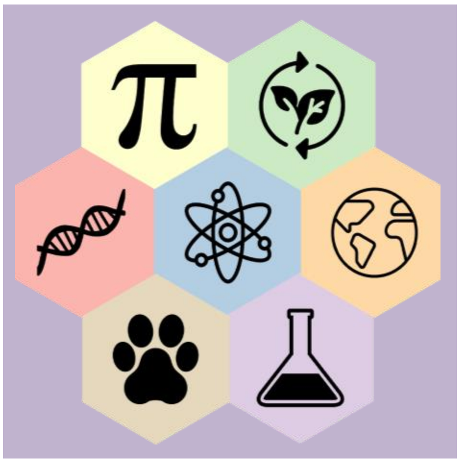
# SCIENCE EARLY CAREER RESEARCH SUMMIT

**PLENARY & INVITED SPEAKERS**

**ECA ORAL & SPEED SESSIONS**

**PRIZES**



Tuesday

4th June 2026

Melbourne Connect

# BOOK OF ABSTRACTS

Brought to you by the Science Early Career Academic Network (SECAN)

THE UNIVERSITY OF MELBOURNE

https://science.unimelb.edu.au/engage/early-career-research-summit

| | |
|---|---|
| **08:30 - 09:00** | **Registration** |
| **Opening Session - Forum 1 (Chair: Sophie Selby-Pham)** | |
| **09:00 - 09:05** | **Opening Announcements & Acknowledgement of Country** |
| **09:05 - 09:35** | **Plenary Speaker: Michael-Shawn Fletcher** |
| **09:35 - 09:55** | **Invited Speaker(s): Teaching ECAs: 1st Year Chemistry Team** |

| **Morning Session** | | | |
|---|---|---|---|
| **Time** | **Stream 1 (Chair: Mandy Freund)** | **Stream 2 (Chair: Marcus Giansiracusa)** | **Stream 3 (Chair: Age Zanca)** |
| **Venue** | **Forum 1** | **Forum 2** | **Forum 3** |
| **10:00-10:20** | **Invited Speaker: Dr Joses Nathanael**<br>*School of Chemistry* | **Invited Speaker: Dr Mia Cobb**<br>*Melbourne Veterinary School* | **Invited Speaker: Dr Tessa Toumbourou**<br>*SAFES* |
| **10:20-10:35** | **Speaker: Elisabeth Vogel**<br>*SGEAS* | **Speaker: Ben Harris**<br>*Biosciences* | **Speaker: June Yong**<br>*Chemistry* |
| **10:35-10:50** | **Speaker: Dale Lonsdale**<br>*Chemistry* | **Speaker: Declan Lafferty**<br>*Biosciences* | **Speaker: Phuong Nguyen**<br>*SAFES* |
| **10:50-11:20** | **Morning Tea** - The Lab and Launch Pad | | |

| **Midday Session** | | | |
|---|---|---|---|
| **Time** | **Stream 1 (Chair: Robert Ryan)** | **Stream 2 (Chair: Rose Macaulay)** | **Stream 3 (Chair: Zahra Islam)** |
| **Venue** | **Forum 1** | **Forum 2** | **Forum 3** |
| **11:20-11:40** | **Invited Speaker: Dr Kristoffer Wild**<br>School of Biosciences | **Invited Speaker: Dr Jamie Burton**<br>SAFES | **Invited Speaker: Dr Hayden Dalton**<br>SGEAS |
| **11:40-11:55** | **Shamali Antoni Baduge (MVS)** | **Liang Ze (SAFES)** | **Elena Kaminskaia (Biosciences)** |
| | **Hasitha Disanayaka Mudiyanselage (MVS)** | **Chathuri Rodrigo (MVS)** | **Tulsi Ram Gompo (MVS)** |
| | **Lok Hang Chan (SAFES)** | **Belay Mino (SGEAS)** | |
| **11:55-12:10** | **Speaker: Joshua Forrest**<br>*Maths and Stats* | **Speaker: Ben Teo**<br>*Maths and Stats* | **Speaker: Giovani Dalla Valle Garcia**<br>*Physics* |
| **12:10-12:25** | **Speaker: Mina Barzegaramiriolya**<br>*Physics* | **Speaker: Naveen Vankadari**<br>*Biosciences* | **Speaker: Veronique Paris**<br>*Biosciences* |
| **12:25-12:40** | **Speaker: Manuel Poretti**<br>*Biosciences* | **Speaker: Saini Samim**<br>*SGEAS* | **Speaker: Israporn Sethanant**<br>*SGEAS* |
| **12:40-12:55** | **Speaker: Benjamin Wagner**<br>*SAFES* | **Speaker: Ashkan Pakzad**<br>*Physics* | **Speaker: Kona Adhikary**<br>*MVS* |
| **12:55-14:00** | **Lunch** - The Lab and Launch Pad | | |

| **Afternoon Session** | | | |
|---|---|---|---|
| **Time** | **Stream 1 (Chair: Caitlyn Perry)** | **Stream 2 (Chair: Ashkan Pakzad)** | **Stream 3 (Chair: Evelyn Huang)** |
| **Venue** | **Forum 1** | **Forum 2** | **Forum 3** |
| **14:00-14:20** | **Invited Speaker: Dr Nisha Mehta**<br>School of Chemistry | **Invited Speaker: Dr Jason Jung**<br>School of Physics | **Invited Speaker: Dr Ritu Taneja**<br>School of Mathematics and Statistics |
| **14:20-14:35** | **Bridget Walker (Biosciences)** | **Putu Henrywaesa Sudipa (MVS)** | **Nirmal Raj Rajendran (SAFES)** |
| | **Bethany Kiss (SAFES)** | **Ishara Pathirage (SGEAS)** | **Dillani Putri Ramadhaningtyas (SAFES)** |
| | | | |
| **14:35-14:50** | **Speaker: Amy Smith**<br>*SAFES* | **Speaker: Robert Ryan**<br>*SGEAS* | **Speaker: Owen Holland**<br>*Biosciences* |
| **14:50-15:05** | **Speaker: Guillermo Garcia Gimenez**<br>*SAFES* | **Speaker: Tahnee Burke**<br>*SGEAS* | **Speaker: Philippa Bell**<br>*SAFES* |
| **15:05-15:20** | **Speaker: Bea Kirk**<br>*MVS* | **Speaker: Kaan Öcal**<br>*Biosciences* | **Speaker: Anna Wittwer**<br>*SAFES* |
| **15:20-15:35** | **Speaker: Li Bi**<br>*SAFES* | **Speaker: Abdul Ghafar**<br>*MVS* | **Speaker: Mia Tam**<br>*SAFES* |
| **15:35-16:00** | **Afternoon Tea** - The Lab and Launch Pad | | |

| **Closing Session (Session Chair: Sophie Selby-Pham)** | |
|---|---|
| **16:00-16:15** | **Christina Ward (Science Library)** |
| **16:15-16:30** | **Nathan Dorey, Ellie Freeman, Claire Smoorenburg (Science Communications and Marketing team)** |
| **16:30-16:45** | **Lucy Zhan (RDU)** |
| **16:45-17:00** | **Closing address by Prof. Moira O'Bryan (Dean - Faculty of Science) and Presentation of Awards** |

# Book of Abstracts

# Invited Speakers

# Locking in Nitrogen for Our Crops and Future Generations

**Joses Nathanael** (Chemistry)

Global food demand is expected to increase substantially over the coming decades as the world population approaches approximately 10 billion. Nitrogen (N) fertilisers are essential for sustaining crop productivity and supporting global food security. However, the current nitrogen use efficiency (NUE) is relatively low, with only around 50% of applied N typically taken up by crops. The remaining N is lost through processes such as ammonia ($NH_3$) volatilisation, nitrate ($NO_3^-$) leaching, and greenhouse gas emissions (such as nitrous oxide, $N_2O$), contributing to air pollution, deterioration of water quality, and loss of biodiversity.

To improve NUE and reduce environmental impacts, a range of mitigation strategies has been explored, including controlled-release systems and chemical inhibitors. Within the N cycle, urease and nitrification inhibitors slow N transformation in soils, extending nutrient availability for plant uptake and reducing N losses. As chemists, our approach focuses on the design and formulation of inhibitor technologies, together with their practical implementation under real-world agricultural conditions.

This presentation will highlight recent work from our group on inhibitor development, application onto urea granules, and challenges associated with storage stability. By retaining N within the soil-plant system, these technologies aim to “lock in nitrogen” for today’s crops and future generations, without further harming our skies and seas.

# Taking the Lead on Happy Dog Science

**Mia Cobb** (MVS)

The evidence for how dogs help human health and wellbeing is copious. Dogs support people with disabilities, assist in border security, law enforcement and emergency response, contribute to mental and physical health outcomes, and occupy a family place in the lives of millions of Australians. What has received considerably less scientific attention is the reflected question: what do dogs need to live a good life? Animal welfare science has made real progress in identifying and mitigating negative welfare states in animals. But the conditions that allow dogs to flourish, to experience positive emotions, to do the things that are meaningful to them - remain understudied. This talk introduces Happy Dog Science - an emerging research focus at the Animal Welfare Science Centre, University of Melbourne, that takes positive pupper welfare seriously. Drawing on interdisciplinary themes including analytical chemistry, behavioural science, and contemporary welfare assessment frameworks including the Five Domains Model, this talk outlines what a rigorous positive canine welfare research agenda looks like and why it matters - for dogs, for the industries and communities that depend on them, and for the broader question of public trust in how animals in our care are treated. It describes active international collaborations with researchers in the United States and United Kingdom that are building this evidence base, and reflects on how support that enables novel discovery research, outside the constraints of traditional funding frameworks, opens up questions that might otherwise go unasked. If we want communities to be confident that dogs living and working with people are genuinely well, we need the science to demonstrate it.

# ‘Gold mining is our only option now’: a feminist political ecology analysis of five decades of landscape and livelihood change in Central Kalimantan’s degraded peatlands

**Tessa Toumbourou** (SAFES)

Indonesia’s biodiverse tropical peatlands are globally important terrestrial carbon stores that play a critical role in climate regulation and regional hydrology. Yet decades of extractive land use have profoundly transformed these ecosystems and the lives of the people who depend on their resources. This presentation examines five decades of environmental and livelihood change in Central Kalimantan, Indonesia, tracing how successive waves of resource extraction and development have reshaped peatland landscapes and generated uneven social outcomes.

Drawing on 42 life-story interviews with older women and men, alongside a comprehensive household survey in two rural communities in Central Kalimantan, I trace overlapping phases of frontier expansion: swidden farming and forest-product collection (1950s-60s), industrial logging (1970s-early 2000s), the failed Mega Rice Project (1996-1998), shifting state-, private-, and donor-led restoration schemes (2000s-2020s), and the recent rise of informal gold mining.

I show that peatland degradation is not the outcome of a single phase of industrial land use, but of layered projects linked to political-economic forces that overlay and cumulatively impact the same landscapes, producing increasingly uneven livelihood trajectories most significantly across gender, generation, and wealth. Many of the few more lucrative livelihood activities available locally – including edible bird’s nest cultivation or equipment lending for informal gold mining – are expensive to enrol in, so households who accumulated capital during earlier extraction booms who are now better positioned to invest in these. In contrast, younger, poorer and more recently arrived men are increasingly drawn into hazardous forms of extractive labour, including temporary migration for informal gold mining. At the same time, women in these households take on growing responsibilities for sustaining families amid ecological decline and economic and food insecurity.

By linking long-term environmental transformation with differentiated social outcomes, this study highlights how global and national political-economic pressures shape contemporary livelihood and social inequalities in tropical peatlands. The findings underscore the importance of historically informed and socially inclusive approaches to ecological restoration and climate mitigation.

# Climate change and the cost-of-living squeeze in desert lizards

**Kristoffer Wild** (Biosciences)

Climate warming can induce a cost-of-living “squeeze” in ectotherms by increasing energetic expenditures while reducing foraging gains. We used biophysical models (validated by 2685 field observations) to test this hypothesis for 10 ecologically diverse lizards in African and Australian deserts. Historical warming (1950–2020) has been more intense in Africa than in Australia, translating to an energetic squeeze for African diurnal species. Although no net impact on Australian diurnal species was observed, warming generated an energetic “relief” (by increasing foraging time) for nocturnal species. Future warming impacts will be more severe in Africa than in Australia, requiring increased rates of food intake (+10% per hour active for diurnal species). The effects of climate warming on desert lizard energy budgets will thus be species-specific but potentially predictable.

# From damp to dangerous: understanding landscape flammability

**Jamie Burton** (SAFES)

Fire does not simply occur; it requires the right conditions, and vegetation dry enough to burn is a critical part of the equation. Fuel moisture content lies at the heart of landscape flammability, yet understanding its relationship with fire activity, and accurately predicting it across landscapes, remains a major challenge. My research addresses these questions through a combination of laboratory experiments, field studies, and large-scale desktop analyses, with the aim of improving our ability to predict fire behaviour and support more effective fire management.

# Volcanoes: Messengers from the Deep

**Hayden Dalton** (SGEAS)

Kimberlites are the deepest-derived magmas on Earth and the primary transporters of diamonds to the surface. They provide a unique mechanism to probe the evolution of the planet's physically inaccessible interior. I will demonstrate how we can use the composition of these enigmatic volcanic rocks to understand deep-Earth processes. Expanding on this deep-Earth approach, I will present findings from investigations into strongly contrasting volcanic events from East Africa, aiming to constrain when these eruptions occurred, how they evolved, and where they originated. These silica-rich volcanoes produce gas-rich, viscous magmas and large-volume explosive eruptions, making them some of the most hazardous forms of volcanism. Ultimately, I will show how a comprehensive understanding of these East African eruptions yields critical insights into the recurrence intervals of dangerous volcanic activity and helps refine the timeline of human evolution.

# Advancing Computational Tools for Sustainable Solutions in Biotechnology and Catalysis

**Nisha Mehta** (Chemistry)

The aim of this McKenzie Fellowship-supported project is to develop robust, transferable, and computationally efficient quantum-chemical and classical simulation tools for metal-containing chemical systems, addressing a long-standing bottleneck in accurately modelling electronically complex systems relevant to catalysis, drug discovery, sustainable chemistry, and biotechnology.

Understanding the structure, reactivity, and dynamics of complex molecular systems at the atomic level remains a major challenge in chemistry and the life sciences. While experimental techniques continue to advance rapidly, they often lack the spatial and temporal resolution needed to directly probe electronic structure, short-lived reactive intermediates, and dynamical processes. Computational approaches, particularly electronic structure theory and molecular dynamics simulations, provide a powerful complementary framework for investigating these phenomena.

By combining quantum-chemical methods with molecular dynamics simulations, this project aims to develop scalable and accurate computational approaches capable of describing complex metal-containing systems in chemically and biologically relevant environments. These tools will enable improved understanding of electronic structure, reaction mechanisms and thermodynamic properties, while supporting the rational design of catalysts, functional materials, and therapeutic compounds. The computational framework developed will establish a reliable in silico screening platform for inhibitors of metallo-β-lactamases, zinc-dependent enzymes that inactivate nearly all β-lactam antibiotics.

# Enhancing Seizure Prediction with High Resolution Single Unit Recordings

**Jason Jung** (Physics)

High-resolution single-unit recordings can enhance epilepsy management by providing detailed insights into brain activity. Implantable devices for brain activity recording have shown potential in forecasting seizure risk, enabling early intervention through targeted stimulation or medication adjustments before seizure onset, unlike responsive neurostimulation (RNS), which responds only after a seizure begins.

Cortical excitability is a key biomarker for seizure prediction, measurable with high-resolution single-unit electrodes alongside conventional EEG and ECoG recordings. Our 'Elatus' multi-electrode array (MEA) design features 25 small (7 μm) carbon fiber electrodes embedded in a diamond substrate, allowing long-term recordings of individual neuronal activity and complementing large-scale EEG/ECoG data for improved seizure prediction accuracy. In vivo experiments in the rat cortex using a seizure-inducing agent (PTZ) and the antiepileptic drug Levetiracetam revealed significant changes in branching ratios, a key metric of brain criticality. PTZ increased branching ratios, pushing the brain into a supercritical state, marked by abnormal exponential growth of neural activity, while Levetiracetam stabilised the ratios, returning the brain to a critical or subcritical state. Integrating high-resolution single-unit recordings with EEG and ECoG systems could enhance seizure forecasting and support more targeted treatment strategies.

# Belonging Before Achievement: Why Education-Focused Research is a STEM Research Imperative

**Ritu Taneja** (Maths and Statistics)

STEM researchers dedicate their careers to solving society's most pressing challenges. Yet one challenge often remains hidden in plain sight: why do capable students disengage, underperform, or leave STEM altogether? While universities invest heavily in advancing scientific discovery, far less attention is given to understanding the educational environments that shape the next generation of scientists, researchers, and innovators.

Education-focused research seeks to address this challenge. It asks not only what students learn, but how they learn, why they persist, and what enables them to thrive. These questions are becoming increasingly important as universities welcome more diverse student cohorts, navigate rapid technological change, and respond to growing concerns around student wellbeing, engagement, and retention.

This study investigates the role of evidence-informed teaching practices in supporting students during the critical transition from school to university. Using a mixed-methods approach, the research draws on student feedback, engagement data, assessment outcomes, and reflective teaching practices collected across large bridging mathematics cohorts. The study examines how scaffolded assessment, authentic disciplinary contexts, collaborative learning, and timely feedback influence students' confidence, motivation, and sense of belonging within STEM.

Preliminary findings suggest that belonging is not simply a by-product of academic success; it is often a prerequisite for it. Students who experience connection, relevance, and support are more likely to engage deeply with learning, persist through challenges, and develop confidence in their academic abilities. These findings highlight the importance of designing learning environments that support not only knowledge acquisition but also students' identities as future STEM professionals.

For early-career academics, this raises an important question: if we value evidence in our laboratories, field sites, clinics, and research groups, why should teaching rely on anything less? Education-focused research is not a departure from STEM research—it is an extension of it. By applying rigorous inquiry to understanding how students learn and succeed, we can strengthen the very foundation upon which future scientific discovery depends. Perhaps the most important question is not whether education-focused research belongs in STEM, but whether STEM can afford to ignore it.

# Oral Contributions

# A Host-Free In Vitro Membrane Feeding System for an Emerging Tick Vector, *Haemaphysalis longicornis*

**Abdul Ghafar** (MVS)

*Haemaphysalis longicornis* is a parthenogenetic three-host tick of increasing veterinary and public health importance and is the principal vector of *Theileria orientalis* in Australasia. Experimental research on this species has been constrained by reliance on live vertebrate hosts, limiting scalability, standardisation and ethical feasibility. This study established a reproducible, host-free in vitro membrane feeding system for adult and nymphal stages. Ticks were fed using a silicone membrane-based system under controlled laboratory conditions. Field-collected adult females were evaluated across six independent experiments for attachment, engorgement, oviposition, egg hatchability and bloodmeal-to-egg conversion efficiency. Nymphal feeding performance was assessed across five experiments. Adult feeding was robust, with 67% (35/52) attachment and 74.3% (26/35) engorgement. Engorged females reached a mean weight of 161 mg and produced a mean egg mass of 67 mg (40% conversion efficiency), with >92% hatchability. Nymphs showed consistently high performance, with 88.4% (76/86) attachment, 97.4% (74/76) engorgement and 90.5% (67/74) moulting success. Engorgement typically occurred within 3–5 days post-attachment, and moulting within 2–4 weeks post-detachment. This system enables controlled, ethical and scalable experimentation and provides a powerful platform for studies of tick physiology, vector competence, acaricide screening and pathogen–vector interactions.

# Integrated strategic bushfire management in a changing climate

**Amy Smith** (SAFES)

Fire regimes are being altered in many parts of the world due to climate change. Changes to fire regimes increase the risk of damage to a broad range of values, including housing, biodiversity, carbon stores, and infrastructure. In response, land and fire management agencies have adopted a suite of risk-reduction strategies such as fuel management through thinning, mulching, and prescribed burning, as well as active suppression and utilisation of a strategic fuel break network for both suppression and prescribed burning activities. While such actions have demonstrated potential to reduce bushfire risk, their effectiveness depends critically on the strategic placement, timing, and type of intervention. Implementation challenges include high financial cost, limited spatial and temporal efficacy, and the growing complexity of fire behaviour under a changing climate. This research uses future climate projections and fire simulation modelling to investigate the most effective approaches for achieving social, economic, and environmental outcomes. The outcomes of this research will help identify cost-effective approaches that are resilient to future uncertainty and capable of reducing risk across Victoria’s diverse landscapes.

# Establishing a model sebaceous skin microbiome to study interspecific microbial interactions in vitro

**Anna Wittwer** (SAFES)

The skin harbours a microbial ecosystem consisting of commensal bacteria, fungi, viruses, archaea, and mites. Three microenvironments comprise the skin surface: sebaceous, moist, and dry. The sebaceous microenvironment is largely populated by bacteria from the genera *Cutibacterium*, *Staphylococcus*, *Corynebacterium*, and *Streptococcus*, as well as *Malassezia* fungi. *Cutibacterium acnes* is particularly dominant in the microbiome of healthy sebaceous skin. Imbalances of the skin microbiota are linked to the development of acne, among other conditions. While external factors play a major role in these perturbations, interactions between members of the skin microbiome are also implicated.

First, a defined medium containing synthetic analogues of key growth substrates (sweat and sebum) has been optimised to facilitate the independent and combined cultivation of four selected skin strains: *Cutibacterium acnes* ATCC 6919, *Staphylococcus epidermidis* ATCC 12228, *Corynebacterium tuberculostearicum* ATCC 35692, and *Malassezia restricta* ATCC 4611. Then we measured the growth response of each strain in response to different concentrations of cell-free supernatant pre-conditioned by the growth of the other strains (4 x 3 combinations).

Given that the four strains studied were selected for their predominance in sebaceous skin, preferences for sweat were higher than expected. Most strains exhibited a tendency to flocculate in liquid media, which made measuring cell densities via absorbance difficult. Preliminary data also suggest that aside from *S. epidermidis*, the selected skin strains are slow-growing in the conditions tested.

# Breast density in phase-contrast breast CT compared to mammography: a mastectomy specimen study

**Ashkan Pakzad** (Physics)

Breast cancer is the most common cancer in women, and breast density is an established risk factor. In clinical practice, breast density is assessed from mammograms, where tissue overlap together with reader judgment remain practical limitations. X-ray phase contrast CT (PCT), performed at the Australian Synchrotron, produces high-contrast 3D images of soft tissue, without compression and without increasing the radiation dose compared to 2D mammography.

We collected PCT scans of fresh mastectomy specimens and trained and applied a deep learning model to automatically separate glandular (dense) and adipose (fatty) tissue in the 3D volumes. From these segmentations we derived two metrics: glandularity (the glandular volume fraction) and heterogeneity (how unevenly glandular tissue is distributed throughout the breast). We compared both metrics against independent density assessments from four radiologists on corresponding mammograms.

Radiologists showed strong agreement with each other, while the PCT-derived glandularity measure showed moderate agreement with radiologist assessments. Though glandularity and heterogeneity were correlated, around a quarter of the variation in tissue heterogeneity was not explained by overall density alone, suggesting that spatial arrangement of glandular tissue carries additional information beyond the simple glandularity measure.

In this specimen study, objective and fine-graded measurements of glandularity and heterogeneity may complement radiologist readings and could offer greater precision. These metrics may have applications in cancer risk assessment and patient-specific radiation dose estimation.

# Accuracy of Visual Condition Scoring in Sheep: A comparison with manual assessment

**Bea Kirk** (MVS)

Many past studies have addressed best management practices to improve ewe and lamb survival on Australian sheep farms. These findings have been effective in informing industry programs.

Thanks to a wide extension network of industry programs, manually assessing ewe body condition score, by feeling the spine and short ribs and assigning a score on a 1-5 scale, is a widely accepted on-farm practice. This allows producers to monitor whether ewes' nutritional requirements are being met on both a flock and individual basis and identify sheep that have additional requirements.

One finding during interviews conducted as part of my PhD on ewe condition score and mortality is that some producers may assess ewe body condition 'by eye' (termed here 'visual condition scoring'), rather than manually. We have found no published data comparing visual assessment of body condition with traditional manual assessment. This comparison would be expected to be complicated by factors such as wool length and genotype.

We propose to compare the accuracy of visual condition scoring with traditional 'manual' assessment in sheep with different wool lengths and genotype. We also seek to find out whether producer factors (e.g. experience) affect the accuracy of visual condition scoring, and why producers choose one method over another. These insights may help increase uptake of best management practices, or offer suggestions on how to modify delivery of current extension programs.

# What’s in Our Poo? Building a Comprehensive Chemical Map of the Human Microbiome

**Ben Harris** (Biosciences)

The gut microbiome plays a central role in human health, with dysbiosis associated with many acute and chronic diseases, including inflammatory bowel disease, gastrointestinal cancers, and mental health disorders. While these associations are increasingly recognised, the underlying causes remain poorly understood. A key missing piece is a comprehensive understanding of the metabolites produced by gut microbes and their interactions with immune cell function.

Here, we present a deep metabolome profiling platform designed to systematically characterise the entire metabolome of the human gut microbiome. A 16-person cohort of human faecal samples were subjected to multi-stage extraction and preparative fractionation, followed by several chromatographic separations coupled to high-resolution mass spectrometry. This approach enables broad coverage across chemically diverse metabolite classes.

To integrate this data, we developed an interactive R Shiny application (MAPS: Metabolite Annotation Propagation and Synthesis) that consolidates and refines metabolite annotations derived from multiple mass spectrometry workflows. By combining targeted and non-target approaches, this platform improves both identification confidence and metabolome coverage, addressing a major bottleneck in metabolomic analysis. Using this platform, we have confidently characterised over 12,000 metabolites, forming what is, to our knowledge, the most comprehensive database of the human metabolome reported to date.

# Loopy Belief Propagation

## **Ben Teo** (Maths and Stats)

I consider a new approach ("loopy belief propagation") for fitting Gaussian models on a phylogenetic network to explain the data observed across present-day species for a continuous univariate or multivariate trait.

We previously showed (https://doi.org/10.48550/arXiv.2405.09327) that a trait evolution model coupled to network can be readily cast as a probabilistic graphical model, so that the likelihood can be efficiently computed using a dynamic programming framework ("belief propagation") defined on an auxiliary graph ("cluster graph") that is tree-structured. Even so, maximum likelihood estimation can grow computationally prohibitive for large complex networks.

Belief propagation can be applied more generally to non-tree ("loopy") cluster graphs to compute a factored energy approximation to the log-likelihood. "Loopy" belief propagation may provide a more practical trade-off between estimation accuracy and runtime. However, the influence of cluster graph structure on this trade-off is not precisely understood.

We conduct a simulation study using our Julia package PhyloGaussianBeliefProp (https://juliaphylo.github.io/PhyloGaussianBeliefProp.jl/stable/) to investigate how varying the maximum cluster size of a cluster graph affects this trade-off. We discuss recommended choices for maximum cluster size, and prove the equivalence of likelihood-based and factored-energy based estimates for the homogeneous Brownian motion trait model.

The talk is based on our preprint (https://doi.org/10.48550/arXiv.2512.18139). I will introduce the key concepts from the ground up.

# Implications of Active Forest Management for arboreal mammals

**Benjamin Wagner** (SAFES)

After native timber harvesting ended in Victoria's state forests in 2024, forests are left as a mix of different ages and histories of use. However, we have limited knowledge about how native tree-dwelling mammals—such as critically endangered Leadbeater's Possum, and the iconic, but endangered southern greater glider, as well as koalas, and other glider and possum species—are using these forests today and in the future.

We tested the use of thermal drones as a new way to detect and monitor these nocturnal animals. Drones can cover large areas (100–200 hectares) and detect animals more effectively than traditional methods like spotlighting on foot, which can be time-consuming, covers less ground, and can miss rare species. Our study found that drones detected more animals and more species, offering a clearer picture of where animals live, what forests they use and in what numbers.

We then used such drones to survey forests of different ages—from freshly logged areas to forests 45 years post-harvest—as well as nearby undisturbed forests. This helped us understand how animals are recovering after logging, and which species are returning to younger forests.

These findings help us better understand how native animals respond to forest disturbance over time and provide valuable information for managing wildlife as Victoria moves beyond native forest logging.

# Computational chemistry: using the electron density to make better models for quantum chemistry

**Dale Lonsdale** (Chemistry)

Theoretical chemistry at the quantum level usually involves solving for the electronic structure of atoms and molecules. This amounts to solving the (electronic) Schrodinger equation given some approximations (i.e. the level of theory) and ideally any introduced error is small and purely quantitative. Obtaining an estimate of, and reducing, the associated error range is a major and active field of research. For small systems consisting of a few atoms, this is trivial. Anything larger, e.g. dozens of atoms, and the so-called "level of theory" (read: computational complexity) used to solve the equations must necessarily be lowered, as modern supercomputers are simply not powerful enough. Inherent in their construction, the inaccuracy owing to a lower level-of-theory cannot be known a priori. Ironically, much of the field of theoretical chemistry relies on empirically benchmarking many such "levels of theory" against a dataset of known results. Only thereafter can error ranges be established and extrapolated to similar chemical systems. Our current work is to explore the idea of using underutilised metrics when conducting benchmarking studies. Traditional metrics use the energy as obtained by solving the Schrodinger equation. Herein, we investigate using the calculated electron density --- a direct experimental observable that is more computationally demanding to obtain and more finicky to work with as compared to traditional energy-based metrics. This talk will present an overview of benchmarking in theoretical chemistry, the problems associated with it, their real-world impacts, and how our contributions may help.

# Improving Harvest Index in Alpine Strawberry for Space Agriculture

**Declan Lafferty** (Biosciences)

Space travel is tough, but it’s better with strawberries! At the ARC Centre of Excellence in Plants for Space, we’re re-engineering alpine strawberries (*Fragaria vesca*) to be a zero-waste, "complete use" crop for deep space missions. My research focuses on improving harvest index (HI), the ratio of edible to vegetative biomass.

Two major traits influencing HI are flowering time and runner production. Early flowering shifts resource allocation towards fruiting earlier in development. However, excessively early flowering limits vegetative growth, reducing photosynthetic capacity and ultimately constraining yield. To address this trade-off, a series of constitutive promoters with varying strengths are being evaluated to fine-tune flowering time and optimise biomass allocation.

Runner production presents a second major constraint. Runners are vegetative structures used for clonal propagation but arise from the axillary meristem (AXM) at the direct expense of fruiting structures. Consequently, HI is strongly determined by AXM fate decisions. Runnerless phenotypes in alpine strawberry are caused by mutations in GA20ox4, a key gibberellin biosynthesis gene. Building on this, I am developing a heat-inducible synthetic switch to enable controlled, on-demand runner production. Heat-inducible promoters are currently being characterised in *F. vesca*.

Together, this work aims to optimise HI to improve crop efficiency, contributing to sustainable food production systems for long-duration space missions.

# Impacts of spatially compounding heatwaves or droughts on production and trade of key food crops

**Elisabeth Vogel** (SGEAS)

Simultaneous climate extremes, such as heatwaves or droughts, across the world's key agricultural production regions are a major food security risk as they can cause concurrent harvest failures and trigger cascading effects via export reductions and food price spikes. Previous studies have primarily investigated the drivers and probabilities of such multi-breadbasket failures, however, the effects on importing countries via trade networks are less clear.

Our study quantified the exposure of food-importing countries to multi-breadbasket failures due to spatially compounding climate extremes, taking into account country-specific consumption patterns and trade relationships. We identify most important food products that contribute most to caloric intake in each country, and quantify the effect of spatially compounding extremes across crop producing countries on the combined production and export of these major crops from origins countries. The results of our study highlight the importance of considering the role of food trade in understanding the impacts of climate extremes on food supply in importing countries; and could be used by decision-makers to identify critical vulnerabilities in the consumption and food trade patterns of individual countries.

# Shadows of the Cosmos: The Theoretical Hunt for Dark Matter

## **Giovani Dalla Valle Garcia** (Physics)

Despite decades of astronomical observations, the vast majority of the universe's matter remains a mathematical necessity rather than a detected reality. To a theorist, dark matter represents the most significant "hole" in our understanding of fundamental physics. It is the invisible scaffolding upon which all visible structure is built, yet its identity remains one of the greatest unsolved puzzles in science.

In this talk, I will pull back the curtain on Dark Matter phenomenology, exploring how we translate grand cosmological mysteries into concrete particle models.

We will discuss:

- The Evidence: Why the motion of stars and the echoes of the Big Bang require a new form of matter.
- The Models: From "Heavy" (WIMPs) to "Light" (Axions), how we hypothesize the properties of something we cannot see.
- The Search: How we design experiments to catch a single, incredibly rare interaction between the dark sector and the world we know.

This session will focus on the logic, the challenges, and the excitement of trying to map the invisible.

# Identification of regioselective flavonoid O-methyltransferases in Eucalyptus leaves

## **Guillermo Garcia Gimenez** (SAFES)

Flavonoids are key plant specialised metabolites that play diverse roles in plant physiology and ecology. Beyond their in planta functions, flavonoids possess health-promoting properties with direct applications in the food and pharmaceutical industries. Methylated flavonoids have received increasing attention due to their enhanced medicinal efficacy compared to compared to non-methylated counterparts. *Eucalyptus* spp. are rich sources of methoxyflavanones in their leaves exhibiting diverse O- and/or C-methylation patterns and abundance. However, the enzymes responsible for flavonoid methylation, as well as other steps in the flavonoid biosynthetic pathway, remain largely unknown. Here, we performed a comparative leaf transcriptomic analysis of two *Eucalyptus* species with contrasting flavonoid profiles, leading to the identification of five candidate O-methyltransferases (OMTs), designated OMT1, OMT2, OMT3, OMT4 and OMT5. The candidate OMTs were cloned and heterologously expressed to characterise their methylation activity, regioselectivity and specificity using a panel of flavonoid substrates. Enzymatic assays showed marked functional diversity, ranging from broad and multi-step methylation (EeOMT1 and EeOMT5) to more selective and position-specific activity (EeOMT2, EeOMT3 and EeOMT4). Differences were also observed in substrate preference between flavanones and flavones, and distinct 3’/4’ regioselectivity patterns. The minor conversion of pinocembrin to alpinetin via 5-O-methylation by EeOMT2, a flavanone with known pharmacological activities, was investigated. A preference for pinocembrin chalcone over pinocembrin, as a substrate was observed in EeOMT2 kinetic assays, suggesting an alternative route within the biosynthetic pathway. Overall, our findings provide a foundation for the metabolic engineering of tailored methylated flavonoids for industrial applications.

# Geological evidence for recurrent magnitude ≥ 6.0 earthquakes on the Para fault beneath the Adelaide Central Business District, South Australia

**Israporn (Grace) Sethanant** (SGEAS)

The Para fault in Adelaide, South Australia, forms a prominent topographic scarp and represents a prominent seismic hazard to the Central Business District (CBD). Its earthquake magnitude potential and rupture history are poorly constrained. Here, we integrate historical and modern borehole data with new surficial geological and fault mapping across the Adelaide CBD to characterise fault traces, earthquake displacements, and slip rates.

Our mapping identifies a fault scarp that displaces Late Pleistocene sediments, with an average fault slip of 1.1 ± 0.5 m. This displacement implies an earthquake of at least magnitude 6.0, and possibly ≥ 6.8. Previously published radiocarbon ages from an unfaulted river terrace indicate that the most recent earthquake predates 8–3 ka. Under Australian National Committee on Large Dams criteria (activity within the last 35 ka), the Para fault may qualify as an ‘active fault’. Up to five major sub-faults appear to comprise the fault zone, with traces inferred to underlie critical infrastructure including hospitals, the airport, and tunnels. Slip rates derived from borehole stratigraphy and Monte Carlo simulations are 65.9 (+5.9/−5.2) m/Myr (Late Pliocene) and 77.4 (+7.6/−6.8) m/Myr for (Early Pleistocene), with a mean of 72.0 (+8.4/−7.3) m/Myr. Combined with constraints on the most recent earthquake, these rates imply recurrence intervals of > 56 kyr. This study provides a transferable framework for characterising earthquake behaviour on faults in slowly deforming, urban settings. By providing slip-rate estimates with their full uncertainty distributions, we enable end-users to select slip-rate values tailored to specific hazard models.

# Designing for nature doesn't cost the Earth

**Jacinta Humphrey** (SAFES)

A key barrier to creating nature positive cities is the unknown cost of implementing and maintaining novel urban designs. To address this gap, we sought to estimate the relative cost of implementing a set of Biodiversity Sensitive Urban Design actions in a greenfield community development in peri-urban Melbourne, Australia. We proposed 18 actions intended to enhance habitat and reduce threats for native fauna, while also supporting human health and wellbeing. Actions ranged from different planting designs to installing habitat analogues and elevated watering points for wildlife. With the assistance of the landholder, we recruited six experts whose knowledge spanned engineering, landscape architecture, urban design, integrated water management, urban planning, urban heat mitigation and public lighting. Using expert elicitation, we asked these specialists to compare each action to a business-as-usual (BAU) scenario, categorising the cost as cheaper, similar, slightly more, significantly more, or prohibitively more expensive than BAU. An online workshop then guided the experts to reach a consensus regarding the relative cost of each action. Overall, our experts concluded that 83% of actions assessed (15/18) were likely to cost the same or only slightly more than BAU, suggesting that Biodiversity Sensitive Urban Design is both feasible and relatively affordable to integrate into new developments.

# Membrane Lipid Dynamics in Macrophage Chemotaxis

**Joshua Forrest** (Maths and Stats)

Macrophages play an important role in the body's innate immune system. They digest smaller external threats, promote healing of internal wounds, and recruit other macrophages using chemokines (chemical signals).

These chemokines bind to specialised receptors on the cell membrane that trigger downstream signals. The receptor CXCR3 in macrophages, for example, is activated by the chemokines CXCL9 and CXCL11. These signals activate membrane-bound phospholipids (PI) which recruit actin remodelling proteins to the cell wall. These membrane lipids can therefore act as a "compass" that point towards the chemical signal and guide the direction of cell motility.

The membrane lipids appear to "lock in" the upstream signal by limiting the ability to change course. How quickly does a macrophage identify the direction of chemotaxis? How does a macrophage respond to competing or conflicting chemotaxis signals? What chemokine concentration is required to override an existing signal?

To answer these questions, we developed a mathematical and computational model of macrophage chemotaxis that combines the internal signalling network cascades with a model of spatially diffused chemokines. We use this model to compare chemotaxis performance under different parameter values and initial conditions. In particular, we measure the relative strength and efficiency of each signal, and the persistence of chemotactic movement in the presence of conflicting signals.

# Unlocking Photodetection Mode Switching from a Simple Lateral Design

**June Yong** (Chemistry)

Achieving multi-mode photodetection within a single device is crucial for nextgeneration optical communication systems, where multidimensional optical information must be efficiently and safely transmitted, processed, and encrypted. Yet, integrating multiple distinct photoresponse modes and dynamically switching between them in real-time typically requires complex architectures or device stacking, which limits scalability and practicality. In this talk, we present a simple lateral photodetector based on a single semiconductor layer directly integrated on a standard SiO2/Si substrate, enabling three well-defined and light-controllable detection modes: transient spikes, continuous square wave, and a hybrid transient-continuous state. This multimodal behaviour emerges from the cooperative interplay of substrate-mediated capacitive coupling, generating ultrafast spike responses (~53 ms), and photovoltaic-driven photoconductive transport responsible for steady-state photocurrents. By modulating illumination intensity and wavelength, the relative contribution of these mechanisms is precisely tuned, allowing real-time switching among three photoresponse states without altering the device structure or bias. Using this lightprogrammable behaviour, we further demonstrate a light-controlled triple-channel secure optical communication platform featuring time-varying encryption keys and multi-modal information encoding and decoding. This work introduces a simple yet powerful strategy for achieving multi-mode photodetection within a single photoactive layer, representing a significant step toward compact, efficient, and intelligent optical communication technologies.

# The business case for foot and mouth disease elimination in Nusa Tenggara Barat, Indonesia

**Kona Adhikary** (MVS)

After a long absence, FMD re-emerged in Indonesia in 2022 and, at the time of writing, the disease is endemic. The government had published guidelines to control and eliminate FMD. For FMD control and elimination programs to be successful, it is essential for stakeholders to have a good understanding of the likely benefits and costs arising from the programs. In this study, we aimed to conduct a cost-benefit analysis of FMD elimination in the province of Nusa Tenggara Barat province, Indonesia. Initially, 10,000 commercial beef farms and 200,000 smallholder farms were simulated. The economic analysis was conducted using two models: (1) a total economic cost model; and (2) a benefit-cost analysis model. FMD positive farms per year was calculated using the exponential decay function (Serway et al., 1989) and seasonal fluctuation (Kumpai and Modnak, 2025). The average cost of FMD for a commercial beef and smallholder farms were 15.6 million IDR and 1.41 million IDR per year respectively. The total cost of the elimination programme for the province was around 162,153 million IDR per year with 83% of the total provincial cost due to vaccination. The benefit cost ratio of elimination by 2035, 2040 and 2045 were 0.924, 0.926 and 0.924 respectively. As BCR is below 1, a lack of financial incentive may impact negatively on progress towards elimination of FMD in Indonesia. Integration of FMD control measures so that it becomes part of a broader animal health program is likely to improve the business case for FMD elimination.

**Reference**

Kumpai, P., Modnak, C., 2025. A mathematical model elucidating the seasonal transmission dynamics of brucellosis in bison. Advances in Continuous and Discrete Models 2025.

Serway, R., Moses, C., Moyer, C., 1989. Modern Physics. Saunders College.

# Adaptive strategies of soil viruses in oligotrophic arid environments

**Li Bi** (SAFES)

Background: In natural environments, viruses must adapt to changing conditions such as variations in nutrient and water availability. However, our understanding of viral adaptation to different soil conditions remains limited.
Methods: We compared soil viral adaptations in nutrient-limited arid inland regions versus nutrient-rich humid coastal regions using viromics.
Results: Our results provide new evidence that viruses employed diverse strategies to persist in oligotrophic arid environments. These strategies include (i) a higher prevalence of potential lysogenic viruses; (ii) a broader host range to enhance infection chances; (iii) encoding specific auxiliary metabolic genes to enhance viral fitness by boosting host resilience against nutrient limitation and aridity; and (iv) maintaining higher micro-diversity and more genes under positive selection to improve viral responses to inhospitable conditions.
Conclusion:
Altogether, we provide new evidence that soil viruses have evolved diverse strategies to survive and proliferate in nutrient-limited and arid environments. These findings have implications for bacteriophage engineering, potentially leading to the development of innovative viral strains better adapted to changing environmental conditions.

# Genome evolution and adaptive potential of symbiotic algae Ostreobium in coral bleaching recovery

**Manuel Poretti** (Biosciences)

In the last decades, climate changes led to global acidification and temperature increase of ocean waters, causing massive events of coral bleaching and mortality. Some coral species showed resilience and recovery responses to bleaching, providing an ideal system to study adaptation to environmental stresses. Our current understanding of coral resilience is primarily based on the coral host and its associated endosymbiotic algae and bacteria living in coral tissue, though these symbionts represent only a minority of the holobiont biomass. Novel research of the calcium carbonate coral skeleton is revealing surprisingly high biodiversity, with over 300 strains of the symbiotic algae *Ostreobium* discovered to date. Notably, *Ostreobium* is the most abundant coral photosymbiont and is hypothesised to buffer corals from the negative effects of bleaching. Through 16S rRNA sequencing, we identified distinct *Ostreobium* strains potentially adapted to high-light environments, suggesting they may play a key role in coral bleaching recovery. Here, we present the first high-quality *Ostreobium* genome assembly, revealing one of the most complex and transposable element (TE)-rich genomes among green algae. Through comparative genomics and transcriptomic analyses, we investigate the role of TEs and structural variants in adaptation to heat and light stress, with particular focus on how *Ostreobium* may contribute to coral bleaching recovery.

# Pricing Frequency Restrictions Curb the Initiation of Collusion

**Mia Tam** (SAFES)

We experimentally test the impact of pricing-frequency restrictions on the price level in a 60 minute, real-time duopoly market. Our unregulated market allows for price changes at any time. We compare this to a real-time market where currently chosen prices are implemented at fixed intervals. Average price levels are significantly lower with price-frequency restrictions. With the help of two additional treatments, we rule out the size of strategic risk, and the decreased possibility of communicating through prices, as drivers of lower price levels in the restricted markets. Instead, discrete pricing periods reduce the ability to successfully initiate collusion by making it harder to establish common knowledge of the mutual willingness to collude.

# Engineering Nanodiamond Surfaces for Enhanced Quantum Biosensing: Achieving Millisecond Spin Relaxation Times

**Mina Barzegaramiriolya** (Physics)

Fluorescent nanodiamonds (FNDs) containing nitrogen-vacancy (NV) defects are emerging as powerful quantum sensors for nanoscale biological imaging and diagnostics. A key measurement protocol, $T_1$ relaxometry, detects fluctuating magnetic fields from target molecules by measuring the spin relaxation rate of the NV defects. However, the sensitivity of this technique is fundamentally limited by magnetic noise originating from the nanodiamond surface, which causes rapid spin relaxation and reduces the baseline $T_1$ time.

In this work, we demonstrate that precise control of the FND surface chemistry can dramatically suppress this noise and enhance sensor performance. We systematically investigate the effect of surface oxidation and core-shell structures on the $T_1$ relaxation times of 100 nm FND ensembles. By applying a controlled silica coating using the Stöber method, we achieved a greater than three-fold increase in the spin relaxation time, improving from $T_1 = 320 \pm 9$ us for commercial bare particles to $T_1 = 1.00 \pm 0.06$ ms for our silica-coated FNDs. Using FT-IR and NEXAFS spectroscopy, we identified that changes to surface functional groups and a reduction in $sp^2$ carbon density are the primary drivers of this enhancement. These findings establish that rational surface engineering can produce bulk-like $T_1$ relaxation times in nanoscale diamonds without requiring complex quantum control sequences, paving the way for highly sensitive, next-generation quantum biosensors.

# Human genetic factors and serine proteases regulate coronavirus infection, insights new drug discovery

**Naveen Vankadari** (Biosciences)

The COVID-19 pandemic, caused by SARS-CoV-2, leads to severe acute respiratory distress syndrome (ARDS). A crucial aspect of coronavirus infection is its unique cell entry mechanism, which involves the processing of its spike glycoprotein. The SARS-CoV-2 spike glycoprotein binds to the host receptor ACE2 and is activated by the host serine proteases Furin and TMPRSS2 through proteolytic cleavage, enabling subsequent viral entry. This study integrates structural, molecular, clinical, and computational approaches to elucidate how TMPRSS2 and Furin recognize and activate the SARS-CoV-2 spike. First, we report the structure of **Furin in complex with the SARS-CoV-2 spike glycoprotein**, revealing how Furin binds to and cleaves the S1/S2 region of the spike. Second, we identified **TMPRSS2 cleavage sites within the S2 domain** of the SARS-CoV-2 spike and determined the structure of its complex, including the catalytic triad. Furthermore, through whole-exome sequencing, we identified a genetic mutation, **rs12329760 (V160M) in the *TMPRSS2* gene**, which is associated with a decreased infection rate in clinically diagnosed COVID-19 patients. Similarly, our analysis revealed that **genetic variants/alleles in *Furin*** modify the binding affinity for the viral spike glycoprotein, potentially explaining some of the observed diversity in infection susceptibility. These findings provide critical insights into the mechanisms and modes of action of Furin and TMPRSS2, which are hallmarks of increased viral virulence and invasion. This comprehensive understanding aids in the development of potential inhibitors targeting this infection pathway, offering promising avenues for high-quality intervention strategies against coronavirus infections.

# Attack of the clone: genomic analysis of Russian wheat aphid in Australia points to invasion by a single clone

**Owen Holland** (Biosciences)

The Russian wheat aphid (*Diuraphis noxia*) is a global pest of cereal crops, first detected in Australia in 2016. *D. noxia* causes leaf damage by feeding, with leaves often rolling and providing protection for the aphids which can protect against pesticides and natural enemies. The manipulation of bacterial endosymbionts in other aphids is a powerful strategy for conferring desirable traits in the aphid host for pest management. Research in this space requires extension to *D. noxia* to manage the pest in Australia, but genomic variation of the host can impact presence and efficacy of desired traits. We aimed to characterise genetic stability of established colonies from wild populations, and variation between Australian populations, as well as international virulence phenotypes, deemed "biotypes". We sequenced and genotyped genomic loci in *D. noxia* lines isolated from 14 infested Australian locations. We show Australian *D. noxia* colonies are almost identical ($\Delta D = 0.002 – 0.021$), likely represented by the invasion of a single clone. In contrast, Australian aphids were genetically distinct from international biotypes ($\Delta D > 0.038$, $P < 0.05$). This study provides reference *D. noxia* genotypes for ongoing investigations into endosymbiont-based control of the *D. noxia* clone in Australia. However, despite strong phenotypic differences, biotypes are not associated with changes in the genome, suggesting other adaptive mechanisms at play, and leaves Australian crops vulnerable to unknown drivers of biotype emergence. Thus, I will also discuss steps required for understanding pathways driving biotype emergence, which must be considered when designing endosymbiont-based pest management strategies.

# Everyday Nature in Urban Streetscapes

## Philippa Bell (SAFES)

Road verges represent a significant proportion of public green space, often with simplified vegetation that offers little value to urban fauna. In Melbourne, Australia, residents are permitted to plant gardens in the portion of residential road verge adjacent to their private property. Referred to as a ‘nature strip,’ these residential road verges are public land that is privately managed. Local councils throughout Greater Melbourne encourage nature-strip gardening for biodiversity benefits; until recently the habitat value of these gardens had not been formally quantified.

I assessed the value of nature-strip gardens for bee, beetle and butterfly biodiversity in the in Melbourne’s north through the experimental addition of habitat gardens in a before-after-control-impact study. Additionally, I explored the attitudes and perceptions of residents and councils towards these gardens. Here, I applied a mixed-methods approach, surveying 510 residents and interviewing four council employees to uncover barriers and drivers of nature-strip gardening in Melbourne.

Through a combination of ecological and social research, I demonstrated that gardens on nature strips can contain the necessary habitat features to attract a greater abundance and species richness of insects compared with the traditional lawn verge. Additionally, I identified a strong appetite for nature-strip gardening to increase the ecological and aesthetic value of streetscapes. This research emphasises the need to recognise road verges as a vital component of urban green space and provides new evidence that can inform policy and practice to enhance biodiversity outcomes from these under-utilised spaces.

# Rheology Across Disciplines: From Material Flow to Sensory Experience

**Phuong Nguyen** (SAFES)

Rheology is the study of material deformation and flow under applied forces. Although it has been widely adopted in engineering disciplines, its potential remains underutilised in many areas of scientific research. This presentation highlights the versatility of rheology as a powerful analytical tool across a range of scientific fields, including food science, crop science, biomedical, and pharmaceutical research. In food science, rheological techniques are increasingly employed to investigate food microstructure and its dynamic evolution during processing and formulation. Rheology also plays a critical role in linking physical properties to perceived texture and sensory mouthfeel during consumption. By combining conventional rheology with tribo-rheological measurements, it is possible to probe both flow behaviour and lubrication properties of foods as a function of film thickness. These measurements closely mimic in-mouth conditions during eating, providing insights into how foods behave as they transition from bulk to thin films within the oral cavity.

In this work, dairy products such as milk and yoghurt with different formulations were studied as representative models for liquid and semi-solid foods. Bulk rheological properties were found to be associated with the perception of thickness as food first enters the mouth. In contrast, tribo-rheological characteristics were strongly linked to sensory attributes governed by thin food films, including creaminess, fattiness, dryness, and mouth-coating. Overall, the results demonstrate that the combined use of rheology and tribo-rheology provides a robust framework for predicting and tailoring sensory mouthfeel, enabling more targeted food design at the early stages of formulation development.

# Are air pollution regulations inadvertently harming the Great Barrier Reef?

**Robert Ryan** (SGEAS)

The International Maritime Organization (IMO) regulated the sulfur content in shipping fuel to less than 0.5 % in 2020. This has brought air pollution benefits for port cities along with a significant cut in global sulfate aerosol emissions in marine areas. This is believed to have resulted in significant direct and indirect impacts on downwards shortwave radiation over the ocean, effectively 'de-masking' a portion of the global warming caused by rising greenhouse gas emissions. In this work we used the Weather Research and Forecasting model coupled to chemistry (WRF-Chem) to calculate the effect of the IMO's sulfate regulations on shortwave radiation and hence and coral bleaching susceptibility at the Great Barrier Reef (GBR). The GBR is already under severe threat from climate change due to increasing ocean temperatures, but incoming direct solar radiation is also understood to be a trigger for coral bleaching. Our study indicates that the 80 % reduction in sulfate aerosol due to the 2020 regulation change may have resulted in up to 11 $Wm^{-2}$ of enhanced downwards shortwave radiation at the GBR sea surface, during the February 2022 lead up to a mass bleaching event. This significantly reduces the approximately 14 $Wm^{-2}$ masking of downwards shortwave radiation provided to the GBR, in the 2022 scenario with higher ship sulfate emissions. Combining our WRF-Chem output with results from coupled ocean-reef-atmosphere simulations suggests that such large reductions in aerosol masking could enhance coral bleaching susceptibility by up to 3 degree heating weeks.

# From crystals to eruptions: Decoding how volcanoes wake up

**Saini Samim** (SGEAS)

The Turkana Basin in northern Kenya, within the East African Rift System, preserves volcanic ash layers interbedded with fossil-bearing sediments linked to early human evolution. While these ash layers are widely used as chronological markers to build evolutionary timelines, they also record the processes occurring within magma systems prior to eruption in a region often considered the cradle of humankind.

A central question in volcanology is: what triggers volcanic eruptions? Understanding explosive eruptions is critical not only for modern hazard assessment, but also for evaluating how volcanism may have shaped past landscapes and environments inhabited by early humans. Here, we address this by investigating pumice—light, highly vesicular volcanic rocks—and their constituent feldspar and pyroxene crystals, as well as volcanic glass, which together archive magma evolution.

High-resolution LA-ICP-MS analyses of ash particles and pumice glass reveal contrasting pre-eruptive behaviours. Some eruptions are triggered by mixing between compositionally distinct magma types, while others reflect the rapid tapping of multiple coexisting magma bodies. In addition, high-resolution LA-ICP-MS mapping of feldspar and pyroxene captures crystal-scale chemical zoning, recording processes such as magma recharge, mixing, and storage. Combined with high-precision $^{40}$Ar/$^{39}$Ar geochronology, these data indicate that crystals can reside in magma reservoirs for tens of thousands of years prior to remobilisation and eruption.

Together, these results demonstrate that eruptions in the Turkana Basin are driven by dynamic, long-lived magma systems, which may have acted as an additional external influence, alongside climatic variability, in shaping hominin environments.

# Martian Meteorites: Insights from the Red Planet

**Tahnee Burke** (SGEAS)

Martian meteorites represent the only physical samples of Mars that can be examined in advanced Earth laboratories therefore provide valuable insights into how the Red Planet works. The phosphates, apatite and merrillite, are accessory phases in all martian meteorites. Given that shergottites are divided into enriched, intermediate, and depleted subgroups based on bulk differences in light rare earth element (LREE) abundance and isotopic compositions, an understanding of phosphate mineral behavior is essential to deciphering the petrogenetic differences between these groups because they are the main REE-bearing phases. We show that it is possible to classify shergottites from a single representative thin section using apatite to merrillite ratios (A10/M, where A10 is apatite abundance × 10) and K-feldspar to phosphate ratios (K10/P, where K10 is K-feldspar abundance × 10). Calculating these ratios provides a quick and straightforward method of chemically classifying shergottites that avoids destroying samples for bulk rock REE analysis. Additionally, the oxidation state of S in apatite has recently been established as an oxybarometer, on the basis that apatite incorporates S in multiple oxidation states, including reduced sulfide ($S^{2-}$), and oxidised sulfite ($S^{4+}$) and sulfate ($S^{6+}$). Established correlations between oxygen fugacity ($fO_2$) and S-XANES spectra were used to calculate $fO_2$ at the time of apatite crystallisation, revealing a large variance in S oxidation state and oxygen fugacity both *across* all samples and *within* individual samples. Thus, detailed examinations of the phosphate minerals provide crucial insights into the final stages of shergottite crystallisation in their associated volcanic systems.

# Evidence-based mosquito control within a One Health framework

## **Veronique Paris** (Biosciences)

Buruli ulcer is an emerging neglected tropical disease with high case numbers in south-eastern Australia caused by *Mycobacterium ulcerans*. Recent research has revealed a complex One Health transmission system involving environmental reservoirs, wildlife hosts, and mosquito vectors. Understanding this multi-host system is critical for developing effective and evidence-based vector management strategies. Here, I present an integrated research program combining population genomics, field ecology, and vector control interventions to better understand and manage the role of mosquitoes in Buruli ulcer transmission in Victoria, Australia. First, genomic analyses of the Australian backyard mosquito *Aedes notoscriptus* reveal patterns of population structure and unexpected long range dispersal across urban landscapes. These findings provide important insights into mosquito movement and help define the spatial scale at which vector control strategies need to operate. Second, I present results from a large-scale mosquito control intervention targeting *Ae. notoscriptus* populations in Melbourne's inner north-west suburbs. This intervention demonstrated that targeted mosquito suppression can significantly reduce vector abundance and was associated with the first documented reduction in human Buruli ulcer cases. Finally, I discuss ongoing genomic research revealing the presence of two distinct mosquito genotypes that co-occur in the same geographic areas but remain reproductively isolated. These cryptic lineages of *Ae. notoscriptus* show strong genetic differentiation despite occupying the same urban environments. Understanding how these lineages differ in their ecology, dispersal, and potential vector competence may provide important insights into the persistence of Buruli ulcer transmission hotspots and the design of more targeted vector management strategies. Together, these studies highlight how integrating genomics, ecology, and public health interventions within a One Health framework can generate actionable insights for managing vector-borne diseases in complex urban environments. Addressing these challenges cannot be achieved within isolated research silos, but instead requires interdisciplinary collaboration across genomics, ecology, epidemiology, and public health to fully understand and manage transmission dynamics.

# Speed Talks

# Low tolerance of two pest aphids to a fungal entomopathogen regardless of chemical resistance status and endosymbiont presence

**Ashritha Prithiv Sivaji Dorai** (Biosciences)

Endosymbiotic bacteria can have diverse effects on the phenotypes of host aphids, that include heat tolerance and fecundity but their effects on fungal entomopathogen tolerance is mostly uncharacterized. Endosymbiont manipulation through microinjection could be used as biological control of aphids, but this depends on the absence of other adverse effects. Novel transinfections of endosymbiont *Rickettsiella viridis* in the green peach aphid *Myzus persicae* (Hemiptera: Aphidinae), result in decreased fecundity and heat tolerance without impacts on chemical tolerance. Here we extend this testing to the fungal entomopathogen, Beauveria bassiana, and also consider the oat aphid *Rhopalosiphum padi* transinfected with endosymbiont *Regiella* as well as a native *Regiella* infection in *M. persicae*.

In the green peach aphid, low concentrations of *B. bassiana* caused complete mortality within 16-20 days, regardless of chemical resistance status of the aphid clone or the presence of *Rickettsiella* or *Regiella* endosymbiont infections. For *Regiella* infected oat aphids, there were only minor effects of this infection on the susceptibility of the aphid to *B. bassiana*. These findings have implications for pest management studies; for instance, green peach aphids infected with *Rickettsiella*, that are chemically resistant may be effectively controlled with *B. bassiana*, and oat aphids infected with *Regiella*, with potentially reduced virus transmission may still be controlled with entomopathogens. The findings suggest that *Rickettsiella* and *Regiella* as biocontrol tools for aphids have no undesirable consequences with respect to entomopathogen-based control.

# Steady-State 3D Thermal Modelling of the Onshore Gippsland Basin

**Belay Mino** (SGEAS)

The onshore Gippsland Basin in southeastern Australia contains significant geothermal energy potential associated with and aquifer hosted within a thick Cenozoic-aged sandstone beneath coal-bearing units. This study developed a 3D steady-state conductive heat flow model to investigate the temperature and thermal energy distribution in the aquifer. A 3D geological framework was constructed using borehole data, structural interpretations, topography, and geophysical constraints. Numerical simulations of conductive heat flow were conducted using Underworld3, incorporating spatially variable anisotropic thermal conductivity and volumetric heat generation. Model boundary conditions include land surface temperatures at the top, borehole-constrained temperatures at depth, and insulating lateral boundaries. The results demonstrate that strong thermal conductivity contrasts, particularly within Cenozoic coal units, significantly influence heat flow and subsurface temperature patterns. Thick coal deposits act as effective thermal insulators, resulting in elevated temperatures at relatively shallow depths. The modelled temperature at the top of the aquifer ranges from approximately 14 to 65 °C. The findings constrain the likely energy content and regional extent of the geothermal energy resource and provide a foundation for future geothermal energy extraction and utilisation in the onshore Gippsland Basin.

# When Wildlife Moves In: Mapping Building Use and Human Tolerance for Evidence-Based Design

**Bethany Kiss** (SAFES)

Animals have long inhabited our buildings alongside us, but our understanding comes from isolated studies, such as reports of a possum in the roof or a bat in our walls. Yet we lack a systematic understanding: which building features serve as habitat, for which species, and how do humans respond to this cohabitation? Analysing 2,399 Wildlife Victoria rescue records from Victoria, Australia (2013-2022), we documented 36 native species using 28 different building features for nesting, sleeping, and foraging. Mammals dominated (78%), including brushtail possums (26%), ringtail possums (24%), microbats (16%), and bare-nosed wombats (10%), followed by birds (17%) and reptiles (2%). Building cavities were most frequently used (40%), followed by shelters (19%), external surfaces (16%), interior rooms (10%), and utility services (6%). Species showed habitat-analogous preferences: arboreal mammals favoured upper cavities while ground-dwellers used foundation spaces. To understand human tolerance, we manually coded perceptions (positive/neutral/negative) and desired actions (stay/leave/no preference) from call descriptions. Chi-square analyses revealed species-specific perception patterns: ringtail possums received 49% positive responses versus 45% negative for bare-nosed wombats. Structural equation modelling demonstrated that building location, species type, and behaviour influenced desired action both directly and indirectly through welfare risk perception as a mediator. A "safety paradox" emerged: animals perceived as unsafe generated simultaneously higher positive feelings (welfare concern) and removal requests. Interior spaces generated 5.2 times higher negative responses than exterior features, with perception mediating approximately 65% of the location-action relationship. These findings provide the first comprehensive inventory of wildlife-building relationships and human tolerance patterns, enabling transition from reactive management to proactive, evidence-based architectural design that intentionally accommodates native wildlife while minimising human-wildlife conflict.

# Just the tip of the death cap: We need to talk about the other killer fungi

**Bridget Walker** (Biosciences)

After being caught up in a high-profile murder trial, death cap mushrooms have recently gained significant media attention. The toxicity of these mushrooms does warrant a membership to the 'killer fungi' club, although unless you're an ill-informed scavenger or eating a beef wellington prepared by Erin Patterson, the risk they pose to human health is relatively small. Rather than mushrooms, the killer fungi club is made up primarily of yeasts and moulds which cause invasive infections that claim the lives of ~2.5 million people annually. Contributing to this high death toll, is a shortage of safe and effective antifungal drugs to treat these invasive infections, and a growing number of fungi that are resistant this limited range. New antifungal agents that can combat these fungi are therefore urgently needed, and the World Health Organisation has recently called for a global effort to prioritise research into these killer fungi to facilitate this. Unlike the poisonous mushrooms, these infectious fungi continue to live and replicate within the human body, and to do that they must be acquiring nutrients from their human host. How they do this exactly is not well understood, but likely to be critical for these fungi to cause disease. To address this knowledge gap and investigate whether disrupting fungal metabolism could be a new strategy for treating these infections, I have been studying genes involved in regulating metabolism in a pathogenic fungus that infects humans. My results show that fungal metabolism is regulated, not only based on available nutrients, but also in response to human body temperature, suggesting that they are relying on specific nutrients to cause disease. Understanding the strategies (or motives) of these killers is the key to outsmarting them, and from this work it seems that we are on the right track.

# Comparative genomics of Ornithobacterium spp. isolated from free range layer chickens with respiratory infections unveils marked genetic diversity and putative new species

**Chathuri Rodrigo** (MVS)

The bacterium *Ornithobacterium rhinotracheale* causes upper respiratory tract infections (URTI) in commercial poultry worldwide. Efficient diagnostic and control of this emerging pathogen require accurate understanding of its classification, prevalence and distribution. The present study explores the genetic diversity of sixty-seven organisms presumptively identified as *Ornithobacterium* and recovered from chickens with URTIs in Australian free-range layer farms. Rep-PCR fingerprinting revealed wide diversity of isolates between and within farms and sites of infection. Forty representative isolates were sequenced entirely and compared to published genomes. Sequence alignments of the rpoB gene supported their classification into the genus *Ornithobacterium*, and 16S rRNA analysis revealed 98.08 % to 100 % identity with *O. rhinotracheale* type-strain DMS15997. However, most isolates gave non-interpretable profiles with the current Multi Locus Sequence Typing (MLST) scheme. Average Nucleotide Identity (ANI) analysis separated the dataset into four genetically divergent clusters. Most of the published *O. rhinotracheale* genomes, including DMS15997, belonged to the largest group, whereas the other clusters contained isolates with ANI values ranging from 84 % to 92 % against DMS15997, suggesting the presence of new species or sub-species. Pan-genome analysis was consistent with these observations, identifying only a small set of core genes (n = 254) in the dataset, while delineating distinct subsets of accessory proteins for each ANI cluster. Core single nucleotide polymorphism phylogeny confirmed further the substantial genetic diversity of the isolates. This study underlines the complex epidemiology and taxonomy of *Ornithobacterium*-associated URTIs in poultry farms and is expected to improve diagnostic and control programs for this pathogen.

# The composition of polyphenols and interactions within polyphenolic mixtures affect permeability and transport across intestinal cells

**Dillani Putri Ramadhaningtyas** (SAFES)

Plant polyphenols are widely studied for their antioxidant properties and their beneficial effects on human health; however, their bioavailability is influenced by factors such as physicochemical properties and the food matrices. This study investigated the influence of polyphenol interactions on intestinal transport using moringa plant as a model system in human intestinal cells (Caco-2 cell monolayers). Different mixtures of polyphenol extracts were prepared by ultrasound-assisted extraction using methanol, ethanol, and acetone at varying solvent–water ratios. Intestinal transport of 10 polyphenols was evaluated across Caco-2 cell monolayers, with apparent permeability coefficients ($P_{app}$) and % transported quantified in the apical-to-basolateral direction to assess bioavailability. Regression modelling demonstrated that the $P_{app}$ of polyphenols, such as gallic acid, syringic acid, sinapic acid, caffeic acid, catechin, epicatechin, and quercetin, was significantly influenced by the concentrations of co-existing compounds, with strong predictive models ($R^2 \geq 70\%$). This indicates inter-compound interactions that modulate permeability within complex extracts. Transport studies revealed generally low intestinal permeability for polyphenols ($P_{app} \approx 0.1–5 \times 10^{-6}$ cm/s; <10% transported), with more lipophilic compounds, such as ferulic acid, displaying higher permeability, whereas hydrophilic compounds, such as gallic acid, showed the lowest permeability. Overall, these findings highlight that polyphenol interactions, physicochemical properties, and extraction conditions collectively influence intestinal transport. Therefore, bioavailability assessment of polyphenols needs to be considered alongside the other polyphenols in the plant food to predict effects upon human health.

# Topography, microclimate and fine-scale thermal heterogeneity influence pollinator foraging behavior

**Elena Kaminskaia** (Biosciences)

Plant-pollinator mutualisms are at risk due to climate change. In addition to coarse-scale climate data, accurate assessment of these risks must incorporate extensive fine-scale microclimatic variation experienced by pollinators in their environment and modulated by diverse landscapes. However, our understanding of microclimate effects on pollination is still lacking.

To bridge this gap, we explored and quantified the relationships between topography, microclimate, and pollinator foraging behavior. We identified key landscape characteristics modulating local microclimates and assessed relative contribution of topography and microclimate to pollinator foraging behavior.

We conducted observations of plant-pollinator interactions in a range of diverse landscapes and microclimates in Tasmania, recording topographic and microclimatic variables along with pollinator behavior (visitation rates and handling time). In addition, we recorded pollinator operative temperature (Te) and sampled flower patch surface thermal heterogeneity.

We found that topography and microclimate were strongly associated with pollinator behavior. Pollinator Te and visitation rates increased at higher solar radiation and air temperature, identifying these microclimatic factors as key drivers of behavior. Surface thermal heterogeneity, modulated by air temperature and solar radiation emerged as another factor strongly contributing to pollinator behavior. On flower patches with high surface thermal heterogeneity, where pollinators were more likely to encounter sub-optimal temperatures, we observed lower visitation rates and increased handling times.

Our findings could improve the accuracy of predictions regarding the effects of climate change on pollination services as well as contribute to our fundamental understanding of ecosystem functioning.

# In vitro coinfection dynamics of *Mycoplasma gallisepticum* and infectious laryngotracheitis virus

**Hasitha Disanayaka Mudiyanselage** (MVS)

Upper respiratory tract infections involving multiple bacterial and viral pathogens are considered major drivers of increased disease severity and transmission dynamics that complicate both diagnosis and treatment. The ability of some pathogens to establish latent or chronic infections further increases the risk of coinfections, especially when primary infection induces immunosuppression. This study investigated the coinfection dynamics of two poultry respiratory pathogens, infectious laryngotracheitis virus (ILTV) and *Mycoplasma gallisepticum* (MG) via in vitro models. Material and methods: Chicken tracheal organ cultures were infected with MG and then superinfected with ILTV. Tracheal histopathology, pathogen growth, and ciliary activity were assessed at 0, 24, 48, and 72 hours after viral superinfection. Sequencing of mRNA was performed on tracheal rings collected 24 hours after ILTV superinfection. Results: Coinfection resulted in statistically lower viral genome copies by 2 days post coinfection, whereas MG replication remained unchanged. RNA-seq analysis revealed the coinfected group had the largest number of significant differentially expressed genes, with unique genes and enriched gene ontologies. Although these were primarily MG-driven inflammatory responses, with the expression of genes responsible for cytokine and chemokine signalling pathways, the presence of ILTV appears to impact certain MG associated pathways in coinfection. Genes associated with ciliary function and cellular structure were down regulated during coinfection, consistent with the observed reduction in ciliary beating, and higher histopathology scores in response to coinfection. Conclusions: These findings provide insights into herpesvirus-mycoplasma interactions and viral interference during coinfection in chickens and may help to advance our understanding of mixed infections.

# Neoarchean apatite reveals late-stage Fortescue magmatism in the Rosemary Island gabbro, Dampier Archipelago, Pilbara Craton

**Ishara Pathirage** (SGEAS)

Constraining the timing of mafic magmatism in zircon/baddeleyite-poor systems remains challenging, where conventional geochronometers are absent or disturbed. This study presents an integrated apatite U-Pb and Lu-Hf geochronological investigation of the Rosemary Island gabbro from the Dampier Archipelago, Pilbara Craton, to establish a robust emplacement age and evaluate isotopic system behaviour. Whole-rock Pb-Pb regression yields an age of around 2,550 Ma, interpreted to reflect post-emplacement isotopic disturbance rather than crystallisation. In contrast, apatite forms a texturally and compositionally coherent magmatic population. Both HR-ICP-MS U-Pb and LA-ICP-MS Lu-Hf data yield emplacement ages of circa 2,680 Ma, indicating that the two independent systems record the same magmatic event. Integration with the regional tectonostratigraphic framework reveals that the gabbro is younger than the Gidley Granophyre (2725 ± 3 Ma; Wingate, 1999) and represents a late-stage intrusive phase of the Neoarchean Fortescue large igneous province. The emplacement age overlaps the Jeerinah Formation (2713-2629 Ma; Hickman, 2023), demonstrating that younger Fortescue Group rocks are preserved in the Dampier Archipelago than previously recognised. These findings highlight the reliability of apatite U-Pb and Lu-Hf geochronology for constraining emplacement ages of mafic intrusions and establish the Rosemary Island gabbro as a new temporal marker for late-stage Neoarchean magmatism and tectonic reorganisation in the Pilbara Craton.

# Can we quantitatively predict bacterial fitness?

**Kaan Öcal** (Biosciences)

All organisms compete for survival, driven by the processes of genetic mutation and natural selection. For bacteria and other microorganisms, evolutionary fitness is largely determined by their growth rate. Yet despite the fundamental importance of this quantity, growth rates are typically measured in laboratory experiments, and our ability to predict them from the underlying biology remains limited. I develop methods to quantitatively predict bacterial growth rates and fitness by combining ideas from biology, statistical physics and machine learning. This allows us to understand how bacteria optimise their fitness in different environments, and provides an evolutionary lens into bacterial behaviour. I will showcase this approach by analysing how bacteria forage for food, and how different ways in which bacteria respond to antibiotics shape their long-term fitness.

# Blue berry extract alters gut microbiota and gut resistome under ampicillin treatment

**Ze Liang** (SAFES)

The increasing prevalence of antibiotic resistance highlights the need for dietary strategies to modulate the gut microbiota and resistome. This study investigated the effects of blueberry extract and its microencapsulated form on gut microbial composition and antibiotic resistance dynamics under ampicillin treatment. Firstly, the phenolic profile of blueberry extract was characterized, identifying key bioactive compounds associated with antimicrobial activity. The extract was subsequently encapsulated into microspheres, and their physicochemical properties, including particle size, morphology, encapsulation efficiency, and stability, were evaluated.

An in vitro colonic fermentation model using human fecal microbiota was employed to assess the impact of encapsulated extracts. Short-chain fatty acids (SCFAs) were quantified to evaluate microbial metabolic activity. Results demonstrated that encapsulated blueberry extract significantly promoted SCFA production, particularly acetate and butyrate, compared to free extract under antibiotic stress.

High-throughput sequencing and resistome analysis revealed that ampicillin treatment disrupted microbial diversity and increased the abundance of antibiotic resistance genes (ARGs). However, supplementation with encapsulated blueberry extract partially restored microbial diversity and reduced the relative abundance of key ARGs. Notably, beneficial taxa such as *Bifidobacterium* and *Faecalibacterium* were enriched, suggesting a prebiotic-like effect.

Overall, microencapsulation enhanced the stability and efficacy of blueberry phytochemicals, enabling targeted modulation of the gut microbiota and resistome. These findings provide insights into the potential of functional food-based interventions to mitigate antibiotic-induced dysbiosis and resistome expansion.

# Plant-microbe interaction of wheat in response to low nitrogen conditions

**Lok Hang (Rex) Chan** (SAFES)

N deficiency in soil constrains plant growth, which beneficial soil bacterial communities may potentially alleviate. However, there is limited knowledge of the plant-bacteria interactions of wheat cultivars with different N-use efficiency (NUE) under N deficiency.

We investigated the responses of root-associated bacterial communities and root metabolites of two wheat cultivars (cv. Mace and Gladius) with reported high and low NUE, respectively, using a glasshouse experiment and a hydroponic experiment with three N levels.

The rhizosphere bacterial community of Mace shifted under N deficiency but not in its root endosphere. Conversely, the rhizosphere bacterial community of Gladius remained unchanged under N deficiency but shifted in its root endosphere. The metagenomic analysis illustrated increased detection of genes related to bacterial growth and motility in the rhizosphere of Mace, but not of Gladius, under N deficiency. A four-fold increase in octadecanoic acid in the root of Mace, but not Gladius, under N deficiency, suggesting the potential role of octadecanoic acid in shaping the rhizobacterial community in Mace with higher reported NUE.

Our study highlights the divergent responses of wheat-bacterial interaction under N deficiency between cultivars. The increase in octadecanoic acid secretion, potentially shaping the rhizobacterial communities and enhancing their growth under N-limited conditions.

# Barley Head Loss: A Farmer's Problem and a Breeder's Challenge

**Nirmal Raj Rajendran** (SAFES)

Barley head loss is an important but under-recognised problem in Australian grain production, especially under hot, dry and windy conditions near harvest. It occurs when the peduncle, the uppermost stem internode below the spike, breaks and causes the ear to detach before or during harvest. This leads to yield loss and creates a major challenge for both farmers and breeders. Despite its practical importance, head loss has received limited research attention, mainly because reliable phenotyping tools and clear selection strategies have not been available. This study aimed to develop a practical framework for selecting barley genotypes with improved head retention. Field experiments were conducted across multiple environments to capture variation in head loss and related traits. A major outcome of this work was the development of a modified Instron-based mechanical phenotyping platform, designed specifically to test peduncle strength and flexibility under a biologically meaningful loading system. Unlike conventional approaches, this method allowed more realistic assessment of structural failure relevant to barley head loss. The platform generated repeatable measurements that helped distinguish strong, flexible and susceptible genotypes. Using these mechanical data together with field phenotypes and agronomic traits, a selection model was developed to identify genotypes with lower head loss risk. This model provides a practical way to combine field performance with biomechanical evidence for breeder-oriented decision making. Overall, this work offers a new phenotyping and selection strategy for barley head loss and provides a strong foundation for breeding more resilient cultivars under increasingly variable harvest conditions.

# Antimicrobial resistance (AMR) and antimicrobial use (AMU) among meat chicken farmers in Bali, Indonesia

**Putu Henrywaesa Sudipa** (MVS)

AMR in animals leads to the development and spread of resistant microorganisms that can impact humans directly, through the food chain, or via the environment. This problem is driven by improper dosing, incomplete treatments, and limited awareness about appropriate antimicrobial use (AMU). A total of 140 farmers who contracted with various poultry companies with closed-house management systems across Bali were surveyed to investigate this issue. The result showed 61% of farmers were unaware of the terms AMR and AMU, although 51% recognised that antimicrobial use restriction exists in Indonesia. Amoxicillin (29%) and trimethoprim-sulfamethoxazole (38%) are the most used antimicrobials, and 53% of farmers used them at inappropriate dosages. 89% of farmers avoided antibiotic use in the finisher period, and 95% obtained antimicrobials from veterinarians or company consultants. Among commonly used biosecurity practices, disinfectant spray (79%) was the most common. This study showed that poultry farmers in Bali still lack awareness of AMR and AMU practices. Improving farmer and veterinarian awareness and monitoring AMU practices were essential for preventing the development of AMR in the future.

# Novel Hidden Satellites and their Evolutionary Dynamics in X-ray Emission Revealed by XR-HERFD

**Ramesh Rijal** (Physics)

Advances in high-resolution X-ray spectroscopy are enabling deeper insight into many-body interactions in condensed matter systems. Here, we report a methodological and experimental advance that allows direct observation of previously unresolved features in manganese and zinc X-ray emission spectra. By combining our in-house developed binary data splicing approach with an extended-range high-energy-resolution fluorescence detection (XR-HERFD) technique, we achieve ~50% improvement in spectral resolution and signal intensity. Measurements performed at the I20-Scanning beamline (Diamond Light Source, UK) reveal, for the first time, statistically robust "Hidden Satellite" structures embedded within the Mn $K\alpha_{1,2}$ emission lines. These features evolve systematically with incident photon energy and are further isolated and validated using principal component analysis (PCA), with statistical significance exceeding $50\sigma$. The Hidden Satellites contribute significantly to the total emission intensity, challenging the long-standing assumption of a constant many-body reduction factor ($S_0^2$). These results reveal unexpected spectral complexity and establish a new framework for interpreting X-ray spectroscopic data.

# In Vivo Characterisation of a Feline Herpesvirus-1 Vectored Immunocontraceptive Vaccine (FHV-GZeG) In Domestic Cats

**Shamali Antoni Baduge** (MVS)

Continuous population growth of feral cats (*Felis catus*) threatens Australia's ecology, economy, and health. Virally vectored immunocontraception is proposed as a sustainable alternative to current population control methods. In this preliminary study, the immunocontraceptive potential of a recombinant FHV-1 vaccine expressing zona pellucida 3 (ZP3) and gonadotropinreleasing hormone (GnRH) was characterised in both previously FHV-1 vaccinated (vac) and unvaccinated (unvac) laboratory cats. Two infection trials were conducted, each with a negative control group (n = 3) and an infection group, with 3 cats intranasally inoculated with the FHVGZeG vaccine and 1 in-contact cat. Virus shedding was detected in nasal and conjunctival swabs of infected cats, and in the conjunctival swabs of in-contact cats by day 4 post-infection. Mild to moderate clinical signs (watery eyes, sneezing, coughing) were observed in 2/3 infected-vac and all infected-unvac cats. No in-contact cats showed clinical signs. Significant serum antibody levels against the transgenic reporter protein were detected in infected-vac cats by day 21, but notin the in-contact cat at any time point. The infected-unvac cats and the in-contact cat showed significant GFP antibody titres by day 14 and 21, respectively. GnRH and ZP3 antibody titres were more variable, with some cats developing high titres. Reproductive tissue histopathology revealed reduced Leydig cell counts in some infected-vac males, but no significant changes in seminiferous tubular diameters or germinal epithelial heights. Zona pellucida loss, thinning, and aberrant formation were evident in infected-unvac females.

# *E. coli* genomics in healthy Nepali poultry extends our understanding of critically important antimicrobial genotypes and potentially a key pathotype of poultry

## **Tulsi Ram Gompo** (MVS)

Genomic surveillance of antimicrobial resistance (AMR) in Nepali poultry is limited. This study has characterised genomic diversity and the AMR genotype of *E. coli* from healthy chickens in Nepal.

We sequenced 434 *E. coli* isolates obtained from faecal or caecal samples from poultry holdings across Nepal. Genotypic characterisation tools applied included MLST (sequence type (ST)), AbriTAMR (AMR genes), EzClermont (phylogroup), and APECtyper (Avian Pathogenic E. coli (APEC) pathotype associated genes, leading to colibacillosis). The core genome phylogeny was constructed to visualise the genotypic features among the E. coli isolates.

Phylogroups B1 (41%) and A (39%) predominated. There were 146 distinct STs identified, including ST155 (11%), ST48 (9%), ST10 (4%), ST117 (3%), ST73 (3%), ST23 (2%) and ST162 (2%) and 29 new STs were confirmed (on Enterobase). Almost half (44%) of the isolates carried an APEC-associated plasmid. Genetic evidence of resistance for critically important antimicrobials, was detected for quinolones (86%; gyrA, parC mutations and qnrS), third-generation cephalosporins (6%; blaCTX-M) and colistin (4%; mcr-1). Comparative genomics revealed three distinct clusters, widely distributed *E. coli* lineages.

A diverse population of *E. coli* was detected in sampled healthy poultry. High proportion of determinants of resistance to fluroquinolones was identified, suggesting high use of this antimicrobial class in poultry production. Genomic surveillance of these isolates has provided evidence that APEC plasmid is widely distributed in healthy chickens along with resistance to critically important antimicrobials. These findings will inform immediate need for AMR management and strategies to minimise economic impact of colibacillosis.