



Wild and Comparative Immunology (WACI) Conference 2026



About the workshop

The 5th Wild and Comparative Immunology Conference will be held in Hobart, Tasmania on 18-19 March. Registration will again be free and will include morning tea, lunch, and afternoon tea for both days! This is possible through the generous support of the Tall Foundation, the [Save the Tasmanian Devil Appeal](#), and the Menzies Institute for Medical Research at the University of Tasmania. The website and conference registration system has been maintained using funds from the [Ceva Wildlife Research Fund](#). Thank you to Elsevier journals *Developmental and Comparative Immunology*, *Comparative Immunology Reports*, and *Developmental and Comparative Immunology*, *Comparative Immunology Reports* for contributing \$750 for best student talks awards! Please contact andy.flies@utas.edu.au if you are interested in sponsoring the event.

To diversify the conference topics, the organising committee is currently accepting nominations for conference themes. The devil vaccine research team will hold half day workshop on the morning of Friday, 20 March 2026 as part of an ongoing grant ARC Linkage Project grant. The grant will provide travel funding for several international and domestic speakers.

When

The workshop will take place in Hobart, Tasmania on 18-19 March, 2026.

Venue

[The Old Woolstore Hotel](#) – [Merino Room](#)

Phone: 03 6235 5355

Program

Wednesday, 18 March 2026

0830 - 0900	Workshop registration open and group photo Location: The Old Woolstore Hotel – Merino Room
Session 1	Novel insights into marsupial immunity Session chair: Andy Flies
0900 – 0905	Welcome to WACI 2026 and Acknowledgement of Country
0905 – 0920	Matt Clement – CEO Bonorong Wildlife Sanctuary Introduction of participants and group photo
0920 – 0930	Pierre-Marie Borne - Ceva Wildlife Research Fund Platinum sponsor of WACI2026
0930 – 0950	Ruth Pye - Immune recognition of a transmissible cancer in Tasmanian devils with MHC-I deletion
0950 – 1005	Lee Campbell - Wommmunology: Defining Innate Immune Signalling Pathways in the Common Wombat
1005 – 1020	Tiing Jen Loh - A non-peptide antigen recognition pathway in Marsupials: Structural and Ligand analysis of UT molecules
1020 – 1030	Question and discussion

1030 – 1100	Morning Tea - provided at the venue
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Session 2	Student talks Session chair: Camila Espejo
1100 – 1110	Anna Langguth - Immune system changes during torpor and winter hibernation in southern hemisphere bent-winged bats: implications for white-nose disease/ syndrome sensitivity
1110 – 1120	Hannah Qin - Using extracellular vesicles to investigate immune responses to helminth infection in African buffalo
1120 – 1130	Imogen Dumville - The diversity of pathogens in a koala and lack of concordance between sample types.
1130 – 1140	Prithul Chaturvedi - Monitoring native wildlife using a remote animal microchip scanner (RAMS)
1140 – 1150	William Zhang - Identifying Bacterial Adhesive Domains to Enhance Antigen Retention in Mucosal Fish Vaccines
1150 - 1200	Questions

1200 - 1300	Lunch – provided at the venue
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Session 3	Immunology of aquatic and marine organisms Session chair: Jerome Le Nours
1300 – 1330	Brian Dixon - Development of an antigen presentation assay using rainbow trout (<i>Oncorhynchus mykiss</i>): From cloning genes to functional assay
1330 – 1345	Amanda Patchett - Single cell RNA-sequencing of gill pathologies in Salmonids reveals localised immune modulation and suppression
1345 – 1400	Andrew Wood - Investigating the role of adaptive immunity in salmonids using rag1 knockout models
1400 – 1415	James Wynne - CRISPR/cas9 knockout of TLR5 genes in trout
1415 – 1430	Questions and discussion

1430 – 1500	Afternoon tea - provided at the venue
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Discussion	How to quantify immunosuppression? Session chair: Andy Flies
1500 – 1600	Breakout groups and discussion
1600 – 1630	Posters Ivona Mladineo - Helminth-derived anisaxin A-2S modulates mice macrophages via VPAC1–PKA–IL-10 ax

Thursday, 19 March 2026

0830 - 0900	Arrival and networking Location: The Old Woolstore Hotel – Merino Room
Session 4	Vaccines, therapeutics Session chair: Alex Kreiss
0900 – 0915	Peter Timms – Registration of a chlamydia vaccine for koalas
0915 – 0930	Andrew Flies – Identifying and overcoming barriers to wildlife vaccines
0930 – 0945	Tonie Rocke – Oro-topical vaccines for wild bats could reduce disease risk
0945 -1000	Freya Russell - Delayed release vaccine implant for use of vaccination against <i>Chlamydia pecorum</i> in koalas
1000 – 1030	Questions and discussion

1030 – 1100	Morning Tea - provided at the venue
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Session 5	Ecoimmunology and diagnostics Session chair: Chrissie Ong
1100 – 1115	Anuk Kruawan - Determining sensitivity and specificity of SHERLOCK diagnostics for the field detection of DFT1 and DFT2
1115 – 1130	Chrissie Ong - Identification of tumour antigens for vaccines against the Tasmanian Devil Facial Tumour Disease
1130 – 1145	Ogundana Ebenezer Kehinde - Molecular Surveillance of West Nile, Akabane, Wesselsbron and Middelburg Viruses in Peri-urban wildlife of southern Nigeria.
1145 – 1155	Questions and discussion

1155 – 1245	Lunch - provided at the venue
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Session 6	Keynote speaker at Menzies Institute for Medical Research Session chair: Andy Flies
1245 - 1300	Walk to venue – 17 Liverpool St
1300 – 1330	Maria Croyle – Vaccine formulations
1330 – 1400	Louise Rowntree – Infectious disease and T cell immunology
1400 – 1415	Walk back to WACI2026 venue – The Old Woolstore

1415 – 1500	Afternoon tea - provided at the venue
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Session 7	Innate immunity Session chair: Amanda Patchett
1500 – 1515	Anjali Gowripalan - Using poxviruses as oncolytic therapies against transmissible tumours in devils
1515 – 1530	Camila Espejo - A constitutive pro-inflammatory immune environment enhances anti-tuberculosis immunity in helminth susceptible African buffalo
1530 - 1545	Matthew Perrott - Pathogenesis of wobbly possum disease: tissue distribution and the role of microglia
1545 – 1600	Nicholas Gherardin – Innate lymphoid cells
1600 - 1610	Questions and discussion
1610 - 1630	Group discussion and planning

Friday, 20 March 2026 – Limited to collaborators on Menzies devil vaccine grants

0830 - 0900	Menzies grant investigators strategy session Location: The Forest , room 1017, Melville St, Hobart, 7000 Meet a Menzies team member at reception
Session 8	Devil vaccine trial strategy Session chair: Andy Flies
0900 – 0920	Review of previous vaccine trials and update from the field
0920 – 0930	Current resources (antibodies, genomes, baits...)
0930 – 0950	Captive vaccine trials – what to measure?
0950 – 1010	Field (clinical) trial design – where, when and how many?
1010 - 1030	Where to draw the line?

1030 – 1100	Morning Tea - provided at the venue
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Session 9	Where to from here? Session chair: Andy Flies
1100 – 1200	Discussion
1300 - ?	Visit to the Bonorong Wildlife Sanctuary
1600 - ?	Social gathering?

WACI 2026 invited speakers

Prof Brian Dixon (University of Waterloo)
 Dr Camila Espejo (Yale University)
 Dr Louise Rowntree (Peter Doherty Institute)
 Prof Maria Croyle (University of Texas, Austin) - pending
 Prof Peter Timms (University of the Sunshine Coast)

WACI 2026 organising committee

Andrew Flies (Menzies, UTAS) andy.flies@utas.edu.au 0468667547
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 Anuk Kruawan (Menzies, UTAS) anuk.kruawan@utas.edu.au
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SESSION 1: NOVEL INSIGHTS INTO MARSUPIAL IMMUNITY

Immune recognition of a transmissible cancer in Tasmanian devils with MHC-I deletion

Ruth Pye

Menzies Institute for Medical Research, University of Tasmania, TAS, AU

Abstract

“Devil facial tumour disease (DFTD), caused by transmissible cancers, has decimated the wild Tasmanian devil (*Sarcophilus harrisii*) population. Devil facial tumour 1 (DFT1) cancer cells have spread due to low major histocompatibility complex class I (MHC-I) diversity in the species, as well as epigenetic regulation of MHC-I proteins on DFT1 cells to evade allograft responses. Tumour regression, recovery from disease, and immune recognition of DFT1 cells have been documented in a small number of cases. Here we tested the hypothesis that antibody response to DFT1 was associated with dissimilarity of host and tumour MHC-I types. We found that most individuals with antibodies against DFT1 cells do not share any alleles with DFT1 at the MHC-I UA locus. In addition to allelic mismatches, deletion of the UA locus increases the likelihood of immune response against DFT1 cells. Strikingly, we show that loss of the UA locus is being selected for at long-term disease sites. We conclude that deletion of an entire MHC locus provides some protection against DFT1. However, not all individuals that generate antibody responses are protected from DFT1, and loss of UA is not sufficient to ensure survival. Our study provides the first evidence of a complete gene loss in a species in response to a disease threat. Further evolutionary loss of MHC-I diversity will increase the species’ risk of future disease epidemics and further jeopardise the long-term viability of the species.”

See <https://www.biorxiv.org/content/10.1101/2025.03.20.644438v1> for co-authors

Wommmunology: Defining Innate Immune Signalling Pathways in the Common Wombat

Lee Campbell

University of Sydney, NSW, AU

Little is known about how marsupial cells sense and respond to pathogens. To address this gap, we established mixed primary cell cultures from tracheal explants of the common wombat (*Vombatus ursinus*). We designed stimulation experiments to profile activation of innate immune pattern recognition receptors (PRRs). Cells from three individuals were exposed to the common PRR-stimulating agonists lipopolysaccharide (LPS; bacterial), poly(I:C) (viral RNA mimic), poly(dA:dT) (viral DNA mimic), and zymosan (fungal). RNA was collected at 0, 12, and 24 hours post-stimulation and processed for RNA-sequencing. Preliminary analyses will provide the first dataset on PRR-driven innate immune responses in marsupial airway cells, with the potential to reveal both conserved and species-specific features of pathogen recognition. Establishing marsupial respiratory cell models represents a critical step toward mapping innate immune signalling in an understudied lineage and extending our understanding of PRR pathways and their regulation beyond eutherian mammals.

A non-peptide antigen recognition pathway in Marsupials: Structural and Ligand analysis of UT molecules

Tiing Jen Loh

Monash University, VIC, AU

The discovery of UT family, MHC-I related genes found only in marsupials and monotremes has raised significant interest in understanding their immunological roles. UT genes display low polymorphism, restricted tissues-specific transcription, and homology modelling suggests they may function as MHC-I-like molecules capable of presenting non-peptide antigens, similar to human MR1 and CD1. Despite their evolutionary significance, the structures of UT molecules and the identities of their ligands have remained unknown. Using a mammalian expression system, UT genes from *Monodelphis domestica* and *Sarcophilus harrisii* were recombinantly expressed. Mass spectrometry and X-ray crystallography were then employed to define the molecular basis of ligand presentation by these UT molecules. High-resolution crystal structure of the *Monodelphis domestica* UT5 and *Sarcophilus harrisii* UT25 revealed the presence of an endogenous lipid ligand. Our study provides the first molecular insights into the evolutionary ancestry of this unique class of mammalian immune receptors and identifies the potential types of ligands that can be presented by UT molecules.

SESSION 2: STUDENT TALKS

Immune system changes during torpor and winter hibernation in southern hemisphere bent-winged bats: implications for white-nose disease/ syndrome sensitivity

Anna Langguth
University of Melbourne, VIC, AU

Bats are important reservoirs for zoonotic pathogens, and understanding how environmental cues influence their biology is critical amid threats from habitat loss and diseases such as white-nose syndrome (WNS). However, little is known about how seasonality influences immunity in southern hemisphere bats.

We investigated the effects of torpor and winter hibernation on immune function in eastern and southern bent-winged bats (*Miniopterus orianae oceanensis* and *M. o. bassanii*) in southeastern Australia. Blood from over 500 individuals revealed significant winter immunosuppression, modulated by climate and year. In 52 bats sampled before, during, and after torpor, total white blood cell counts declined sharply during torpor but recovered rapidly afterward. Experimental exposure to the fungal antigen Zymosan suggested that white blood cells respond by migrating into tissues while plasma innate immune factors are not used, with challenged torpid bats also arousing more frequently.

These results show that even brief/ shallow torpor, and relatively mild southern hemisphere winters, substantially influence bat immune function. Australian bats may be susceptible to WNS during hibernation, though milder winters could reduce disease impacts. Our work highlights how energy conservation during winter trades off against immunity, shaping bats, vulnerability to emerging pathogens and providing essential data for disease risk assessments.

Using extracellular vesicles to investigate immune responses to helminth infection in African buffalo

Hannah Qin
Yale University, USA

In natural systems, co-infections are common and can significantly influence disease outcomes. In African buffalo (*Syncerus caffer*), gastrointestinal helminths (parasitic worms) and bovine tuberculosis (BTB) frequently co-occur. Previous research has shown that buffalo resistant to helminths clear worm infections more effectively, but paradoxically experience faster BTB progression and higher BTB-associated mortality than helminth susceptible individuals. These findings suggest that immune mechanisms conferring helminth resistance may compromise BTB control. To investigate the mechanistic basis of helminth resistance in buffalo, we examined immunological differences between helminth resistant and helminth susceptible individuals using extracellular vesicles (EVs), lipid-bound particles that carry protein signatures of host immune function. EVs were isolated from the serum of 18 buffalo (7 resistant, 11 susceptible) over the course of an experimental helminth infection. Samples were collected at baseline (Day 0), acute infection (Day 14), and chronic infection (Day 35). Helminth susceptible buffalo had higher baseline EV protein concentrations and showed more variation in EV protein concentration over time than resistant buffalo. These contrasting temporal patterns suggest that susceptible and resistant buffalo respond to helminth infections differently in terms of protein secretions. Ongoing data analyses will identify specific proteins and pathways underlying these differences, providing insight into the immunological basis

The diversity of pathogens in a koala and lack of concordance between sample types

Imogen Dumville

University of the Sunshine Coast, QLD, AU

In koalas, chlamydial disease (*Chlamydia pecorum*) is a primary threat. However, *C. pecorum* does not operate in isolation in koalas, multiple other pathogens, including KoRV-B, KoRV-D, PhaHV-1 and PhaHV-2 is known in multiple populations. However, these pathogens, interactions, their impact on disease, and their ability to be detected non-invasively, has not yet been extensively studied.

I will discuss the differences in swab and scat sample pathogen loads and diversity, through examination of 90 swab:scat pairs. Wide ranges of scat sensitivity and specificity were observed across pathogens, with *C. pecorum* and KoRV-B results being incongruent between sample types. Despite this, detection of Chlamydia in both swabs and scats correlated with current disease, enabling the use of non-invasive scats in conservation applications. Our results also demonstrated the impacts of coinfection, as when pathogens were examined in combination, only the combined presence of *C. pecorum* and KoRV-B in scat associated with disease. Conversely, the presence of KoRV-D in swabs was associated with host health. This work underscores the importance of holistic pathogen research, focusing on pathogen-pathogen and pathogen-host interactions, as well as providing evidence to support the application of non-invasive sampling in koala conservation.

Monitoring native wildlife using a remote animal microchip scanner (RAMS)

Prithul Chaturvedi

Menzies Institute for Medical Research, University of Tasmania, TAS, AU

Declining populations of Tasmanian devils (*Sarcophilus harrisii*) and Eastern quolls (*Dasyurus viverrinus*) in the past two decades have disrupted ecosystems of the island state. This can primarily be attributed to climate change, habitat loss, disease, and introduced pest species. Distribution of smaller species populations like the antechinuses (*Antechinus minimus*, *Antechinus swainsonii* and *Antechinus vandycki*) is sparsely studied. Much of our knowledge on native animals depends on trapping trips. Here, trapped individuals are assessed for health and microchipped before release. However, these trips are labour-intensive and costly to organise and hence are conducted annually at each selected site. We have developed a remote animal microchip scanner (RAMS) to monitor tagged wild animals for an extended period. This system comprises of a microchip scanner and a smart bait dispenser with an artificial intelligence-enabled camera fitted to a standard devil trap made using polyvinyl chloride (PVC) pipe. The dispenser can target individuals for vaccination and supplemental feeding based on microchip scanning. The device can be setup to dispense baits based on species using an image classification model trained on trail camera images. Alongside this, the onboard camera captures images with the tube, standard white background. These images can be used in training a facial recognition model for untagged individuals. Field scientists can remotely receive updates on activities from RAMS on an online dashboard using long-range wide area network of the smart dispenser. We have successfully trialled RAMS on captive and wild individuals.

Identifying Bacterial Adhesive Domains to Enhance Antigen Retention in Mucosal Fish Vaccines

William Zhang

Commonwealth Scientific and Industrial Research Organisation (CSIRO), AU

Vaccines are crucial for preventing disease outbreaks in finfish aquaculture. Immersion (bath) vaccination is an efficient delivery method, allowing simultaneous vaccine administration to large numbers of fish and reducing stress compared to injection. However, immersion vaccines often produce weak immune responses due to poor antigen uptake across the protective mucosal-skin barrier. In contrast, many bacterial pathogens readily attach to host mucosal surfaces using specialised adhesive proteins. To improve antigen retention of mucosal vaccines, we employ bioinformatic approaches to characterise bacterial muco-adhesive domains and use these as the foundation for engineering chimeric binding antigens. Through proteome-wide screening, we identified adhesive and mucosal binding protein domains from major fish pathogens, including *Aeromonas salmonicida*, *A. hydrophila*, *Tenacibaculum maritimum*, *Vibrio anguillarum* and *Yesinia ruckeri*. Several domains were conserved across multiple pathogens, while others were pathogen specific. Twelve binding domains were selected for gene synthesis and will be cloned into *E. coli* expression systems. ELISA and dot blot immunoassays, and cell binding assays, will be used to measure binding of these domains to mucus and gill epithelia. These findings form the basis for constructing chimeric adhesive antigens designed to improve antigen retention during immersion vaccination. Future work will evaluate their performance in salmonid vaccine trials.

SESSION 3: IMMUNOLOGY OF AQUATIC AND MARINE ORGANISMS

Development of an antigen presentation assay using rainbow trout (*Oncorhynchus mykiss*): From cloning genes to functional assay

Brian Dixon

University of Waterloo, CA

Antigen presentation and cytotoxic T cell responses play a vital role in combating intracellular infections and are well-studied in mammals, however, their functions in teleost fish remain less refined. This study developed a primary cell-based assay to explore antigen-specific cytotoxic responses in rainbow trout. Dorsal fin cells were exposed to heat-inactivated viral hemorrhagic septicemia virus (VHSV) IVb and then co-cultured with splenocytes from trout previously injected with the same heat-inactivated VHSV. Cytotoxicity was measured using a lactate dehydrogenase (LDH) release assay, while immune marker expression was analyzed by flow cytometry. Results showed that dorsal fin cells expressed elevated levels of MHC-I and MHC-IIa, and reduced CD3CE μ and IgM levels, indicating active antigen presentation and involvement in adaptive immunity. Co-cultures of VHSV-stimulated fin cells with activated splenocytes resulted in significantly increased LDH release at 12 hours, relative to controls. Additionally, splenocytes from VHSV-injected fish demonstrated stronger cytotoxic responses compared to native fish, suggesting antigen-specific activity. To investigate the role of MHC-I in this response, an anti-MHC-I antibody was used to block MHC-I molecules on dorsal fin cells prior to co-culture. This blockade significantly decreased LDH release, confirming the essential role of MHC-I in antigen-specific recognition. These results indicate that activated splenocytes

Single cell RNA-sequencing of gill pathologies in Salmonids reveals localised immune modulation and suppression

Amanda Patchett

Commonwealth Scientific and Industrial Research Organisation (CSIRO), AU

Pathogen-associated gill pathologies are a significant burden on fish health. Characterised by gill colonisation with one or more aetiologic pathogens, these pathologies arise due to the localised host immune response and can lead to cardiovascular compromise and eventual mortality. Strategies for disease mitigation, such as vaccination, can be ineffective, and alternatives like antibiotics can produce environmental impacts. Symptomatic treatment using immune-targeted therapies could provide an alternative for broadly treating disease, potentially triggering immune memory for sustained pathogen protection. To better understand immune-modulation in the gills of infected hosts, we performed single-cell RNA sequencing on bacteria-associated pathologies from farmed Atlantic salmon (*Salmo salar*). Over 31,000 cells from healthy gill tissue, focal lesions, diffuse lesions and adjacent gill tissue were sequenced at a depth of more than 30,000 reads per cell. Analysis of mapped reads revealed localised infiltration of myeloid and lymphocytic cells into diseased tissue and identified up-regulation of pro-inflammatory and immunosuppressive genes. Meta-analysis of additional total RNA-sequencing datasets revealed similar patterns of immunosuppression across multiple pathogenic diseases in Atlantic salmon. The identified immune pathways are potential broad-spectrum targets for disease treatment in Salmonids. Future studies will assess their therapeutic potential using in vitro and in vivo models.

Investigating the role of adaptive immunity in salmonids using rag1 knockout models

Andrew Wood

Commonwealth Scientific and Industrial Research Organisation (CSIRO), AU

In aquaculture, vaccination is a major disease prevention strategy, but effective vaccines remain elusive for some pathogens. The immune system of teleost and salmonid fishes differs from mammals, and further knowledge is needed to improve disease control strategies in aquaculture. Using gene editing, we are investigating the immune system in trout by knocking out key immune pathways. Rag1 is a protein encoded by the rag1 gene that is critical for V(D)J (variable, diverse, and joining regions) recombination, and consequently the maturation of T and B cells required for adaptive immune responses. Using CRISPR-Cas9 gene editing we have created populations of rag1 knockout rainbow trout (*Oncorhynchus mykiss*) and brown trout (*Salmo trutta*). Our rag1 knockout trout lack V(D)J recombination and do not respond to vaccination due to a lack of mature T and B cells. Future work will focus on measuring immune responses in the absence of an adaptive immune system.

CRISPR/cas9 knockout of TLR5 genes in trout

James Wynne

Commonwealth Scientific and Industrial Research Organisation (CSIRO), AU

Sensing of pathogen associated molecular patterns (PAMPs) is a key step in the development of an effective immune response against pathogens. Toll-like receptor 5 (TLR5) recognises bacterial flagellin and through its TIR domain initiates the activation of signalling pathways such as NF-kappa B which in turn stimulates the transcription of proinflammatory cytokines which have various roles in immune function and anti-microbial effects. Bony fish are unique in that they contain both a membrane bound (known as TLR5M) and a secreted form of TLR5 (known as TLR5S) which lacks the transmembrane and TIR domains. While the role of TLR5M appears conserved across animals the role of TLR5S remains more unclear. Utilising CRISPR/cas9 gene editing in both cell lines and whole fish the present study generated TLR5M and TLR5S knockouts (KO) for studying the function of these genes. Our results confirm TLR5M as the major receptor for bacterial flagellin. Furthermore, TLR5S KO appears to heighten the immune response providing further evidence that this receptor acts a decoy to suppress innate immune response.

SESSION 4: VACCINES, THERAPEUTICS

Registration of a chlamydia vaccine for koalas

Peter Timms

University of the Sunshine Coast, QLD, AU

Discussion of the recent registration of the koala chlamydia vaccine as a registered veterinary vaccine with the Australian Pesticides and Veterinary Medicines Authority

Identifying and overcoming barriers to wildlife vaccines

Andrew Flies

Menzies Institute for Medical Research, University of Tasmania, TAS, AU

In 2019, our team launched an ambitious plan for an oral bait vaccine to prevent devil facial tumour disease (DFTD). By 2022, our team had developed an adenovector-based vaccine that was functional in the laboratory for in vitro assays. We began preparing federal and state permit applications in 2022. By the end of 2025 we had achieved the major licenses and permits required for in vivo vaccine trials of a genetically modified virus in Tasmanian devils. This talk aims to layout a roadmap for other teams to navigate the regulatory environment more efficiently, and plan for pool data in successive trials for filing an APVMA minor use veterinary product application.

Oro-topical vaccines for wild bats could reduce disease risk

Tonie Rocke

United States Geological Survey (USGS.gov), USA

Reservoir-targeted vaccination of wild animals has been used to curtail disease spread for the benefit of humans and other animals (e.g. rabies in terrestrial carnivores) and has also been used for conservation of endangered species (e.g. avian flu in condors). So far, vaccination has not been attempted to manage disease in wild bats (Chiroptera) that are considered primary reservoirs for zoonotic pathogens (e.g. rabies, Nipa, Hendra and Ebola viruses), largely due to their unique feeding behaviors and lack of adequate delivery methods. However, recent studies in *Myotis* spp. in the U.S. that causes high morbidity and mortality from a fungal disease (white nose syndrome-WNS) that attacks bats while they are hibernating, indicates vaccination may be a feasible option for managing this and other diseases in bats. Using raccoon poxvirus, genetically altered to express pathogen-specific antigens, we have developed and tested oral vaccines to manage WNS in *Myotis* spp. and rabies in vampire bats (*Desmodus rotundus*) and have shown both to be safe and efficacious. Oro-topical delivery methods are being developed, taking advantage of these species's natural tendencies for allogrooming, which allows for transfer and consumption of the vaccine by roost mates, a more efficient and safer method of vaccine distribution.

Delayed release vaccine implant for use of vaccination against *Chlamydia pecorum* in koalas

Freya Russell

Queensland University of Technology, QLD, AU

Chlamydia is an obligate intracellular bacterial pathogen responsible for disease and infertility across multiple species including the Koala (*Phascolarctos cinereus*). Vaccination to prevent chlamydial infections could provide an alternative to antibiotics and we have developed a vaccine that has proven to be safe and immunogenic in captive-bred koalas. This vaccine was also tested in a wild population in Elanora, QLD. Due to the need for two shots to elicit complete protection and the complications this can cause, we have shifted to developing a delayed release vaccine implant. Here we investigate immunological responses from 16 captive-bred koalas to compare the traditional prime/boost vaccination method and the experimental prime/implant vaccination schedule. Through ELISA analysis of serum and flow cytometry analysis of in vitro stimulated peripheral blood mononuclear cells (PBMCs), we have found that the prime/implant regime produced equivalent humoral and cell-mediated immunity when compared to the traditional prime/boost vaccination method and therefore is a good alternative for wild populations.

SESSION 5: ECOIMMUNOLOGY AND DIAGNOSTICS

Determining sensitivity and specificity of SHERLOCK diagnostics for the field detection of DFT1 and DFT2

Anuk Kruawan

Menzies Institute for Medical Research, University of Tasmania, TAS, AU

The Tasmanian devil (*Sarcophilus harrisii*) population has undergone a major decline in the wild due to epidemics of two clonally transmissible cancers, devil facial tumour 1 (DFT1) and devil facial tumour 2 (DFT2). Understanding the distribution and prevalence of DFT1 and DFT2 is challenging, as they can only be detected in the field once tumours are large enough to be visually observed. Although PCR-based diagnostics are available, they are not readily field-deployable. To overcome these limitations, we developed an ultrasensitive, rapid, and field-deployable diagnostic tool based on the Specific High-Sensitivity Enzymatic Reporter Unlocking (SHERLOCK) technique, which combines an isothermal nucleic acid amplification with CRISPR-based target recognition and reporter cleaving. We tested over 300 swab samples collected from 114 wild Tasmanian devils across the state. In addition, we evaluated multiple swab types for sample collection and found that forensic flocked swabs outperformed other swab types. Importantly, the assay demonstrated high sensitivity and specificity with a low false-positive and false-negative rates. This SHERLOCK-based diagnostic enables active surveillance and management strategies for devil facial tumour disease that are not currently feasible using existing methods.

Identification of tumour antigens for vaccines against the Tasmanian Devil Facial Tumour Disease

Chrissie Ong

Menzies Institute for Medical Research, University of Tasmania, TAS, AU

The devil facial tumour disease (DFTD) is a unique case of transmissible cancers (DFT1 and DFT2) that have overcome the major histocompatibility complex class I (MHC-I) barriers to evade immune recognition. Most devils succumb to DFTD, with rare evidence of antibody responses or immune cell infiltration into the tumours. Conversely, sporadic tumour regressions in wild devils are associated with antibodies against MHC-I molecules on DFT1 cells, identifying a potential vaccine target.

Genetic mismatches in the polygenic and polymorphic MHC-I alpha chain between host and tumour, and tumour peptides bound on MHC-I are potential antigens for anti-DFT immune response. We aimed to identify the specific target(s) of anti-DFT1 immunity to guide vaccine development.

A panel of MHC-I antigens consisting of individual alleles expressed in DFTs, with and without bound peptides, were generated recombinantly to assess the antibody targets in devils with strong anti-DFT response. Our results showed that host devil antibodies recognised mismatched MHC-I alleles independent of bound peptides and syngeneic MHC-I molecules in the presence of bound peptides. This suggests that both MHC-I mismatches in the alpha chain and MHC-I bound peptides are candidate vaccine targets and may play a role in regulating the immune response to DFTs and transmissible cancers.

Molecular Surveillance of West Nile, Akabane, Wesselsbron and Middelburg Viruses in Peri-urban wildlife of southern Nigeria

Ogundana Ebenezer Kehinde

Redeemer's University Nigeria, NG

Arboviruses are arthropod-borne RNA viruses with major public health, veterinary, and economic impact. Among them, West Nile virus (WNV), Akabane virus (AKAV), Middelburg virus (MIDV), and

Wesselsbron virus (WSLV) are significant for their febrile and neurotropic potential in humans and animals. While WNV and AKAV are well-studied, MIDV and WSLV remain under-reported, particularly in Nigeria despite regional detections in South Africa.

This study screened peri-urban wildlife in southern Nigeria, including African giant rats, bats, cattle egrets, and squirrels, for molecular evidence of these viruses. A total of 320 tissue samples (spleen and liver) from 160 animals across Enugu, Ebonyi, Ondo, and Osun States were analyzed using RT-qPCR.

All samples tested negative for MIDV and WSLV. However, two bat samples from Osun and one cattle egret from Ondo were positive for AKAV, while one squirrel tested positive for WNV. African giant rats showed no infection.

Findings indicate that bats may serve as potential reservoirs for arboviruses in southern Nigeria, highlighting the importance of expanded genomic surveillance to better understand their epidemiology and zoonotic risks.

SESSION 6: KEYNOTE SPEAKER AT MENZIES INSTITUTE FOR MEDICAL RESEARCH

From Lab Scale to Grand Scale: Battling Threats to Public Health with Pharmaceutical Science

Maria Croyle

The University of Texas at Austin, USA

Bio: Dr. Croyle joined the UT Austin College of Pharmacy in 2000 to establish a research program that relies upon principles of formulation and drug delivery, physical chemistry, structural biology, immunology and pharmacology to understand how viruses can be used as medicines. She has received grants from the NIH, the Canadian National Research and Technology Initiative and many industry partners to support her work and has published over 60 peer-reviewed manuscripts in journals such as Science Advances, Communications Medicine and Molecular Pharmaceutics. She has served on expert panels for the National Institutes of Health, the United States Pharmacopeia and the Academy of Finland. Her group was the first to report long-term protection from a needle free vaccine for Ebola using technology that was licensed to spin out company, Jurata Thin Film. Dr. Croyle served as CSO of Jurata (2019-2023) and received the Lyda Hill Impact Prize in Engineering from the Texas Academy of Medicine, Engineering, Science and Technology for the creation of a pilot line that accelerates global distribution of vaccines. Most recently she has been elected as fellow of the National Academy of Inventors and the American Association of Pharmaceutical Scientists. Throughout her career she has mentored over 100 pharmacy and PhD student students attaining positions in industry, regulatory agencies and academia and brought pharmaceutical science to mainstream audiences in a National Geographic episode on pandemics.

The COVID-19 pandemic highlighted how pharmaceutical formulations and technology can impact the global distribution of vaccines and biological drugs. It also created a resurgence in the development of methods for administration of needle-free vaccines. This presentation will identify physical and chemical factors that impact the stability of vaccines and how development of a needle free Ebola vaccine addressed these and other immunological issues through the development of a film-based platform technology that culminated in the first report detailing the durability of a single dose Ebola vaccine evaluated in a large animal model. The remainder of the presentation will demonstrate how the technology could be produced rapidly on a large scale for global distribution.

CD8+ T cell immunity directed at Influenza viruses in First Nations peoples

Louise Rowntree

University of Melbourne, Doherty Institute, VIC, AU

Bio: Dr Louise Rowntree is a Group Leader and NHMRC EL1 Fellow with extensive expertise in viral immunology in vulnerable populations, within the Department of Microbiology and Immunology, The University of Melbourne and the Peter Doherty Institute for Infection and Immunity. Louise completed her PhD at Monash University investigating human cross-reactive CD8+ T cells in viral infections. She then joined Prof Anthony Purcell's Laboratory (Monash) to further explore T cell cross-reactivity between viral and self-antigens and identify immunoreactive peptides. Louise has been a key senior member of Prof Katherine Kedzierska's Laboratory at the Doherty Institute since 2019, where her work focuses on dissecting anti-viral responses in high-risk groups, including First Nations people, pregnant women, elderly, children and patients with co-morbidities, with an emphasis on T cell epitope identification and T cell responses associated with severe disease.

SESSION 7: INNATE IMMUNITY

Using poxviruses as oncolytic therapies against transmissible tumours in devils

Anjali Gowripalan

The Australian National University, ACT, AU

Devil facial tumour (DFT) disease is a threat to Tasmanian devils for which there is no therapeutic relief. Previous work from our group found a 100-fold greater susceptibility of DFT1 and DFT2 cells to vaccinia virus (VACV) compared to healthy devil fibroblasts and we proposed this virus as an oncolytic therapy for DFT disease. Transcriptomic analysis suggested that the selective VACV growth in devil tumour cells might be due to low expression of a known antiviral factor, FAM111A, which is abundant in fibroblasts. In support of this, knockdown of FAM111A expression in fibroblasts, rescued virus growth 10-fold. Additionally, devil FAM111A appeared more potent than human FAM111A. We demonstrated that this is due to different localisation in cells, with human FAM111A needing to escape the nucleus to attack VACV replication centres in the cytoplasm, whereas devil FAM111A is always cytoplasmic. Finally, we showed that the VACV protein I3, which is known to be the target of human FAM111A, is strongly degraded by the devil homologue. Therefore, we propose that FAM111A, which is widely expressed in healthy devil but not DFT cells, at least partly explains the tumour specificity of VACV, supporting the development of this potential anti-DFT virotherapy.

A constitutive pro-inflammatory immune environment enhances anti-tuberculosis immunity in helminth susceptible African buffalo

Camila Espejo

Yale University, USA

Co-infections shape disease outcomes in complex ways. In African buffalo (*Syncerus caffer*), gastrointestinal helminths and *Mycobacterium bovis* (bTB) frequently co-occur. Paradoxically, helminth resistant buffalo show rapid bTB progression and higher mortality than susceptible counterparts, even without active infection. To investigate this phenomenon, we experimentally infected 26 wild-caught, bTB-free buffalo with helminth larvae and quantified systemic immune responses at baseline, acute, and chronic infection. Animals were pre-classified as helminth resistant or susceptible based on egg-shedding profiles. Susceptible animals showed elevated IL-10 at chronic infection yet maintained strong positive correlations between pro-inflammatory cytokines (TNF- α , IL-12, IFN- α) at all timepoints, whereas resistant buffalo showed weaker or negative correlations. These patterns suggest susceptible individuals maintain coordinated Th1/pro-inflammatory responses during helminth infection that may confer advantage against bTB. Supporting this, a principal component axis defining Th1/pro-inflammatory phenotype was positively associated with bTB-specific IFN- α and IL-12 production in susceptible, but not resistant animals. Furthermore, functional assays revealed enhanced antimicrobial capacity in susceptible individuals: macrophages produced more nitric oxide, monocytes produced more reactive oxygen species and showed greater phagocytic activity, mechanisms linked to improved bTB control. Our findings show that helminth susceptible buffalo maintain coordinated pro-inflammatory responses and enhanced antimicrobial functions that may explain their bTB advantage.

Pathogenesis of wobbly possum disease: tissue distribution and the role of microglia

Matthew Perrott
Massey University, NZ

Wobbly possum disease (WPD) is a systemic condition, clinically characterized by weight loss and ataxia. High levels of viral RNA have been previously detected in macrophage-rich tissues such as liver, spleen, and kidney, but moderate to low levels of viral RNA were also present in many other tissues 1. The aims of the current study were to investigate the presence of WPD in previously untested tissues and to determine the type of cells infected in the brain to help elucidate the pathogenesis of neurological dysfunction.

WPD antigens were detected in macrophages within bone marrow and lung, further expanding the tissue-tropism of the virus. In the nervous system, WPD virus was rarely associated with peripheral nerves and the optic nerve. No viral antigens were detected in the retina, cranial nerve VIII or vestibular apparatus. Viral antigens were most consistently identified in the leptomeninges and in the cerebellum, where they co-localized with the antibody marker for microglia (Iba-1). In addition, the number of microglia was increased in WPD-infected possums compared with controls. Astrocytes were not associated with WPD virus and were not upregulated. We conclude that neurological deficits in WPD are due to an upper motor neurone-based ataxia and microglia dysfunction.

What's cooking? The effect of temperature on the immune response

Julie Old
Western Sydney University, NSW, AU

Animals have evolved to live in different environs, with some having adapted specialised features to support survival in adverse conditions, whilst others adapt behaviourally. Maintaining a body temperature to optimise unique metabolic and physiological processes is essential. Temperature impacts the immune system differentially, with lower temperatures impacting the adaptive immune response, but not the innate response. A reduction in adaptive immune capacity at lower temperatures can be due to a failure to effectively assemble MHC and may be a result of modifications of the plasma membrane structure or its viscosities. Ensuring the effectiveness of the adaptive immune response through optimal temperature regulation may support immunological fitness, ultimately enhance conservation and biodiversity of wildlife species, and improve welfare outcomes for production animals, and ourselves.