New Zealand Society for Parasitology

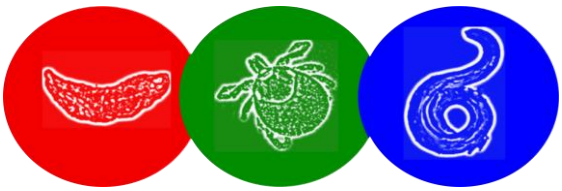
50th Conference
31st May – 1st June 2023
&
PAD Advisory day
2nd June 2023

Conference hosted by:

toitū OTAGO SETTLERS MUSEUM

PAD hosted by:

agresearch
āta mātai, mātai whetū



The society thanks our amazing 2023 sponsors for their generous support:

Conference programme

DAY 1
WEDNESDAY 31st MAY
Toitu Otago Settlers Museum

Time	Speaker and talk
12:30 PM	Registration opens @ Toitu Otago Settlers Museum – 31 Queens Gardens, Dunedin
1:00 PM	Welcome
	SESSION 1 – Sponsored by Elanco
1:10 PM	**KEYNOTE: Michelle Taylor** – The ectoparasite *Varroa destructor* and why honey bees need our help
1:50 PM	**Robert Poulin** – What's in a name? Taxonomic and gender biases in the etymology of new species names
2:10 PM	**Bronwen Presswell** – Short and sweet: an analysis of the length of parasite species names
2:30 PM	AFTERNOON TEA – Sponsored by PGG Wrightson
	SESSION 2
3:00 PM	**Simão Correia** – Host-parasite interactions: new insights on trematode impacts on their bivalve hosts
3:15 PM	**Laura Saywell** – Investigating the role of extracellular vesicles in *in vitro* growth of *Cryptosporidium parvum*
3:30 PM	**Xuhong Chai** – Decay of parasite community similarity with host phylogenetic and geographic distances among deep-sea fish (grenadiers)
3:45 PM	**Jerusha Bennett** – Parasites of concern in our coastal seabirds
4:00 PM	**Priscila Salloum** – Incorporating the microbiome dimension in host-parasite interactions
4:15 PM	**Daniela de Angeli Dutra** – Revealing the drivers of parasite diversity: territorial and biodiversity hosts raise haemosporidian regional diversity worldwide
4:30 PM	**Kyle Shanebeck** – Semi-aquatic mustelids as sentinels for parasites of zoonotic concern, and the pathobiology of larval Alariasis in river otter and mink of Western Canada
4.45 PM	**Bridget Lamont** – Tracking and Treatng *Cryptosporidium* in Aotearoa
5:00 PM	Day 1 close
6:00 PM	Arrive at **Staff Club**, University of Otago (See Page 6 for dinner details) sponsored by Elanco
6:30 PM	Entrée served
7:00 PM	Buffet served
8:00 PM	Quiz – you are a parasite; find your way through the life cycle
9:00 PM	Student prize
9:30 PM	Bar closes
10:00 PM	Depart

Conference programme

DAY 2
THURSDAY 1st JUNE
Toitu Otago Settlers Museum

Time	Speaker and talk
8:30 AM	Registration opens @ Toitu Otago Settlers Museum – 31 Queens Gardens, Dunedin
8:55 AM	Housekeeping
	SESSION 3 – Sponsored by Donaghys
9:00 AM	**KEYNOTE: Emma Chen**– It is in their Blood - a Tale of Avian Malaria in Yellow-eyed Penguins/Hoiho
9:40 AM	**KEYNOTE: Michelle Taylor** – The changing focus of controlling *Varroa destructor*
10:00 AM	**Augusto Simoes-Barbosa** - 2024 NZSP/ASP-ICAP: across the ditch and to the world
10:15 AM	MORNING TEA – Sponsored by Nexan Vetmed
	SESSION 4 – Sponsored by Alleva
10:45 AM	**Augusto Simoes-Barbosa** – In attention to holistic relationships between the host, parasite, and the microbiome: the case of *Trichomonas vaginalis*
11:00 AM	**Bruce Russell** – Update on Zoonotic Malaria
11:15 AM	**Sean Daly** – Spot-On Drenches in Sheep for Control of Gastrointestinal Parasites and Lice
11:30 AM	**Kathryn McRae** - Phenotypes for host resistance to gastrointestinal nematodes
11:55 AM	**Andrew Dowling** – Highlights from my PhD study on the effects of Fasciola hepatica in dairy cattle
12:25 PM	LUNCH – Sponsored by Elanco
	SESSION 5 – Sponsored by BI
1:30 PM	**Colin McKay** – Sheep lice – the forgotten parasite?
2:05 PM	Closing remarks and thanks from us!
2:10 PM	Day 2 close

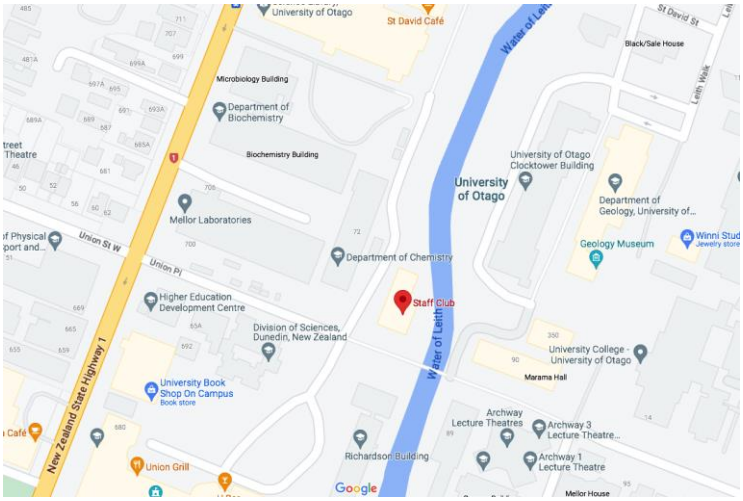
PAD Advisory Day

DAY 3
FRIDAY 2nd JUNE
AgResearch Mosgiel

Time	
8:30-9:00 AM	Arrive at Cullen Room @ AgResearch (Invermay) 176 Puddle Alley, Mosgiel 9092 CLICK HERE FOR LOCATION
	SESSION 1
9:00-9:45 AM	**Bill Pomroy** - Combination theory – Putting it in perspective
9:45-10:30 AM	**Andrew Dowling and Trevor Cook** – Options for treating adult cattle for internal and external parasites
10:30-11:00 AM	MORNING TEA – Sponsored by Zoetis
	SESSION 2
11:00-12:30 PM	**Andy Greer** – Practical use of TST
12:30-1:15 PM	LUNCH – Sponsored by PGG Wrighsons
	SESSION 3
1:15-1:45 PM	**Trevor Cook** – Monitoring lambs on a clean feed – a pilot
1:45-2:45 PM	**Emma Dangen, Anne Ridler, Trevor Cook, Andy Greer and Bryon Vollweiller** – Farmer motivation for making change on farm
2:45-3:15 PM	AFTERNOON TEA – Sponsored by Alleva
3:15-3:45 PM	**Greg Mirams** - FECPAK data mining
3:45 PM	Day 3 close

Conference Dinner

UNIVERSITY OF OTAGO
STAFF CLUB
Te Wharekai o kā Kaimahi



Location: Otago Staff Club CLICK HERE FOR LOCATION

6:00 PM	Arrive at Otago Staff Club
6:30 PM	Entrée served
7:00 PM	Buffet served
8:00 PM	Quiz – you are a parasite; find your way through the life cycle
9:00 PM	Student prize
9:30 PM	Bar closes
10:00 PM	Depart

Dinner and drinks are sponsored by Elanco

Buffet menu

Entrée
Salmon tartar, whipped feta, smoked spiced paprika oil, lavosh, roquette

Main
Manuka smoked lamb rump with roast cauliflower puree & mint pistachio pesto (GF)
Harissa chicken breast with thyme and lemon mousse & saffron beurre blanc (GF)
Goats cheese feta, cos, roasted pear & pecan salad with lime and avocado oil (GF)
Fresh beans, broccoli, spinach & spring onions (GF, V+)
Roast cashew and root vegetable korma (V)
Cumin scented potato salad (V)

Dessert
Chocolate torte & fresh fruit (V)
Freshly brewed coffee, selection of teas and herbal infusions

Our 2023 Keynote Speakers

Michelle Taylor has been at the forefront of varroa research for the past 20 years. She will be giving two talks, one 40min talk to start the conference off at 1:10pm on Wednesday 31st May and another at 9:40am on Thursday 1st June

The ectoparasite *Varroa destructor* and why honey bees need our help
Michelle Taylor
Day 1 – Wednesday 31st May @ 1:10pm

The changing focus of controlling *Varroa destructor*
Michelle Taylor
Day 2 – Thursday 1st June @ 9:40am

Scan this QR code for more…

Plant & Food Research
Rangahau Ahumāra Kai

Varroa image from Wikipedia

Our 2023 Keynote Speakers

Emma Chen is a wildlife veterinarian working at Dunedin's wildlife hospital. Her daily roles are to provide triage and high-standard care for native New Zealand Wildlife, many of which are highly endangered.

It is in their Blood – a Tale of Avian Malaria in Yellow-eyed Penguins/Hoiho

Emma Chen

Day 2 – Thursday 1st June @ 9:00am

Avian malaria is caused by the vector-borne haemoparasite Plasmodium spp., which affects nearly all taxa of birds worldwide, and has caused significant impact on populations that have not co-evolved with the protozoan organism. Penguins seem to be more susceptible to the disease.

Yellow-eyed penguins / Hoiho (*Megadyptes antipodes*) are nationally endangered and predicted to become extinct on mainland New Zealand in the next few decades. Infectious diseases including avian malaria play a significant role in their ongoing decline. Dunedin Wildlife Hospital (DWH) has been involved with conservation efforts of Hoiho since opening in January 2018.

Avian malaria has been reported in Hoiho since the 1940s, however only sporadic deaths were recorded prior to the 2017/2018 season. Significant flooding and favourable weather conditions for mosquito breeding in 2017/2018 led to the worst recorded malaria season for Hoiho, with 29 confirmed deaths due to this disease. Climate change, the associated surge in vector availability and reduced host fitness due to stress from starvation or injuries are possible causes for the increased number of cases in recent years.

This presentation will give a brief overview of the life cycle of Plasmodium spp., the disease it causes, and the challenges in managing avian malaria in the endangered Hoiho population. A few additional weird and wonderful clinical cases involving parasites of native wildlife will also be included.

Scan this QR code to go to the Wildlife Hospital Website!

Hoiho image from NZ Birds Online

Presentation Abstracts

What's in a name? Taxonomic and gender biases in the etymology of new species names

Robert Poulin, Cameron McDougall and Bronwen Presswell

Department of Zoology, University of Otago, Dunedin, New Zealand

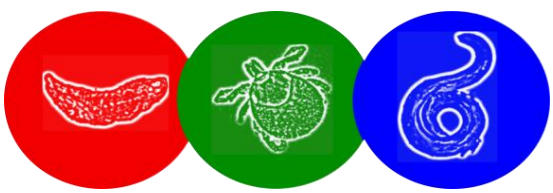
As our inventory of Earth's biodiversity progresses, the number of species given a Latin binomial name is also growing. While the coining of species names is bound by rules, the sources of inspiration used by taxonomists are an eclectic mix. We investigated naming trends for nearly 2900 new species of parasitic helminths described in the past two decades. Our analysis indicates that the likelihood of new species being given names that convey some information about them (name derived from morphology, host, or locality of origin) or not (named after an eminent scientist, or for something else) depends on the higher taxonomic group to which the parasite or its host belongs. We also found a consistent gender bias among species named after eminent scientists, with male scientists being immortalised disproportionately more frequently than female scientists. Finally, we found that the tendency for taxonomists to name new species after a family member or close friend has increased over the past twenty years. We end by offering suggestions for future species naming, aimed at honouring the scientific community's diversity and avoiding etymological nepotism and cronyism, while still allowing for creativity in crafting new Latin species names.

Short and sweet: an analysis of the length and parasite species names

Robert Poulin, Daniela de Angeli Dutra, Bronwen Presswell

Department of Zoology, University of Otago, Dunedin, New Zealand

In its advice to taxonomists, the International Commission on Zoological Nomenclature(ICZN) recommends that scientific species names should be compact, memorable, and easy to pronounce. Using a dataset of over 3000 species of parasitic helminths described in the past two decades, we investigate trends in the length of Latin specific names (=epithets) chosen by taxonomists. Our results reveal no significant temporal change in the length of species epithets as a function of year of description, with annual averages fluctuating around the overall average length of just over 9 letters. We also found that lengths of species epithets did not differ among the various host taxa from which the parasites were recovered. However, acanthocephalan species have been given longer species epithets than other helminth taxa. Finally, although species epithets were shorter than genus names for three-quarters of the species in our dataset, we detected no relationship between the length of species epithets and that of genus names across all species included, i.e., there was no evidence that shorter species epithets are chosen to compensate for long genus names. We conclude by encouraging parasite taxonomists to follow the recommendations of the ICZN and choose species epithets that are, as much as possible, compact and easy to remember, pronounce and spell.



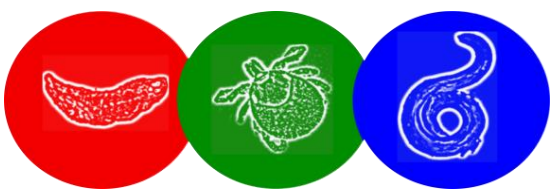
Presentation Abstracts

Host-parasite interactions: new insights on trematode impacts on their bivalve hosts

Simão Correia, Sergio Fernández-Boo, Manuel Vera, Robert Poulin, Luísa Magalhães

University of Aveiro, Portugal

Bivalves are important resources for coastal communities and ecosystems, providing both economic and ecological benefits. However, in many coastal systems where bivalves have a prominent ecological influence (as ecosystem engineers for instance) and represent an important source of income to local communities, the natural stocks have been negatively impacted by overfishing, ineffective management, environmental degradation, and emergent diseases. The role of trematode parasites in this stock decrease is often disregarded due to lack of overt signs of disease. This is true for final and second intermediate hosts (bivalves included) but not for the first intermediate host (usually a bivalve), where infection can lead to castration or death. Nevertheless, sub-lethal effects in the final and second intermediate hosts are likely able to have cascading impacts on communities and ecosystems with unpredictable economic and ecological losses. Using the European edible cockle (Cerastoderma edule) as trematode first intermediate host model and the New Zealand cockle (Austrovenus stutchburyi) as second intermediate host model, the present study aimed to identify the impacts of trematode infection on individual hosts and on offspring gene expression, as well as the wider ecosystem impacts. Innovative methodologies, such as comparative transcriptomics and epigenetics were applied to both models, sampling the haemolymph (for RNA extraction and analysis of gene expression) and digestive gland or foot (for DNA extraction and analysis of methylation) to study the bivalves' immune system and transgenerational impacts, respectively. Preliminary results identified differences in gene expression and methylation levels between infected cockles (with the trematode Bucephalus minimus) and non-infected individuals. Similar results were observed for the offspring of infected individuals, indicating inheritance of information across generations. The results from both species can be used to compare the potential global impacts of trematode parasite outbreaks on bivalve hosts and ecosystem functioning, assisting the development of novel modelling approaches to control disease outbreaks.



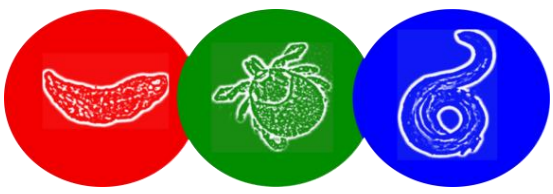
Presentation Abstracts

Investigating the role of extracellular vesicles in *in vitro* growth of *Cryptosporidium parvum*

Laura Saywell, Bridget Lamont, Professor Bruce Russell & Dr Rémy Mushin

Cryptosporidium Research Team, University of Otago

Globally, diarrhoeal disease is a significant cause of mortality, particularly in children under two years of age. There are many aetiologic factors responsible for diarrheal infections including the apicomplexan parasite *Cryptosporidium*. In developing countries, *Cryptosporidium* is particularly deadly amongst HIV-positive patients and children younger than five years. In Aotearoa, *Cryptosporidium parvum* thrives amongst our vast livestock industry, causing seasonal human outbreaks that coincide with lambing and calving seasons. Unfortunately, there is no vaccine for cryptosporidiosis and current treatments are only effective in immunocompetent individuals. This lack of efficacious treatments is partially due to neglect in *Cryptosporidium* research, which has been heavily limited by the lack of a continuous *in vitro* culture system. Despite these obstacles, recent advances of *in vitro* culture systems have unlocked the ability to explore the *C. parvum* life cycle and behaviour in a host cell-free environment. One area that is yet to be investigated is how *C. parvum* communicates with other parasites and host to coordinate complex events triggered at specific stages of the life cycle. Extracellular vesicles have been identified as cell-to-cell communication vehicles in many organisms, including *Cryptosporidium*'s close relatives, *Plasmodium* and *Toxoplasma*. However, it is currently unknown if *C. parvum* produces extracellular vesicles, and if these extracellular vesicles have an effect on the various life cycle stages of this parasite. In our lab, we hypothesize that *C. parvum* does produce extracellular vesicles, and we intend to use a host cell-free culture system to isolate and characterize these extracellular vesicles. We also intend to determine the effect of *C. parvum*-derived extracellular vesicles on stages of the parasite's life cycle. Additionally, we will isolate extracellular vesicles from mammalian host cells, HCT-8, to investigate any potential effects directed by HCT-8-derived extracellular vesicles on the *C. parvum* life cycle. This work will enhance our understanding on the life cycle of *C. parvum*.



Presentation Abstracts

Decay of parasite community similarity with host phylogenetic and geographic distances among deep-sea fish (grenadiers)

Xuhong Chai, Jerusha Bennett, Robert Poulin

Department of Zoology, University of Otago, Dunedin, New Zealand

Parasite community studies are an important aspect of community ecology, having contributed much knowledge about patterns and processes of species assembly in nature. However, our understanding of which macro- ecological and evolutionary processes have shaped parasite communities (i.e., assemblages of different parasite species within the same host) comes from only few host-parasite systems. A thorough understanding of these concepts requires a much more comprehensive investigation of a broader range of host-parasite systems from various ecosystems. The present study focuses on New Zealand grenadiers (deep-sea fish of the family Macrouridae) and their endoparasites on the Chatham Rise, a model system for deep-sea parasitological studies not previously investigated in New Zealand.
The overarching aim of this project was to test the effects of host phylogeny and geography on the structure of endoparasite communities in grenadiers. We hypothesised that host phylogeny determined the presence/absence of parasites in different fish species, whereas both host phylogeny and geographical distances among sampled populations affected the prevalence and mean abundance of parasites. The study yielded several important findings. First, grenadiers from the Chatham Rise harbored a surprisingly high diversity of digeneans, cestodes and nematodes, with different species of grenadiers having different parasite assemblages. Second, in line with the main aim, we found that similarity in presence/absence of parasites was only affected by the phylogenetic relatedness among grenadier species, whereas both phylogenetic distance among grenadiers and geographic distance between sample locations influenced the similarity of parasite communities based on prevalence and mean abundance. Most importantly, this study highlighted the significant effect of host phylogeny in shaping their parasite assemblages, a factor previously neglected in studies of deep-sea systems.

Parasites of concern in our coastal seabirds

Jerusha Bennett, Bronwen Presswell, Robert Poulin

Department of Zoology, University of Otago, Dunedin, New Zealand

Kia ora NZSP members! At most previous NZSP conferences, members of our Parasitology Research Group from the University of Otago advocate for the inclusion of parasites in ecological research for their crucial roles played in the structure and functioning of healthy natural systems. In doing so, over the last few years we have also identified some parasites we believe to have high potential to either cause disease or death to their hosts. Therefore, instead of a talk about an ecosystem-level approach to the importance of parasites, this year I'll kōrero about the specifics of some newly discovered parasites infecting a range of New Zealand seabirds. First, I'll introduce an eye parasite that infects over 50% of all gull individuals in Otago. Then, I'll talk about a new species of nematode we found in the lungs of various penguin species. Lastly, I'll introduce a problematic parasite we recently re-discovered in New Zealand for the first time since it caused a mass mortality event of an estimated over 200,000 petrels in the 1970s. What does the presence of these parasites mean for the future of seabirds in New Zealand?

Presentation Abstracts

Incorporating the microbiome dimension in host-parasite interactions

Priscila Salloum, Fátima Jorge, Robert Poulin

Department of Zoology, University of Otago, Dunedin, New Zealand

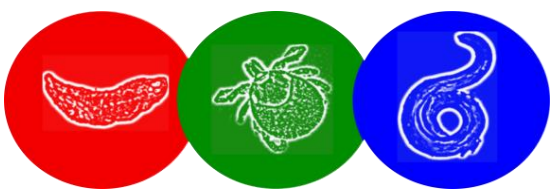
We often consider the eco-evolutionary dynamics of host-parasite interactions as a two-racers contest: on the one hand, natural selection favours hosts resistant to parasitic infections; on the other hand, parasites that can bypass such resistance have a fitness advantage. However, like most living organisms, microbes associate with both hosts and parasites, potentially modulating host defense and parasite virulence and transmission. Incorporating the microbiome dimension in this two- player evolutionary game is incredibly complex, but it starts by characterising the microbiome of both hosts and their parasites. In this short talk, I will present the tale of four parasitic trematodes that use the same mud snail species as an intermediate host. Differences in the microbiota composition and bacterial abundance among the four trematodes and between trematodes and their mud snail host support the hypothesis that parasites do not simply acquire microbes randomly from a pool available in their environment (or in their host). Ultimately, microbe-parasite associations that may favour microbial transmission (and evolution) are most likely tightly intertwined in the host-parasite evolutionary race.

Revealing the drivers of parasite diversity: territorial and biodiverse hosts raise harmosporidian regional diversity worldwide

Daniela de Angeli Dutra

Department of Zoology, University of Otago, Dunedin, New Zealand

Biodiversity varies across the world and is influenced by multiple factors, such as environmental stability and past historical events (e.g., Panama Isthmus). At same time, organisms with unique life-histories (e.g., parasites) are subject to unique selection pressures that structure their diversity patterns. Parasites represent one the most successful life-strategies, impacting directly and indirectly the ecosystem by cascading effects on host fitness and survival. Here, I focused on a highly diverse, prevalent, and cosmopolitan group of parasites (avian haemosporidians) to investigate the main drivers of regional parasite diversity on a global scale. To do so, I compiled data from four global datasets on (i) avian haemosporidian (malaria and malaria-like) parasites, (ii) bird species richness, (iii) avian functional traits, and (iv) climate data. Then, using generalized mixed models, I evaluated potential drivers of haemosporidian diversity. I found that haemosporidian diversity is driven by both host regional diversity and functional traits, and by environmental conditions. In other words, parasite diversity increased with increasing host richness and higher numbers of resident and territorial birds. Further, greater temperature seasonality was also positively correlated with parasite diversity. Hence, regions harboring the greatest resident/territorial avian diversity (e.g., neotropics) and/or higher temperature seasonality (e.g., North America) generally harbor the highest diversity of haemosporidian parasites. Overall, I demonstrated that haemosporidian parasite diversity is intrinsically associated with their hosts' diversity and functional traits.

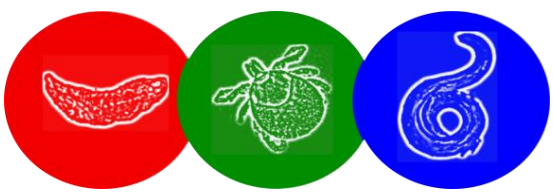


Semi-aquatic mustelids as sentinels for parasites of zoonotic concern, and the pathobiology of larval Alariasis in river otter and mink of Western Canada

KM Shanebeck, P Thomas, S Green, C Lagrue

University of Alberta, Canada

Semi-aquatic mustelids are ideal sentinels for freshwater and marine ecosystems. As mesocarnivores that dominate aquatic ecosystems, they are at high risk for infection by a variety of parasites and are potential vectors for terrestrial predators and scavengers. Studies investigating the populations of North American river otter (*Lontra canadensis*) and mink (*Neogale vison*) are limited, though they are integral parts of riparian ecosystems and are commercially trapped in Canada. Similarly, little is known about wild populations of zoonotic parasites of concern in Canada and research is limited for species associated with sublethal or subclinical effects. This study investigated the parasitic populations of river otter and mink provided by licensed fur trappers in Alberta and British Columbia, Canada. Necropsies revealed parasites of concern both for wildlife and human populations. Most prevalent were infections of mesocercarial *Alaria mustelae* (Trematoda: Diplostomidae) which infected over 70% of animals sometimes concurrently with infection by adults, showing mink and otter to both be competent definitive as well as paratenic hosts. Mesocercaria were associated with chronic peritonitis likely due to ectopic migration of the larval parasites and moderate to severe multisystemic inflammation and fibrosis which likely contributed to some degree of morbidity and suboptimal nutritional condition. Infections by mesocercaria of *A. alata* have been reported to cause similar pathology in humans, while infections by *A. mustelae* have not previously been reported as a major threat to aquatic wildlife or people. Other zoonotic species of concern included infection by *Versteria* sp. (Cestoda: Taeniidae) which causes similar disease pathology to *Echinococcus* sp. and Toxoplasma gondii which was found in the brains of 30% of Albertan otters. Our data highlights a serious gap in knowledge around helminth communities in Western Canada and the threat related to vulnerable communities. Ongoing research is needed to assess the risk of infection by *Versteria* sp., *T. gondii*, and *A. mustelae* for indigenous communities and fur trappers who handle these organisms.



Presentation Abstracts

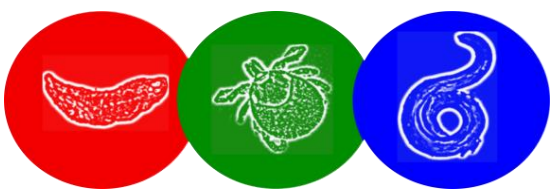
Incorporating the microbiome dimension in host-parasite interactions

Bridget Lamont, Professor James Ussher, Dr Daniel Pletzer, Professor Bruce Russell and Dr Remy Muhsin

Department of Microbiology and Immunology, University of Otago, Dunedin, New Zealand

Cryptosporidium spp. is a genus of intestinal apicomplexan parasites, capable of infecting a range of mammals (including humans), often causing an acute diarrheal disease known as cryptosporidiosis. In developing nations, poor sanitation, malnourishment, and high rates of HIV infection, have created the ideal niche for *Cryptosporidium* to thrive. Interestingly, Aotearoa has comparatively higher rates of cryptosporidiosis than other developed countries, with these mostly zoonotic outbreaks coinciding with the spring lambing/calving season. Despite its importance, cryptosporidiosis remains a neglected disease, with fundamental research hindered by the absence of a tractable *in vitro* continuous culture of this parasite. In this study, we provide a promising methodology for the subtyping of *Cryptosporidium parvum* positive clinical isolates in Aotearoa. We then perform a subtyping analysis to produce a robust methodology for multi-locus subtyping using various specific gene loci known to be highly polymorphic regions of the *Cryptosporidium* genome. This subtyping work will aid in tracking transmission and surveillance of circulating species around the region.

In this study, we also leverage a newly optimised *in vitro* drug screening platform to investigate, for the first time, the anti-cryptosporidial activity of newly developed synthetic peptoids with potent antimicrobial activity. Using our *in vitro Cryptosporidium* testing platform, from a library of 18 peptoids, we have shortlisted two peptoids, TM9 and TM19 which both have activity against the asexual stages of *C. parvum.* However only TM9 showed no cytotoxic effects against mammalian host cells. Due to the complex nature of the parasitic life cycle, TM9 must be screened against various life cycle stages. This includes determining TM9's effect on the parasites ability to invade host cells and its ability to block the egress of merozoites (intracellular parasitic stage) from host cells. *Cryptosporidium* has asexual and sexual life cycle stages; therefore studies are needed to determine the ability of TM9 to interrupt the sexual cycle. Once this is complete TM9 will then be tested in an *in vivo* mouse model. This study will provide the basis for development of a specific peptoid treatment against cryptosporidiosis in NZ farms, with the overall hope it can be used to combat cryptosporidiosis in Aotearoa.



Presentation Abstracts

2024 NZSP/ASP-ICAP: across the ditch and to the world

Augusto Simoes-Barbosa

School of Biological Sciences, University of Auckland

In this presentation, I am thrilled to share my enthusiasm for the organization of the 2024 NZSP Annual Meeting and invite your opinions and contributions. Our annual meeting will be held jointly with the Australian Society for Parasitology in Auckland, New Zealand. Adding to the excitement, the 7th edition of the International Conference on Anaerobic Protists (ICAP) will also take place during this time, bringing together approximately 100 international scientists specializing in anaerobic protozoan parasites. The talks from the ICAP will be integrated into our joint event, creating a unique opportunity for New Zealand parasitologists to present and discuss the local scientific advancements with an esteemed international audience.

Mark your calendar: 26-29 August 2024.
Faculty of Engineering bldg. 401 at the University of Auckland, conveniently located at 20 Symonds Street in Auckland, New Zealand.

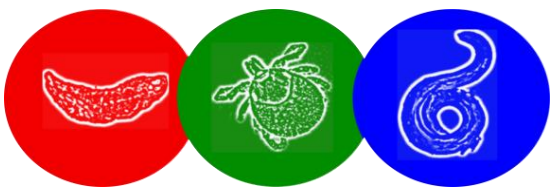
To stay tuned for the latest developments on the 2024 NZSP/ASP-ICAP, register your interest at https://icap2024.org/
If you are keen on contributing to the scientific organization committee, kindly reach out to me at a.barbosa@auckland.ac.nz. Your support and involvement are greatly appreciated.

In attention to holistic relationships between the host, parasite, and the microbiome: the case of *Trichomonas vaginalis*

Augusto Simoes-Barbosa

School of Biological Sciences, University of Auckland

Trichomonas vaginalis is a protozoan parasite that specifically targets the mucosal lining of the urogenital tract in humans. This extracellular parasite is responsible for causing trichomoniasis, which is recognized as the most prevalent non-viral sexually transmitted infection worldwide. Trichomoniasis is often accompanied by vaginal dysbiosis, characterized by a reduction in beneficial lactobacilli and a flourish of anaerobic bacteria. This correlation suggests a holistic relationship between the host, parasite, and the microbiome, indicating the coevolution of genes and phenotypic traits. Our research reveals that *T. vaginalis* has acquired NlpC/P60 genes from bacteria through horizontal gene transfer. These genes encode endopeptidases targeting peptidoglycan with potential implications in shaping the vaginal microbiome. In mixed cultures, these NlpC/P60 enzymes help *T. vaginalis* to reduce populations of lactobacilli. Conversely, *T. vaginalis* and dysbiotic vaginal bacteria exhibit mutually beneficial characteristics in terms of dispersion, substrate adhesion, and growth. By delving deeper into the intricate relationship between the host, *Trichomonas*, and the microbiome, we can gain valuable insights that hold the potential to develop alternative treatments for trichomoniasis.



Presentation Abstracts

Update on Zoonotic Malaria

Rossarin Suwanarusk and Bruce Russell

Department of Microbiology and Immunology, University of Otago, Dunedin, New Zealand

Zoonotic malaria, also referred to as simian malaria or monkey malaria, is a specific form of malaria that can be transmitted from non-human primates, particularly old world monkeys, to humans. This phenomenon carries significant implications for public health, particularly in Southeast Asia. In countries like Malaysia, zoonotic malaria has become the predominant form of malaria in humans. Infections caused by Plasmodium knowlesi, the primary zoonotic malaria parasite in the region, can result in severe illness and, if left undiagnosed and untreated, even death. Consequently, understanding zoonotic malaria is of utmost importance in preventing outbreaks and epidemics among human populations. Over the past five years, three additional zoonotic malaria parasites—P. cynomolgi, P. inui, and Plasmodium fieldi —have emerged in Malaysia, Indonesia, Thailand, and Cambodia. Although these newly identified zoonotic malaria causes have not demonstrated the same severity of illness as P. knowlesi, it is crucial to comprehend the reasons behind this phenomenon, particularly in areas where efforts are underway to eliminate human malaria. Exploring zoonotic malaria provides valuable insights into the transmission dynamics and evolutionary patterns of malaria parasites. By studying the interactions between non-human primate reservoir hosts, mosquito vectors, and humans, scientists can enhance their understanding of the complex ecological factors that contribute to malaria transmission. This knowledge, in turn, can inform the development of more effective interventions and strategies for malaria control and elimination. This talk aims to present the latest information on the threats and opportunities associated with zoonotic malaria. It will delve into the current understanding of zoonotic malaria in Southeast Asia, highlighting the implications for public health and emphasizing the importance of ongoing research in this field. By delving into the complexities of zoonotic malaria, we can pave the way for improved prevention and control measures, ultimately reducing the burden of malaria on human populations.

Spot-On Drenches in Sheep for Control of Gastrointestinal Parasites and Lice

Sean Daly

Donaghys Ltd

In 2010 following a discussion between the Donaghys Managing Director and a North Canterbury farmer Donaghys began investigating the potential for a topical anthelmintic for sheep to reduce the labour required to drench sheep.

As well as being easy to use the product also needed to be a combination product. Eprinomectin and levamisole were chosen as the active ingredients. For application, a spot-on method was chosen with the product being applied to skin level bypassing wool which could prevent absorption of the active ingredients into the blood stream. Between the shoulder blades was selected as the application site as it was easily accessible in the standing sheep. Scorpius Elite can use a normal oral drench gun or pour on gun to apply the product to skin level. Scorpius Elite contains 15 g/L of eprinomectin and 26 g/L of levamisole and is given at a dose volume of 1 mL/2.5 kg. This equates to a dose rate of 6 mg/kg and 10.4 mg/kg for eprinomectin and levamisole respectively. Scorpius Elite has a meat withhold of 16 days and a milk withhold of 35 days.

Donaghys have continued to invest in innovation with topical anthelmintics and are currently developing an abamectin based product which has displayed considerable efficacy against the sheep body louse *Bovicola ovis*. As well as improving efficacy against lice, substitution of abamectin to eprinomectin will also have cost of goods benefits reducing the cost of the drench to farmers.

Donaghy's manufacture the Scorpius range and their oral drenches for sheep and cattle at their factory in South Dunedin.

This report summarises the efficacy studies completed to date with Scorpius Elite and Tison Attack.

Presentation Abstracts

Phenotypes for host resistance to gastrointestinal nematodes

Kathryn McRae and John McEwan

AgResearch

Despite the availability of numerous strategies for the control of parasites in sheep, farmers throughout the world have continued to rely heavily on the use of anthelmintic treatments. Sustainable, long-term management of parasites requires a more integrated approach, and breeding sheep with an increased ability to resist infection is a potentially important part of this strategy. In New Zealand, there are three options for breeding for response to parasite infection, namely internal parasite resistance (WormFEC), internal parasite resilience, and CarLA parasite resistance.

Highlights from my PhD study on the effects of *Fasciola hepatica* in dairy cattle

Andrew Dowling[1], Bill Pomroy[2], Laryssa Howe[2], Kevin Lawrence[2], Ian Scott[2]

[1]PGG Wrightson Ltd, 1 Robin Mann Place, Christchurch [2]Massey University, Palmerston North

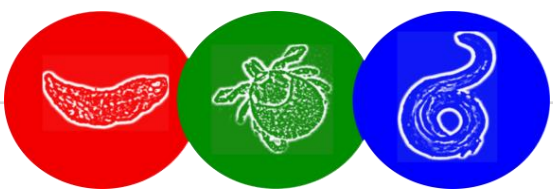
The liver parasite *Fasciola hepatica,* a trematode parasite, causes liver pathology affecting livestock production. I will present some of the highlights from my studies.
In 37 naturally infected cattle, using a multivariable linear regression model the coproantigen ELISA value was found to have a correlation with the natural log of fluke count fluke burden ($p=0.01$) with an adjusted $R^2=0.61$. Liveweight was shown to decrease by 20.4kg for each unit increase in the natural log of fluke count ($p=0.2$).
There was an apparent lack of impact of treatment of cows in the autumn on the prevalence of fluke infection in dairy herds in the spring of the same calendar year, in a region of New Zealand considered to be endemic for liver fluke infection. In 388 herds, the autumn and spring IDEXX diagnostic category had a weighted kappa = 0.58 (95%CI 0.52-0.64) indicating a *moderate agreement*. In herds with a high prevalence of infection, drenching in the autumn did not appear to impact the fluke population as determined by spring testing.
A small, but repeated, reduction of milk fat percentage was associated with liver fluke infection.
There is no gold standard field test for liver fluke infection. Analysis of diagnostic tools using Bayesian latent class modelling calculated the coproantigen ELISA to perform very well.
The need for future studies will also be discussed.

Sheep lice – the forgotten parasite?

Colin McKay

Elanco, New Zealand

An overview of aspects of control of what was once the most economically important parasite of sheep in New Zealand, namely the biting louse *Bovicola ovis*.



Presentation Abstracts
POSTER

Parasitic manipulation and the role of the microbiome on phenotypic changes in amphipods *T. serrulata*

Célia Koellsch-Amet

Department of Zoology, University of Otago, Dunedin, New Zealand

Parasitic infection often induces changes in host morphology, physiology or behaviour - known as parasite manipulation - making parasitism an important source of intraspecific variation. This parasitic manipulation is thought to be a means for the parasite to increase its trophic transmission to the definitive hosts. Parasite manipulation is often associated with the concept of “extended phenotype”, as parasite genes generate phenotypic expression in the body and behaviour of their host, whether through changes in metabolism or gene expression or simply in response to infection. However, the phenotypic and behavioural manipulation induced by the parasite is variable. Recently, host and parasite-associated microbial communities (microbiomes) have begun to be considered as potential modulators of parasite-induced phenotypic change in their hosts. Parasites most often have multidimensional effects on their hosts, including changes in behavioural, physiological, morphological and metabolic characteristics that increase their chances of transmission. Species of all major parasitic taxa are thought to alter the microbiome of their host, although it is not known whether the changes they make are beneficial or not. The hypothesis that parasites use microbes as a biological weapon to increase their virulence has been put forward as a “disruptive strategy”, but the microbiomes associated with parasites are still largely unknown. More and more studies are emerging on the subject, but host microbiomes are still receiving more attention from researchers. Thus, our current research aims to fill this gap, with the mission to assess the role of the microbiome in the phenotypic variability of the acanthocephalan and cestode-parasitized amphipod *Transorchestia. serrulata*, compared to uninfected amphipods. We analyse behavioural and phenotypic changes previously observed in amphipods of this species through the pronounced variation in body coloration as well as the alteration of behaviour at very small spatial scales in *Transorchestia serrulata* (before considered as *Transorchestia chiliensis*) following parasitic infection (Lagrue et al. 2016) and attempt to find the origin of this phenotypic modification taking into account the role of the microbiome.

Célia’s poster will be available to view between sessions throughout Day 1 and Day 2.

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