Symposium room 1), CP1 (Wed, 2023/9/6 10:30-11:45; Symposium room 1), CP2 (Wed, 2023/9/6 11:00-11:45; Symposium room 2), CP5 (Wed, 2023/9/6 15:00-16:00; Symposium room 1)
Johnson, G.J.	244	S3 (Wed, 2023/9/6 15:00-15:15; Symposium room 2)
Jones, Lisa	199	CP11 (Thu, 2023/9/7 15:30-16:30; Symposium room 1)
Jones, M K	240	CP14.1 (Fri, 2023/9/8 14:00-14:30; Symposium room 1)
Jones, Malcolm	169, 172	CP1 (Wed, 2023/9/6 10:30-11:45; Symposium room 1), CP4.2 (Wed, 2023/9/6 14:15-14:35; Symposium room 1)
Jones, Malcolm K.	109	CP16 (Fri, 2023/9/8 15:30-16:30; Symposium room 1)
Jones, Menna	205	CP7 (Thu, 2023/9/7 10:30-11:30; Symposium room 1)
Jonsdottir, T	118	CP14.1 (Fri, 2023/9/8 14:00-14:30; Symposium room 1)
Judd, Jenni	226	W9 (Fri, 2023/9/8 15:00-16:30; Workshop room 3)
Kalthoff, Cecilia	227	CP16 (Fri, 2023/9/8 15:30-16:30; Symposium room 1)

Kaushansky, Alexis	227	CP16 (Fri, 2023/9/8 15:30-16:30; Symposium room 1)
Keatley, Sarah	251	W1 (Wed, 2023/9/6 10:30-12:00; Workshop room 3)
Kelava, S	218	CP7.1 (Thu, 2023/9/7 11:30-12:00; Symposium room 1)
Kelly, Ashton	124	CP1.1 (Wed, 2023/9/6 11:45-12:00; Symposium room 1)
Keokhamphavanh, Boualy	251	W1 (Wed, 2023/9/6 10:30-12:00; Workshop room 3)
Khieu, V	234	CP12 (Fri, 2023/9/8 10:30-11:15; Symposium room 2)
King, A.J.	244	S3 (Wed, 2023/9/6 15:00-15:15; Symposium room 2)
Kirke, A.K.	244	S3 (Wed, 2023/9/6 15:00-15:15; Symposium room 2)
Knight, Breanna	251	W1 (Wed, 2023/9/6 10:30-12:00; Workshop room 3)
Knight, Breanna	136	CP15.1 (Fri, 2023/9/8 14:00-14:15; Symposium room 2)
Konečný, L.	265	CP1.2 (Wed, 2023/9/6 12:00-12:05; Symposium room 1)
Kopp, S R	240	CP14.1 (Fri, 2023/9/8 14:00-14:30; Symposium room 1)
Korman, Rachel	257	S5 (Thu, 2023/9/7 13:00-14:00; Symposium room 2)
Kotze, A C	240	CP14.1 (Fri, 2023/9/8 14:00-14:30; Symposium room 1)
Kyne, P.M.	244	S3 (Wed, 2023/9/6 15:00-15:15; Symposium room 2)
Lai, Keng Heng	228	CP9.1 (Thu, 2023/9/7 14:00-14:15; Symposium room 1)
Laing, Roz	129	CP13.1 (Fri, 2023/9/8 11:30-11:45; Symposium room 1)
Lakvin Fernando, Asela	214	CP5 (Wed, 2023/9/6 15:00-16:00; Symposium room 1)
Lam, Alex	122	CP13.1 (Fri, 2023/9/8 11:30-11:45; Symposium room 1)
Laman, Moses	217	CP9.1 (Thu, 2023/9/7 14:00-14:15; Symposium room 1)
Larkins, Andrew	250	W1 (Wed, 2023/9/6 10:30-12:00; Workshop room 3)
Larkins, Andrew	201	CP12 (Fri, 2023/9/8 10:30-11:15; Symposium room 2)
Larkins, Andrew	119	CP12.2 (Fri, 2023/9/8 11:45-12:00; Symposium room 2)
Lau, Colleen	245	P1 (Wed, 2023/9/6 8:45-10:00; Plenary Room)
Lau, Colleen L	197	CP8 (Thu, 2023/9/7 11:00-11:45; Symposium room 2)
Lee, Joanne	258	S9 (Fri, 2023/9/8 15:00-15:30; Symposium room 1)
Lee, Rogan	190, 127	W7 (Fri, 2023/9/8 10:30-12:00; Workshop room 3), CP12.2 (Fri, 2023/9/8 11:45-12:00; Symposium room 2)
Lehane, Adele	132	CP5.1 (Wed, 2023/9/6 16:00-16:30; Symposium room 1)
Leonardi, Steven Santino	105	CP12.2 (Fri, 2023/9/8 11:45-12:00; Symposium room 2)
Leong, Dickson	261	CP1.1 (Wed, 2023/9/6 11:45-12:00; Symposium room 1)
Liffner, Benjamin	100	CP4.1 (Wed, 2023/9/6 14:00-14:15; Symposium room 1)
Liffner, Benjamin	227	CP16 (Fri, 2023/9/8 15:30-16:30; Symposium room 1)
Lignereux, L	220	CP7.1 (Thu, 2023/9/7 11:30-12:00; Symposium room 1)
Lim, Pailene	206	CP9 (Thu, 2023/9/7 13:00-14:00; Symposium room 1)
Lin, Belinda B	230	W7 (Fri, 2023/9/8 10:30-12:00; Workshop room 3)

Lin, Enmoore	217	CP9.1 (Thu, 2023/9/7 14:00-14:15; Symposium room 1)
Lindner, Scott	227	CP16 (Fri, 2023/9/8 15:30-16:30; Symposium room 1)
Ling, Dawson	103	CP13 (Fri, 2023/9/8 11:00-11:30; Symposium room 1)
Littler, Dene R.	261	CP1.1 (Wed, 2023/9/6 11:45-12:00; Symposium room 1)
Liu, Boyin	100	CP4.1 (Wed, 2023/9/6 14:00-14:15; Symposium room 1)
Liyanage, Tharaka	164	CP15.1 (Fri, 2023/9/8 14:00-14:15; Symposium room 2)
Loukas, Alex	241	CP4.2 (Wed, 2023/9/6 14:15-14:35; Symposium room 1)
Macháček, T.	265	CP1.2 (Wed, 2023/9/6 12:00-12:05; Symposium room 1)
Maguire, Capella S.	143	CP5 (Wed, 2023/9/6 15:00-16:00; Symposium room 1)
Maia, M	236	CP12.1 (Fri, 2023/9/8 11:15-11:45; Symposium room 2)
Maier, Alex	258	S9 (Fri, 2023/9/8 15:00-15:30; Symposium room 1)
Maier, Alexander G.	253	S6 (Thu, 2023/9/7 15:00-15:30; Symposium room 1)
Mao, Emma	182	CP13.2 (Fri, 2023/9/8 11:45-12:00; Symposium room 1)
Marais, Richard	187	CP13.2 (Fri, 2023/9/8 11:45-12:00; Symposium room 1)
Martin, Alynn	205	CP7 (Thu, 2023/9/7 10:30-11:30; Symposium room 1)
Mason, Kylie	230	W7 (Fri, 2023/9/8 10:30-12:00; Workshop room 3)
Mastud, Pragati	238	CP5.1 (Wed, 2023/9/6 16:00-16:30; Symposium room 1)
Mationg, Mary Lorraine	215	CP12.1 (Fri, 2023/9/8 11:15-11:45; Symposium room 2)
Maue, Michael	243	S5 (Thu, 2023/9/7 13:00-14:00; Symposium room 2)
McArthur, Clare	229	CP12 (Fri, 2023/9/8 10:30-11:15; Symposium room 2)
McArthur, Clare	232	CP12.1 (Fri, 2023/9/8 11:15-11:45; Symposium room 2)
McCann, Kirsty	154, 153	CP1.1 (Wed, 2023/9/6 11:45-12:00; Symposium room 1), CP8 (Thu, 2023/9/7 11:00-11:45; Symposium room 2)
McCarthy, James	124	CP1.1 (Wed, 2023/9/6 11:45-12:00; Symposium room 1)
McGee, James	227	CP16 (Fri, 2023/9/8 15:30-16:30; Symposium room 1)
McGuire, Helen	124	CP1.1 (Wed, 2023/9/6 11:45-12:00; Symposium room 1)
McHugh, Connor	181	CP4.2 (Wed, 2023/9/6 14:15-14:35; Symposium room 1)
McHugh, Connor	241	CP4.2 (Wed, 2023/9/6 14:15-14:35; Symposium room 1)
McHugh, Emma	214	CP5 (Wed, 2023/9/6 15:00-16:00; Symposium room 1)
McKay-Demeler, Janina	129	CP13.1 (Fri, 2023/9/8 11:30-11:45; Symposium room 1)
McKew, Genevieve	157	W8 (Fri, 2023/9/8 13:00-14:30; Workshop room 3)
McMorran, Brendan	168	CP9 (Thu, 2023/9/7 13:00-14:00; Symposium room 1)
McMorran, Brendan J.	194	CP9.2 (Thu, 2023/9/7 14:15-14:30; Symposium room 1)
McShane, Lauren	179	W7 (Fri, 2023/9/8 10:30-12:00; Workshop room 3)
Mencke, Norbert	242, 243	S5 (Thu, 2023/9/7 13:00-14:00; Symposium room 2), S5 (Thu, 2023/9/7 13:00-14:00; Symposium room 2)

Miles, Kim	241	CP4.2 (Wed, 2023/9/6 14:15-14:35; Symposium room 1)
Miller, Kate	199	CP11 (Thu, 2023/9/7 15:30-16:30; Symposium room 1)
Morgan, John	225	W8 (Fri, 2023/9/8 13:00-14:30; Workshop room 3)
Mueller, Ivo	217	CP9.1 (Thu, 2023/9/7 14:00-14:15; Symposium room 1)
Muhi, Stephen	230	W7 (Fri, 2023/9/8 10:30-12:00; Workshop room 3)
Mustafa, Bahar E	180	CP3.1 (Wed, 2023/9/6 14:15-14:30; Symposium room 2)
Naung, Myo	217	CP9.1 (Thu, 2023/9/7 14:00-14:15; Symposium room 1)
Nazir, Kashif	141	CP4.2 (Wed, 2023/9/6 14:15-14:35; Symposium room 1)
Nguyen, Loan	125	CP2.1 (Wed, 2023/9/6 11:45-12:00; Symposium room 2)
Nguyen, TT	236	CP12.1 (Fri, 2023/9/8 11:15-11:45; Symposium room 2)
Nie, Xiaoqi	111	CP13.2 (Fri, 2023/9/8 11:45-12:00; Symposium room 1)
Niles, Jacquin	260	P4.1 (Fri, 2023/9/8 9:15-10:00; Plenary Room)
Noordin, Rahmah	171	W8 (Fri, 2023/9/8 13:00-14:30; Workshop room 3)
O'Connor, Suji	216	CP11 (Thu, 2023/9/7 15:30-16:30; Symposium room 1)
O'Donoghue, Finn	264	CP4.2 (Wed, 2023/9/6 14:15-14:35; Symposium room 1)
O'Donoghue, Peter	101	CP7.1 (Thu, 2023/9/7 11:30-12:00; Symposium room 1)
O'Handley, Ryan	219, 220, 212, 221	CP3.1 (Wed, 2023/9/6 14:15-14:30; Symposium room 2), CP7.1 (Thu, 2023/9/7 11:30-12:00; Symposium room 1), CP13 (Fri, 2023/9/8 11:00-11:30; Symposium room 1), CP15.2 (Fri, 2023/9/8 14:15-14:30; Symposium room 2)
Oliveira, Rafael	194	CP9.2 (Thu, 2023/9/7 14:15-14:30; Symposium room 1)
Page, Wendy	263	P4 (Fri, 2023/9/8 8:30-9:15; Plenary Room)
Patankar, Swati	238	CP5.1 (Wed, 2023/9/6 16:00-16:30; Symposium room 1)
Paul, Shatabdi	252	CP12.2 (Fri, 2023/9/8 11:45-12:00; Symposium room 2)
Paun, Andrea	213	CP8 (Thu, 2023/9/7 11:00-11:45; Symposium room 2)
Peck, Ashleigh	138	CP12.2 (Fri, 2023/9/8 11:45-12:00; Symposium room 2)
Pekin, Kaitlin	161	CP9.2 (Thu, 2023/9/7 14:15-14:30; Symposium room 1)
Perkins, N R	239	CP2.1 (Wed, 2023/9/6 11:45-12:00; Symposium room 2)
Peterková, K.	265	CP1.2 (Wed, 2023/9/6 12:00-12:05; Symposium room 1)
Ploeger, E	118	CP14.1 (Fri, 2023/9/8 14:00-14:30; Symposium room 1)
Power, Cecilia	152, 185, 196	CP6 (Wed, 2023/9/6 15:15-16:30; Symposium room 2), CP6 (Wed, 2023/9/6 15:15-16:30; Symposium room 2), CP6 (Wed, 2023/9/6 15:15-16:30; Symposium room 2)
Power, Michelle	199, 231	CP11 (Thu, 2023/9/7 15:30-16:30; Symposium room 1), CP11 (Thu, 2023/9/7 15:30-16:30; Symposium room 1)
Power, Michelle	229	CP12 (Fri, 2023/9/8 10:30-11:15; Symposium room 2)
Power, Michelle	232	CP12.1 (Fri, 2023/9/8 11:15-11:45; Symposium room 2)

Power, Rosemonde	139	CP10 (Thu, 2023/9/7 14:00-14:30; Symposium room 2)
Prasad, Aparna	238	CP5.1 (Wed, 2023/9/6 16:00-16:30; Symposium room 1)
Preston, Sarah	199, 207, 184	CP11 (Thu, 2023/9/7 15:30-16:30; Symposium room 1), CP15.1 (Fri, 2023/9/8 14:00-14:15; Symposium room 2), CP15.2 (Fri, 2023/9/8 14:15-14:30; Symposium room 2)
Primavera, Veronica	227	CP16 (Fri, 2023/9/8 15:30-16:30; Symposium room 1)
Proietti, Carla	124	CP1.1 (Wed, 2023/9/6 11:45-12:00; Symposium room 1)
Rae, Angus	258	S9 (Fri, 2023/9/8 15:00-15:30; Symposium room 1)
Ralph, Stuart	100	CP4.1 (Wed, 2023/9/6 14:00-14:15; Symposium room 1)
Ralph, Stuart	214, 187	CP5 (Wed, 2023/9/6 15:00-16:00; Symposium room 1), CP13.2 (Fri, 2023/9/8 11:45-12:00; Symposium room 1)
Ralph, Stuart	223	CP14 (Fri, 2023/9/8 13:00-14:00; Symposium room 1)
Ralph, Stuart A	204	CP5.1 (Wed, 2023/9/6 16:00-16:30; Symposium room 1)
Raming, Klaus	243	S5 (Thu, 2023/9/7 13:00-14:00; Symposium room 2)
Ramu, Palaniappan	264	CP4.2 (Wed, 2023/9/6 14:15-14:35; Symposium room 1)
Randhawa, I	239	CP2.1 (Wed, 2023/9/6 11:45-12:00; Symposium room 2)
Ray, Maddy	202	CP7.1 (Thu, 2023/9/7 11:30-12:00; Symposium room 1)
Raza, Ali	125	CP2.1 (Wed, 2023/9/6 11:45-12:00; Symposium room 2)
Razook, Zahra	217	CP9.1 (Thu, 2023/9/7 14:00-14:15; Symposium room 1)
Ringwaldt, Elise	205	CP7 (Thu, 2023/9/7 10:30-11:30; Symposium room 1)
Rivory, Phoebe	127	CP12.2 (Fri, 2023/9/8 11:45-12:00; Symposium room 2)
Ross, Kirstin	233	W8 (Fri, 2023/9/8 13:00-14:30; Workshop room 3)
Roy, Pradip	144	CP2 (Wed, 2023/9/6 11:00-11:45; Symposium room 2)
Rug, Melanie	258	S9 (Fri, 2023/9/8 15:00-15:30; Symposium room 1)
Ruscher, Roland	241	CP4.2 (Wed, 2023/9/6 14:15-14:35; Symposium room 1)
Russell, Rhiannon	200	W7 (Fri, 2023/9/8 10:30-12:00; Workshop room 3)
Ryan, Una	123	CP5.1 (Wed, 2023/9/6 16:00-16:30; Symposium room 1)
Saliba, Kevin	111, 140	CP13.2 (Fri, 2023/9/8 11:45-12:00; Symposium room 1), CP14.1 (Fri, 2023/9/8 14:00-14:30; Symposium room 1)
Samarawickrama, Gangi R.	109	CP16 (Fri, 2023/9/8 15:30-16:30; Symposium room 1)
Santos, Jaever	224	CP7 (Thu, 2023/9/7 10:30-11:30; Symposium room 1)
Santos, John Harvey	125	CP2.1 (Wed, 2023/9/6 11:45-12:00; Symposium room 2)
Saunders, T.M.	244	S3 (Wed, 2023/9/6 15:00-15:15; Symposium room 2)
Schmitz-Linneweber, Christian	258	S9 (Fri, 2023/9/8 15:00-15:30; Symposium room 1)
Schneider, Molly P.	261	CP1.1 (Wed, 2023/9/6 11:45-12:00; Symposium room 1)
Scholz, Tomáš	256	P3 (Thu, 2023/9/7 17:00-17:45; Plenary Room)
Shami, Gerald J.	100	CP4.1 (Wed, 2023/9/6 14:00-14:15; Symposium room 1)

Shanley, Harrison	117	CP3 (Wed, 2023/9/6 13:00-14:15; Symposium room 2)
Sheorey, Harsha	179	W7 (Fri, 2023/9/8 10:30-12:00; Workshop room 3)
Shield, Jennifer	159	W9 (Fri, 2023/9/8 15:00-16:30; Workshop room 3)
Shuaib, Mohammad Jamiu	150	CP9.2 (Thu, 2023/9/7 14:15-14:30; Symposium room 1)
Siddiqui, Ghizal	100	CP4.1 (Wed, 2023/9/6 14:00-14:15; Symposium room 1)

2023 Annual Conference of the Australian Society for Parasitology Inc.

September 5-8, DoubleTree by Hilton Hotel Esplanade Darwin, NT, Australia

Conference Organisation

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Maxine Smith, James Cook University
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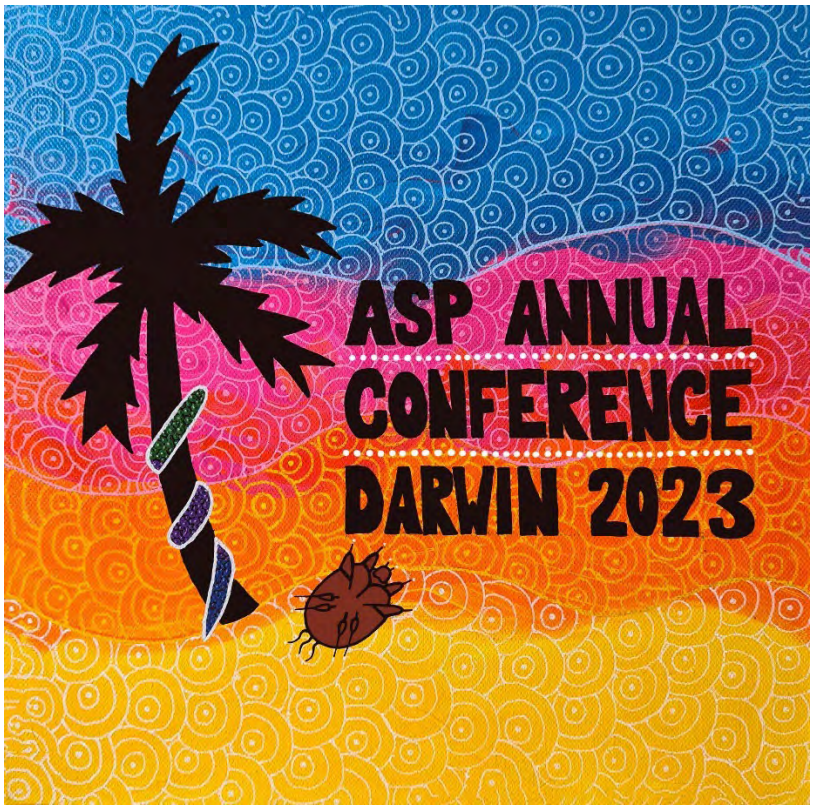
Conference Logo



Our wonderful conference logo was designed by Jayde Hopkins, an indigenous artist based in Darwin, Northern Territory. Jayde is a proud Gurindji and Woolwonga woman born and raised in the NT. Jayde is studying a Bachelor of Biological Sciences with aims to become an infectious disease researcher and is passionate about science communication and loves using art as a teaching tool. As an artist Jayde specialises in vibrant colours, utilising dot painting and more contemporary techniques to paint the natural world. Since 2020 Jayde has been creating artwork with her business Nawula Almaren Aboriginal Art. Jayde spoke to Deb Holt, the 2023 ASP Conference co-chair, about art.

Jayde describes the story behind the painting:

"After looking at previous conference logos, my aim for this painting was to marry place with parasite. I wanted to include elements of the Top End with parasites relevant to the area. In the painting background I have included an iconic Territory sunset with rich, vibrant colours. In the foreground, to the left of the wording, is a local helminth (*Strongyloides stercoralis*) wrapped around a tropical palm tree. (Size not to scale – but could you imagine!). Crawling from the palm to the words detailing the conference is a scabies mite, ready to burrow its way into our hearts…or skin."

"Through my work at Menzies School of Health Research this year, I have been undertaking a major project entitled, 'Menzies Art Gallery of Scientific Discovery'. I've created a series of paintings based on new discoveries by Menzies researchers. This has been an incredible opportunity as a scientist and artist, I was able to meet most of the researchers and work directly with the novel organisms in the lab, growing bacteria on agar and Gram staining for reference images to inform my artwork. I was honoured when my painting of *Staphylococcus argenteus* was chosen for the cover image of the October 2022 edition of Microbiology Australia."

And people can view Jayde's other work in Darwin and online!

"Yes! If you would like to visit in person, I have a few paintings displayed for sale at Saltwater @ Bundilla, the cafe/restaurant located at the Museum and Art Gallery of the Northern Territory (19 Conacher Street, The Gardens). Otherwise to view my full collection online you can check out my website " https://www.nawula-almaren-aboriginal-art.com.au/

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Virbac Australia is one of the largest subsidiaries of the Virbac group. In Australia, Virbac employs around 260 personnel covering R&D, Manufacturing, and Sales and Marketing. Virbac Australia has an annual sales turnover in excess of A$100 Million.

Research and Development in Australia

Virbac Australia R&D focuses on ruminant parasiticides and vaccines but is also interested in other areas such as nutrition, pain and welfare. Virbac Australia invests in research, development and licensing in order to bring new products to the Australian market. Virtually all R&D investment by Virbac Australia involves local clinical trials.

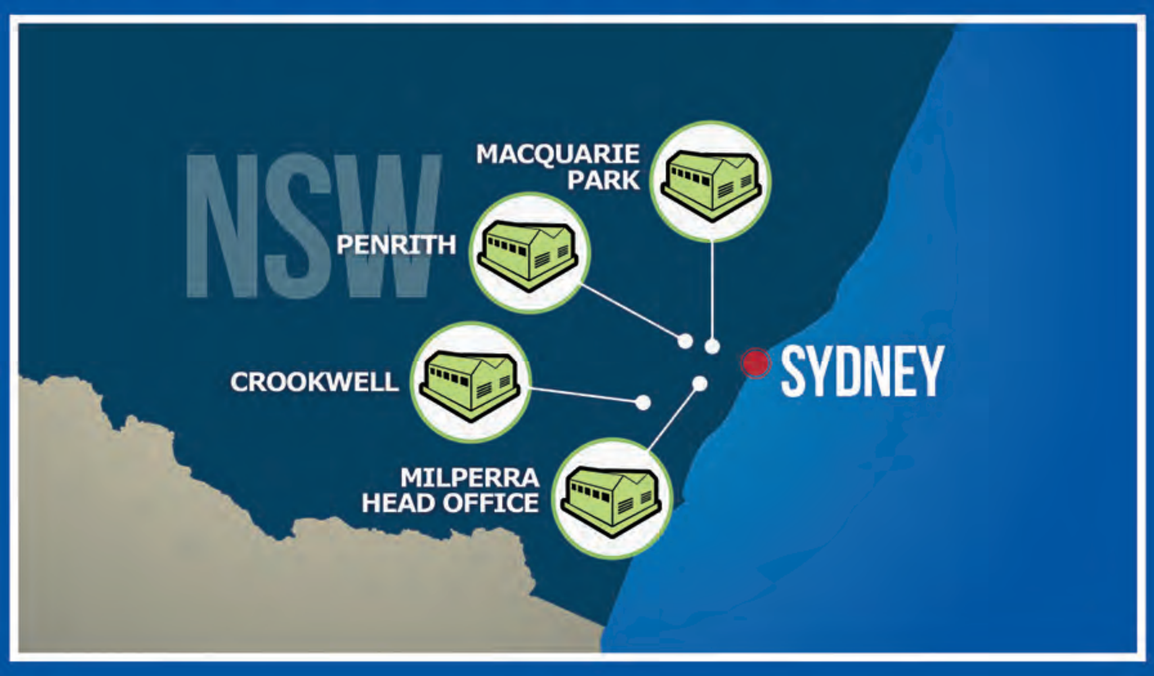
Innovative ideas originating in Australia which are relevant to other animal health segments, such as companion animals, may be developed in other Virbac R&D centres. This depends on the specialised expertise required for each project.

Virbac is one of the few animal health companies that have both Manufacturing and Research & Development facilities in Australia.

Manufacturing in Australia

As a reflection of animal diversity, veterinary drugs are produced in various forms – including oral tablets and pastes, dermatological and parasiticide products specially formulated for topical application, medicated in-feed pellets, sterile injectable vaccines, slow-release implants, antibiotics and other pharmaceutical agents. This broad range of pharmaceutical dosage forms requires specific production facilities.

Virbac Australia's three production sites cater for a range of diverse manufacturing requirements: the Crookwell site in rural NSW manufactures Rilexine™ antibiotic tablets for cats and dogs, Virbamec™ cattle and sheep parasiticides, the Equimax™ horse-wormer range and a number of other product lines; the Virbac plant at Penrith in Sydney manufactures the SingVac™ and Websters™ cattle and sheep vaccines and the Cydectin™ cattle and sheep parasiticide products; Macquarie Park, also in Sydney, is the site of production of the Suprelorin™ and Ovuplant™ slow-release implants for reproductive control in various species. Virbac is continuing to invest in and enhance the process capability of all its production facilities so that new and improved products can be made available to the animal health market.



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For information about Post-Doctoral Fellowships at New England Biolabs please visit: **https://www.neb.com/about-neb/careers**

2023 ASP Conference Mini Programme
[Yellow Highlight = ASP Student Presenter]

Time	Tuesday 5 Sep	Wednesday 6 September			Thursday 7 September			Friday 8 September		
7:00-8:30		Student Breakfast Event								
8:30-10:00	ASP Council Meeting	Introduction: Deb Holt **Welcome to Country** ***P1 One Health Plenary Lectures*** (Ballroom) Chair: Amanda Ash Banchob Sripa Colleen Lau			***BMM 2023 Bancroft Mackerras Medal Award and Lecture*** ***P2 Plenary Lectures*** *(Ballroom)* Chair: Rebecca Traub ***IJP Lecturer*** Matt Grigg			***P4 Plenary Lectures*** *(Ballroom)* ***Strongyloides Plenary Lecture 1*** Chair: Jenni Judd Wendy Page ***IJP:DDR Invited Lecturer*** *(Ballroom)* Chair: Kevin Saliba Jacquin Niles		
10:00 – 10:30		Morning Tea			Morning Tea			Morning Tea		
10:30 – 12:00		**W1 One Health Workshop** Chair: Mal Jones Mal Jones, Amanda Ash, Darren Gray, Rebecca Traub, Andrew Larkins	**CP1 CP1.1 CP1.2 Omics & Informatics** Chair: Katja Fischer 15 min: 131, 175, 173, 169, 198 5 min: 154, 124, 261	**S1 CP2 CP2.1 Livestock sponsored by Virbac** Chair: Aleta Knowles 30 min Invited: Ala Tabor 15 min: 144, 113, 134	**W4 Bioinformatics Workshop**	**CP7 CP7.1 Biodiversity & Wildlife** Chair: Michelle Power 15 min: 205, 211, 224, 112, 5 min: 101, 218, 110, 220, 202, 176	**S4 CP8 CP8.1 Epidemiology & Diagnostics** Chair: Kamil Braima 30 min Invited: Sarah Auburn	**W7 Strongyloides Workshop** Chair: Harsha Sheorey 190, 200, 230, 179	**S7 CP13 CP13.1 CP13.2 Drugs & Drug Resistance** Chair: Benedikt Ley Invited 30 min: Kamala Ley-Thriemer 15min: 212, 103	**CP12 CP12.1 CP12.2 Zoonoses and Public Health** Chair: Narelle Dybing 15 min: 229, 234, 201 5 min: 215, 235, 232, 177, 236, 195

			3 min: 265	5 min: 125, 192, 239			15 min: 213, 197, 153 5 min: 151, 183, 102		5 min: 122, 129, 135 3 min: 111, 174, 187, 182, 166	3 min: 127, 119, 138, 105, 252
12:00-13:00		Lunch			Lunch			Lunch		
13:00-14:30	Registration	**W2 One Health Workshop** Chair: Darren Gray Vito Collelo, Amanda Ash, Andrew Thompson	**S2 CP4 CP4.1 CP4.2 Immunology & Pathogenesis** Chair: Brendan McMorran 30 min Invited: Rintis Noviyanti 15 min: 120, 126 5 min: 100, 146, 222 3 min: 181, 172, 241, 141, 106, 264	**CP3 CP3.1 Livestock sponsored by Virbac** Chair: Aleta Knowles 15 min: 104, 208, 163, 117, 114 5 min: 188, 219, 180	**W5 Bioinformatics Workshop**	**CP9 CP9.1 CP9.2 Immunology & Pathogenesis** Chair: Steven Kho 15 min: 116, 168, 128, 206 5 min: 217, 209, 228 3 min: 150, 147, 161, 194, 158,	**S5 CP10 Veterinary Parasitology sponsored by Vetoquinol** Chair: Clare Anstead 30 min Invited: Norbert Mencke 30 min Invited: Rachel Korman 15 min: 139, 162	**W8 Strongyloides Workshop** Chair: Catherine Gordon 225, 171, 157, 233	**CP14 CP14.1 Drugs & Drug Resistance** Chair: Brad Sleebs 15 min: 133, 191, 142, 223 5 min: 118, 140, 148, 108, 155, 240	**S8 CP15 CP15.1 CP15.2 Companion Animals sponsored by Elanco** Chair: Liisa Ahlstrom 30 min Invited: Rebecca Traub 15 min: 107, 203 5 min: 136, 207, 164 3 min: 115, 121, 184, 149, 221
14:30-15:00		Afternoon Tea			Afternoon Tea			Afternoon Tea		

15:00-16:30		**W3 One Health Workshop** Chair: Rebecca Traub Roundtable Discussion	**CP5 CP5.1 Protozoan Biology** Chair: Paul Gilson 15 min: 130, 214, 143, 156 5 min: 132, 165, 204, 123, 237, 238	**S3 CP6 Aquatic** Chair: Di Barton 15 min Invited: Amy Kirk 15 min: 152, 196, 185, 193, 160	**W6 Bioinformatics Workshop**	**S6 CP11 Education & Outreach** Chair: Sarah Preston 30 min Invited: Alex Maier 15 min: 216, 231, 210, 199	**W9 Strongyloides Workshop** Chair: Kirsten Ross 159, 170, 226, 178	**S9 CP16 Microscopy** Chair: Danny Wilson 30 min Invited: Melanie Rug 15 min: 189, 109, 227, 145
16:30-17:00		Pre-AGM Prosecco break			Pre-Plenary Prosecco break		Pre-Plenary Prosecco break	
17:00-17:30		**ASP Presidential Address**			***P3 IJP:PAW Lecturer*** *(Ballroom)* Chair: Andrew Thompson		***P5 Strongyloides Plenary Lecture 2*** *(Ballroom)* Chair: Wendy Page	
17:30-17:45		**2023 Annual General Meeting of the ASP**			Tomas Scholz		Zeno Bisoffi **Award of Student Prizes**	
17:45-19:00					***ASP Public Outreach Event from 630pm @ Bustard Town, 15 Knuckey Street***		*Free time*	
19:00-19:30	**Welcome Reception 700pm-900pm**						**Conference Dinner 700pm-11pm**	
19:30-		***Student Social Evening***						