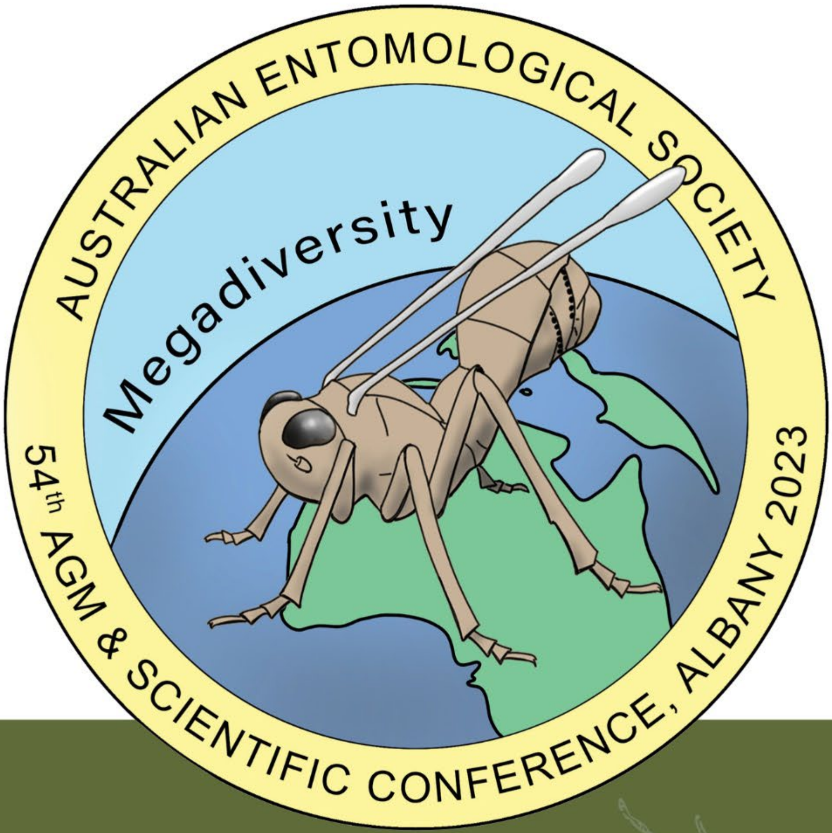

THE 2023 AUSTRALIAN ENTOMOLOGICAL SOCIETY

54th Annual General Meeting & Scientific Conference

12th - 16th November 2023

Albany Entertainment Centre, ALBANY WA

Australian
Entomological
Society

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Conference welcome

The Australian Entomological Society (AES) conference organising committee would like to welcome you to the 2023 conference in regional Western Australia, in the beautiful coastal town of Albany, this 13–15th November.

The Albany area is also known as boodja (country) of the traditional Menang-Noongar people. The Menang people called it Kinjarling or 'place of rain' and evidence of Aboriginal presence in the area dates back to more than 25,000 years, including traditional fish traps (>7,500 years old) which can still be seen in Oyster Harbour, east of Albany.

Albany is Western Australia's oldest European settlement (1826) and Darwin's last stop from 6–13th March 1836 before leaving Australia, where he infamously declared that "*Since leaving England I do not think we have visited any one place so very dull & uninteresting*". Darwin, however, hadn't scratched the surface with his few days of autumn collecting around Albany as, since then, an amazing floral diversity has been uncovered and much of the southwest's insect diversity remains yet to be described. The extent of the diversity in the region prompted its inclusion in Myer et al.'s (2000) original 25 global biodiversity hotspots.

Thus, this year's theme of **Megadiversity** is appropriate for both the region, and invertebrates more generally. We envision that many presentations will attest to the invertebrate megadiversity from the southwest, and beyond. We are thrilled that so many people wanted to join us in Albany, with this year's face-to-face conference marking four years since the last before the pandemic (in Brisbane 2019) and 13 years since the last Western Australian conference. It is a fitting backdrop of spectacular spring scenery and taxonomic diversity in which to celebrate entomology.

With 171 official registrants and several distinguished guests, we hope that you have a fantastic conference full of collaboration and networking discussions!

Melinda Moir
Local conference organising committee member, and AES President

Committees

Local organising committee

Dr Melinda Moir, Department of Primary Industries and Regional Development

Ms Laura Fagan, Department of Primary Industries and Regional Development

Dr Nikolai Tatarnic, Western Australian Museum

Permanent AES organising committee

Prof. Philip Weinstein, The University of Adelaide

Dr Murray Fletcher, Retired, NSW Department of Primary Industries

Ms Patricia Slattery, Flinders University

Symposium conveners

Pollination Prof. James Cook

Bush Blitz Ms Jo Harding and Dr Kate Grarock

Entomological Education Dr David Merritt and Dr Helen Spafford

Session chairs

Invasive Species Ms Laura Fagan and Dr Mark Schutze

Viruses and Vectors Dr Piotr Trebicki

Physiology, Behaviour and Evolution Dr Wei Xu and Prof. Leigh Simmons

Ecology & biology Dr Kirsti Abbott

Anthropogenic impacts & conservation Dr Lachlan Jones and Dr Richard Glatz

Endosymbionts and microbes Mrs Elsie Kinnaird and Dr Vineeta Bilgi

Pollination Prof. James Cook and Dr Katja Hogendoorn

Taxonomy and Systematics Prof. Nate Lo and Dr Nik Tatarnic

Pest management and control Ms Donna Chambers and Ms Svetlana Micic

Collaborations, Engagement & Extension Dr Volker Framenau

General information

SOCIAL FUNCTIONS

Sunday 12th Nov
Welcome Reception. Albany Entertainment Centre, 16.30 - 18.30

Monday 13th Nov
Poster Session. Albany Entertainment Centre.16.30 - 17.30
Student night. Stirling Club. 14 Stirling Terrace, Albany. 19.00 - 22.00

Tuesday 14th Nov
Conference Dinner, Hilton Garden Inn. 19.00 - 22.00

REGISTRATION DESK TIMES
Sunday 12 November from 16:30
Monday – Wednesday from 08:00

INTERNET: Please ensure you have enough data for your internet needs. Internet access through the venue may be available but cannot be guaranteed.

SPEAKERS AND ASSISTANCE: Speakers, please ensure that you take your USB to Tristan at the Speakers Assistance Desk (beside the registration desk) well before your session so that your presentation can be loaded and checked. Ideally, you would do it the day before your presentation during morning tea or lunchtime. Please do not leave this until the last moment.

NAME BADGES: Delegates are requested to wear their name badges at all times during the conference.

MESSAGES: During conference hours **Secretariat** Phone: 0439 149 495 (Ruth Speldewinde).
Please check the notice board by the Registration Desk regularly for messages.

TAXI SERVICE:
Albany City Cabs and Transport
https://albanycitycabs.com.au/
(08) 9841 7000

INSURANCE: the Australian Entomological Society does not accept responsibility for personal accidents, theft and/or damage to the property of conference delegates or accompanying persons.

Conference Organiser
Ruth Speldewinde
Mobile: 0439 149 495

Key sponsors and partners

This conference wouldn't be possible without the support and assistance of our sponsors and partners.

Gold Sponsors

UWA Albany Campus has provided the Great Southern community with access to higher education and research opportunities since 1999. Over 20 years later, the University offers full undergraduate degrees in Arts, Commerce, Science and supports the first year of most majors. The UWA Smart Start program offers an alternative pathway to university entrance for people living in the Great Southern region and postgraduate degrees are offered through the expertise of local research academics. UWA Albany Campus is situated in a biodiversity hot spot featuring some of the most spectacular flora, fauna, scenery and beaches in Australia. The campus is located in the heart of Albany, rich with heritage, history and culture. Affordable, modern and purpose-built accommodation is within easy walking distance of the campus.

UWA Albany provides an opportunity to learn in a high-tech environment with a close-knit, caring university community that supports students throughout their study. Students have the valued experience of learning from internationally recognised experts and academics in various fields whilst enjoying unique experiences as part of their course. A multidisciplinary approach develops critical thinking and creates a valuable foundation of skills and adaptability for a fulfilling, future career.

Bush Blitz is Australia's largest nature discovery program – a unique multi-million dollar partnership between the Department of Climate Change, Energy, the Environment and Water, Parks Australia, BHP and Earthwatch Australia to document plants and animals across Australia. Since the program began in 2010 Bush Blitz has discovered more than 1700 new species and has added thousands of species records to what is already known, increasing our scientific knowledge to help us protect our biodiversity for generations to come.

There are many plants and animals still to be discovered by science. There are an estimated 580,000-680,000 species in Australia, but three-quarters of this biodiversity is yet to be identified. Forty-five per cent of continental Australia and over 90 per cent of our marine area have never been comprehensively surveyed by scientists. Our expeditions target plant and animal groups thought to have the most undiscovered species, including spiders, insects, molluscs and lichens.

The Bush Blitz team sits with Parks Australia and works closely with the Australian Biological Resources Study. Earthwatch Australia delivers education and outreach components of the Program.

Bush Blitz involves specialist taxonomists, indigenous communities, rangers and landowners, teachers, students and BHP employees. Together they are making an extraordinary contribution to the protection of our country's natural heritage.

The Harry Butler Institute, Murdoch University is an environmental research Institute working towards outcomes based on excellence in both scientific research and industry best practice. Honouring the legacy of Australian naturalist, educator and environmental advocate, Harry Butler AO CBE, the Institute is a place where human development and biodiversity can coexist.

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BUSINESS
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Funded by the Western Australian Government through Tourism Western Australia, the City of Perth and member partners across the State, Business Events Perth has been securing high value conferences and incentive groups for Western Australia for 50 years. Their charter is to market, in conjunction with local organisations, Western Australia nationally and internationally as a destination for conventions, exhibitions and incentive travel groups. Business Events Perth wants you to hold your conference in WA and helps you to make it happen. Their bank of in-house expertise and industry knowledge ensures that a meeting, incentive or exhibition planner will have access to current market intelligence, local support and assistance to help bring an event to Western Australia. The great State of WA has so much to offer and Business Events Perth knows what you need to stage a successful event. Contact Business Events Perth to help make your next conference the huge success you want it to be.

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A+
CITY OF
Albany

The City of Albany, spanning 4,312 square kilometres, offers urban and rural living. It manages extensive infrastructure, including 1,600kms of roads, 250kms of pathways, 438kms of kerbing, and 35 hectares of gardens, playgrounds, and sports fields.

Diverse amenities like a library, leisure centre, airport, town hall, day care, and visitor centre cater to the community.

The region's exceptional biodiversity, the renowned National Anzac Centre, boutique dining, whale watching, fishing, and cultural events create an exceptional lifestyle for residents and unforgettable experiences for visitors.

Welcome Event Sponsor

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MUSEUM

The Western Australian Museum is the State’s premier cultural organisation, housing WA’s scientific and cultural collection. For more than 120 years the Museum has been making the State's natural and social heritage accessible and engaging through research, exhibitions, and public programs.

Today, the Museum has seven public locations across our State – and a Collections and Research Centre that houses more than eight million objects.

With more than 500,000 pinned specimens and an uncounted number in ethanol, the Museum’s entomology collection contains representatives of all kinds of insects, chiefly from Western Australia, but including specimens from other Australian states and elsewhere in the world.

Through extensive fieldwork, the WA Museum contributes to significant research outcomes that deepen our understanding of Western Australia's unique environment, and aid in the conservation of biodiversity.

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We proudly manufacture some of the finest entomological equipment available worldwide, right here in Australia.

We are situated in the Northern Rivers of New South Wales, from where we supply products throughout Australia and the rest of the world.

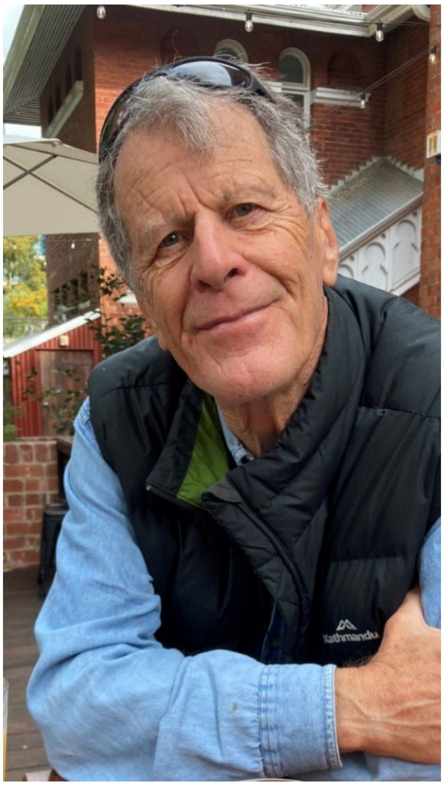
Keynote and invited speakers

Dr Sonya Broughton

Sonya Broughton joined the then Western Australian Department of Agriculture in 1989 as a technical officer working on the Queensland fruit fly eradication effort, in particular the mass rearing and sterilising of flies for use in the Sterile Insect Technique. Sonya then competed her PhD at the University of Queensland researching insects used for lantana biocontrol, and subsequently worked as the Eradication Entomologist on the papaya fruit fly outbreak in far north Queensland. After returning to WA and the Department of Agriculture and Food as it was known by then, Sonya spent the next 16 years conducting research on Mediterranean fruit fly and other horticultural pests including thrips, aphids and mites. She led projects to screen and trial agrichemicals for use in bait and cover sprays, trap trials, evaluation of mass trapping as a control technique, and implementation of area wide management. She has also been involved in implementing integrated pest control programs for several horticultural crops in Western Australia. During the last six years, Sonya has played key roles in several pest and disease incident responses in Western Australia including Queensland fruit fly in the Perth metropolitan area, Mediterranean fruit fly in the Ord River Irrigation Area, citrus canker, tomato potato psyllid, browsing ant, and cucumber green mottle mosaic virus. She has also contributed to nationally significant plant pest incident responses in other states and territories.

This extensive experience with plant pests and diseases culminated in 2019 with Sonya rising to the role of Chief Plant Biosecurity Officer for Western Australia, in the freshly renamed Department of Primary Industries and Regional Development. In this role, Sonya is responsible for the biosecurity and protection of plants and plant industries across Western Australia. The Plant Biosecurity team that she leads manages the risks posed by plant pests and diseases, minimising their impact and leading emergency responses in the event of pest or disease outbreaks. Sonya represents WA at national biosecurity forums, advising government and industry on strategy, policy, and practical reforms in plant health. She is a member of several national committees including Australia’s Plant Health Committee – the peak government plant biosecurity policy and decision-making forum in Australia, chair of the Australian Fruit Fly Technical Advisory Committee, and a member of Australia’s National Fruit Fly Council. Her experience, and current role as Chief Plant Biosecurity Officer for WA, have given her a relatively unique overview of the long-term trends of invasive insects across Australia.

Dr William (Bill) Humphreys



Dr William (Bill) Humphreys, Adjunct Professor, School of Biological Sciences, University of Western Australia; Associate, Western Australian Museum.

Bill is an Associate of the Western Australian Museum and an Adjunct Professor at The University of Western Australia. Immediately after graduating from University of Wales he worked on the Royal Society Expedition to Aldabra Atoll (now part of the Seychelles) and then on the Kenyan fringing reef focussing on echinoderms. He completed his PhD at the Australian National University on the ecology and physiology of wolf spiders (Lycosidae) and subsequently worked on possum and small mammal ecology in Victoria and northern New South Wales based at La Trobe University, Melbourne. He continued wolf spider work from Bath University, UK, conducting field work in Greece and Croatia (then Yugoslavia). He moved to the Western Australian Museum in 1988 where he was involved in biological survey work of the Eastern Goldfields and mesomammals of the Mitchell Plateau (Ngauwudu), Kimberley. Eventually, he was lured into caves by the presence, in the unlikely desert setting, of an arachnid (Schizomida) and expanded the taxonomic coverage by sampling the water table. He eventually specialised in subterranean biology, initially in the caves of Cape Range and Barrow Island and then the Kimberley before starting to examine the groundwater fauna accessible only down boreholes. This work spread throughout the Yilgarn and Pilbara facilitated by, even enabled from, the presence of mineral exploration boreholes in a landscape otherwise lacking caves. The Yilgarn proved particularly interesting owing to the presence of hundreds of isolated groundwater calcrete aquifers found within the extensive palaeodrainage system. Working with colleagues from the University of Adelaide, he has described three sympatric genera of amphipods and more than 100 species of flightless, eyeless subterranean diving beetles (Dytiscidae), by far the most diverse such fauna globally and these have become the focus of diverse physiological, behavioural, ecological and evolutionary studies by numerous authors.

The diversity and notable biogeographical relations of these faunas led to interaction with the EPA and eventually to subterranean fauna becoming an integral part of any environmental Impact assessments in Western Australia. As a result, in this highly mineraliferous State, he has revealed a remarkable diversity of subterranean fauna in this now arid region, largely of species from lineages derived from humid temperate and tropical forests.

He has published about 235 papers, 5 edited books and 37 book chapters.

Dr Cathy Byrne

Dr Cathy Byrne is the senior Curator of Zoology at the Tasmanian Museum and Art Gallery, where she manages a small team of curators and technicians who manage the large collection of Tasmanian animal specimens (over 500,000 specimens) and conduct zoological research. Zoology also participates in many educational public programs promoting Tasmania's unique biodiversity. Cathy is a lepidopterist by trade, and describing and classifying new species of native moths constitutes most of her research at the museum. The national Bush Blitz project has been a pivotal part of the collection of Lepidoptera species for Dr Byrne's curation of the Tasmanian collection, understanding the Tasmanian fauna and taxonomic research.

Cathy has worked on Australian Lepidoptera for almost twenty years and is the only lepidopterist in a paid position in Australia. There is never any shortage of work as there are approximately 21,000 species of moths in Australia with around half of this number undescribed. Her early work on the family Geometridae revolutionised the higher classification of the family and revised the taxonomy of a large proportion of the Australian geometrid fauna. Currently, she is describing new species from a genus of beautiful geometrid moths called satin moths from the genus *Thalaina* and has published many papers on Lepdioptera taxonomy and ecology during her career. She also recently produced an interactive key for the identification of the caterpillars of Australian moths and butterflies. Currently Cathy is the chair of the Council of Heads of Australian Faunal Collections and represents this peak body on many national fora relevant to the support of the nationally distributed faunal collections, taxonomic research and publishing zoological data online.

Conference program

Information Disclaimer: The speakers, topics and times are correct at the time of publishing.
In the event of unforeseen circumstances, the organisers reserve the right to alter or
delete items from the Conference Program

Venue Key: AEC = Albany Entertainment Centre | HGI = Hilton Garden Inn | UWA = UWA Albany Campus

Sunday 12th November		
8.30-14.30 UWA	Australian Entomological Society Board meeting	
13.30-16.00 UWA	*Austral Entomology* Editors Board meeting	
16.30-18.30 AEC	Registration, Welcome Reception: AES President's address (Melinda Moir), UWA representative address (Steve Hopper), WA Museum CEO address (Alec Coles) With invited guests Jeremy Friend (South Coast Regional Manager, Department of Biodiversity and Attractions), Catherine Salmaggi (Manager, Museum of the Great Southern), Scott Neil (Museum of the Great Southern)	

Monday 13th November		
Time	AEC Main Room	Hilton stream
8.00-8.30	Registration desk open	
8.30-9.00	Official opening of conference, Welcome to Country, President's address. With special guest Vernice Gillies	
9.00-9.45	Plenary - Sonya Broughton CPBO	
9.45-10.00	Pat Marks presentation	
10.00-10.30	Morning tea	

Monday 13th November (cont.)		
	General session: Invasive species **Laura Fagan chairing**	**General session: Viruses and Vectors** **Piotr Trebicki chairing**
10.30-10.45	Steinbauer: Holding the biosecurity front line	Xu: A streamlined sampling approach to quantify the invertebrates associated with the Yellow Canopy Syndrome of sugarcane
10.45-11.00	Lassaline: Untangling the web: Dynamics of the Australian terrestrial invertebrate trade	Aftab: Identification of flying aphid species in Victorian grain crops
11.00-11.15	Schutze: A review of the introduced scale insects of Australia	Trebicki: The native Australian spittlebug, *Bathyllus albicinctus*, a potential vector of exotic *Xylella fastidiosa*
11.15-11.30	Cousins: Polyphagous shot hole borer – eradicating an invasive exotic beetle from Western Australia	Selleck: Investigating cercopoid (froghopper and spittlebug) diversity in eastern Australian orchards and vineyards
11.30-11.45	Szito: Morphological identification of the Polyphagous Shot Hole Borer, *Euwallacea fornicatus* (Coleoptera: Curculionidae)	Nancarrow: Transmission efficiency of Australian cereal viruses by four aphid species
11.45-12.00	Gloag: The aftermath of a founding bottleneck: invasive Asian honey bees in Australia	Peck: Adapting to big city life: Using mosquito biodiversity to monitor parasite and virus abundance in urban and peri-urban areas.
12.00-12.45	LUNCH	AES Education committee meeting
	General session: Invasive species **Mark Schutze chairing**	**General session: Physiology, Behaviour & Evolution** **Wei Xu chairing**
12.45-13.00	Theo Evans: modelled worldwide potential distribution of two of the world's most widespread termite invaders	Paris: How often are male mosquitoes attracted to humans?
13.00-13.15	Martoni: Complementarity of morphological and molecular identifications of ants (Hymenoptera: Formicidae) for biosecurity.	Hart: To hair or not to hair, that is the question: the effectiveness of urticating hairs as a defence in the face of larval mortality
13.15-13.30	Tobin: An integrative approach to uncovering the distribution of the pest nitidulid Carpophilus truncatus in Australia	Xu: Functional characterization of moth sensory neuron membrane proteins (SNMPs)

Monday 13th November (cont.)		
13.45-14.00	Steinbauer: Partners in crime: Facilitation of foraging and predation by European wasps through access to a new source of honeydew	McGenniskin: Phylogenetic and environmental determinants of oothecal structure in Australian mantises (Mantodea)
14.00-14.15	Fagan: Safeguarding borders to protect biodiversity	Lewis: Lifetime and reproductive consequences of short-term anthelmintic exposure to female dung beetles
14.15-14.20	Fenner (rapid fire): On the trail of the green snail	Anderson (rapid fire): The density and evenness of dung beetle assemblages increase ecosystem multifunctionality
14.20-14.50	Afternoon tea	
14.50-15.00	Photo shoot of AES conference participants: Pia Scanlon	
	General session: Ecology & biology **Kirsti Abbott chairing**	**General session: Physiology, Behaviour & Evolution cont.** **Leigh Simmons chairing**
15.00-15.15	Brassard: The impacts of fire on ant communities varies among vertical strata: results from a long-term fire experiment in an Australian tropical savanna.	Dashevsky: Venomics of spider wasps (Hymenoptera: Pompilidae)
15.15-15.30	Townsend: Response of carrion-associated flies (Diptera) to mass mortality events in an Australian alpine ecosystem	Lymbery: Warfare in ants and video games
15.30-15.45	Rahman: Developing an age-stage and two-sex life table of the lesser-known Australian fruit fly Northern Territory fruit fly Bactrocera aquilonis (May) from different hosts	Smart: Unravelling the three axes of termite antipredator traits: a comparative analysis of the morphological, chemical, and behavioural defences of Australian mound building termites.
15.45-16.00	Tierney: Nesting biology of alpine *Exoneura* bees: an important high altitude pollinator	Rabia Ali: Self and conspecific host discrimination in the egg parasitoid *Trichogramma pretiosum*
16.00-16.15	Thomas: Using morphometrics to study the ecology and life history of an iconic New Zealand Stag beetle	Heddle: Dung derived from different pasture types influence progeny size
16.15-16.30	Mavende: The effectiveness of automated suction traps in monitoring beneficial parasitoid wasps	Bayless: Contextualising multiple origins of parasitism in acalyptrate fly phylogenomics
16.30-17.30	Poster session	
19.00-22.00	Student Event Night 2023	

Tuesday 14th November		
Time	AEC Main Room	Hilton stream
8.20-8.30	Welcome and Housekeeping	
8.30-9.15	Plenary - Bill Humphreys	
	General session: Anthropogenic impacts & conservation **Lachlan Jones Chairing**	**General session: Endosymbionts and microbes** **Elsie Kinnaird chairing**
9.15-9.30	Tsyrlin: Molecular methods for the other 95% of animal diversity	Bilgi: Evaluation of entomopathogenic fungi against Mediterranean fruit fly.
9.30-9.45	Tweed: Identifying and filling the gaps in the conservation of island endemic insects: a case study from Norfolk Island	Soleimannejad: Novel endosymbionts effects on interaction between grain crop aphids and parasitoids
9.45-10.00	Yagui: Restoring declining species through translocations: A test case using flightless grasshoppers in an urban setting	Tan: Efficacy of microbes from honeybees and the small hive beetle pest to develop traps that affect beetle attraction and oviposition choice
10.00-10.15	Petersen: Ecology and conservation of significant butterflies *Ogyris subterrestris petrina* and *Jalmenus aridus*	Williamson: The role and acquisition of gut bacteria in an Australian native bee
10.15-10.45	Morning tea	
	General session: Anthropogenic impacts & conservation cont. **Richard Glatz chairing**	**General session: Endosymbionts and microbes cont.** **Vineeta Bilgi chairing**
10.45-11.00	Gibb: Rainforest litter invertebrates decimated by high severity burns during Australia's gigafires	Ansermin: *Rickettsiella*, an endosymbiont of aphids, affects microhabitat selection in the green peach aphid, Myzus persicae
11.00-11.15	Jones: Body size of North American solitary bees resilient to warming temperatures in Rocky Mountain wildflower meadows	Dorai: Understanding microbial communities within aphids and their interactions with insecticides
11.15-11.30	Glatz: Enigma moth parasitoid, *Ovaustra aurantia* (Hymenoptera: Braconidae): third partner in a specific tri-trophic interaction at high risk of co-extinction	Qazi: Endosymbionts..manipulators of reproduction in parasitoid wasps?
11.30-11.45	Bell: Building streetscape habitat to enrich biodiversity	Ross: Deleterious endosymbionts for aphid (Hemiptera: Aphididae) control

Tuesday 14th November (cont.)		
11.45-12.00	Arriaga Jiménez: IUCN SSC - Dung Beetle Specialist Group	Whittle: Parental control of offspring microbiota in *Aedes aegypti* mosquitoes
12.00-12.15		Gill: Importance of considering the holobiont in aphid populations for research
12.15-13.00	LUNCH	AES Conservation committee meeting
	Symposium: Pollination **James Cook chairing**	**General session: Taxonomy and Systematics** **Nate Lo chairing**
13.00-13.15	Menzies: eDNA and invertebrate pollinator community comparison: an EPICC survey method comparison study and community analysis	de Souza Castanheira: Taxonomy and systematics of the 'backobourkiine' spiders, a putative new subfamily of orb-weavers (Araneae, Araneidae)
13-15-13.30	Tierney: The tyranny of distance: bee pollination services in the Australasian realm	Prado: Taxonomy and systematics of the artoriine wolf spiders (Araneae: Lycosidae): is *Artoria* monophyletic?
13.30-13.45	Slattery: Disparate continental scale patterns in the floral host breadth of Australian colletid bees (Colletidae:Hymenoptera)	Piper: Population genomics of the Queensland Fruit fly (*Bactrocera tryoni*) species complex.
13.45-14.00	Milla: A hundred years of vegetation changes in Kosciuszko National Park reflected in the pollen record of insect specimens	Mills: Diversity of Australian archaeococcoid scale insects: implications for taxonomy and biological control
14.15-14.30	Cook: Exploring the diversity of Australia's fig-pollinating wasps	Morgan: Taxonomy and systematics of *Chasmoptera* (Neuroptera: Nemopteridae: Nemopterinae): assessing the species status of Western Australia's only spoon-wing lacewing genus.
14.30-14.45	Encinas-Viso: Genetics and ecology of the alpine allodapine bee Exoneura spp.	
14.45-15.15	Afternoon tea	
	Symposium: Pollination cont. **Katja Hogendoorn chairing**	**General session: Taxonomy and Systematics cont.** **Nik Tatarnic chairing**
15.15-15.30	Gilpin: How are flowering plants and pollinators affected by fire and the indirect consequences for pollination services within orchards.	Paphatmethin: Molecular phylogeny of Australian micro-moths in the superfamily Gelechioidea (Lepidoptera)

Tuesday 14th November (cont.)		
15.30-15.45	Gloag: Male bees visit flowers too: understanding the life history and pollen transport of Tetragonula males	Rodriguez: Phylogenomics and taxonomy of the genus Leioproctus (Colletidae)
15.45-16.00	Hilton: Host plant pollination by Australian Heliozelidae (Lepidoptera: Adeloidea)	Zwick: High-throughput collection genomics: Generating DNA reference sequences at scale
16.00-16.15	Hogendoorn: The use of solitary bees in protected cropping	Lo: Evolution and systematics of *Panesthia lata*, an endangered cockroach from the Lord Howe Island Group, and related taxa
16.15-16.30	Taniguchi: To identify native insect species that help avocado flower pollination in Western Australia	Slater-Baker (rapid fire): Investigating the biodiversity and systematics of Australian ‘mummy wasps’ (Braconidae: Rogadinae)
		Beaver (rapid fire): Systematics of the genus Clania, with a preliminary phylogeny of the Australian Bagworm Moths (Lepidoptera: Psychidae)
16.30-17.30	AES AGM	
19.00-23.00	Dinner - Hilton	

Wednesday 15th November		
Time	AEC Main Room	Hilton stream
8.25-8.30	Welcome and Housekeeping	
8.30-9.15	Plenary - Bush blitz speaker Cathy Byrne	
	Phil Carne prize finalist talks x 3:	
9.15-9.35	Heddle - The interaction between *Onthophagus binodis* and cattle dung pH	
9.35-9.55	Contos - Whole-of-community invertebrate rewilding: Leaf litter transplants rapidly increase beetle diversity during restoration;	
9.55-1015	Patricia Henriquez-Piskulich - Dazzled by shine: gloss as an antipredator strategy in fast moving prey	
10.15-10.45	Morning tea	
Wednesday 15th November (cont.)		

	Symposium: Bush blitz **Kate Grarock chairing**	**General session: Pest management and control** **Donna Chambers chairing**
10.45-11.00	Harding/Grarock: Over a decade of species discovery with Bush Blitz	Chambers: Cup half-full: Managing the world’s worst coffee pest, Coffee Berry Borer (*Hypothenemus hampei* (Ferrari); Coleoptera: Curculionidae: Scolytinae) in Papua New Guinea
11.00-11.15	Braby: Systematics, diversification and evolutionary history of butterflies in the tribe Candalidini (Lepidoptera: Lycaenidae)	Bawa: Review of potential use of pheromones for canegrub control in Australian sugarcane: past research and future opportunities
11.15-11.30	Evangelista: Phylogenomics of endemic Australian Ulopinae (Hemiptera: Cicadomorpha: Cicadellidae)	Rahman: Insect response to canola with modified sterol metabolism
11.30-11.45	Leijs: Fourteen years of Bush Blitz native bee surveys: new species and a DNA barcode reference library for Australian bee species.	Regmi: Performance of fall armyworm reared on various horticultural crops
11.45-12.00	Tatarnic: Sticky assassins – the evolution of resin use in Australian assassin bugs (Hemiptera: Reduviidae)	Sarkar: The predator community of tomato potato psyllid, *Bactericera cockerelli* in Western Australia and their field predation
12.00-12.15	Kearney (rapid fire): Yalata-Fowlers Bay Bush Blitz Orthoptera: Caelifera	Farrell: The Future of Banana IPDM - Microbial and Biological Pest Control
12.15-13.00	LUNCH	AES Collection committee meeting
	Symposium: Bush blitz cont. **Cathy Byrne chairing**	**General session: Pest management and control** **Svetlana Micic chairing**
13.00-13.15	Ward: Fluffy bums and their aliens: The distribution and abundance of passionvine hopper, Scolypopa australis (Walker) (Hemiptera: Ricaniidae), parasitoids in Victoria	Micic: Finding French Anystis Mite (FAM), 30 years after its release in grain growing areas of Western Australia
13.15-13.30	Martoni: Biodiversity of the Norfolk Island psyllids (Hemiptera: Psylloidea)	Thia: Genomic investigations of demography and pesticide resistance evolution in an invasive mite pest
13.45-14.00	Constant: What about Platybrachys & c. planthoppers one century after Henry Hacker? (Hemiptera: Eurybrachidae)	Nguyen: Insecticide resistance in Australian serpentine leaf miner, Liriomyza huidobrensis (Blanchard, 1926) (Diptera: Agromyzidae)
14.00-14.15	Yeates: Diversification, cospeciation and host-use evolution in Australian *Fergusonina* (Diptera: Fergusoninidae) galling flies feeding on Myrtaceae	Schmidt: Global, asynchronous sweeps at multiple resistance genes in Aedes mosquitoes

Wednesday 15th November (cont.)		
14.15-14.30	Moir: Checking the pulse: assessing insect diversity, taxonomy and threat status in south-west Australia	Severtson: Determining the economic impact of native budworm (Helicoverpa punctigera) in cereal crops in Western Australia
14.30-15.00	Afternoon tea	
	Symposium: Entomological education **David Merrit and Helen Spafford chairing**	**General session: Collaborations, Engagement & Extension** **Volker Framenau chairing**
15.00-15.15	David Merritt (UQ) The past and the future of entomological education in Australia	Framenau: To describe or to document: making a case for the Fauna Portal using money spiders (Araneae: Linyphiidae)
15.15-15.30	Greg Holwell (NZ) Entomology teaching and learning in Aotearoa New Zealand: past, present and future	Kearney: Digitising a Key chapter in Australia’s entomological history: grasshopper collections of the ANIC
15.30-15.45	Kirsti Abbott (MAGNT) A Brief History of Entomological Education in Australian Museums	Bikaun: Harnessing citizen science for enhanced Varroa surveillance in Western Australia
15.45-16.00	Lyn Cook (UQ) Challenges and benefits of AI for insect identification in tertiary level courses	van der Mescht: Beekeeper experience and training are associated with beneficial practices that prevent the spread of American foulbrood (Paenibacillus larvae)
16.00-16.15	Andy Howe (USC) Insect Investigators: a school-based citizen science project on arthropod diversity	Guthrie: MyPestGuide® - Making taxonomy sexy again by connecting scientists with an engaged community
16.15-16.30	PANEL DISCUSSION - Helen Spafford	Schutze: The AES Collection Committee arisen from the ashes of CHAEC
16.30-16.45	PANEL DISCUSSION - Helen Spafford	Ridsdill-Smith (rapid fire): An important and victorious science: the International Congresses of Entomology
16.45 - 17.30	Awards presentation & wrap up - Hand over to Cathy Byrne to speak about 2024 conference	
17.45	Conference conclusion	Vacate the venue AEC by no later than 6.30pm on Wednesday 15th November

Thursday 16th November		
7.00-16.00	Optional Field trip - Stirling Ranges and Twin Creeks	

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A Brief History of Entomological Education in Australian Museums

Abbott, K. (1), G. Monteith (2), K. Walker (3) & N. Tatarnic (4)

(1) Museum and Art Gallery of the Northern Territory, Conacher St, The Gardens, NT 0801; (2) Queensland Museum, South Bank, South Brisbane, QLD 4101; (3) Melbourne Museum, Nicholson St, Carlton, VIC 3053; (4) Western Australian Museum, Kew St, Welshpool, WA 6106.

A traditional image of a natural history museum often depicts colourful butterflies, giant beetles and spiny mantids jam-packed into wooden drawers. In these displays their ecology, behaviour and significance remain a mystery but their beauty has inspired artists and naturalists for centuries. Fast forward to a modern museum and entomology is more than beautiful specimens in a drawer. Entomological education programs in Australian museums stem from exhibitions, collections and curatorial expertise, and have ranged from national workshop series to on-Country learning, loan kits, school incursions and animal husbandry books. While there have been hundreds of examples of education programs that include insects at State institutions, this presentation will highlight case studies from Museums Victoria (MV), Queensland Museum (QM), Western Australia Museum (WAM) and Museum and Art Gallery of the Northern Territory (MAGNT) that illustrate the incredible investment and impact made over the past 40 years in entomological focused education.

Identification of flying aphid species in Victorian grain crops

Aftab M (1), P. Trebicki (2,3), N. Nancarrow (1,2) & B. Rodoni (4,5)

(1) Agriculture Victoria, Horsham Centre, 110 Natimuk Road Horsham, VIC 3400, Australia; (2) School of Agriculture and Food, The University of Melbourne, Parkville, VIC Australia; (3) Applied BioSciences, Macquarie University, Sydney, NSW Australia; (4) Agriculture Victoria, AgriBio Centre, Bundoora, VIC Australia; (5) School of Applied Systems Biology, La Trobe University, Bundoora, VIC Australia.

Aphids pose a significant threat to grain crops through direct feeding damage and as virus vectors. The hot and dry southern Australian climate keeps aphid populations low during the summer but in some years, given the right conditions, they can persist in high numbers. High pupation levels in autumn or early winter increase the risk of virus spread to emerging crops. Effective virus management relies on aphid monitoring but reliable aphid population data is only available for selected locations in Victoria. Aphids were monitored using yellow sticky traps from January to December in 2021, their numbers were counted, and majority of the specimens were identified to species level. Seventeen aphid species were identified, five were abundant: Russian wheat aphid (RWA, *Diuraphis noxia*), plum aphid (*Brachycaudus helichrysi*), green peach aphid (*Myzus persicae*), oat aphid (*Rhopalosiphum padi*) and corn aphid (*R. maidis*). The population of RWA was highest. Seven species were trapped in low numbers: pea aphid (*Acyrthosiphon pisum*), turnip aphid (*Lipaphis pseudobrassicae*), cabbage aphid (*Brevicoryne brassicae*), blue- green lucerne aphid (*Acyrthosiphon kondoi*), cowpea aphid (*Aphis craccivora*), lettuce aphid (*Nasonova ribisnigri*), and tulip bulb aphid (*Dysaphis tulipae*). The presence of another five species was negligible: green sowthistle aphid (*Hyperomyzus lactucae*), spotted alfalfa aphid (*Therioaphis trifolii forma maculata*), ornate aphid (*Myzus o*rnatus), silver birch aphid (*Euceraphis betulae*) and mealy plum aphid (*Hyalopterus pruni*). The population of oat and corn aphids peaked in mid-October. The populations of green peach aphid and plum aphids peaked between mid-October to mid-November. The population of RWA peeked in mid-November to end of November. These results highlight that aphid monitoring is important before the application of any control measures.

Self and conspecific host discrimination in the egg parasitoid *Trichogramma pretiosum*

Ali, R., V. M. Alvarez, P. W. Taylor , S. Akter , R. Regmi , B. Mainali

Applied Biosciences, Macquarie University, North Ryde, NSW 2122

The effectiveness of biocontrol agents in managing pest populations depends on their ability to efficiently locate and target specific pests while minimizing interactions with non-target organisms. Host discrimination, capacity to differentiate parasitized host from the non-parasitized ones, plays a crucial role in achieving this objective by enabling optimal resource allocation. It has been suggested that the evolution of host discrimination is driven by the need to enhance the reproductive success of female parasitoids marking preferred hosts. *Trichogramma pretiosum* (Hymenoptera: Trichogrammatidae), a commercially available egg parasitoid, has potential in managing the fall armyworm (FAW) *Spodoptera frugiperda* which has recently established in Australia and posed a serious threat to horticultural crops. Efficacy assessment of *T. pretiosum* in discriminating self- and con-specific hosts is essential for its reproductive success along with higher rate of parasitism of the host. We conducted a study to investigate the self- and con-specific host discrimination in commercially produced *T. pretiosum* on eggs of Australian population of FAW. The study compared the behaviours of self- and con-specific gravid females under choice and no-choice conditions and recorded all behavioural events using high-definition digital video cameras. The recorded videos were analysed using event recorders J-watcher and BORIS software. Furthermore, we examined the influence of superparasitism on oviposition behaviour and assessed parasitism rate and sex ratio in relation to superparasitism. The findings indicated that *T. pretiosum* possesses host discrimination abilities, with self-females exhibiting more pronounced rejection behaviours. Superparasitism was found to impose significant time costs on ovipositing females, but it did not significantly affect the parasitism rate or sex ratio of *T. pretiosum*. Overall, the study concluded that *T. pretiosum* can discriminate between parasitized eggs during competition among self- and con-specific females. As a gregarious parasitoid on FAW eggs, *T. pretiosum* could be an effective biocontrol agent for managing FAW populations.

The density and evenness of dung beetle assemblages increase ecosystem multifunctionality

Anderson, D.J. (1,2), J.D. Berson (1,2), R.K. Didham (1,2), T.A. Evans (1) & L.W. Simmons (1)

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Humanity depends upon natural ecosystem functions, but just how organisms perform ecosystem functions is debated. There are numerous components of biodiversity, with early ecosystem function research focussing on the role that species richness plays in driving a single ecosystem function. In general, positive, asymptotic relationships have been reported, indicating functional redundancy with increased species richness. However, recent research is now indicating that a broader view of the biodiversity-ecosystem function relationship is possible by assessing additional components of biodiversity and multiple ecosystem functions.

We used artificial assemblages of dung beetles (Coleoptera: Scarabaeidae) to investigate two overlooked components of biodiversity, density and species evenness, and their influence on the performance of multiple ecosystem functions. The ecosystem functions measured were: the reduction of cattle dung (which fouls pasture), the reduction of dung moisture content (which limits nuisance dung-breeding flies), as well as plant shoot growth and plant root growth. Our artificial assemblages were comprised of various mixtures of three summer-active species of similar size: *Onthophagus taurus*, *Onthophagus binodis* and *Euoniticellus fulvus*. These assemblages were placed in free-draining pots in a glasshouse for 13 weeks.

We found that when dung beetles were present, up to 71% of the dung was removed from the soil surface, the moisture in the remaining dung reduced by 63% and ryegrass shoot and root growth increased by around 200% each. Increasing beetle density increased dung removal, decreased dung moisture content and increased total shoot weight. Increasing evenness increased dung removal and decreased dung moisture, but had no influence on shoot and root growth.

These results indicate the larger, more complete value that dung beetles provide to agroecosystems, and the need to consider multiple metrics and functions when conducting biodiversity-ecosystem function research.

Rickettsiella, an endosymbiont of aphids, affects microhabitat selection in the green peach aphid, *Myzus persicae.*

E. Ansermin, P. Stott Ross & A. Hoffmann

Pest and environmental research group, University of Melbourne, Bio21 institute, 30
Flemington Rd, Parkville VIC 3052.

The green peach aphid, *Myzus persicae* (Sulzer) (Hemiptera, Aphididae), is a widespread insect that has captured the interest of researchers because of its economic importance in the agricultural sector. It is a pest to more than 400 plant varieties, many of which are important crops and ornamentals. Control of this pest has mainly involved agrichemicals, but pesticide resistance and environmental issues have raised the need for exploring novel control options. Recent efforts to control this pest in a sustainable way have brought attention to bacteria living in symbiosis in the body of the aphid. These endosymbionts can provide the host with benefits as well as costs, particularly when novel bacteria are introduced into hosts. Past research on endosymbionts mainly focuses on common life-history traits, while behavioural alterations have been neglected. Here we explore the effect of the secondary endosymbiont *Rickettsiella viridis* on *Myzus persicae* in terms of microhabitat selection. We find that aphids hosting *Rickettsiella* lack the characteristic preference for the abaxial surface of bok choy leaves, suggesting a modification of the aphid's behaviour. Ongoing experiments aim to determine if endosymbiont-induced changes in behaviour and body colour affect the host's susceptibility to predation, its activity, and probing behaviour. Our results have implications for the use of endosymbionts in aphid pest control programs, and their role in aphid evolution.

Dung Beetle Specialist Group (IUCN SSC), Red Lists to facilitate conservation efforts

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The Dung Beetle Specialist Group (DBSG) was proposed and officially accepted in 2022 by the International Union for Conservation of Nature Species Survival Commission (IUCN SSC). Red listing is a critical tool for conservation biologists, providing an assessment of a species' risk of extinction. The IUCN Red List has become a benchmark for global conservation efforts. The DBSG aims to develop IUCN Red Lists for dung beetles worldwide, providing valuable information on their conservation status and potential threats to their survival. Dung beetles are important ecosystem engineers who are critical in nutrient cycling and maintaining healthy soils. The DBSG recognizes their vital role in maintaining ecological balance and biodiversity and works towards their conservation. The DBSG brings together experts from different countries, with a wealth of knowledge on dung beetles. This collaboration is essential in creating comprehensive Red Lists that broadly understand their distribution and population trends worldwide. Such lists are critical in prioritizing conservation actions and identifying critical habitats for species survival. Invertebrates, such as dung beetles, are often overlooked in conservation efforts, so having a specialist group dedicated to them is crucial. The DBSG works towards raising awareness about the importance of dung beetles, and will provide expert advice and guidance to policymakers, conservation practitioners, and the general public. Establishing the Dung Beetle Specialist Group is a significant step towards improving dung beetle conservation efforts globally and in Australia.

Apis florea an emerging threat to Australia

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The Red dwarf honey bee, *Apis florea* Fabricius, 1787 is native to southern Asia and parts of the Middle East. Their workers range from 7 – 10 mm in size, with a red-brown abdomen and black and white bands. They are a social open nesting species characterised by a single vertical comb which can be hanging from vegetation or human structures. *Apis florea* colonies aggressively target resources and will readily abscond to areas with more favourable conditions. They are non-aggressive to humans and exhibit cryptic nesting making colonies hard to detect. *A. florea* has successfully invaded Singapore, Peninsula Malaysia, Indonesia, East Africa, Taiwan, and the rest of the Middle East. In the last 3 years there have been four known incursions into Australia. The Brisbane (2020), Perth (2021) and Melbourne (2022) incursions were quickly detected and eradicated before they could establish. The most recent incursion was detected in March 2023 on the Burrup Penisula in Western Australia, and is under active eradication, with 12 colonies being destroyed to date. *Apis florea* poses a threat to Australia through direct competition for resources with native wildlife and the European honey bee (*Apis mellifera*). *Apis florea* has been reported to rob European honey bee hives in other countries and is known to act aggressively towards them when foraging. They can carry viruses exotic to Australia and brood mites including *Euvarroa sinhai*. While the ability for *E. sinhai* to cross into *A. mellifera* is uncertain it has been present in the last three incursions of *A. florea* and is known to vector some bee viruses. *Apis florea* poses a clear threat to the Australian bee industry and the environment, and the frequency of incursions is a great concern.

High molecular weight DNA purification from arthropods

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Ticks transmit the greatest diversity of pathogens of any vector arthropod. For this reason, ticks are a significant focus for DNA analysis, not only their DNA but also because they harbour host and microbiome content. Traditionally, successful PCR amplification can be obtained from low input copy number and fragmented DNA. However, many next generation sequencing methods require high quality and quantity DNA.

In this study, various tissue disruption techniques (liquid nitrogen bead homogenisation, slicing with a scalpel blade, and undestroyed), amount of tissue (whole ticks, bisected ticks, and legs only), and extraction kits (Qiagen Blood and Tissue and Qiagen MagAttract) were compared to evaluate the quantity and fragmentation of purified genomic DNA from adult female ornate kangaroo ticks, ***Amblyomma triguttatum.*** In terms of DNA quality, the use of liquid nitrogen bead homogenisation of tick tissue resulted in highly fragmented genomic DNA, while slicing ticks generated longer genomic DNA. Further quality improvements were observed when the slicing disruption method was combined with the Qiagen MagAttract Kit. Regarding DNA quantity, whole ticks extracted using the Qiagen Blood and Tissue kit produced the highest yield of DNA; homogenisation, slicing, non-destructive extraction methods yielded 7.09, 8.07 and 0.01 ng/µL of DNA per mg of tissue, respectively. Additionally, bead homogenised tick legs yielded 0.71 ng/µL per mg of tissue, while sliced whole ticks using Qiagen MagAttract yielded 2.57ng/µL per mg of tissue.

The findings of this study indicate that while applications requiring higher quantity of DNA regardless of fragmentation (i.e. for traditional targeted PCR applications) either application will produce sufficient genomic data, for applications requiring a high molecular weight DNA input (whole genome or long-read sequencing applications), it is more beneficial to homogenise the entire specimen using a scalpel blade than use liquid nitrogen bead homogenisation.

Review of potential use of pheromones for canegrub control in Australian sugarcane: past research and future opportunities.

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In Australia canegrub larvae, which include 20 species of Melolonthine scarab beetle species, feed on the sugarcane root system. The resultant damage lowers crop yield and sugar content. Since the early 1900s, canegrubs have posed a considerable problem for the Australian sugarcane sector. They continue to be the most important insect pest of sugarcane, resulting in significant economic losses with an estimated cost of over $40 million annually. For decades, the most effective management approach for canegrubs has been chemical insecticides, which effectively lower the pest population, thus avoiding economic loss. However, the use of some chemical insecticides has led to significant environmental issues, such as soil and water pollution and the emergence of insecticide resistance in canegrubs. Current and future initiatives for canegrub management are motivated by sustainability and environmental responsibility. In response to these concerns, pheromone-based control techniques have gained some attention as potential alternatives to traditional chemical insecticides. This approach could potentially lead to the disruption of the adult beetle behaviour through the action of either repellent or attractant properties of chemical pheromones. In other agricultural industries pheromone-based pest control methods have been shown to be effective, environmentally friendly, and non-toxic to other beneficial organisms. We discuss in this review, the history, advances, and efficacy of sugarcane pest pheromone research in Australia. We also highlight the challenges and limitations of using pheromones to manage canegrubs and suggest potential research avenues.

Contextualising multiple origins of parasitism in acalyptrate fly phylogenomics

Bayless, K. & D. Yeates

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Improved sampling of fly genomes and transcriptomes makes it possible to address previously intractable challenges. Life history transitions to phytophagy and parasitoidism have occurred multiple times in acalyptrate fly larvae (Diptera: Schizophora). To construct this dataset, we sequenced representatives of hundreds of key fly taxa. We inferred compelling phylogenetic hypotheses of three major lineages based on 3000 nuclear protein coding gene markers. An expanded Sciomyzoidea was robustly recovered as sister to all other Schizophora. In Sciomyzoidea, parasitoid lineages group together contradicting morphology-based classification. Sciomyzidae, parasitoids of aquatic molluscs, are more closely related to conopoid insect parasitoids than to aquatic sciomyzoids. Tephritoidea represents a lineage with variously modified egg-laying oviscapts. Parasitoidism evolved multiple times within Tephritoidea; bird parasites were placed within carrion-feeding Piophilidae and a lineage attacking scarab larvae rendered plant-feeding Tephritidae non-monophyletic. The aculeate oviscapt used to damage plant tissue predates phytophagy and was concurrently adapted for parasitoidism. Within Ephydroidea, morphologically modified Cryptochetidae scale parasitoids and Braulidae bee lice are close relatives to Drosophilidae, an extraordinarily diverse family which includes genetic model organisms and agricultural pests. A phylogenetic framework incorporating multiple lineages for the first time revealed that while braulids and cryptochetids are placed within Drosophilidae, they are not close relatives of bee or scale parasitoid drosophilids. These novel inferences examined in light of natural history and functional morphology reveal the complex origins of parasitoidism. Exploring parameter space and taxonomic subsampling suggest that contrasting molecular evolutionary regimes confound some relationships. Improving taxon sampling and refining natural history trait data are powerful tools to reduce this potential bias. Funding from the Australian Biological Resources Study is supporting revisionary studies of enigmatic Cryptochetidae. Numerous new species are being described with museomics illuminating parasitoid host records in order to improve the taxon sampling and phylogenetic trait data underpinning acalyptrate fly evolutionary studies.

Building streetscape habitat to enrich biodiversity

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Urbanisation is occurring at an extraordinary rate and scale, and the habitat loss and fragmentation associated with urbanisation is considered a major threat to biodiversity, including insect diversity, worldwide. Nevertheless, the urban landscape provides many unique opportunities for conservation, with repeated calls throughout the literature for creative conservation actions in novel urban green spaces.

This study focusses on nature strips, as they are an abundant and underutilised green space in Melbourne. Traditionally composed of lawn and a street tree, these spaces provide few resources to the insects that rely on a complex understory and/or shrubby vegetation for food, shelter and nesting habitat. While there is evidence that increasing habitat availability in more traditional urban greenspaces (e.g. parks and golf courses) can assist in biodiversity conservation, there has been little prior research on the biodiversity value of habitat additions on nature strips.

This study uses a paired Before-After-Control-Impact (BACI) design to explore the value of nature strip habitat gardens for insect biodiversity. Habitat gardens are curated specifically for the set of insect species known to inhabit the area, and include resources for adult and juvenile nutrition, nesting and shelter. Come along as I present the experimental design and data collection methods, and outline how I managed resident and council expectations and preferences to manipulate habitat on 14 nature strips in the City of Merri-bek.

Harnessing citizen science for enhanced Varroa surveillance in Western Australia

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The parasitic varroa mite (*Varroa destructor*) is considered the most significant threat to honey bee (*Apis mellifera*) health globally. In 2022, varroa mites were detected in beehives throughout the mid-north coast of New South Wales, highlighting Australia's vulnerability to undetected incursions. Western Australia's (WA) Department of Primary Industries and Regional Development maintains an active bee surveillance program that uses sentinel hives at ports, and conducts apiary inspections at pollination, trade, compliance, and outreach events. However, the Department's resources are limited and only a small percentage of WA's 57,000 registered beehives are visited by government apiary inspectors each year. Since the launch of the Australian Honey Bee Industry Biosecurity Code of Practice in 2016, all beekeepers have been encouraged to check their apiaries for exotic mites twice per year. To assess beekeeper participation and improve data collection, the Department launched a Microsoft Forms-based varroa surveillance reporting survey in March 2023, which coincided with the national Bee Pest Blitz April campaign. The reporting tool and campaign have successfully mobilised a significant number of beekeepers to actively contribute to surveillance efforts, effectively doubling the Department's annual varroa surveillance dataset and geographic coverage. Between 9 March and 10 May 2023, the Department's form successfully collected varroa surveillance data from 539 (11%) of WA's registered beekeepers who surveyed a total of 1,782 beehives. No varroa were detected in WA, providing greater confidence in the state's varroa-free status. Perhaps more importantly, the reporting component of the campaign has prompted many beekeepers to reconsider ineffective passive surveillance methods, acquire surveillance equipment, and adopt active roles in bee health surveillance. The Department aims to increase participation in its collaborative bee surveillance approach and will continue building industry capacity for surveillance through outreach and education activities. To learn more about reporting bee pests and surveillance in WA, visit www.agric.wa.gov.au/reportbeepests.

Alternative disinfestation for market access of crops affected by tomato potato psyllid and Mediterranean fruit fly

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(2) AgHort Solutions Pty. Ltd., Doubleview, WA 6018.

Abstract: Tomato potato psyllid (TPP, *Bactericera cockerelli*), is a serious pest of solanaceous crops and some Convolvulaceae crops and is currently limited to Western Australia (WA). Another destructive pest species that also shares some host plants with TPP is the Mediterranean fruit fly (Medfly, *Ceratitis capitata*), which is endemic to WA. Both species are associated with significant economic losses indirectly affecting market access of horticulture commodities. Industry stakeholders in the eastern states and territories are concerned about the impact of both pests if these were to spread to their jurisdictions. The current strategy is to confine both pests to their current distribution, prevent their spread, surveillance, and minimise their impact on domestic and international trade. Presently, methyl bromide (MB) fumigation is used as an endpoint postharvest treatment option against TPP and Medfly in most produce. So, developing additional treatments against both pests in their common host crops would support trade from WA.

Three alternative treatments were investigated: low dose MB (LDMB), ethyl formate (EF)/Vapormate® and phytosanitary irradiation (PI). Eggs of TPP on tomato, and Medfly in capsicum, chilli, eggplant, and tomato were found to be the most tolerant stage in LDMB trials. Several treatment doses were identified that were effective in killing more than 30,000 insects with no survivors and satisfied the quarantine standard of 99.99% control in large-scale trials. Four LDMB doses against Medfly eggs in red capsicum and two new shorter dose rates against TPP eggs were identified. Effective dose rates of EF, Vapormate® and PI against TPP life-stages were also identified. The information generated in this research will help to gain and maintain access to interstate markets and negotiate international access and trade. It will ensure continuity of supply of WA grown produce to consumers and containment of TPP to its current distribution range.

Evaluation of entomopathogenic fungi against Mediterranean fruit fly

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Department of Primary Industries and Regional Development, South Perth, WA 6151.

Abstract: Mediterranean fruit fly (Medfly, *Ceratitis capitata*) is an economically important endemic pest species in Western Australia (WA) that attacks a wide range of fruits, vegetables, and nuts. It is associated with serious economic losses indirectly affecting market access and trade of horticulture commodities. Medfly management options in WA typically include bait spraying (protein and insecticides), cover sprays, mass trapping and lure-and-kill, sterile insect technique (SIT), sanitation, and area wide integrated pest management (IPM). Similarly, eradication programs target the adult stage, with a single pesticide, Spinosad, currently available for use in urban and peri-urban areas. Entomopathogens as biocontrol agents (BCAs) are an integral part of IPM however, currently, biocontrol as an IPM tool to manage Medfly in WA remains to be developed. The Research Roadmap, Strengthening Australia's Fruit Fly System Research Program acknowledges BCAs as a high priority research area providing an opportunity to evaluate the potential of entomopathogens against fruit fly.

The overarching aims of this proof-of-concept research were to widen the currently limited knowledge on the effectiveness of entomopathogenic fungi (EPF) that are commercially available in Australia as potential BCAs of Medfly. The project focussed on three core areas of research: susceptibility of Medfly life stages to EPF including effects on adult survival with and without bait, effects on oviposition and semi-field or field performance of EPF. Mortality due to mycoses was used as a measure of success in bioassays designed to assess Medfly susceptibility. A proof-of-concept auto-dissemination device was designed for horizontal transmission that used EPF dust in wild type and SIT flies. Data indicated that EPF products caused egg mortality and had larvicidal, pupicidal, and adulticidal activity, and deterred oviposition. Results demonstrated for the first time that EPF dust in auto-disseminator could effectively be transferred from bodily contact and impacted survival of adults.

Systematics, diversification and evolutionary history of butterflies in the tribe Candalidini (Lepidoptera: Lycaenidae)

Braby, M.F. (1,2)

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The tribe Candalidini is restricted to Australia and mainland New Guinea and its adjacent islands. Although it represents a large radiation of Papilionoidea within the Australian region, recent taxonomic investigations indicate considerable uncertainty in the composition of genera and in the number of species. The age and evolutionary history of the group is largely unknown. A phylogeny of the Candalidini based on a molecular data set (13 loci) in conjunction with morphological evidence was therefore undertaken to provide a robust framework for a revised classification. In this new classification, four genera and 42 species are recognised. Among the genera, one genus is newly described (*Eirmocides* Braby, Espeland & Müller, 2020), two genera are reinstated from synonymy (*Erina* Swainson, 1833; *Cyprotides* Tite, 1963), and five genera are placed in synonymy (*Holochila* C. Felder, 1862; *Nesolycaena* Waterhouse & R.E. Turner, 1905; *Adaluma* Tindale, 1922; *Zetona* Waterhouse, 1938; *Microscena* Tite, 1963). At the species level, five taxa (3 species, 2 subspecies) are newly described, three taxa (subspecies) are treated as distinct species, and one species is placed in synonymy. A dated phylogeny using Bayesian inference in BEAST2 and biogeographical and habitat analyses based on the DEC model in BioGeoBEARS indicated that the ancestor of the Candalidini most likely evolved in rainforest habitats of the mesic biome in situ on the Australian plate of Southern Gondwana during the Eocene (c. 43 Ma). A major period of diversification occurred in the Miocene, which coincided with aridification of the Australian continent, followed by a further episode of radiation in montane New Guinea during the Plio-Pleistocene.

The impacts of fire on ant communities vary among vertical strata: results from a long-term fire experiment in an Australian tropical savanna

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The effects of fire on fauna are often primarily indirect, driven by fire-induced changes in habitat structure. Extensive research on the effects of fire on ant communities has identified fire-induced changes to woody cover (habitat openness) as a major driver of species richness and composition. However, most studies only consider epigaeic (foraging on the soil surface) species and little attention has been paid to species inhabiting other vertical strata (subterranean, leaf litter and arboreal). The impacts of fire on ant communities are likely to vary markedly among vertical strata because of differences in both mortality during fire and the extent of change in microhabitat structure. Here, we use a long-term field experiment to quantify the effects of fire on the abundance, richness and composition of ant assemblages of different vertical strata in a highly diverse tropical savanna. We first document the extent to which each stratum harbours distinct assemblages. We then assess how the assemblage of each stratum responds to fire-related predictors (i.e., fire frequency, fire activity and woody cover). We found that each stratum harbours a distinct ant assemblage and that they showed predictably different responses to fire. Leaf-litter and epigaeic ants were the most sensitive to fire because fire directly affects their microhabitats, whereas subterranean ants were the least sensitive because of the insulating effects of soil. Our results show that co-occurring species of the same taxonomic group differ in their response to fire depending on the stratum they inhabit. As such, understanding the effects of fire on entire communities requires consideration of the fire-response of species in all vertical strata.

Cup half-full: Managing the world's worst coffee pest, Coffee Berry Borer (*Hypothenemus hampei* (Ferrari); Coleoptera: Curculionidae: Scolytinae) in Papua New Guinea

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Coffee is the second largest agricultural export in Papua New Guinea (PNG). It is the primary source of household income for many highland communities, more than 2.5 million people. National production has declined to less than one million bags per year. The recent arrival of Coffee Berry Borer *Hypothenemus hampei* highlights the urgency of improving farmers' technical knowledge to address this devastating pest. Coffee Berry Borer is the most serious and destructive insect pest of coffee production in the world, and while currently absent from Australia, it poses a significant biosecurity threat.

Coffee Berry Borer (CBB) has now become well established in several coffee production areas of PNG and priorities now focus on managing the pest. An ACIAR project was commissioned in 2019 aimed to limit CBB damage and protect the coffee industry by managing CBB infestations with world's best practices and to find long-term sustainable IPM solutions. The project is a partnership between the Department of Agriculture and Fisheries Queensland, the PNG Coffee Industry Corporation and the Australian Centre for International Agricultural Research.

A best management practice package was developed through an expert review panel and is currently being delivered to industry and growers throughout the highlands of PNG, with training events to deliver the management package. Several on-farm demonstration trials have been set-up and extension materials are being distributed. A CBB training manual has been jointly developed with Curtin University. Feedback from training events has been positive and continues to be sought after by the coffee industry within PNG.

What about *Platybrachys* & c. planthoppers one century after Henry Hacker? (Hemiptera: Eurybrachidae)

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The family Eurybrachidae forms a characteristic component of the planthopper fauna of Australia, well known by their conspicuous egg masses covered in white wax on trunks of *Eucalyptus*, *Acacia* etc. Eurybrachids often superficially resemble lanternflies (without cephalic process) and are distributed in Old World tropics and subtropics with 15 of 42 genera and 53 of 200 species (25+% of the family) in Australia, which actually represents the centre of hyperdiversification of the family. The first Australian species were described in 1775 by Fabricius, and the first biological data only mentioned that they lived on *Eucalyptus*.

In 1924, Australian entomologist Henry Hacker documented some species of *Platybrachys* Stål, 1859 around Brisbane, on *Eucalyptus* and *Acacia*. He also proposed new synonymies based on his discovery of the strong sexual dimorphism in two species and provided first insights into the biology, development, predators and parasites of these species.

For my revision of the Eurybrachidae, started in 2004, redefinition and review of existing genera appeared crucial. Confirming Kirkaldy's view (1906) that it was "*badly in need of revision*", the speciose genus *Platybrachys* was recognized as problematic, poorly defined and heterogenous. Hence, two new genera were erected to accommodate *Platybrachys stillata*, and *Platybrachys sanguiflua*, respectively, while *Olonia ornata* was transferred into *Platybrachys*. The scrutiny of remaining species within *Platybrachys* revealed that other species, including *P. signata* from Queensland, don't belong to *Platybrachys*. A new genus is erected for *P. signata* and study of collection material, recent field trips and collaboration with citizen-scientists provided an additional ten new species in this new genus from all over the country, as well as data on morphology, host plants, intraspecific variation and very peculiar mating behaviour.

Whole-of-community invertebrate rewilding: Leaf litter transplants rapidly increase beetle diversity during restoration

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Restoration of degraded areas is now a central tool in humanity’s response to continued species-loss. However, restoration projects often report exceedingly slow or failed recolonisation of fauna, especially dispersal-constrained groups such as invertebrates. Active interventions via reintroducing or “rewilding” invertebrates may assist recolonisation and thus improve restoration outcomes. However, invertebrate rewilding is rarely implemented during ecological restoration.

Our project studied the efficacy of invertebrate rewilding as a means of reintroducing dispersal-constrained species and improving diversity during restoration. Rewilding was conducted by transplanting leaf litter, soil, and invertebrates contained within it, from species rich remnant sites into species poor, and geographically isolated, revegetated farmland sites. We sampled pre- and post-rewilding invertebrate communities in remnant, rewilded revegetation, and control revegetation sites. We analysed morphospecies richness, abundance, community composition, and modelled morphospecies traits (dispersal traits/trophic guild) using a Hierarchical Modelling of Species Communities approach to determine which biological properties facilitated establishment.

Beetle morphospecies richness increased rapidly in rewilded sites and was indistinguishable from remnant communities as early as 7 months post-rewilding. Beetle community similarity in the rewilding sites significantly deviated from the control sites 27 months post-rewilding, however remnant communities remained distinct. Establishment success varied as other taxa did not respond as consistently as beetles within the study timeframe. Additionally, we found predatory morphospecies were more likely to establish post-rewilding than other trophic groups. Our results demonstrate that the simple act of transplanting leaf litter can result in comparatively large increases in species richness during restoration in a short timeframe. We advocate our methodology should be adopted more frequently to address failed community restoration as it was cost-effective and can be easily applied in various restoration settings. However, further efficacy tests and longer study timeframes are needed to ensure effectiveness for a broader range of invertebrate taxa.

Exploring the diversity of Australia’s fig-pollinating wasps

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Figs (*Ficus* species) and fig-pollinating wasps (Hymenoptera: Agaonidae) are famous for their mutualisms and partner species specificity, and it was long thought that every fig species had its own exclusive wasp species. While recent work has revealed many cases where one fig species has multiple (though still few) pollinator species, it remains true that fig wasp diversity is strongly correlated with fig diversity, just not in a 1:1 way. Australia is home to about 45 fig species from two main groups: (1) an endemic Australasian radiation, and (2) a few members of several widespread Asian lineages. Fig wasps from some of group 1 have been studied in Australia and Papua, while wasps from some of group 2 have been studied, but mainly in Asia rather than Australia. These studies reveal that: (1) some figs (e.g. Moreton Bay Fig) do indeed appear to have only one pollinator species. (2) several fig species in Asia and Australia show extensive geographic turnover of pollinator species across the host plant range. (3) A few Australian fig species have multiple pollinator species sympatric at a single site. Consequently, revealing the full diversity of Australian fig-pollinating wasps will require sampling and taxonomic study of wasps from each fig species at multiple sites across its geographic range. However, knowledge of current patterns, sampling effort and some key details of phylogenetic history allow us to predict where we are most likely to find unsampled, or currently unrecognised, pollinator species.

Challenges and benefits of AI for insect identification in tertiary level courses

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Identifying insects to family level and below is challenging and, in higher education, has traditionally been reserved for later-year courses. Artificial intelligence (AI) is rapidly improving in its usefulness for identifying insects and provides an addition to the current toolkit of dichotomous keys, field guides (web- and book-based) and multi-entry keys (such as those produced using LUCID). It is important that students learn to apply all appropriate methods for identifying insects, such as would be used in a workplace, and to be able to evaluate whether the determined identification is likely to be accurate. AI creates a potential quandary: we want students to use all available resources to identify insects accurately but, at the same time, use of AI makes it difficult to assess the actual skills of the student. Image recognition AI, such as that used in Google Lens and iNaturalist, has been available for obtaining identifications of insects for a few years but, in late 2022, ChatGPT and other natural language chatbots capable of personalised and sophisticated responses burst onto the education scene. Despite the hysteria immediately propagated by the mainstream media, some universities are now embracing the technology, albeit with ongoing discourse on how to conduct authentic, verifiable assessment. Here, I will discuss some benefits of using AI in teaching insect identification, and highlight some challenges faced in assessment of students' identification skills when they are able to access and use all the tools available.

Polyphagous shot hole borer – eradicating an invasive exotic beetle from Western Australia

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Polyphagous shot hole borer (PSHB, *Euwallacea fornicatus*: Curculionidae), an invasive exotic woodborer, and its fungal symbiont, *Fusarium* sp. [AF-18], were detected on a residential property in Perth, Western Australia (WA), in August 2021. PSHB is a significant threat to urban forests, attacking over 500 species globally. Amenity and horticulture trees in Israel, California, South Africa, and Vietnam are significantly impacted by this pest, resulting in limb failure and tree death. In WA, 123 host species have been attacked by this beetle since detection, of which half support PSHB reproduction. Currently no registered chemical treatment is available. Treatment is dependent on infestation levels and host species, and completed by pruning affected limbs, or tree removal. DPIRD is working to eradicate PSHB through a nationally agreed phased response plan. A quarantine area and movement restrictions are in place, to support surveillance efforts, and restrict further spread. Traps with an aggregation lure (Quercivorol) have also been deployed across this area to detect and delimit the spread. To date PSHB appears restricted to within the Perth metropolitan area. DPIRD has inspected more than 1.362 million trees and 2,700 traps. Preferred hosts in WA include box elder maple (*Acer negundo*), black locust (*Robinia pseudoacacia*), poinciana (*Delonix regia*), Moreton Bay and Port Jackson figs (*Ficus macrophylla*, *F. rubiginosa*) and coral trees (primarily *Erythrina* x *sykesii*). Some native plant species have been attacked, with individuals typically growing in proximity to high PSHB populations. DPIRD is working closely with local industries, local governments, and the community to conduct and maximise surveillance and tracing activities. This presentation will summarise DPIRD's PSHB response activities, what we know about PSHB in WA, how this outbreak differs from those overseas, and explore some of the challenges and opportunities presented in the effort to eradicate this pest from Western Australia.

Venomics of spider wasps (Hymenoptera: Pompilidae)

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The venoms of spider wasps from the family Pompilidae are (in)famous for two characteristics: the long-term, non-lethal, paralysis of their spider victims and intensely painful defensive stings delivered to potential predators. We report the first gold-standard venomic investigation of these taxa combining mass spectrometric proteomics of the venom itself with RNAseq transcriptomics of the venom glands. These results greatly increase our understanding of the composition of pompilid venoms and have revealed several new toxin families. Our work touches on the evolution of novelty even in a supposedly 'conserved' phenotype and the mechanisms of the characteristic activities of these venoms.

Taxonomy and systematics of the 'backobourkiine' spiders, a putative new subfamily of orb-weavers (Araneae, Araneidae)

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The spider family Araneidae includes medium-sized to large orb-weavers with generally vertical webs. A recent multi-gene molecular study supported a paraphyletic 'Araneinae', indicating the existence of new clades, including the Australasian/Pacific 'backobourkiine' spiders, with most of its species historically misplaced in *Araneus* and *Eriophora*. The backobourkiines are the most speciose and most abundant group of orb-weaving spiders in Australia and include those species commonly referred to as Garden Orb-weavers. They can also be found in Asia, the Pacific and in New Zealand, and recent data suggests its presence in the Afrotropical region.

The backobourkiines now consist of 70 species in 10 genera: *Novakiella* (two species), *Backobourkia* (four species), *Lariniophora* (one species), *Plebs* (22 species), *Hortophora* (13 species), *Socca* (12 species), *Salsa* (seven species), *Leviana* (five species), *Quokkaraneus* (one species) and *Kangaraneus* Castanheira & Framenau, 2023 (three species). As part of our current ABRS-funded revision of the backobourkiines, two more genera are currently being revised: *Acroaspis* (13 species) and *Carepalxis* L. Koch, 1872 (around 14).

This presentation summarises our work on the dominant backobourkiines, including results of detailed phylogenetic analyses based on morphological and genomic data, that aims to clarify some relationships within the group that were poorly supported in previous studies.

Understanding microbial communities within aphids and their interactions with insecticides

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Aphids (superfamily *Aphidoidea,* order Hemiptera) are a major pest of agriculture. The management of aphids in agriculture has relied on pesticides. However, the overuse of pesticides has led to aphids like *Myzus persicae* developing resistance over the years. This issue together with the withdrawal of some pesticides has raised issues around the future control of aphids. Resistance has typically been studied under the context of the host genome. Yet, aphids can be considered as a holobiont consisting of its own host genome and microbiome genome co-existing and interacting with each other to co-evolve. Aphids contain bacterial communities (a part of the microbiome), known as endosymbionts which have evolved with them over time. Endosymbionts have important effects on aphid physiology, such as heat shock resistance and resistance to parasitism and may provide useful targets for novel methods of pest control, but little is known about their contribution to pesticide resistance. By manipulation of the endosymbiont in aphids, the effect on chemical tolerance can be studied. It is important as a novel pest control method with increased resistance may have its implications. Preliminary data on *Myzus persicae* showed no significant difference in chemical tolerance between infected and uninfected strains of the endosymbiont *Rickettsiella.* Evidence of symbiont mediated chemical tolerance has been found in insects but this is still a large knowledge gap for aphids. I provide results on pesticide responses of *M. persicae* and other aphids such as *Rhopalosiphum padi* and *Diuraphis noxia* where deliberate changes in endosymbionts have been implemented. By determining the potential contribution of endosymbionts to pesticide resistance, my research will provide insight into how microbial symbioses can be implemented in the management of pest aphids in agriculture. This may lead to improved strategies for controlling pesticide resistant pests.

Genetics and ecology of the alpine allodapine bee *Exoneura* spp.

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The conservation status of native insect pollinators and their susceptibility to environmental change, such as habitat loss and degradation, are poorly understood. We still lack a thorough understanding of the biology, ecology and genetics of Australian native bees. Alpine insect pollinators are particularly threatened due the effects of climate change on alpine ecosystems globally – reduction of alpine habitats is particularly problematic in Australian contexts because of their already limited altitudinal band (1,850-2,228m). *Exoneura* is a genus of native allodapine bees found throughout temperate Australian habitats that exhibit facultatively social colony organisation and nest in a range of plant substrates. In this talk I will present our findings regarding the genetics and ecology of the alpine bee *Exoneura* (*Exoneura* spp.).

We found that *Exoneura* spp. regularly visits flowers of multiple alpine plant species, and it has a very specific distribution across the elevation gradient. Furthermore, preliminary analyses of Dart-seq genotyping suggest the presence of a single, potentially undescribed, species of *Exoneura*. Additionally, population genetic analysis suggests relatively high population connectivity across the Perisher valley but marked differences of genetic diversity between populations. We conclude that this potentially novel *Exoneura* species is likely to be an important a pollinator within Australian alpine ecosystems and its population viability could be partly threatened by the increase frequency and intensity of extreme climate events.

Phylogenomics of endemic Australian Ulopinae (Hemiptera: Cicadomorpha: Cicadellidae)

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Ulopinae is a distinctive and compelling leafhopper subfamily that is widely distributed across the Afrotropical, Palearctic, Indomalayan and Australasian regions. The ulopine fauna of Australia is entirely endemic and includes two tribes, Ulopini and Cephalelini. A considerable share of the putative phylogenetic diversity of these tribes is endemic to Australia, accounting for 12 of the 34 genera currently recognised worldwide. The evolution of ulopines, including many interesting aspects of their life history, has become increasingly relevant as they are key to understanding the paraphyly of leafhoppers with respect to the treehoppers. This study provides the first glimpse into the true diversity of Australian Ulopinae based on a thorough phylogenomic sampling of multiple subfamily lineages and including specimens collected in Bush Blitz expeditions. Here we infer the phylogeny of the Australian Ulopini with special attention to the genus *Austrolopa*, contextualising their evolutionary history and assessing its species-level classification. These leafhoppers have an outstanding cryptic appearance, and some species lack hindwings, suggesting a diminished dispersal ability. *Austrolopa* previously included two species, one of which (*A. brunensis*) is considered widely distributed throughout Australia. Within a relatively small range from Black Mountain (ACT) to Kosciuszko National Park (NSW), three species were discovered and are being described based on morphological and molecular data, including fully annotated mitochondrial genomes. Our results suggest that ulopines may be narrow-range endemics in montane habitats, potentially confined to small geographic areas and host plants. Our findings illustrate that the Australian Ulopinae are far more diverse than currently circumscribed, and several species of *Austrolopa* are yet to be recognised, some of which in Southeastern Australia may be at risk of extinction from bushfires and habitat loss.

Choosing data for predicting potential distribution of invasive species: *Coptotermes* termites as a test case.

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Predictive models are often used to estimate potential future distributions of invasive species. These models are informed by climate metrics of known distributions, both known endemic and invaded ranges, and then used to predict and map potential invasive distribution. This approach has problems: the endemic distribution may not be well mapped; more data from invaded ranges and human modified landscapes; biological factors that constrain endemic distribution (food resources, disease, predators, competitors) are not included in these models; and inexact species identification.

We considered these issues with two congeneric species of termite. *Coptotermes formosanus* is native to China and Taiwan, and has invaded Japan, islands in the north Pacific and the continental USA; also considered a '100 worst invasive species'. *Coptotermes gestroi* is native to SE Asia and has invaded islands in the Pacific, Indian and Atlantic oceans, and Brazil. Although these termites are found in forests in their endemic ranges, all invaded locations are urban.

We found that potential global distributions based on endemic range climate data were smaller than those based on invaded range climate data. This was due to invaded ranges having higher climate variability; generally cooler and drier than invaded ranges. The urban heat island and humans piping water into cities probably allows both *C. formosanus* and *C. gestroi* to survive in what would otherwise be inhospitable locations. It seems unlikely these termites will spread from currently invaded cities into the surrounding forested landscapes. We did find high climate suitability for both species in uninvaded locations, sugging vulnerability should they arrive.

Finally, we considered the Australian species *C. acinaciformis*, which invaded and was eradicated from Fiji and NZ. This species has a very wide potential global distribution, however it is likely a species complex. Considering just the south-east Australian populations shows a much narrower potential distribution.

Safeguarding borders to protect biodiversity

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Australia, one of the world's seventeen megadiverse countries, demands a firm commitment from all individuals towards environmental conservation due to its high number of endemic species across various taxa. This duty encompasses managing native biodiversity and implementing effective biosecurity systems to monitor invasive species. Identifying invasive species that could become a serious pest would benefit Australia's environment, livelihood, and trade. The MyPestGuide® Reporter app, developed in 2017 as an early detection tool, includes an online portal for coordinating the taxonomic identifications of newly emerging pest threats. Public reports through the MyPestGuide® Reporter app have provided multiple detections of invasive pests and newly discovered species, offering valuable insights into native and introduced species and citizen science lessons. Our analysis of critical biosecurity surveillance information illustrates how biosecurity can effectively address ongoing challenges, safeguarding borders and protecting Australia's megadiversity.

Insect sanctuaries for beneficial predators and parasites in tropical banana

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Conservation of insects that offer biological control is extremely important to control pest populations in agriculture, by helping beneficial insects to establish and succeed within the agricultural ecosystem. This project aimed to use a Conservation Integrated Pest Management approach to alter a north Queensland banana ecosystem to provide more favourable environmental conditions to enhance the population of beneficial insects. This was achieved by incorporating plots of flowering companion plants, referred to as insect sanctuaries. Insect sanctuaries are designated areas that promote beneficial insects by providing additional resources and shelter, free from the disturbances of farming practices (i.e., pesticides or habitat removal). Seven flowering plants were evaluated including dill, fennel, *Salvia*, lemon balm, Thai chilli, garlic chives, and *Impatiens*, against a bare ground control to determine if the abundance and diversity of the insect community could be increased by incorporating an extra layer of plant biodiversity in banana ecosystems. The abundance and diversity of insects attracted to each treatment were monitored for six months (March – September 2022) using sticky traps, pitfall traps, and physical observations. Insect sanctuaries did increase abundance and diversity at the trial site, however, these findings couldn't be distinguished statistically from potential seasonal variation in the insect composition. From these trial findings, *Salvia* and *Impatiens* would likely be suitable plants for insect sanctuaries in bananas, due to their high attraction for natural enemies (predators and parasites) and suppression of some pest groups. Finding the high attraction of beneficial insects to these flowering plants suggests that further studies in this area would be useful to investigate.

The future of banana IPDM – microbial and biological pest control

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The work discussed here forms part of the banana integrated pest and disease management (IPDM) project funded by Hort Innovation using R&D levies from the Australian banana industry. Currently, control of insect pests in banana bunches relies on the use of insecticides applied under the protective bunch cover. There are only a limited number of insecticides currently registered for this use and one of these, chlorpyrifos, is currently under review. We are investigating biological control of the three major pests of banana bunches – banana scab moth (*Nacoleia octasema*), banana rust thrips (*Chaetanaphothrips signipennis),* and banana flower thrips (*Thrips hawaiiensis*) to develop alternative management techniques. Microbial entomopathogens including the fungal genera *Beauveria* and *Metarhizium*, as well as commercially available predatory mites (Montdorensis (*Typhlodromips montdorensis)*, Cucumeris (*Neoseiulus cucumeris)*, Hypoaspis (*Stratiolaelaps scimitus)*, Californicus (*Neoseiulus californicus*) and insects (Orius (*Orius tantillus)* and green lacewing (*Mallada signatus*)) are being tested for control against the three pest species. This research is imperative for the banana industry to provide adequate pest control in the loss of chemistries. The potential outcomes from this research include reducing insecticide resistance, no chemical residues on fruit, safer conditions for applicators, and environment-friendly practices. This research is being undertaken over the next four years in north Queensland and at this stage we are only undertaking small-scale trials under laboratory, greenhouse, and field conditions. The status of these trials and some preliminary results will be discussed here.

On the trail of the Green snail

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Green snail, *Cantareus apertus,* is native to Mediterranean Europe and North Africa, but has become a significant pest in parts of the USA and Australia, where the climate is similar to its native range. An agricultural pest of vegetables and pasture grasses, it is also known to inhabit and feed on native vegetation. After establishing in Perth and south-west WA in the 1980s it remained within a small range until recently, when it was detected near Albany in 2020. In 2011 Green snail was found in Cobram, northern Victoria, where it remains established. Notably, a dark colour morph is present in Albany and Cobram. Exploratory analyses suggests that these two populations are genetically similar, but different to that of the original WA population. Here I will present the recent expansion in Western Australia and our preliminary genetic findings of this exotic pest.

To describe or to document: making a case for the Fauna Portal using money spiders (Araneae: Linyphiidae)

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The Fauna Portal Australia (www.faunaportal.org) is an innovative identification platform conceptualised for invertebrates, although it can be used for any faunal (and floral) group. It offers a unique filter for diagnostic images that allows to examine particular morphological characters in the same view side-by-side at the genus and family level. Geographic filters based on species distribution records further allow restricting the choice of taxa for identification. A simple molecular module allows downloading species-specific sequence data. The Fauna Portal therefore provides a one-stop-shop for species identification, particularly in groups that have been taxonomically treated in scattered publications. For example, based on the research focus of the senior author, all taxonomic images of wolf spiders (Lycosidae), orb-weaving spiders (Araneidae) and mouse spiders (Actinopodidae) are online to support their identification. Almost 1,000 spider species are now online.

In addition, through the application of core taxonomic principles (designation of a reference specimen or 'type' and obligatory diagnosis) the Fauna Portal also facilitates the stable listing of undescribed species using a simple numerical parataxonomic code. Taxonomic hypotheses can therefore be published in real time and are open to public scrutiny. This rapid documentation of biodiversity data has the potential to speed up taxonomy as a stopgap until species are formally described. The principles of the Fauna Portal will be presented using a poorly known spider family as exemplar, the sheet-web or money spiders (Linyphiidae). This is the second largest spider family world-wide based on the number of described species and the current assumption that it is poorly represented in Australia is contested here.

UCE Phylogenomics of the Australasian Sphaeropthalminae (Hymenoptera: Mutillidae)

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The Mutillidae (velvet ants) are a diverse, and often-times abundant, family of parasitoid wasps, characterised by extreme sexual dimorphism and anti-predator adaptations. Females of the group are apterous and often exhibit a suite of defensive traits, namely: a painful venomous sting; the largest sting-to-body ratio of any hymenopteran; a thick slippery exoskeleton; large cuticular spines; olfactory and auditory aposematism; and striking visual aposematism leading to their participation in one of the largest known Müllerian mimicry complexes. Despite their diversity, abundance, ecological importance, and evolutionary significance, mutillids are often underrepresented in our collections and severely understudied, especially in Australia. Most Australian species have been temporarily dumped in the morphologically diverse genus, *Ephutomorpha*, with a mere 4% of described species are known from both sexes, and much of the diversity remains undocumented. Due to the challenging nature of mutillid taxonomy, a comprehensive molecular phylogeny is key to understanding the true diversity and relationships within the Australasian mutillid fauna, at the genus and species level. Here, we use a large morphometric and phylogenomic dataset spanning all currently described Australian genera, to reconstruct the first-ever molecular phylogeny of the Australasian Sphaeropthalminae and elucidate previously unclear generic and species boundaries. Using colour-trait data from 5000 female mutillid wasps (approximately 200 species from 10 genera), we document the presence of four putative mimicry rings in Australia, with strong colour-pattern similarities not due to shared ancestry. However, each mimicry ring exhibited widespread geographic distribution across mainland Australia and significant overlap with all other rings – an unexpected finding given that mimicry signals are often subjected to purifying selection. This study builds on evidence of velvet ants forming large Müllerian mimicry complexes and provides a framework to assess how evolutionary and ecological processes shape present-day patterns of diversity.

Rainforest litter invertebrates decimated by high severity burns during Australia's gigafires

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Climate change is increasing the frequency of extreme fires. In 2019-2020, extreme fires burned 97 000 km^2 of native vegetation in south-eastern Australia, affecting many areas of rainforest, which has historically burned less frequently. One year post-fires, we surveyed litter macroinvertebrates in fifty-two temperate rainforest sites. Sites had experienced increasing levels of fire severity (unburnt, medium severity and high severity). We asked how fire severity affected: 1) litter macroinvertebrate habitats; 2) the abundance of litter macroinvertebrate taxa per unit area; and 3) abundance relative to litter habitat (volumetric density). We also estimated the loss of litter macroinvertebrates across rainforests in the study region. High severity burns supported only a fifth of the litter volume and canopy cover as unburnt sites, lower soil moisture and higher herb cover. Medium burns were intermediate. Macroinvertebrate abundance declined with burn severity: high severity burns supported only 26% of the abundance in unburnt sites; medium severity burns supported 80% of that in unburnt sites. Patterns were similar for all taxa, with millipedes declining most. High severity fires resulted in up to 1.90 million fewer macroinvertebrates per hectare; 0.53 million fewer per hectare of medium burn rainforest. Across the study region, we estimate that 60 billion fewer litter macroinvertebrates persisted in temperate rainforests alone. Volumetric densities of many litter macroinvertebrate taxa in high severity burns were higher than in unburnt sites, suggesting nutrients may be more available post-fire, or that persisting individuals become concentrated in the leaf litter. For less desiccation-tolerant groups (e.g., amphipods, Amphipoda: Talitridae), density declines with increasing severity may reflect the combined impact of low soil moisture and reduced litter cover. Many taxa persisted following high severity fires, but declines were substantial, and taxa differed in their vulnerability. Longer-term monitoring is required to understand the recovery trajectory and impacts on ecological function.

Importance of considering the holobiont in aphid populations for research

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Maintaining populations of invertebrates for experiments normally starts with establishing colonies in a laboratory setting. The success of keeping aphids (Hemiptera: Aphididae) has historically been assessed based on survival determined by colonisation, fecundity, developmental time or ability to breed. The holobiont refers to the host and its associated microorganism communities. Aphids have relationships with their microbiome that can provide their host with essential substances or other advantages as well as costs. Overlooking these during the maintenance of colonies could lead to inaccurate results when biological inferences are being made based on colony material. For species such as *Acyrthosiphon pisum* (Pea aphid), *Sitobion avenae* (English Grain aphid) and *Myzus persicae* (Green Peach aphid) such phenotypic effects associated with endosymbionts have been well established. We intend to extend this pool to determine endosymbiont composition in 11 aphid species. The composition, density and incidence of endosymbionts in these species was monitored, considering time in the laboratory, host plant, and generation. We assessed two commonly used culturing methods with a newly developed method to control aphid development factors and stresses. During the stability assessment some species lost their secondary endosymbionts over time, but no obvious immediate physiological implications were observed. Some species had stable endosymbionts, but stability may depend on host plant. When considering the holobiont, our understanding of the quality of aphids and their limitations improved for use in experimental work. There is also suggestion that phenotypic effects associated with the holobiont in natural populations could be missed in cases where endosymbionts are lost.

How are flowering plants and pollinators affected by fire and the indirect consequences for pollination services within orchards

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Fire affected the apple growing region of Bilpin in 2019, burning large tracts of native forests which surround the orchards, and which are important habitat for pollinators of apple. An experiment to assess flowering plant diversity and associated invertebrate flower visitors within the orchards, the surrounding native vegetation matrix and upon apple at five apple orchards within Bilpin had been underway since September 2017. Subsequently, the fire provided an opportunity to 1) quantify the fire severity around each of the apple orchards and monitor plant recovery through satellite images over time, and 2) assess the impact of fire on the diversity and abundance of plants in flower within the surrounding native vegetation (which was impacted by fire) and to determine the influence of this disturbance on flower visitors to the surrounding native vegetation as well within the orchard. Using permanent quadrats placed within the orchards and surrounding native vegetation matrix we were able to document the flowering plants and pollinator visitors over two years before fire and two years after fire. Using Jaccard's index of similarity we found a 60% overlap in flower visiting insects within the bushland and a 50% overlap in flower visitors within the orchards with both habitats having unique insect species observed before and also after fire. Interestingly, there was only a 23% overlap in plant species observed flowering before and after fire within the surrounding native vegetation with a total of 19 species uniquely observed before the fire and 35 plant species unique to after the fire. Understanding how plant-pollinator interactions are affected by fire is vital to understanding ecosystem recovery and may help to inform land managers to ensure pollination services are provided to pollinator dependent crops.

Enigma moth parasitoid, *Ovaustra aurantia* (Hymenoptera: Braconidae): third partner in a specific tri-trophic interaction with high co-extinction risk

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In 2015, the Enigma moth (*Aenigmatinea glatzella*) was described from Kangaroo Island as the sole member of a new primitive family, Aenigmatineidae. The moth has an obligate association with *Callitris gracilis* (Southern cypress pine) and larvae develop concealed in chambers in wood of small branches. Observations of *A. glatzella* placing eggs beneath minute, adpressed pine leaves, also revealed a braconid wasp that targeted recently laid eggs. This apparent egg-larval parasitisation was confirmed by discovery of adult wasps that failed to emerge from Enigma moth larval chambers. We recently described this wasp as a new genus and species, *Ovaustra aurantia,* in the Gondwanan subfamily Mesostoinae. Given the unusual biology and taxonomic distinctiveness of the moth, *O. aurantia* is highly unlikely to have other hosts. Interestingly, the three protagonists in this specific tritrophic interaction are near-basal taxa in their respective groups.

The Enigma moth is listed as Critically Endangered by the IUCN but is not protected under Australian law. It is clearly at risk of co-extinction given the susceptibility of *Callitris* to fire and its restricted range on Kangaroo Island. *Ovaustra aurantia* must therefore be similarly threatened, and both insects are obvious candidates for listing under the Federal EPBC Act.

Mesostoinae has only about 10 described Australian species and although molecular evidence for the subfamily is strong, there are no clear morphological synapomorphies that underpin it. Further, the host range of members appears to be relatively broad. Within Mesostoinae, relationships between genera are poorly defined with only one strongly supported clade of four endemic New Zealand genera. However, we are gathering morphological and molecular evidence from tens of undescribed putative mesostoines, primarily from Kangaroo Island. We aim to improve characterisation of Australian Mesostoinae, elucidate generic relationships amongst new and described taxa, and define one or more morphological synapomorphies for the subfamily.

Male bees visit flowers too: pollen transport by *Tetragonula* males

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Assessing the foraging behaviour and pollen transport of bees is key to understanding how they contribute to the reproduction of the plants they visit. As only female bees actively collect pollen, the contribution of male bees to pollination is often overlooked. Yet males are also flower-feeders that rely on nectar as flight fuel. Moreover, many bees have sex-differences in life histories, flight ranges and morphology that may result in male and female bees of the same species having unique pollination roles.

In this talk, I will describe recent efforts in our lab to understand the life history and behaviour of male stingless bees in the genus *Tetragonula* (Hymenoptera, Apidae). Males leave the nest when mature and never return to their natal nests. They are typically not observed again until they congregate in mating swarms outside colonies with virgin queens. We find that males of *T. carbonaria* commonly travel >1km to join mating swarms and may travel up to 20km. They therefore have far greater dispersal capabilities than queens and greater foraging ranges than workers (which are typically <500m).

Males captured at mating congregations are often visibly coated in pollen and we find that the typical male carries a similar pollen load to a nectar-foraging worker. Like workers, males are also generalists as they carry pollen from a large diversity of native and non-native plants. Importantly, we found that males retained four times as many pollen grains on their bodies from one day to the next than did workers, presumably because workers efficiently groom themselves and each other inside nests overnight while males do not. Given that up to 50% of all brood may be males in *Tetragonula* colonies during the springtime, the contribution of male *Tetragonula* to pollination in natural and agro-ecosystems is worth considering, particularly as they could vector pollen far greater distances than workers.

The aftermath of a founding bottleneck: invasive Asian honey bees in Australia

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Insect invasions sometimes arise from the accidental introduction of very few individuals. These invasions are characterized by strong founder effects: a loss of genetic diversity relative to the source population. If and how such loss of genetic diversity affects the population dynamics or adaptive potential of invaders remains a source of debate. In this talk, I discuss efforts in our lab to understand the consequences of a founding bottleneck for the invasive population of the Asian honey bee (*Apis cerana*; Hymenoptera, Apidae) in Far North Queensland. This population was very likely founded by a single colony (one mated queen and her workers) in the mid-2000s. Today it numbers an estimated 10,000+ colonies in the Cairns and Tablelands region. Using whole-genome sequencing of bees collected each year of the invasion over a ten-year period (2007-2018), plus those from the source populations of New Guinea and Java, we find loci with signatures of positive selection in the first years post-invasion for the Australian population. Thus *A. cerana* has adapted since its arrival here, despite the severe founding bottleneck and low standing genetic variation. We also show, however, the initial founder event has consequences for the population's rate of range expansion. This is because colonies expanding outwards at the range edges have high genetic load (high proportions of inviable brood due to inbreeding); that is, serial founder effects at range edges amplify the negative effects of the original founding bottleneck, creating local regions of low fitness and slowing the rate of population spread.

Over a decade of species discovery with Bush Blitz

Grarock. K.

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Bush Blitz is Australia’s largest species discovery program. It is a unique multi-million dollar partnership between the Department of Climate Change, Energy, the Environment and Water, Parks Australia, BHP and Earthwatch Australia to document plants and animals across Australia.

There are an estimated 580,000-680,000 species in Australia, with three-quarters of this biodiversity yet to be identified. Forty-five per cent of continental Australia and over 90 per cent of Australia’s marine waters have never been comprehensively surveyed.

Since the Program began in 2010 Bush Blitz has undertaken 50 multidisciplinary expeditions supporting the discovery of almost 2,000 putative new species. Through this large body of work thousands of species records have also been added to public databases, increasing scientific knowledge to help protect Australia’s biodiversity for generations to come.

Although Bush Blitz focuses on flora, and both vertebrate and invertebrate fauna, insects contribute about 60% of these putative new species records. Through Bush Blitz research funding the description of thousands of new species has been supported, of these 39 genera and 685 species are invertebrates.

MyPestGuide® - Making taxonomy sexy again by connecting scientists with an engaged community

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Community observations are vital for monitoring species distributions and detecting harmful pests early on for effective eradication. Timely and accurate taxonomic identifications are essential for policy-making, biosecurity decisions and conservation planning. The MyPestGuide® system consists of a Reporter app, four field guides, and an online community portal to view, map, and manage images of organisms.

The suite of tools connects local communities with Australian scientists, who identify organisms and engage directly with reporters in a two-way conversation about the biological and biosecurity impacts facts of each species. The system fosters scientific and community engagement, promoting new taxonomic collaborations and development of local community pest projects. Since 2017, the MyPestGuide® Reporter app has garnered significant public appeal, receiving over 385,276 reports across all projects, averaging 5,600 reports annually. Taxonomically, there have been 38,895 different organisms verified to the level of Genus by analysis of imagery.

The uptake of MyPestGuide® Reporter reflects the public's desire to know and protect their local natural environment. As a result, reports are helping to infer Australia's freedom from pests and diseases while growing access to new overseas markets.

To hair or not to hair, that is the question: the effectiveness of urticating hairs as a defence in the face of larval mortality

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“Hairy caterpillars”, the larval stage of some moth species, are covered from head to apex in various integumental structures that are commonly considered to be the cause of a delayed itchy manifestation in humans and other vertebrates. As such, these urticating hairs have been interpreted as a form of defence against predators. Very little research about the effectiveness of this ‘defence’ in reducing mortality has been explored and this is partly due to the challenges of observing this mechanism in a naturally occurring predation event, especially given the timing to its effect. Difficulties also exist in measuring the natural mortality rates of insects in the field and identifying if the mortality resulted from predation itself as a variety of other factors are known to cause mortality (for example, the environment, extreme weather events and disease) and predators often leave no evidence. Life tables are a fundamental tool in population ecology used to identify mortality rates by life stages. This can allow us to determine the vulnerable stages of insects and the key factors responsible for their mortality in particular locations. In this study, we extracted data of *Lepidopteran* life tables from various published field-based studies to establish whether the possession of urticating hairs correlates to decreased mortality while also taking into account the contributions of other common caterpillar defences, such as body size, long hairs, feeding habits (internal/external) and gregariousness, to name a few. This knowledge can ultimately bring us one step closer to better understanding the evolution of predator-prey interactions, especially given these particular types of caterpillars can cause health concerns.

Dung derived from different pasture types influence progeny size

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The consumptive material of cattle plays a crucial role in the quality of dung and the consequent reproductive capacity of dung beetles (Coleoptera: Scarabaeidae). Yet, previous studies have failed to identify whether the pasture species or growth stage of the pasture, affects dung beetle populations. Three pasture types (improved native, forage oat, and inter-sown rye/clover) were investigated for influence on subsequent quality of cattle dung, the number of broods and reproductive output measured as brood size (dry weight and ellipsoid volume), development time and F_1 progeny size (beetle length and pronotum width) of *Onthophagus binodis, Euoniticellus africanus* and *E. intermedius*. Nitrogen content of dung was highest in rye/clover derived dung compared to improved native and forage oat. Improved native derived dung had the highest carbon content, energy content, organic matter, pH and insoluble non-starch polysaccharide content. Forage oat had the lowest nutritional content. but the highest moisture content, ash content and soluble non-starch polysaccharide content compared to the other pastures. Ellipsoid volume of broods but not dry weight nor brood production was influenced by dung derived pasture type with smaller broods produced in forage oat compared to improved native derived dung. Pasture type influenced progeny length, with female *E. intermedius,* and males and females of *O. binodis* being 11.4%, 11.2% and 7.3% longer respectively in rye/clover derived dung compared to forage oat dung, while native improved dung did not influence the size. The pronotum width of *O. binodis* F_1 progeny was 9.8% wider when reared from rye/clover dung when compared to forage oat. Rye/clover derived dung provided the best resource for dung beetle reproduction compared with forage oat dung, with improved native dung being in the middle. Cattle diet is an important factor for consideration when evaluating reproductive ability and progeny size of dung beetles, and warrants further investigation.

The interaction between *Onthophagus binodis* and cattle dung pH

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The environment surrounding invertebrates can influence the physiology of larval offspring. Dung beetles provide several significant ecological functions, including dung breakdown, fly control, and nutrient cycling. Cattle diet influences the chemical and physical constituents of dung, of which pH is considered critical. Few studies have assessed this, though a pH of 6.3 is regarded as the lowest threshold for dung beetle reproduction. We investigated the effects of an introduced and widespread dung beetle (*Onthophagus binodis*) on cattle dung pH (7.3, 6.0 and 5.0); and pH on *O. binodis* reproduction, offspring phenotypic traits and development time. Dung beetle presence increased the Δ pH (more alkaline) within dung pads after 96 hours. Dung beetles produced broods in dung with a pH of 5.0, though in fewer numbers. Larval development was delayed in pH 5.0 with an average of 50 days compared to 44 days in dung with pH 6, 7, and the control (7.3). Smaller broods (ellipsoid volume (mm3)) were produced in dung with a pH of 5.0 compared to pH 6.0 and 7.0, and offspring emerging from broods produced from dung with a pH of 6.0 were larger compared to all other pH treatments. Results have shown that dung pH is important for brood production and progeny phenotypic traits of an agricultural ecosystem engineer and that our study refutes earlier studies with reproductive ability evident for *O. binodis* at pH 5 with no evidence to suggest dung pH influences the provisioning of broods.

Gloss as an antipredator strategy in fast moving prey

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Glossy surfaces are found across the tree of life and have been proposed to have both visual and non-visual functions. Previous studies on stationary prey have found mixed results for the role of a glossy appearances in predator avoidance—some have found that glossiness can act as a warning signal or improve camouflage, whereas others have detected no survival benefit. An alternative hypothesis that is yet to be tested is whether glossiness could provide protection for moving prey. Glossy, fast moving animals produce flashes of light that increase in frequency at higher speeds, which could make it harder for predators to track and accurately locate them. We tested this hypothesis by presenting giant rainforest mantids (*Hierodula majuscula*) with glossy or matte targets moving at slow and fast speed. We found that independently of speed, mantids were less likely to strike glossy targets. Additionally, mantids were less likely to track glossy targets and more likely to hit the target with one out of the two raptorial legs that struck rather than both raptorial legs, but only when targets were moving fast. Our results support the hypothesis that a glossy appearance may have a function as an antipredator strategy by reducing the ability of predators to track and accurately target glossy fast moving prey.

Host plant pollination by Australian Heliozelidae (Lepidoptera: Adeloidea)

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Heliozelidae are a family of monotryisan Lepidoptera with approximately 130 described species worldwide. Where studied, the larvae of most described species mine leaves from which they excise an oval case in which to pupate. Over the last 15 years our studies have shown that Australia is a hot-spot for heliozelid diversity with many hundreds of undescribed species that exhibit a wide variety of larval behaviour, including pre-dispersal seed and flower-bud mining, gall-feeding and leaf-mining. Pre-dispersal seed-mining by Australian Heliozelidae has been observed in many Rutaceae genera and in *Hibbertia* (Dilleniaceae). In both plant families, female moths lay their eggs into flowers, and once they hatch, caterpillars consume the developing seeds. Within these groups, the ability of female moths to pollinate the flowers in which their larvae will feed has arisen at least three times independently. In the best studied case, thirteen of eighteen *Boronia* species in a clade, comprising series Heterandrae, series Variabiles and series Persistens of Section *Boronia* are pollinated by Heliozelidae in the genus *Prophylactis* and, in at least some cases, the relationship between the moth and plant appears to be obligate mutual.

The use of solitary bees in protected cropping

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The risks involved in relying on a single species for crop pollination are well understood, but not always heeded. In many developed countries worldwide, plantings around pollination dependent crops aim to support and increase pollinator diversity. By comparison, resilience of pollination in protected cropping has received less attention. In large netted areas, reliance is often completely on honey bees, while the exponentially expanding greenhouse industry nearly solely uses bumblebees for pollination. Similar to the situation with crops out in the open, this narrow reliance involves risks related to breeding difficulties due to lack of resources and species specific pests and diseases.

In the last 70 years, a wealth of solitary bee species have been investigated for their ability to pollinate greenhouse crops, and numerous effective species have been identified. But while the need to expand the portfolio of pollinators in protected cropping is well understood among researchers, the use of solitary bee species in industrial protected cropping remains negligible. In this contribution, we will investigate the traits that determine the suitability of solitary bees as greenhouse pollinators, review the status quo and explore the limitations for deployment in greenhouses.

Entomology teaching and learning in Aotearoa New Zealand: past, present and future

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Entomology has been taught at most of Aotearoa New Zealand's universities both historically and currently. Entomology education has provided solid practical training for generations, leading to high employability for our graduates. The events of recent years forced the teaching of entomology online for most universities and resulted in major changes to curricula and assessment, and particularly to the extent to which students gained practical entomology training. Here I will discuss how entomology was taught pre-2020, and during periods of online lockdown teaching across Aotearoa New Zealand. I will reflect on the challenges faced, the approaches we took, and the lessons we have learned. I will particularly emphasise my own direct experiences teaching entomology at the University of Auckland, and some of the fun (if inferior) ways we managed to provide practical experiences during lockdowns.

Diversity and abundance of potential *Xylella fastidiosa* vectors and related taxa in *Xylella*-susceptible crops and native vegetation in southern New South Wales, Australia

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Xylella fastidiosa (*Xf*) is a bacterium transmitted to plants typically by xylem-feeding spittlebugs (Cercopoidea) and cicadellid leafhoppers (Cicadellinae: Cicadellini and Proconiini). *Xf* and its vectors are considered the single greatest threat to Australian plant biosecurity and horticultural industries due to the predicted economic impact of plant diseases caused by the bacterium (e.g., Pierce's disease in grapes, olive quick decline syndrome and bacterial leaf scorch). Despite this, little is known about the potential of native Australian leafhopper and spittlebug species to be vectors of *Xf* in vulnerable crops. Our project involves gathering baseline data on leafhopper and spittlebug diversity and abundance in the irrigation districts of south-east New South Wales. We focus primarily on the horticultural crops of wine grapes, citrus, cherries, and olives, but also extend our study into native vegetation, as results from two years of trapping in the crops produced almost no xylem-feeding species. The diversity and abundance of leafhoppers and spittlebugs in crops and native vegetation and the possible implications for transmission of *Xf* and other plant pathogens in Australia are discussed.

Insect Investigators: a school-based citizen science project on arthropod diversity

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Insect Investigators is a citizen science project (2021-23) which is documenting and describing Australia's insect diversity by engaging schools with the science of taxonomy.

The project has dual aims: 1) fundamental scientific research on a critical component of our ecosystems, i.e. the description of Australia's wonderful insects, and 2) building awareness of the taxonomic and ecological sciences through engaging schools and regional communities in the process of documenting arthropod biodiversity, and in discovering, recognising, and naming previously undescribed species.

During March 2022, fifty Australian schools in Western Australia, South Australia and Queensland monitored their own Malaise trap, and sent weekly samples to the team at the University of Adelaide, where the catch was sorted and specimens selected for DNA barcoding.

Just over 12000 specimens were successfully sequenced at the University of Guelph Canada (Barcode of Life Data System - BOLD), resulting in over 5400 Operational Taxonomic Units. Over half of these preliminary species are new to the BOLD database and handfuls of species are presently being described by taxonomists. This talk will explore some of taxonomic and ecological data with focus on insects, as well as pedagogical outcomes of the project.

Effects of urbanisation on ant diversity in bushland remnants of a rapidly urbanizing city, Perth, Western Australia.

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Urban areas are expanding rapidly, leading to declines in diversity globally. Remnant vegetation within urban areas provide excellent opportunities for conserving biodiversity within cities. However, long-term persistence of biodiversity within remnants is threatened by habitat loss and fragmentation, increasing isolation, habitat degradation and invasive species. Conservation in these remnants is hampered by a lack of understanding of the responses of wildlife to urbanisation. Ants provide valuable ecosystem services and are a vital component of almost all terrestrial ecosystems, including urban bushland remnants. Understanding the factors that influence their diversity are therefore critical. We sampled ants in 20 urban bushland remnants in the Perth Metropolitan Area. To evaluate the influence of urbanisation) on ant taxonomic and functional diversity and composition we characterised the structure (composition and configuration) of the surrounding landscape and measured habitat (e.g. leaf litter and ground cover) and remnant patch (e.g. area and time since isolation) characteristics. Understanding how these factors affect diversity will improve ant conservation at both a local and landscape level and preserve ecological functions.

Artificial nesting pots encourage nesting by native bees

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The majority of bee species globally nest underground, however above-ground nesting bees have received most of the research attention in regard to creating extra nesting habitat. Evidence has revealed that ground-nesting bees play important ecological roles, and often are important pollinators in agricultural landscapes. However, techniques to attract and promote ground-nesting bees through enhancing nesting resources have been limited, as well as methods to create mobile nesting structures. This study established twelve artificial nesting pots designed to attract *Lasioglossum dotatum*, a native ground-nesting bee species, around glasshouses at Murdoch University in Western Australia across a two-year period (6 nesting pots established in 2022, and 6 in 2023). Within 24 hours of installation across the study period, all nesting pots were colonized, with an average of 36 nesting entrances observed per nesting pot for 2022 and 35 nesting entrances per nesting pot for 2023. The nesting pots were successfully transported into greenhouse spaces and the bees were observed to continue to survive under these conditions. To assess the survival rates of offspring and successful development into adults, the emergence rates were recorded using emergent traps in September 2023. The emerging bees were documented in all nesting pots installed during the previous season. This study has shown that this nest pot design provides suitable nesting space for *L. dotatum*, allowing the next generation to successfully develop and emerge. Further research is needed to understand how to encourage foraging and pollination services within the glasshouse. Overall, this study represents an important step towards understanding and conserving ground-nesting bee populations, and the development of effective infrastructure for their management.

Body size of North American solitary bees resilient to warming temperatures in Rocky Mountain wildflower meadows

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Body size is a critical trait affecting organism survival and reproduction. Environmental stress is often associated with a reduction in body size. For example, agricultural intensification is associated with reduced solitary bee body size, which can be prevented with floral plantings. Global warming is another form of environmental stress which affects timing and abundance of flowering. Thus, such warming could have both direct effects on bee body size and indirect effects through floral resources. To assess how bee body size is responding to warming we use a dataset of bee specimens collected in subalpine meadows in Colorado, USA from 2009-2018 - years with wide variation in temperature and snowmelt timing. Bees were collected using passive trapping and netting every two weeks throughout each flight season. Previous work using 40 years of floral and climate data have shown early snowmelt is associated with early flowering in this ecosystem, as well as an increase in the number of days with low floral abundance. Based on these changes in flowering, we predicted bee body size would decline in a year following earlier snowmelt. For seven solitary or primitively social bee species spanning four families (Halictidae, Andrenidae, Colletidae and Apidae), we measured inter-tegular span of female specimens across the study period, which includes wide variation in snowmelt timing. We found in all of the bee species that body size had very weak correlations with snowmelt timing and winter cold severity, either same year or previous year. This suggests that the length of overwintering has little effect on body size. It also appears that bees provision their offspring with the same quantity of food stores regardless of floral abundance, perhaps instead producing fewer offspring if flowers are scarce. We thus predict body size of these bee species will not be greatly impacted by climate change.

Digitising a Key chapter in Australia’s entomological history: grasshopper collections of the ANIC

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Ken H. L. Key was a significant figure in Australia’s entomological history, through his scientific ideas and through his intense empirical efforts to build a collection of grasshoppers for the Australian National Insect Collection (ANIC). He and his colleagues, especially John Calaby, MJD White and Lew Chinnick, surveyed in Australia for 54 years (1936-1989). We digitized all their 223 field notebooks (2097 pages) and transcribed all the field trips conducted in Western Australia (WA) and Tasmania (47 notebooks, 590 pages), geocoding all sampling sites (8975 geographic coordinates for 503 species) which are now available on the Atlas of Living Australia. I will provide an overview of this work and what it has taught about the history of the grasshoppers, the entomologists and Australia more generally.

Yalata-Fowlers Bay Bush Blitz Orthoptera: Caelifera

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A survey of grasshopper species (order Orthoptera, suborder Caelifera) was conducted between the 25th November and the 1st December, 2021 in the Yalata-Fowlers Bay region. Sites were in part chosen to resurvey areas that were surveyed between 1947 and 1969 by Dr Ken Key and his associates to develop the grasshopper collection of the Australian National Insect Collection. Nineteen resurvey sites and seven additional sites were surveyed during the study period and species presence was recorded as well as details on thermal conditions during the survey. Site photos and macro photos of all taxa were taken. Overall, 29 species of grasshopper were recorded from the area from 22 genera and three families. Comparison of resurvey sites revealed higher overall diversity but no correlation between historical and current site diversity, and little site-specific overlap (max 33%, mean 17%). Some very common taxa in the current survey were absent from previous surveys. The higher present diversity of grasshoppers in the area may reflect historical changes such as relaxed grazing pressure from stock and rabbits.

Untangling the web: dynamics of the Australian terrestrial invertebrate trade

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The trade and keeping of exotic pets has serious implications for Australia's biosecurity and biodiversity conservation. This trade gives rise to a multitude of adverse consequences, including overexploitation of wild populations, introduction of alien species, and spread of disease. Although the impacts of wildlife trade on vertebrates are well-documented, the effects on terrestrial invertebrates are largely unexplored and underregulated in Australia.

In this novel one-year snap-shot study, we investigated the online trade of terrestrial invertebrates in Australia. We collected data from a public classifieds website and 23 Australian online pet stores, identifying 264 species of traded invertebrates. The native *Extatosoma tiaratum* (giant prickly stick insect) was the most traded species, while the families Phasmatidae (stick insects), Formicidae (ants), and Theraphosidae (tarantulas) were the most popular. Among the traded species, three were known to be invasive in Australia, while 87% were native. The conservation status of almost all species traded (92%) has not been evaluated. Finally, we did not observe a saturation in the number of species traded in our one-year study, exemplifying the need for large scale monitoring and risk assessments for Australia's terrestrial invertebrate trade.

Our ongoing research extends beyond this study, investigating additional trade pathways such as physical pet stores and wildlife trade expos. Additionally, we are conducting a case study on honeybee trade in Australia to further understand the potential biosecurity threats associated with this trade. These efforts aim to bridge the knowledge gaps concerning the trade of invertebrates, facilitating their inclusion in policy decision-making.

By understanding the diversity of invertebrate species traded in Australia and the underlying drivers (i.e., consumer demand) behind this trade, we can gain a greater understanding of the risks traded species and their recipient environments are facing. This research contributes to the development of a comprehensive framework that integrates invertebrates into wildlife trade policies and conservation efforts, ultimately safeguarding Australia's unique terrestrial invertebrate fauna and their ecosystems.

Fourteen years of Bush Blitz native bee surveys: new species and a DNA barcode reference library for Australian bee species

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Participation in 13 Bush Blitz (BB) surveys mostly in remote parts of Australia in the last 14 years resulted in a wealth of new information on native bee taxonomy and distributions.

Here we give an overview of the biodiversity encountered and new species recognised. The Bush Blitz surveys and the associated funding for taxonomic work resulted in the descriptions of 131 new species in eight genera and four families. Specimens collected on the BB surveys, private collection trips as well as fieldwork associated with PhD projects, were also used to build on to our DNA barcode reference library of reliable identified Australian native bee species. More than 4070 specimens were sent to the Barcode of Life Data systems (BOLD) for DNA sequencing. The generated DNA barcode data, which is open access in the AUSBS project in BOLD, is meant to be a resource for future bee researchers as a service to assist with the identification of bee specimens.

Currently there are 1085 BINs (Biological Identification Number) recognised in the AUSBS project, which reflects the number of species. Identifying the species is work in progress and is hampered by the fact that less than half of the known species are in identification keys. However, identification of specimens in genera with existing keys, resulted in the recognition of new species, of the sexes of species described under different names, as well as of sexes that had been wrongly associated in the past. In several genera that currently lack identification keys, the number of BINs far outnumbers the number of current available names, indicating additional new species.

ABRS: 50 years of impact in Australian taxonomy

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This year marks the 50th anniversary of the Australian Biological Resources Study, originally established in 1973 to become the national focal point for taxonomy and systematics and make taxonomic information freely available. In this time, the ABRS has awarded a total of $84 million in competitive taxonomic research grants that has enabled the taxonomic community to document, describe and revise Australian biodiversity. We provide several updates on some of the ABRS's recent activities: 1) entomological highlights from the 2022 Australian Taxonomic Capacity Survey documenting current trends in the workforce; 2) progress towards integrating the Australian Faunal Directory and the Australian National Species List, and; 3) an example of a successful media campaign promoting Taxonomist Appreciation Day 2023 and the role of taxonomists to the Minister for the Environment and Water and the public. Given the ABRS's strong track record in enabling taxonomic research, it will continue to mobilise taxonomists and research partners to document and describe Australia's unique biodiversity for the benefit of future generations.

Taxonomic revision of the arbovirus vector mosquito *Culex annulirostris* Skuse, 1889 using museum genomics

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The common banded mosquito *Culex (Culex) annulirostris* Skuse, 1889 is the primary vector of the recent outbreak of Japanese encephalitis virus (JEV) in Australia, among other arboviruses. Although previous sanger-based molecular studies reported putative cryptic species in *Cx. annulirostris*, taxonomic resolution of the species complex has been hampered due to destructive sampling techniques and a lack of authoritatively identified reference specimens. By using genome skimming from only one or two legs, we successfully sequenced the complete mitochondrial genome of specimens to identify mosquito species held in Australian museums or reference collections dating back to 1951. We used mitogenome data integrated with morphological characters to diagnose four cryptic species comprising: *Cx. annulirostris* sensu stricto widespread throughout Australia, with smaller populations throughout Timor-Leste and Australasia; *Culex (Culex) somerseti* Taylor, 1912 stat. rev. (resurrected from synonymy within *Cx. annulirostris*), predominantly eastern Australian; and two undescribed species from Papua New Guinea and north Queensland, Australia, and another from the Solomon Islands. Ancestral state reconstruction revealed recent migration of two independent *Cx. annulirostris* populations from Australia to Papua New Guinea and Timor-Leste, respectively. We also resolved the validity and placement of manuscript names from museum collections and the literature. Adoption of museum genomics will enable improved biosecurity diagnostics of native and exotic species, tracking of historical incursions of vectors using historical collections, and working towards describing the remarkable 170 unnamed mosquito species documented in Australia. Epidemiologists can now complete vector competence testing on each revised species to identify their specific role in disease transmission, including the recent outbreak of JEV in Australia.

Lifetime and reproductive consequences of short-term anthelmintic exposure to female dung beetles

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Macrocyclic lactone based anthelmintics are frequently used to treat gastrointestinal nematode infestations within livestock. These anthelmintics target the glutamate-gated chloride channels present in nematodes which leads to reduced motility and eventual mortality. However, these channels are also present in a wide variety of other fauna, which can lead to detrimental effects in non-target and beneficial invertebrates.

Dung beetles are an example of the non-target organisms affected by these anthelmintics. Most of the research has focused on immediate effects of anthelmintics, however, here we investigated how the short-term exposure of female dung beetles may affect their lifetime reproductive output. We used a single female mesocosm setup under controlled environmental conditions, where half of the females were briefly exposed to dung containing anthelmintic for a period of a week, before returning to anthelmintic-free dung. We measured brood ball production on a daily basis and monitored females for mortality. We additionally measured egg to adult survival of offspring, their pronotum width, sex, and development time.

We found that females exposed to ivermectin had comparable lifespans to control females, but they required a longer reproductive period to have comparable reproductive output. All offspring provisioned with dung containing ivermectin failed to survive to adulthood. However, offspring produced in ivermectin-free dung by females previously exposed to ivermectin had the same probability of survival as offspring from females never exposed to ivermectin. By measuring daily brood ball production over the lifespan of female dung beetles, our results provide insight into not only the sub-lethal effects of ivermectin on dung beetles, but also the life history ecology of dung beetles and potential changes that occur throughout their lifespan. Furthermore, our findings raise the importance of investigating lethal and sub-lethal effects of anthelmintics over a lifetime period to gain clarity into potential impacts of toxicity on non-target organisms.

Pervasive relaxed selection in termite genomes

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Cockroaches are a diverse group of insects that comprise ~4500 species, as well as ~3000 eusocial termite species. In recent years, the first genomes of termites and cockroaches have been sequenced, with the genomic basis of eusociality in termites a key topic of investigation. The two cockroach species whose genomes have previously been reported, *Blattella germanica* and *Periplaneta americana*, are both well known omnivorous pest species. However, the vast majority of cockroaches are not pest species, and play key roles in nutrient recycling in a range of ecosystems. To increase the power of comparative genomic analyses to investigate the biology of cockroaches and termites, the genomes from phylogenetically diverse cockroach species are needed. We have sequenced, assembled and annotated the genomes of two soil-burrowing and one wood-feeding cockroach species *Geoscapheus dilatatu*s, *Neogeoscapheus hanni* and *Panesthia cribrata*. These are the first genomes to be sequenced from the cockroach family Blaberidae, the most speciose cockroach family. We used multiple genomic data types, including PacBio long-read sequences, HiC sequencing and linked-read sequencing to obtain our three assemblies. The completeness and continuity of the resultant genomes varied; *G. dilatatus* was the highest quality, with 98.7% BUSCOs present (93.9% complete, and 4.8% fragmented), and a N50 of ~3.2 Mb. We are currently investigating evolution in cockroaches and termites, including the emergence of specific traits (e.g. eusociality in termites), and assessing major genomic changes within and between groups (e.g. expansion/contractions of significant gene families).

Evolution and systematics of *Panesthia lata*, an endangered cockroach from the Lord Howe Island Group, and related taxa

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The cockroach genus *Panesthia* is represented by two lineages in Australia, arising from separate invasions of the continent by Melanesian ancestors. The more recent of these evolutionary radiations comprises five known species, occurring in the rainforests, sclerophylls and woodlands of the eastern seaboard, as well as the Lord Howe Island Group (LHIG). Concurrent with the cockroaches' dispersal across Australia, global cycles of glaciation caused dramatic turnover of rainforests, and fluctuations in the arrangement of offshore islands. Due to poor sampling in molecular studies, and conflict over the validity of the standing taxonomy, there is little certainty about relationships among species, or about the impact of climatic fluctuations upon their evolution. We undertook a comprehensive phylogenetic analysis of the clade, using mitochondrial and nuclear markers from nearly all known morphospecies and populations. This was supported by a population genetic study of the endangered Lord Howe Island cockroach *Panesthia lata*, using mitochondrial genomes and a panel of nuclear single-nucleotide polymorphisms. Our phylogenetic analyses reveal five unrecognised species of mainland *Panesthia*, and suggest that they have arisen primarily through vicariance as rainforests fragmented during Plio-Pleistocene glacial cycles (~2–6 Ma). Ancestral niche reconstructions also evidence three instances of speciation associated with transitions into drier forest, which have potentially allowed species to disperse more widely across the seaboard. Based on these results, we describe a novel species of *Panesthia*, and propose taxonomic updates to the clade, supported by candidate autapomorphies. Lastly, we show that while *P. lata* colonised the LHIG in a single event ~2 Ma, most of its island populations diverged during the last glacial period (~20–40 ka). This suggests that the species' evolution has involved episodic gene flow across land bridges during sea level lowstands. We also detect high levels of inbreeding in all populations, and outline strategies for their conservation.

Warfare in ants and video games

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Humans are not the only animals that go to war: eusocial insects such as ants do so on a comparable scale. Theoretical models of warfare predict that the value of an army is proportional to two key factors: the strength of each soldier in the army, and army size. In theory, the optimal strategy of investment in army size versus investment in soldier quality should depend on the environment. Simple, open environments should favour superior numbers, whereas complex terrain-based environments should favour stronger soldiers. Here, we provide the first controlled experimental validation of this theoretical prediction.

We first demonstrate this pattern using simulated battles between relatively strong and weak soldiers in a real-time strategy video game. We then validate this result in real animals using an ant model system: small armies of strong native meat ant (*Iridomyrmex purpureus*) workers were more successful in battles against large armies of weak non-native invasive Argentine ant (*Linepithema humile*) workers in complex than in simple battlefields.

Our results provide controlled experimental evidence that optimal army investment strategies depend on environmental complexity. This is a significant advance in the empirical study of nonhuman warfare, particularly in social insects. It is also important for understanding the competitive balance among native and non-native invasive ant species, since invasive ants are typically smaller but more numerous than their native competitors.

Complementarity of morphological and molecular identifications of ants (Hymenoptera: Formicidae) for biosecurity

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In Australia ants are often amongst the most ubiquitous and ecologically influential components of most terrestrial systems, exhibiting an exceptionally high level of endemic diversity. Whilst an increasingly important group for biosecurity, at the species-level there remains a great deal of uncertainty with several of the most diverse, widespread and ecologically dominant genera, in need of revision.

Exotic invasive ant species are amongst the most environmentally and economically devasting biological invaders, easily transported by humans, with traits that allow them to thrive in novel environments and outcompete native species. Distinguishing between exotic species and related natives as soon as possible is essential to reduce the chance of establishment, but the lack of species-level understanding for native species in some genera (e.g., *Nylanderia* and *Pheidole*) can severely delay detection of congeneric exotic species.

Here we obtained DNA using non-destructive extraction methods and compared two high throughput sequencing (HTS) metabarcoding platforms, MiSeq (Illumina) and MinION (Oxford Nanopore), to obtain molecular identifications of ants. We compare costs and levels of sensitivity associated with both platforms, and we make suggestions on their most appropriate use in the context of biosecurity diagnostics. Additionally, thanks to the non-destructive protocols used here, ants could be further examined morphologically, demonstrating the advantages and current limitations of DNA-based identifications. This work highlights the importance of using both morphology and molecular techniques to enhance ant identifications for biosecurity, demonstrating once again how these approaches are complementary and not antithetical to each other.

Biodiversity of the Norfolk Island psyllids (Hemiptera: Psylloidea)

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Norfolk Island is a small, isolated archipelago in the South of the Pacific Ocean, located between Australia, New Zealand and New Caledonia. The history of colonization and land use on the island has resulted in a mosaic of introduced and often degraded habitat with only limited areas of reasonably well-preserved native habitat.

Like most invertebrate taxa, the psyllid fauna of Norfolk Island is poorly known. No psyllids had been formally recorded from Norfolk prior to an extensive quarantine survey undertaken between 2012 and 2014 which also produced the first records for many other taxa. This survey officially recorded a total of six psyllid species belonging to three different families: three Aphalaridae, one Carsidaridae, and two Triozidae. All six were introduced species that had been recorded either from Australia or from New Zealand, or from both countries.

After a more recent survey and extensive targeted collections, we provide additional records that increase the number to 13 species, encompassing four families. Of these, nine species are introduced and four are considered native, with three possibly endemic.

As a result of this work, we generated molecular data, a key to the psyllids of Norfolk Island, and descriptions for two new species, which are the first endemic species from the archipelago. Ultimately, the new records we present enable a better understanding of the psyllid diversity in the South Pacific and allow us to investigate the systematics and distribution of these taxa across Norfolk Island, Australia, and New Zealand.

The effectiveness of automated suction traps in monitoring beneficial parasitoid wasps

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The use of 'Sentinel' automated suction traps for monitoring beneficial parasitoid wasps has emerged as a critical aspect of ecological research and agricultural practices. The introduction of suction traps called 'Sentinels' for monitoring pests' movement and population patterns in 2017 within Australia has contributed to the need to understand beneficial insect abundance concurrently. Parasitoid wasps are a highly diverse, under-described insect group that suppresses insect pest populations. This study explores the benefits of using solar-powered Sentinels in monitoring parasitoid wasps and gaining insight into the diversity of beneficials and their ecological significance within the environment. The Sentinel was placed in the Adelaide Botanical Gardens alongside a Malaise trap to evaluate the differences in the parasitoid diversity caught. Preliminary results of an honours project focussing on the abundance of wasps caught in different trap types and the species diversity across trap types (within one superfamily, the Ichneumonoidea) will be presented. By studying the diversity of beneficials using the Sentinel traps, researchers and primary producers can gain insights into their abundance, species composition and seasonal patterns to improve biodiversity conservation and pest management decision-making. This study emphasises the importance of Sentinel traps, contributing to the advancement of monitoring beneficials concurrently with pests to enhance environmental sustainability.

Phylogenetic and environmental determinants of oothecal structure in Australian mantises (Mantodea)

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Morphological traits are phylogenetically conserved but can also be driven by environmental variables. As large invertebrate predators, mantises are useful indicators of ecosystem health. Although they can be hard to detect, their egg cases (oothecae) are apparent, long-lasting, and may provide a good measure of mantis assemblages. Previous studies have indicated that oothecae are phylogenetically distinct and important to include in taxonomic descriptions of Mantodea. Information on Australian Mantodean oothecae is severely limited. Here, we tested the role of phylogeny and environment in shaping mantis ootheca morphology. We obtained 343 mantis oothecae from 19 genera across the Australian continent. We measured internal and external morphology using Micro-CT and handheld calipers, with climate data from WorldClim. Principal component analysis identified the major axis of variation in morphology to be related to overall size, with the remaining significant dimensions being relative attachment area, internal ootheca size, egg chamber size and relative porosity volume. Linear mixed models revealed that phylogeny was strongly linked with morphology, accounting for up to 93% of variation. For all species and for the genera *Archimantis* and *Pseudomantis*: mean annual temperature was positively correlated with overall size and relative porosity volume, but showed negative correlation with inner ootheca size and relative attachment area, except in *Pseudomantis*, where relative attachment area showed a negative correlation with mean annual temperature range. The other climatic parameters showed no significant relationship to our principal components. Other genera showed no significant responses to environmental parameters, nor did egg chamber size. Oothecae of end-attachment were smaller than those of base-attachment, and relative attachment area varied with substrate. Although variation due to the environment was small relative to that driven by phylogeny, we found some evidence that larger oothecae with smaller relative attachment areas may be better insulated, more thermally stable and less vulnerable to desiccation.

eDNA and invertebrate pollinator community comparison: an EPICC survey method comparison study and community analysis

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Floral visitors and pollinators play a crucial role in maintaining forb and shrub diversity, performing arguably one of the most important ecosystem services in terms of plant reproduction. However, comprehensive sampling of our pollinator communities in Australia is limited and usually constrained to a single order. In 2022 this study performed a comprehensive survey of the invertebrate floral visitors to five grassland flowering species at Illabarook Grassland Flora Reserve in the Victorian Volcanic Plains using eDNA metabarcoding, sweep netting, vane traps, human observation, and cameras to understand how effective metabarcoding is for assessing invertebrate communities. Results based on high-level ordinal analyses indicate that eDNA sampling offers at the very least a comparable survey method for sampling invertebrate communities using processed flower heads and provides an excellent rate of identification per hour of sampling effort. Collected invertebrates are currently being identified to family or lower where possible and direct 16S rDNA & COI mtDNA sequencing of individuals is being undertaken to add this data to BOLD and BLAST databases. Two pollen libraries are under development: (1) a pollen reference library of co-flowering species; and (2) using pollen taken from all captured invertebrates to document the pollinator interactions for the sampled plants within the greater grassland. This talk will present the invertebrate family-level analyses showing how eDNA compares with traditional survey methods in capturing the floral visitor community, along with the general invertebrate pollinator community results.

The past and the future of entomological education in Australia

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I review entomological education in Australia using as a yardstick the status of entomological education in the jubilee year of the Entomological Society of Queensland, 1974. Education was a featured topic in the jubilee publication, which was titled "Changing Patterns in Entomology". Gordon Hooper, head of the University of Queensland (UQ) Department of Entomology at that time presented a paper titled "The Entomologist: His Formal Training"—the title reflects changes in societal and educational attitudes that have occurred since. He pointed out how the number of entomology courses/subjects on offer to science and agriculture students at UQ was steadily increasing. Since 1974, the number of entomology-specific courses/subjects available at Australian universities including the University of Queensland has plummeted. Today, the discussion of the status of tertiary-level entomological education tends to be a lament. I outline the changes in course offerings throughout Australia and review the drivers behind these changes. We need to acknowledge that education is becoming more about helping students manage and contextualise information than it is about lecturing to them. Practical skills might need to be obtained in workshops or at the workplace.

Finding French Anystis Mite (FAM), 30 years after its release in grain growing areas of Western Australia

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French Anystis mite (*Anystis wallacei*) (FAM), a biological control of redlegged earth mites (*Halotydeus destructor*) (RLEM), can control up 70%- 80% of RLEM in spring. Between 1988-1991, 36 release sites for FAM were established from Coorow to Augusta.

Surveys in 2021/22 found FAM only at 10 release sites. Nine release sites were long-term pasture paddocks, of which only two had a history of in-frequent organophosphate insecticide applications. Only at one release site, which had been cropped for the first time in 2021, were FAM found in uncropped weedy refuges in the paddock.

At all release sites, FAM were found to have spread from the original release site only if directly adjacent to the release site was a pasture paddock or a weedy refuge. In release sites that were cropped FAM were not found in weeds along fencelines or lane-ways, only in refuges in the paddock that could not be sprayed such as drains.

Two nursery sites have been established to allow interested parties to collect FAM for release:

1. Manjimup Research Facility (MRF), even though FAM were not released here, FAM spread 1.4 km from the original release site onto MRF;
2. Boyup Brook release site had the highest abundance of FAM found to date, with on average 92 FAM per square metre.

One hundred years of vegetation changes in Kosciuszko National Park reflected in the pollen record of insect specimens

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Kosciuszko National Park is one of Australia's most significant parks, home to rare segments of highly threatened alpine flora and several endangered animals, including the iconic Bogong moth *(Agrotis infusa,* Noctuidae). Until the 1960s, intense stock grazing took place within the park, followed by restoration efforts that included plantings of non-native species. The vegetation today is markedly different, with many endemic species now present in the park. We examined the pollen record from insect specimens collected in the region dating from the early 1920s to 2021, focusing on two major pollinator groups: march flies (*Copidapha maculiventris,* Tabanidae) and native bees (*Lassioglossum*, Halictidae and *Leioproctus*, Colletidae). The results obtained through pollen DNA metabarcoding reflect the changing patterns of vegetation in the park, exhibiting low plant diversity and a predominance of woody shrubs, trees and pasture crops during heavy grazing periods, an increase in *Trifolium* (Fabaceae) species during early restoration stages, and a high diversity of native plants in recent years. Our study demonstrates how biological collections are rich sources of information that can be unlocked to reconstruct past events and understand their impact on our environment.

Diversity of Australian archaeococcoid scale insects: implications for taxonomy and biological control

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Scale insects are small, sap-sucking plant parasites that make up approximately 10% (c. 8300 described species) of the known emipteran fauna. They can be divided into two main informal groups: the archaeococcoids and the neococcoids. Although Australia's neococcoid diversity is relatively well-known and documented, most groups of Australian archaeococcoids are poorly studied and have not been recently revised taxonomically. This is problematic for biocontrol programs, such as when trying to construct non-target species lists to assess the potential prey-specificity risks of native species when exposed to proposed biological control agents. Additionally, the lack of recent systematic studies makes it difficult to know what species to use for prey-specificity testing experiments. Here, we amplify multiple molecular markers (nuclear and mitochondrial loci) from archaeococcoid specimens collected across Australia to test species boundaries and document possibly cryptic diversity within this group of poorly-studied insects.

Checking the pulse: assessing insect diversity, taxonomy and threat status in south-west Australia

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Purported mass loss of insects globally is coinciding with accelerating threats, including megafires, flooding, temperature extremes, urbanisation, and habitat loss. In global diversity hotspots, where endemism is high, and native vegetation highly impacted, many insect species would likely be both endemic and threatened. However, insect diversity, endemicity and threat status are largely unknown in these regions. Here we assess the biodiversity and status of host-dependent insects in the southwest Australian hotspot. We investigated a large number of different insect families (including those that were not host-dependent), consulting with taxonomic specialists, however, we found that much of the information required for basic assessment was too scant. We selected nine insect families across three orders; Tingidae, Achilidae, Derbidae, Dictyopharidae, Triozidae (Hemiptera), Micropterigidae, Heliozidae (Lepidoptera), Boopidae, and Philopteridae (Psocodea). These families had 632+ species, of which 255 (~ 40%) were described. One species was formally listed as threatened, but a further 245 species potentially require conservation management. We found that threatening processes include coextinction (through loss or reduction in host populations), climate change, altered fire regimes, habitat loss, and fragmentation of host populations – with many threats acting synergistically upon species. Taxonomic and resourcing bias has inhibited attempts to describe the insect diversity and biogeography of the region, precluding comprehensive conservation assessments for the majority of insect families that we attempted to explore. Given the scale and intensity of threats faced by a hyperdiverse insect fauna in the southwest Australia biodiversity hotspot, a systematic approach to manage habitats at a landscape scale is most likely to succeed in conserving species in the short-term. Longer term solutions require addressing these taxonomic, geographic and ecological knowledge gaps, thus increasing our understanding of the diversity and conservation needs of all insect families in southwest Australia.

Boosting pest biocontrol using caffeine-fuelled beneficial insects

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Caffeine is naturally present in the nectar of several plant species (e.g., *Citrus* spp., *Coffea* spp., *Camellia sinensis* and the forage legume *Onobrychis viciifolia*). European honey bees (*Apis mellifera*) fed on caffeinated nectar are known to have improved memory for the same flower type thus increasing the chances of pollination. Given that parasitoid wasps and honey bees are closely related flower visitors, and parasitoid wasps are widely used as biocontrol agents, this project will investigate whether caffeinated nectar enhances the performance of several species of parasitoid wasps, including *Trichogramma pretiosum*, in vineyards.

If laboratory studies indicate that the presence of caffeine in a sugar solution improves a parasitoids ability to parasitize its host insect, then we will seek to determine the biologically active concentrations of nectar caffeine that maximises the number of insect pests parasitized by a particular species of wasp parasitoid. Small scale studies in greenhouses, and in the field, will then investigate:

(1) the level of pest control achieved by parasitoids (e.g., *T. pretiosum* reducing the number light brown apple moths [*Epiphyas postvittana*] feeding on the foliage and fruit of grapevines) in settings where grapevines are grown near caffeinated or caffeine-free nectar plants; and

(2) the potential for caffeinated nectar plants to be incorporated into the management of commercial vineyards.

The underlying hypothesis of the research is that caffeine will allow female wasp parasitoids to more effectively learn the kairomones released by insect pests and the herbivore-induced volatile synomones released by plants when attacked by insect pests such as *E. postvittana*.

Insect behavioural studies will use various choice/decision methods (e.g., the ‘y-tube olfactometer’ method) and chemical studies will use ultra high-performance liquid chromatography (UHPLC).

Taxonomy and systematics of *Chasmoptera* (Neuroptera: Nemopteridae: Nemopterinae): assessing the species status of Western Australia's only spoon-wing lacewing genus.

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Chasmoptera is a genus of charismatic spoon-wing lacewings (Neuroptera: Nemopteridae: Nemopterinae) endemic to Western Australia. There are currently only three described species in this genus: *C. hutti* (Westwood 1848), *C. superba* (Tillyard 1925) and *C. mathewsi* (Koch 1967). A defining feature of *Chasmoptera* is their elaborate extended hindwings, with apical dilations arranged in a "ribbon" or "spoon" shape. Little is known of their evolution or biology, though some inferences can be made from Nemopteridae from other continents.

Species identification for this genus has relied predominantly on hindwing morphology, with some forewing and genital morphology. Recent and historical collections of *Chasmoptera* from several different populations differ in appearance from the three described species and have been flagged as putative new species. The aim of this research was to assess the species status of eight discrete *Chasmoptera* populations using morphometric analyses of hindwing shape and mitochondrial (COI, 16S) and nuclear (28S) sequence data. The phylogenetic relationships among the species of *Chasmoptera* were also investigated.

Delimitation analyses identified two likely new species: *Chasmoptera* "AE" and *Chasmoptera* "PG". The unique hindwing morphology of an isolated population near Lake Grace revealed another putative new species, though for this population specimens did not yield any viable DNA data. Morphometric analysis showed that males have greater shape variation in their hindwings than females, consistent with the male hindwings being under sexual selection. K-means clustering presented some shape trends, although the patterns of species delimitation that were defined for the described and putative new species (as identified by hindwing shape) were not maintained. The results of this study present the first molecular phylogeny of *Chasmoptera* and tentatively doubles the number of known species. Further study of Nemopterinae in Western Australia and beyond should be carried out to preserve and protect these rarely encountered lacewings.

Transmission efficiency of Australian cereal viruses by four aphid species

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Aphids (Hemiptera: Aphididae) are vectors of yellow dwarf viruses (YDVs) which are found in cereals worldwide. Both aphids and YDVs can significantly reduce grain yield and are prevalent in cereal fields in south-eastern Australia. The most common cereal aphids in this region are *Rhopalosiphum padi* (bird cherry oat aphid), *Rhopalosiphum maidis* (corn aphid), *Metopolophium dirhodum* (rose grain aphid) and *Diuraphis noxia* (Russian wheat aphid). Several YDV species that had not been reported as present in Australia before have recently been found, however, little is known about the epidemiology of these species in an Australian context. To examine this, three individual glasshouse experiments were conducted to assess how efficiently *R. padi*, *R. maidis*, *M. dirhodum* and *D. noxia* transmit three Australian YDV isolates: barley yellow dwarf virus PAV (BYDV PAV), a barley yellow dwarf virus PAS (BYDV PAS)-like isolate, and barley virus G (BVG), to cereals. Each plant was exposed to a single viruliferous adult aphid for 72 hours then tested for virus presence four weeks later using tissue blot immunoassay. While *R.padi* was the most efficient vector of both the BYDV PAV and BYDV PAS-like isolates to wheat, *M. dirhodum* also transmitted both isolates, but much less efficiently. Additionally, *R. maidis* was the most efficient vector of BVG to barley but more surprisingly, *R. padi* also transmitted BVG, albeit less efficiently than *R. maidis*. Knowledge about the vectors of newly identified YDV species in Australia will help the development of more targeted management practices and therefore reduce the impact of aphids and viruses in grain crops.

Insecticide resistance in Australian serpentine leaf miner, *Liriomyza huidobrensis* (Blanchard, 1926) (Diptera: Agromyzidae)

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Serpentine leaf miner (*Liriomyza huidobrensis)* was first reported invading New South Wales and Queensland vegetable farms and nurseries in late 2020. Since then, it has posed a significant threat to Australian agriculture and horticultural industries.

Chemical control of serpentine leaf miner is difficult due to the larval feeding characteristic of mining inside plant leaf tissue. This lessens or prevents contact with sprayed chemical insecticides. In addition, the continuous use of broad-spectrum pesticides to control concurrent insect species may increase leaf miner resistance.

This study developed novel bioassay methods to test serpentine leaf miner in Australia for response against the chemical insecticides approved to control them. Additionally, we developed a multi-locus amplicon sequencing panel that successfully screened for target-site mutations causing resistance to several insecticide groups in serpentine leaf miner collected from New South Wales and Queensland.

Alarmingly, dose response and DNA-based testing suggest that serpentine leaf miner resistance to many chemicals is likely. Specifically, baseline dose response against dimethoate and imidacloprid for two strains, from New South Wales and one strain, from Queensland showed a similar and potentially resistant type response between strains. Sprayed rates required to achieve 100% mortality in the laboratory were significantly higher than the recommended field rate. LC_{50} estimates ranged from 1.4 (95% fiducial limit (FL) 0.8-2.0) to 2.5 (95% FL 2.1-3.0) g / L against dimethoate and 1.8 (95% FL 1.0-2.8) to 2.0 (95% FL 1.7-2.4) g/L for imidacloprid.

DNA resistance screening via multi-locus amplicon sequencing supported the bioassay as we detected homozygous mutations causing resistance to Group 1A&B Carbamates and Organophosphates, Group 2B Phenylpyrazoles, Group 3A Pyrethroids and Group 28 Diamides.

The novel bioassay method and the high throughput multi-locus amplicon sequencing we have developed efficiently defined the resistance status of this newly introduced leaf miner species. These combined novel bioassay and molecular tools can further help Australian industries monitor the long-term effectiveness of their strategies to control leaf miner.

Funding available for industry-focussed research in honey bees and pollination

B. Oldroyd

Agrifutures Australia, Honey Bee and Pollination Program, Building 007, Tooma Way Charles Sturt University, Locked Bag 588, Wagga Wagga NSW 2650, Australia.

Most of us struggle to get sufficient funding to support our research. But did you know that that there are granting agencies that sometimes can’t get enough suitable applications to expend their budgets? Agrifutures Australia is a Research and Development Corporation that supports a number of Australia’s agricultural industries. The Honey Bee and Pollination Program of Agrifutures supports the beekeeping industry’s needs. The program has an annual budget between $700,000 to $1,000,000, meaning that it can support 2-3 large (c.a. $100,000 p.a.) projects at any one time. It also provides seed funding for R&D ideas via its Industry Development Grants program. The Development Grants program can also provide support for training, for example for Honours and PhD students in industry-focussed projects. Support is generally provided for three years for major projects, and for longer where the project warrants it. Unlike many other programs, there is no requirement for co-funding; where justified, the requested budget is fully funded by Agrifutures Australia. The application process is not onerous; you can realistically complete a preliminary research proposal form online in one afternoon. The panel will then provide feedback as to whether they would be interested in receiving a full proposal. While full applications are more onerous than the preliminary proposal, it is nothing like as complicated as an ARC application for example.

Any research that could benefit the honey bee (*Apis* mellifera) industry will be considered. The Panel has funded many projects of interest to entomologists including honey bee pathology, ecology, pollination biology, bee breeding and genetics and population genetics to name a few. The panel not only provides financial support but also provides mentoring where needed for researchers that are new to honey bees. The panel does not support basic research except where it has strong potential to benefit the honey industry. You can find more information about the work of the panel and its strategic plan at https://agrifutures.com.au/rural-industries/honey-bee-pollination/. If you are interested in working in bees and beekeeping, please come and have a chat with me at my poster.

Molecular phylogeny of Australian micro-moths in the superfamily Gelechioidea (Lepidoptera)

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Gelechioidea, a superfamily of micro-Lepidoptera, is renowned for its incredible species richness, comprising approximately 18,500 described species distributed worldwide. In Australia, it is believed to be home to more than 20% of the world fauna (~4,000 species) and is considered the most diverse. Due to its immense species diversity, the classification at the family and superfamily levels has been unstable, with the number of recognised families ranging from 15 to 24. Moreover, the relationships among families and subfamilies remain poorly understood due to limited taxon sampling, especially from the Australian fauna.

In this study, we used collection genomics to revise the classification of Gelechioidea, with a focus on the Australian fauna and nomenclaturally relevant taxa. We sequenced mitochondrial genomes of the type species of approximately 500 genera and their synonyms, targeting all named gelechioid genera in Australia. Additionally, to ensure comprehensive coverage of the vast majority of the estimated 4,000 Australian gelechioid species, we incorporated approximately 30,000 publicly available COI barcodes. Our maximum likelihood analyses revealed that the superfamily Gelechioidea is monophyletic, while many of the morphology-based divisions of Oecophorinae (Oecophoridae) are not monophyletic. Furthermore, the relationships among families and subfamilies are poorly resolved.

Our project provides an exemplary illustration of how the systematics of mega-diverse organism groups can be addressed. In addition, this first molecular phylogeny of Australian Gelechioidea establishes the basis for a revised classification and a predictive framework for investigating the evolution of traits, such as life history strategies.

How often are male mosquitoes attracted to humans?

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Many mosquito species live close to humans where females feed on human blood. While male mosquitoes do not feed on blood, it has long been recognized that males of some species can be attracted to human hosts. To investigate how commonly male mosquitoes are attracted to humans, we review existing literature and performed human-baited field trials. We then undertook further laboratory and tent experiments to examine attraction to humans in males and females of three common *Aedes* mosquito species. We find that male attraction to humans is restricted to a handful of species including *Aedes aegypti* (Yellow fever mosquito) and *Ae. albopictus* (Tiger mosquito). The presence of male host-seeking behaviour in some species may promote mating success and contribute to these species being globally invasive. Male and female *Ae. aegypti* show similar patterns in preferential attraction between different human subjects. We also demonstrate that mosquito repellents applied to human skin repel male mosquitoes. Our findings provide insights into mosquito evolution and behaviour and have implications for mosquito control programs, particularly those that involve monitoring of the male mosquito population.

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

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

This study will monitor the biodiversity of mosquito species and the prevalence of mosquito-borne parasites and viruses across ten urban and peri-urban locations around Perth's metropolitan area. To compare shifts in mosquito population diversity and disease prevalence across time, traps have been set to represent both the four seasons and the six Noongar seasons. By evaluating seasonal variation, changes in mosquito composition will be evaluated and used to determine alterations in transmission risk related to vector abundance.

Mosquitoes, being hematophagous, will be utilised as a non-invasive surveillance tool to detect MBD. The prevalence of MBD has been determined using viral NGS and PCRs specific to mosquito-borne parasites, such as *Dirofilaria*, *Plasmodium*, and *Haemoproteus*. Mosquitoes are pooled according to date, location, and species, allowing each detection method to be specific to a particular mosquito species. Although this data does not determine the vector's ability for transmission, positive results will indicate the presence of the detected MBD within the location sampled. These results provide insight into local disease risks to humans, domestic animals, and wildlife, and potential disease vectors, which may aid future mosquito control programs.

Current distribution, behaviour, and habitat preferences of the Inland Hairstreak, *Jalmenus aridus* Graham & Moulds, 1988 (Lepidoptera: Lycaenidae) in the Goldfields of Western Australia

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The Inland Hairstreak, *Jalmenus aridus* Graham & Moulds, 1988 (Lepidoptera: Lycaenidae) is recorded only from its type locality at Lake Douglas, 12 km SW of Kalgoorlie. However, a recent mine-site fauna survey near Kalgoorlie uncovered a new breeding population. This prompted a renewed effort, supported by the mining company, to determine if there were more populations nearby. Our paper details the survey efforts and what we have learned about *J. aridus* biology and habitat preferences during two flight seasons. about J. aridus biology and habitat preferences during two flight seasons. Nine sites are now recorded with *J. aridus* spread over an area measuring 120 km north to south, and 40 km east to west. *J. aridus* preferred habit is described with the hope that others will be encouraged to visit Kalgoorlie and discover more populations of this elusive butterfly.

Population genomics of the Queensland Fruit fly (*Bactrocera tryoni*) species complex

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Tephritid fruit flies pose a significant and escalating threat to Australian horticultural industries, with potential new introductions of exotic species, alongside range expansions of endemic pests, jeopardizing crop production and access to international markets. Effectively managing the impacts of these pests into the future requires a comprehensive understanding of their population dynamics, genetic diversity, and dispersal patterns. Recent advances in population genomic analysis, including kinship analyses, offer novel avenues for investigating the spread and dispersal of tephritid fruit flies across a variety of geographic scales in order to inform outbreak response and integrated pest management strategies.

Our research has involved the development and evaluation of novel whole genome sequencing techniques and population genomic methods to elucidate the genetic structure and connectivity between tephritid populations, with a specific focus on the *Bactrocera tryoni* (Diptera: Tephritidae) species complex. Through analysis of genome-wide polymorphism data from multiple populations across the entire geographic range of the complex, our research provides new insight into the evolutionary history, distribution, and taxonomic status of each species, with implications for market access.

This work serves as a foundation for a new project under the Australian Horticultural Market Access Research Partnership, which aims to augment our understanding of tephritid fruit fly biology and management through the integration of regulatory market access research, in-field insect pest management, and genomic investigations. The findings from this research program will have significant implications for ongoing management of endemic and exotic fruit flies in Australia, facilitating the design of tailored surveillance programs, biosecurity measures, and targeted control strategies based on the specific demographic and dispersal patterns of these economically important pests.

Taxonomy and systematics of artoriine wolf spiders (Araneae: Lycosidae): is *Artoria* monophyletic?

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The genus *Artoria* currently represents the most speciose genus of wolf spiders in Australia represented by 42 described species and possibly another 120–150 undescribed species. Like most other genera in the subfamily Artoriinae, it includes comparatively small spiders of less than 10 mm body length which are generally found in leaf litter and near creeks and other water bodies, largely in the Bassian and Torresian Australian bioregions. The genus has also been reported from Asia, the Pacific, New Zealand and Africa. Morphological and molecular evidence suggests, however, that *Artoria* is paraphyletic although this assumption has never been tested with rigorous phylogenetic methods. This presentation will introduce our ABRS-funded taxonomic and systematic revision of the Australian and world-wide artoriine taxa with special reference to the genus *Artoria*. We will completely revise the Australian and New Zealand faunas of the genus and will test its monophyly with morphological and molecular methods, in particular with respect to other artoriine genera such as *Artoriopsis*, *Anoteropsis*, *Notocosa*, *Syroloma*, *Lycosella*, *Navira* and *Lobizon*.

Endosymbionts…. manipulators of reproduction in parasitoid wasps?

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Aphids (Hemiptera: Aphididae) and Lepidopteran pests are major crop pests that cause severe economic losses in Australian grain industry. Pesticide overuse has driven insecticide resistance in pests (Thia *et al*., 2023). To control insect pests, parasitoid wasps are considered as promising biocontrol agents, but their effectiveness relies on their mode of reproduction. Endosymbiotic bacteria such as *Wolbachia*, *Cardinium*, *Rickettsia* and *Arsenophonus* are known to alter host reproduction in insects, and this can be used to increase the efficacy of biocontrol agents like parasitoid wasps by inducing asexual reproduction. However, there has been limited research on the diversity of endosymbionts in parasitoid wasps within Australian agricultural crops. To understand the phenotypes of these endosymbionts in nature, we need to know where these endosymbionts are found. The benefit of characterizing the diversity of endosymbiotic bacteria within and among natural populations of aphid and lepidopteran parasitoids of Australian grain crops will help to develop an effective (thelytokous) strain of parasitoid wasp. Therefore, in this study, our aim is to survey a wide range of grain crops across the southeastren parts of Australia, with a particular focus on the Victorian region. To date, we have surveyed 12 different species of lepidopteran parasitoids, which belong to four superfamilies, as well as nine different species of aphid parasitoids, which belongs to two superfamilies. Among the lepidopteran parasitoids, we observed *Wolbachia* to be the most prevalent infection in *Diadegma semiclausum* (Hymenotera:Ichneumonidae) , *Cotesia gloemrata* (Hymenoptera: Braconidae), *Eriborus* sp. (Hymenotera:Ichneumonidae). and *Copidosoma sp*. (Hymenoptera: Braconidae).

Insect response to canola with modified sterol metabolism

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In Australia, canola is the third largest crop and Western Australia is the major canola growing state producing about 40% of the nation's 2.7 million tonnes each year. With times, canola has been attacked by a wide range of insects and pests. Among them, green peach aphid (GPA), *Myzus persicae* and diamondback moth (DBM), *Plutella xylostella* are the most notorious ones. The widespread use of chemical insecticides and pesticides has led to the development of resistance in targeted species. To address the above issues, an innovative, more efficient and environmentally friendly approach to control insect pests is needed, one approach is to develop genetically modified (GMO) canola with modified sterol level in canola. Sterol especially phytosterol is an important component for harbivorous insects. Phytostrols are associated with insect life cycle, development, reproduction, and feeding preferences. It has been reported that insects' life cycle can be affected by modified sterol profile but little attention has been paid to modified sterol profile in canola.

This project aimed to investigate insect (GPA and DBM) responses (feeding preference, effect on life cycle, and molecular responses) to canola with modiflied sterol profile. Three genetically modified (GMO) canola lines, along with wild type canola as controls, has been used in this study. To examine the feeding preferences of insects between GMO and control canola, choice-feeding bioassay has been carried out. Priliminary results showed that there was no significant differences of GPA feeding preference between GMO canola and control canola. This study will improve our understanding of insect-plant interactions and help develop more sustainable and eco-friendly management practices.

Performance of fall armyworm reared on various horticultural crops

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The fall armyworm (FAW) *Spodoptera frugiperda* (JE Smith), a polyphagous pest that recently invaded Australia, poses a significant threat to horticulture production and trade. Although reports of FAW infestations in different horticultural crops have been documented, the extent of damage and the potential for establishment in specific crops remain unclear. Understanding FAW's performance on different hosts can help to ascertain risk and facilitate the development of efficient FAW management strategies. To address this knowledge gap, we investigated larval development and fecundity of female FAW from larvae fed on various natural hosts, including beans, capsicum, okra, strawberry, and sweetcorn. FAW larvae exhibited longer larval and pupal developmental time on strawberry, capsicum, and okra than on bean and sweetcorn. Adult females from capsicum-, strawberry-, and okra-fed larvae produced fewer eggs than those from beans- and sweetcorn-fed larvae. Notably, no larvae hatched from the eggs of adult females from capsicum-fed larvae, suggesting that this crop prevented the pest from completing its life cycle. These findings enhance our understanding of FAW development and female fecundity on some major horticultural crops that are susceptible to infestation. Furthermore, this knowledge can contribute to the development of targeted management strategies for controlling this pest.

An important and victorious science: the International Congresses of Entomology

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The history of the International Congresses of Entomology (ICE) provides fascinating snapshots of the development of the science of entomology over the last 100 years. The editors of this book worked with 22 international authors to describe each of the 25 Congresses held from 1910-2016 in 20 different countries. Australians have had a strong presence in ICE for the past 50 years, and like many delegates I have attended multiple Congresses; my first, ICE XIV, in Canberra 1972, followed by six more including ICE XXV in Orlando 2016. The Congresses continue to be the largest in-person meeting for the science of entomology. ICE I in Brussels 1910 attracted 254 delegates from 24 countries, while ICE XXV in Orlando attracted 6,671 delegates from 101 countries.

Holding Congresses in different countries has allowed “entomologists of the world to gain an appreciation for how the challenges and opportunities for insect science vary from place to place, to form connections, professional and personal, and to function as a global community of scholars and practitioners” (p273). More recently delegate demographics have broadened “with increasing participation on the part of formerly under-represented groups, including women, students, and early career professionals” (p273). “ICE may provide the best opportunity to bring the case for evidence-based science in policy decision-making directly to decision-makers” (p275). The theme of the next ICE XXVII in Kyoto, Japan in August 2024, “New discovery through consilience”, emphasises that evidence from independent unrelated sources can converge on strong conclusions; a continuing important output from ICE.

James Ridsdill-Smith, Phyllis Weintraub, Max Whitten, and May Berenbaum (editors) 2022. An Important and Victorious Science: The International Congresses of Entomology. Entomological Society of America, 276pp. (Thomas Say Publications in Entomology-Memoirs). ISBN 978-0-9776209-3-7.

Phylogenomics and taxonomy of the genus *Leioproctus* (Hymenoptera: Colletidae)

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The colletid bee genus *Leioproctus* is the largest bee genus in Australia, comprising over 300 species. Despite its ubiquity, the monophyly of the genus and its subgenera has been disputed, and numerous species remain undescribed. In this study, we aimed to determine the boundaries of *Leioproctus*, closely related genera of Neopasiphaeinae (Hymenoptera: Colletidae), and subgenera by sequencing Ultra Conserved Elements (UCE) from 40 fresh and museum specimens, encompassing 34 species, 11 subgenera, and three genera. For 36 of these samples, we used hybridisation capture to enrich for 2590 ant-specific UCEs. For the remaining samples, we utilized a whole-genome sequencing approach to recover UCEs. UCE loci were retrieved, aligned, and concatenated from the assemblies derived from these two approaches using Phyluce. On average, we recovered 1,609 loci per sample with a mean length of 576 bp, resulting in a 75% complete matrix containing 1487 loci. We generated a maximum likelihood tree using iqtree2 and employed the ultrafast bootstrap method to obtain node support values. The resulting phylogeny does not support the monophyly of *Leioproctus* s.l. or *Leioproctus* s.s. (UFB < 0.8). However, the monophyly of all other subgenera sampled is supported (UFB > 0.8). Further sampling, especially within *Leioproctus* s.s., is required to improve the taxonomy of this ubiquitous bee genus, which could potentially lead to the description of hundreds of new species.

Deleterious endosymbionts for aphid (Hemiptera: Aphididae) control

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Endosymbiotic bacteria that live inside insects have a variety of effects on their hosts and can be used to control insect populations. For example, transinfections of *Wolbachia* endosymbionts are now being used to reduce dengue transmission by mosquitoes, but there has been limited progress on applications using other endosymbionts. Here we develop a novel pathway to application in aphids (Hemiptera: Aphididae) by transferring the endosymbiont *Rickettsiella viridis* to the major crop pest *Myzus persicae*. *Rickettsiella* infection greatly reduced aphid fecundity and modified aphid body color, from light to dark green. Despite inducing host fitness costs, *Rickettsiella* spread rapidly through caged aphid populations via plant-mediated horizontal transmission. The phenotypic effects of *Rickettsiella* were sensitive to temperature, with the loss of body color modification at high temperatures, a reduction in aphid heat tolerance, and temperature-dependent spread through populations. *Rickettsiella* shows potential to spread through natural *M. persicae* populations by vertical and horizontal transmission. Establishment of *Rickettsiella* could reduce crop damage by modifying population age structure, reducing population growth and providing context-dependent effects on host fitness. Our work highlights the importance of plant-mediated horizontal transmission and interactions with temperature as drivers of endosymbiont spread in asexual insect populations.

The predator community of tomato potato psyllid, *Bactericera cockerelli* in Western Australia and their field predation

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The tomato potato psyllid, *Bactericera cockerelli* (Hemiptera: Triozidae) is an invasive pest in Australia which can cause severe economic loss in the production of solanaceous crops. In early 2017, it was first detected on mainland Australia in Perth, Western Australia. In this study we identified the species of *B. cockerelli* predators occurring in fields of Solanaceae in Western Australia. Sampling was done using sweep netting technique in fields in some of the major Solanaceae growing regions of Western Australia in 2021 and 2022. To monitor the prey and predator populations yellow sticky traps were also placed in the sampling locations. Species specific primers were developed to detect DNA of *B. cockerelli* in predators that had fed on *B. cockerelli*. The primers were then used to screen which of the predators collected from the field had been feeding on the target prey, *B. cockerelli*. A broad taxonomic rang of predators were collected from the two years of field sampling. Chrysopidae was the most abundant followed by Coccinellidae. Monitoring with yellow sticky traps revealed that the predator populations in the field increased when *B. cockerelli* population were higher. The predators from the field which we analysed belonged to 7 insect taxa, 45% were positive to *B. cockerelli* DNA and Coleopteran predators were more common. These findings highlight the predator community, which can be used in implementing the eco-friendly and sustainable pest management options for invasive *B. cockerelli* in Western Australia.

Advances in macro and micro photography to improve biosecurity capabilities for invertebrates

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Exotic invertebrate incursions can negatively impact the environment, agriculture, horticulture and our way of life. Diagnostic imaging can facilitate invertebrate identification, contributing towards faster eradication and reducing the likelihood of pests establishing.

Here I review the available imaging methods for producing the best quality invertebrate diagnostic photos for biosecurity. A comparison between two types of high-tech imaging systems and two types of mid-range phone camera setups was undertaken to determine differences in image quality, versatility, and cost effectiveness. The setups consisted of;

1. a phone camera with a clip-on macro lens,

2. a phone camera held against a stereomicroscope eyepiece to achieve higher magnification levels,

3. an off-the-shelf, high-end motorised stereomicroscope imaging setup, and

4. a custom-built imaging system using a digital, full-frame mirrorless camera and multiple individually sourced components.

Results showed the custom-built system delivered superior image quality and allowed more versatility. Components could also be upgraded at a lower cost. However, the off-the-shelf system provided faster and more automated results that less tech-savvy individuals could achieve acceptable outcomes with, albeit at the expense of image quality, level of detail and a higher upfront cost. Whilst a phone camera is a very cheap option, images produced with both setups were inadequate to make reliable species identifications for most invertebrates due to inferior image quality and lack of depth of field.

In conclusion, utilising either high-tech system will increase biosecurity capabilities including identification tools such as the Pest and Disease Image Library (PaDIL) and value-add to institutions housing insect collections, by digitally preserving aging specimens and creating a permanent record for future reference, even if the imaged specimen has long deteriorated along with the determining taxonomist.

Global, asynchronous sweeps at multiple resistance genes in *Aedes* mosquitoes

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Aedes aegypti (yellow fever mosquito) and *Ae. albopictus* (tiger mosquito) are highly invasive pests with global distributions that together confer the world's dengue burden. Insecticide-based management has led to the evolution of insecticide resistance in both species, which can show a complex genetic architecture and unexpected geographical patterns. Here we report global asynchronous sweeps on two chromosomes containing resistance genes. Sweeps at the voltage-sensitive sodium channel gene (VSSC) on chromosome 3 correspond to a single substitution in *Ae. albopictus* and three substitutions in *Ae. aegypti*, including two at the same nucleotide position (F1534C). In *Ae. aegypti*, we identify a second swept region on chromosome 2, containing 15 glutathione S-transferase (GST) epsilon genes with significant copy number variation across populations and where three distinct haplotypes have swept through the Indo-Pacific region, the Americas, and Australia. VSSC and GST sweeps had similar broad geographical patterns but local patterns indicate these likely swept at different times. Although evolutionary research on resistance in *Aedes* has focused more on VSSC mutations, these findings highlight the global significance of GST genes and open new avenues of research into their evolution and function.

It’s so cute! Réunion planthopper detected in Australia

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The Réunion planthopper, *Euroxenus vayssieresi* (Bonfils, Attie & Reynaud, 2001) (Hemiptera, Issidae, Issinae, Sarimini) was described from Réunion Island (Mascarene Islands) in 2001 and has since been recorded from Hawaii (2021), and Ghana - Western Africa (2022). The planthopper is likely invasive in Hawaii and Ghana, with anthropogenic dispersal suspected through movement of infested live plants. It is unknown whether *E. vayssieresi* is native to Réunion Island, but the tribe Sarimini likely evolved in the Oriental region, as supported by morphological and molecular analyses.

In May 2021 and 2022, a Northern Australia Quarantine Strategy (NAQS) entomologist observed large numbers of planthoppers in an herb and vegetable garden at the Department of Agriculture, Fisheries and Forestry Cairns regional office (Cairns airport precinct, Queensland). They were tentatively identified as an Australian endemic *Chlamydopteryx* sp.. In July 2022 specimens were sent for identification to one of us (Moir). The planthopper was morphologically identified, and confirmed by molecular analysis, as the exotic Réunion planthopper, *E. vayssieresi*. This was the first known Australian incursion of the planthopper. Subsequently, further detections have been made in suburban Cairns (Aug-Nov 2022) and Darwin (Northern Territory, Sept 2022). In November 2022, the Consultative Committee on Emergency Plant Pests determined that the Réunion planthopper did not meet the definition of an Emergency Plant Pest and no further action was recommended.

We have observed the Réunion planthopper feeding on the following hosts: *Beta vulgaris* (Amaranthaceae), *Aloe vera* (Asphodeloidaceae), *Lactuca sativa*, *Zinnia* sp. (Asteraceae), *Eruca vesicaria* ssp. *sativa* (Brassicaceae), *Dianthus* sp. (Caryophyllaceae), *Ocimum basilicum*, *Salvia officinalis* (Lamiaceae), *Vigna* sp. (Fabaceae), *Solanum lycopersicum*, *Solanum melongena* (Solanaceae) and *Grevillea baileyana* (Proteaceae).

The family Issidae appears relatively poorly represented in Australia. However, the ambiguity of *E. vayssieresi* when first detected demonstrates the need for a taxonomic revision of the Australian fauna, particularly in the tropical north.

A review of the introduced scale insects (Hemiptera: Sternorrhyncha: Coccomorpha) of Australia

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Over 860 species of scale insects, or coccoids (infraorder Coccomorpha), are recorded from Australia, some of which are significant pest species in agriculture, horticulture, and forestry. The status of several species as native or introduced remains unclear, as is whether certain introduced species remain extant in the Australian environment given the most recent collection records may be decades old. Such information is critical for basic research on native taxa, for pest management, and for the purposes of biosecurity and market access, especially given that published locality data are mined to populate widely used databases such as ScaleNet.

We systematically reviewed the literature and collection records to provide an up-to-date checklist, including information on which species are introduced and, where possible, the timing of their first detection. We interrogated questionable records and geographic locality data and found several instances of errors or misinterpretations that resulted in previously recorded exotic species now considered absent from Australia (in some cases having never occurred here). Further, we assessed whether some taxa previously considered as introduced are likely native to the continent. Finally, we documented recent detections of exotic species in Australia, noting the circumstances of their detection in assessing their probability of establishment, and provide an assessment of the high biosecurity risk species yet to be detected on our shores, highlighting the importance of ongoing surveillance.

This checklist provides biosecurity practitioners and taxonomists with an authoritative list of introduced coccoids, that now represent approximately 16% of all species recorded in Australia.

The AES Collection Committee arisen from the ashes of CHAEC

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The AES Collections Committee, or AES ColCom for short, was formed in 2022 and following a period of quiescence by its forerunner, CHAEC (Council of Heads of Australian Entomological Collections). The committee is evenly represented by most of Australia's major 'biodiversity' (e.g., museums) and 'biosecurity' (e.g., agricultural departments) collections, with committee members hailing from every state and territory.

As laid bare in the committee's mission statement, the AES ColCom seeks to advance and disseminate entomological collections-based knowledge and research on Australian insects for the benefit of all. The committee supports Australian and regional collections in maintaining best practice and the highest standards in curation, collection management, and in the sharing of information and specimens.

This presentation provides a brief introduction of how the committee came about, who are its members, what we've been up to, how we can serve the wider entomological community, and how you can contribute towards our objectives in supporting and developing Australia's entomological collections.

Investigating cercopoid (froghopper and spittlebug) diversity in eastern Australian orchards and vineyards

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Cercopoid hemipterans, also known as froghoppers or spittlebugs, are relatively understudied, and poorly characterized in Australia. This is surprising considering they are xylem-feeders, meaning they have the potential to transmit xylem-limited diseases. For example, in Europe, the meadow spittlebug (*Philaenus spumarius*) contributes greatly to the spread of *Xylella fastidiosa*, a xylem-limited bacterium with a host-plant list of over 600 species. *Xylella* does not occur in Australia, however overseas it significantly affects economically important plants such as almonds, peaches, citrus, cherries, olives, and grapes, among many others.

There are large gaps in what we know of cercopoid diversity around horticultural production areas in Australia. We have been addressing this through a current *Xylella* Vectors Project, with Agriculture Victoria and NSW DPI monitoring and surveying citrus, cherry, olive, and grape growing areas in south-eastern Australia. The surveillance focuses on the presence of native froghoppers and spittlebugs, which may contribute to the spread of *Xylella* if the disease reaches Australia.

While studying the life history and feeding mechanics of potential insect vectors, we are also investigating effective collecting methods, plant associations, and cercopoid distributions in Australia as a whole. We have found just two species of froghopper in three years of orchard/vineyard trapping using sticky mats, pan traps and sweep-netting. Only a single species, *Bathyllus albicinctus*, was collected in numbers significant enough to be considered a high-risk potential *Xylella* vector. Due to the small species diversity uncovered in these areas, we have also collated data from Australian agricultural institutes and museum reference collections to further explore cercopoid diversity. By investigating the possible local vectors of this disease, we hope to improve our preparedness for potential eradication of *Xylella* if that becomes necessary. Our research highlights the value of in-depth knowledge of species diversity in combating agricultural and biosecurity risks and issues.

A myriad of new species of the Tartessini (Hemiptera, Cicadellidae, Tartessinae) leafhoppers from Queensland

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The Tartessini leafhoppers, a tribe of the subfamily Tartessinae, are distinctive small to medium sized leafhoppers, up to 12mm in length, typically with a heart-shaped pronotum. The tribe is mostly known from Australasia (Australia and Papua New Guinea), with some species from South East Asia. These adaptable leafhoppers, inhabit environments ranging from arid and semi-arid to tropical rain forest regions. Despite being widespread in Australia, little is known about the biology of these plant feeding insects.

In her comprehensive taxonomic revision of the Tartessini, Faith Evans in 1981, described 37 new species and 19 new genera from Australia, resulting in a total of 69 species and 22 genera currently described from the country. The largest number of species (48) are recorded from Queensland with around 55% of those, only recorded from that state.

Species of Tartessini can appear very similar to each other. There are few external morphological features to distinguish between species, and associating the females with male specimens of the same species or even genus is problematic, due to superficial uniformities. Study of the male genitalia structures, however, readily separates species, and reveals distinctive and elaborate features.

In this study, leafhoppers were collected by sweeping and light trapping, over eight weeks, during three separate field trips in eastern Queensland, (2019-2022). This led to an unexpected impressive increase in the known species of Tartessini from Queensland and identified a stunning 30 new species which are being described and illustrated (Semeraro & Constant, *unpublished*). This represents a +60% increase in the number of species known in Queensland and +40% increase in the total number of species described in this tribe from Australia. This study highlights the incredible species richness of the Tartessini, but is likely only the tip of the biodiversity iceberg for this group in Australia: hundreds are expected.

Determining the economic impact of native budworm (*Helicoverpa punctigera*) in cereal crops in Western Australia

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Helicoverpa punctigera, commonly known as the native budworm, is a major pest of crops in Australia. While its agricultural host species are well known, recent reports from growers and advisors in Western Australia suggested that *H. punctigera* larvae were being found in wheat crops, a non-traditional host, with population estimates exceeding 20 larvae per 10 sweeps of an insect sweep net and damage evident to flag leaves and heads. Through pheromone-based moth trapping, crop inspections, glasshouse trials and a field cage trial, we investigated the behaviour of *H. punctigera* moths and larvae on, and potential economic damage to, wheat crops in the northern grainbelt of Western Australia. Surprisingly, similar number or more moths were detected in traps in wheat crops compared to nearby canola or lupin host crops during 2021 and 2022. However, glasshouse trials showed that moths are deterred from laying eggs on tillering or heading wheat whether paired with a traditional host such as faba bean or lupin or isolated with wheat only. Choice and no-choice trials with larvae indicated a preference for traditional hosts over wheat, but with some damage to flag leaves and glumes experienced when wheat was in head. When isolated with wheat only, most larvae starved to death and survivors had smaller pupae, indicating reduced performance. Results support the preference-performance hypothesis that species choose hosts that provide the best larval development. Although results point to agronomic practices such as wild radish weed control influencing the likelihood of *H. punctigera* larvae presence in wheat crops, we suggest that climate change, especially increased summer rainfall in central Australian migration source areas, is increasing moth pressure onto traditional, and now non-traditional, crops further down the migration route.

Investigating the biodiversity and systematics of Australian ‘mummy wasps’ (Braconidae: Rogadinae)

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Rogadinae is a subfamily of parasitoid wasps belonging to the megadiverse family Braconidae. Rogadines are commonly known as ‘mummy wasps’, as members of the subfamily share the unique trait of mummifying their caterpillar hosts as the larvae develop. These wasps are found throughout Australia, however only a fraction of their estimated diversity is formally documented. A particularly poorly studied tribe, the Betylobraconini, was only found to belong to Rogadinae within the last decade following molecular work. Betylobraconini is largely endemic to Australia and surrounding regions, however the biology of all members of the tribe remains completely unknown, and their likely hosts can only be speculated based on morphology and the habits of related taxa. This project employs a combination of DNA barcoding, Phylogenomics and morphological approaches to explore the diversity of the Australian Rogadinae, and forms a foundational taxonomic and systematics framework for further work. With a focus on members of the Betylobraconini, the project also aims to provide a better understanding of the biology and evolutionary history of this poorly understood group.

Disparate continental scale patterns in floral host breadth of Australian colletid bees (Colletidae: Hymenoptera)

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Plant-bee networks are rarely, if ever, studied quantitatively at continental scales, yet these have the potential to inform how biota and ecosystems are assembled beyond narrower regional biomes. The short-tongued bee family Colletidae comprises the major component of bee diversity in Australia, with three major subfamilies: the Neopasiphaeinae, Hylaeinae and Euryglossinae. We use museum data (>27,000 records) to record binary interactions between these bees (from each of these subfamilies, resolved to subgenera) and plants (resolved to genera).

The resulting networks were analysed using bipartite graphs and associated indices of network structure. The three bee subfamilies showed markedly different network structures with their floral hosts. Euryglossinae had strong interactions with Myrtaceae and an otherwise relatively narrow host breadth, Neopasiphaeinae had little signal of host specialisation above genera and a very broad host breadth, and Hylaeinae appeared intermediate in network structure. Furthermore, Euryglossinae is more speciose within Australia (404 species, or ~ 25% of described Australian bee fauna) than Hylaeinae and Neopasiphaeinae, but these differences do not correspond to the stem ages of the three subfamilies, suggesting that time-since-origin does not explain bee species diversity or floral host breadth. Patterns of host breadth persist after rarefaction analyses that correct for differing numbers of observation records. We suggest that visitation networks could be influenced by evolutionary constraints to expansion of floral host breadth, but it is also possible that many bee-plant interactions are shaped by bees exploiting floral traits that are driven by non-bee fauna operating at large biogeographical scales.

Unravelling the three axes of termite antipredator traits: a comparative analysis of the morphological, chemical, and behavioural defences of Australian mound building termites

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Predation is a powerful selective force driving the evolution of diverse antipredator traits. Termites (Blattodea: Isoptera) are one group that have evolved an arsenal of diverse antipredator defences to maximise survival when faced with predators, ranging from highly modified mandibles, to specialised cephalic appendages that eject a toxic entangling agent. Others simply exude chemical secretions in conjunction with mandibular weapons, whilst others sacrifice themselves for the good of the colony by rupturing specialised glands. The sheer diversity of antipredator adaptations that we see in termites, provide a fascinating avenue for exploring the evolutionary history of a complex social insect. Mechanical and chemical components of various termite weapons have received some attention, but the associated defensive behaviours and the evolutionary history of such traits have been neglected, thus limiting our ability to understand the evolution of a species' entire antipredator repertoire.

Using field-based behavioural assays, whereby we simulate an artificial mound breach by a predator, we aim to quantify termite antipredator behaviours in a phylogenetically controlled, comparative framework, as well as determine whether defensive behaviours have coevolved with morphological and chemical defences, using 20 Australian mound building termite species as a model. Preliminary data suggests that the defensive response of Australian mound building termites is highly variable amongst species. Soldier and worker numbers, time to response and duration of response as well as specific defensive behaviours exhibited differed greatly between species depending on weapon type. Although this work is in its infancy, it can help increase our understanding of how and why complex antipredator defence strategies have evolved as well as explain how behavioural, morphological, and chemical defensive traits interact to form a species' antipredator repertoire.

Novel endosymbionts effects on interaction between grain crop aphids and parasitoids

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Aphids have established a long-term mutualism with the obligate microbial symbiont *Buchnera aphidicola* (Bacteria; Erwiniaceae), which provides them with essential amino acids lacking in plant phloem. Aphids also harbor numerous heritable facultative endosymbionts that may induce either beneficial or detrimental effects on aphids under certain ecological conditions. Aphid-parasitoid interactions can be greatly affected by facultative endosymbionts. Here we assessed the effects of the facultative endosymbiont, *Rickettsiella viridis* (Bacteria; Legionellales), on potential parasitism by *Aphidius colemani* (Hymenoptera; Braconidae), using a newly developed infected line of *Rhopalosiphum padi* (Hemiptera; Aphididae), and compared them to the line lacking this secondary endosymbiont. We also tested whether infection with *R. viridis* affects parasitism status of *Diarretiella rapae* (Hymenoptera; Braconidae) against *Diuraphis noxia* (Hemiptera; Aphididae). We found that *R. viridis* provides neither *R. padi* nor *D. noxia* with significant protection against *A. colemani* and *D. rapae*. Moreover, our results suggest that parasitoids facilitate horizontal of facultative endosymbionts in grain crop aphids. These results will help inform the advantages and costs associated with this newly generated infection which may play an important role determining its efficiency as biocontrol agent in integrated pest management.

Developing an age-stage and two-sex life table of the lesser-known Australian fruit fly Northern Territory fruit fly *Bactrocera aquilonis (May)* from different hosts

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Bactrocera aquilonis (May) (Diptera: Tephritidae), a dacine Australian fruit fly is endemic to northwestern region of Western Australia. Laboratory based life-table data for this species was generated from four hosts: zucchini, lemon (Meyer), apple (Granny smith) and carrot media (standard media) under constant temperature 26±1 ° C and RH 60±10 % conditions. Egg hatching rate *in vitro* and *in situ* survival rates ($S_{\chi j}$) of other life stages (larvae to adults) of the fruit fly showed a host-type influence. The reproductive capacity (fecundity) and its duration (survival time) for this fruit fly species were used to estimate female age-stage specific fecundity (f_χ), age-specific fecundity (m_χ) and the age-specific maternity ($l_\chi m_\chi$) values required for calculation of demographic parameters. Finite rate of increase ranged from 1.056 to 1.07 (λ day^{-1}), generation time (T) from 59.12 to 70.31, intrinsic rate of increase from 0.054 to 0.0685 (r day^{-1}) and net reproductive rate (R_0) from 44.6 to 58.5. Peak reproductive value (v_χ) of an individual to future population was reached around 40-50 days post-infestation being the highest for those reared from zucchini and carrot media (~80 day $^{-1}$). Regardless of substrates, this species was able to maintain a relatively high reproductive capacity for at least 40 days. Life expectancy (e_χ) of an individual reached its highest at the onset of oviposition and was between 80 to 100 days depending on substrates. *B. aquilonis* is not considered pest of economic importance to horticultural production and fruit fly sensitive markets. However, this can potentially change with a major shift in his host preference and its distribution under climate change. The temporal age-stage population survival data generated in this study will be valuable in predicting population abundance and distribution, as well as designing in-field control strategies.

The future of online platforms in entomology education: a panel discussion

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Universities around the world rapidly shifted to primarily online platforms for entomology courses during the COVID-19 pandemic. This was challenging for many entomology instructors who often included a significant hands-on element as part of their units. Now in the post-pandemic era, face-to-face instruction has returned to most institutions and there is an opportunity to retain the valuable aspects of online teaching in entomology curricula. A panel of entomology educators from Australia and New Zealand will discuss how they have handled the transitions between online and face-to-face teaching. The panel will consider the future of online platforms in entomology education and issues related to academic integrity.

Partners in crime: Facilitation of foraging and predation by European wasps through access to a new source of honeydew

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Australia is adopted home to a suite of well-established and more recent invasive pest insects. Recent invaders are the focus of concerted eradication efforts whereas the well-established invaders are usually not. Moreover, the impact of invasive pest insects on native insects is not documented. The European wasp (*Vespula germanica*) first became established in Tasmania in 1959 and later in numerous locations on the Australian mainland between 1977-78. It now occurs throughout most of southeastern Australia. By contrast, the Giant pine scale (*Marchalina hellenica*) was first discovered in Adelaide and Melbourne in 2014. While the infestation in Adelaide was successfully eradicated, the infestation in Melbourne persists. Giant pine scale has been the focus of an eradication program because it represents a threat to the profitability of commercial pine plantations. However, because it produces copious honeydew (a resource not previously associated with pine plantations), the species also represents a serious environmental threat because European wasps recruit readily to this carbohydrate. The consequences for native insects of the formation of such nutritional mutualisms have been well documented, e.g. in the beech forests of New Zealand where *V. germanica* is also established. We present novel data on honeydew foraging by *V. germanica* as well as the insect prey of this destructive vespine wasp.

Holding the biosecurity front line

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DAFF's Technical Response team work on Australia's biosecurity front line, managing incursions and established infestations of exotic pests on Commonwealth controlled land at and near the border. Working closely with other DAFF and State biosecurity teams, our job is to stop exotic invasive pests, which can hitch a ride in or on imported cargo, containers or packaging, becoming established and causing enormous damage to our agriculture, environment and way of life. The Technical Response team began operations in July 2021 and since then has managed and contributed to a large number of biosecurity responses, including the African black sugar ant (*Lepisiota incisa*) infestation in Perth, locating and destroying feral honey bees (*Apis mellifera* – potential hosts to spread varroa mite) at first ports of entry, numerous brown marmorated stinkbug (*Halyomorpha halys*) detections in Sydney and Melbourne and an incursion of milk snail (*Otala lactea*) in imported cars at the Port of Brisbane. This presentation will provide an insight into the operational environment of our team and the challenges it faces in the future.

Morphological identification of the Polyphagous Shot Hole Borer, *Euwallacea fornicatus* (Coleoptera: Curculionidae)

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Ambrosia beetles are a group of unrelated Scolytinae and Platypodinae weevil clades defined by a shared ecological strategy: fungus farming. Xyleborini is the most important and species-rich tribe of ambrosia beetles. This group contains more invasive pests than all other ambrosia beetle groups combined. One of the economically most significant pests, *Euwallacea fornicatus* was recently detected in the Perth metropolitan area of Western Australia and is currently under eradication. *E. fornicatus* is a species complex currently encompassing four species and there is little doubt that more will be discovered. All lineages within the species complex are currently considered morphologically nearly identical. Unfortunately, the morphometric investigations point out some overlapping features making their morphological separation very unreliable. This highlights the shortcomings of species concepts based solely on type-specimen morphology. There are other species within the genus, which are also very difficult to identify.

Due to the relatively high numbers of by-catch, separation of *Euwallacea* species from native Australian Scolytinae and Platypodinae woodborers is very important. In this talk I will outline some useful features that enable us to separate these species quickly and reasonably reliably.

Unidentified weevil causing crop damage in the Dongara and Mingenew region of Western Australia

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An unidentified pest weevil (Curculionidae) was reported damaging canola crops in the Dongara and Mingenew region, Western Australia. It was first reported to Department of Primary Industries and Regional Development (DPIRD) entomologists in July 2013 and then sporadically over the past decade until more severe and widespread damage of canola seedling crops was reported in 2021 and 2022. Growers indicated that canola on heavy fine cracking clay soils appeared to be more favourable to the weevil than crops on sandy soils. It has been dubbed the Dongara weevil referring to the first place from which it was reported.

Curculionidae, is the largest insect family, encompassing over 83,000 named species and at least another estimated 220,000 species yet to be discovered and named. Finding a “new” pest species is significant, with several possible scenarios leading to its presence. The unidentified weevil could be an exotic species that is not a pest in its place of origin, or it could be a native species, with unusual morphological features, that has suddenly switched from endemic plant hosts to cultivated crops.

The Dongara/Mingenew weevil is likely not a native species (R. Oberprieler pers. comm.). Initial molecular work indicated that most of the closest hits are North American weevil species, however at 83-86% it is meaninglessly low.

A joint investigation between DPIRD, Mingenew Irwin Group and Murdoch University of the new weevil pest will assist with the development of effective management strategies and diagnostic tools to correctly identify the pest.

Efficacy of microbes from honeybees and the small hive beetle pest to develop traps that affect beetle attraction and oviposition choice

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The small hive beetle, *Aethina tumida* is a major pest to Australian apiculture as their larvae consume the honey, brood, and pollen produced by honeybees in hives. During consumption, the larvae contaminate the honey and cause the honey to ferment, thereby jeopardising honeybee colonies across the warm and humid coastal strip between Victoria and North Queensland. To control beetle populations, beetles and their eggs that are laid may be trapped to reduce their damage on honeybee hives. As a signal of honeybee hives for beetles to feed and lay eggs, locations with microbial odours associated with honeybee hives tend to be selected by beetles. With microbial odours derived from honeybee gut bacteria (*Gilliamella apicola* and *Snodgrasella alvi*) and a fungal species from whole beetles (*Kodamaea ohmeri*), we investigated the effects of these microbial strains on the attraction and egg-laying (oviposition) choice of beetles. With beetles of different sexes, mated status, and age, single individuals were placed in laboratory 'Y-mazes' and grouped beetles in boxes with two locations for selection, either a microbial treatment broth or control broth without microbes. For attraction choice, the locations selected were recorded each hour across three hours of beetle observation. For oviposition choice, the number of eggs laid in each location was recorded after 72 hours. Preliminary results of beetle attraction and oviposition data and their analyses will be presented at the conference, to discuss the efficacy of the microbial odours and their possible combinations to develop beetle traps. The approach of our study will contribute to the development of innovative and cost-effective traps for the long-term integrated pest management of small hive beetles, with massive implications for Australian apiculture, agriculture, economy, and food security.

To identify native insect species that help avocado flower pollination in Western Australia

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Inadequate pollination is a major reason for poor and erratic avocado yields. The European honeybee, *Apis mellifera*, serves as the principal avocado pollinator, but they do not have a high preference for avocado flowers, and alternative pollinators are desirable. Consequently, the pollination services they provide could be more optimal. Reliance on this single pollinator species is risky because *A. mellifera* is threatened by many pests and diseases, such as the ectoparasitic mite Varroa destructor. When the devastating Varroa mite invades Western Australia, a significant proportion of *A. mellifera* will be lost, with subsequent consequences to fruit production. Therefore, research is required to assess the viability of alternative or complementary insect pollinators to ease the pressure on *A. mellifera* and Beekeepers and protect Australia's crop industries. The research is to utilise field observation, bioassay, and molecular biology techniques to identify the WA insect species that are the best candidates for avocado pollinators.

The pollination research was conducted between 2019-2021 in two regions of Western Australia. Pan and vane traps were also used to determine the insect communities in the orchards. As pollinators, 13 Hymenoptera and five Diptera species were found in the orchards. Specimens were collected for taxonomy and DNA barcoding. To continue, this research will improve our understanding of WA avocado pollinators and significantly strengthen the WA avocado industry. In addition to the honey bee, *A. mellifera*, native bees and other insect pollinators are valuable pollinators of wild plants and other horticultural crops.

Sticky assassins – the evolution of resin use in Australian assassin bugs (Hemiptera: Reduviidae)

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As their name suggests, assassin bugs (Hemiptera: Heteroptera: Reduviidae) are predatory insects, feeding mainly on other invertebrates. Various specialised hunting behaviours have evolved in the family, one of the more unusual of which is “sticky trap predation”, whereby individuals use sticky exudates – either produced by the insect or collected from the environment – to enhance predation. The latter is most common in the subfamily Harpactorinae, where many species are known to coat themselves with sticky resin collected from various plants. Until recently, such tool use in the Australian fauna has only been documented in a single species. Based on field observations and museum specimens, we show that such behaviour is in fact more widespread, and using molecular analyses we then place the evolution of sticky trap predation in a phylogenetic context.

Genomic investigations of demography and pesticide resistance evolution in an invasive mite pest

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The redlegged earth mite (*Halotydeus destructor*; Trombidiformes; Penthaleidae) is an invasive mite pest in Australian agriculture. After invading from South Africa in the 1920s, this mite has spread across Australia's major grain-growing region and has evolved resistance to pesticides commonly used for its control. Genomic data are helping address long-standing questions about demographic processes that structure redlegged earth mite populations and the genetic mechanisms of pesticide resistance. We used a whole-genome pool-seq approach to study populations of redlegged earth mite in Australia that varied in their resistance to pesticides. High-resolution genomic markers allowed us to discern a pattern of regional population structure between western and eastern populations. This provided evidence against the previously held hypothesis of a single homogeneous Australian population. Our genomic data allowed us to identify new target-site mutations in the *para* and *ace* genes for pyrethroid and organophosphate resistance, and helped reveal duplication events in the *ace* gene that may also contribute to pesticide resistance. Genomic data have thus provided valuable insights into the evolutionary dynamics of resistance, its spread across populations, and the potential for molecular monitoring of field populations, in invasive redlegged earth mite. These findings hold promise for enhancing management of this pest and developing targeted strategies for its control.

Using morphometrics to study the ecology and life history of an iconic New Zealand Stag beetle (Lucanidae)

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Stag beetles (Lucanidae) are famous for having enlarged mandibles that they use in contests over access to mating opportunities. The genus, *Geodorcus*, is a group of large bodied flightless stag beetles endemic to New Zealand. Most of the species have ranges restricted to small islands or mountains, with the exception of the Helm's stag beetle, *G. helmsi*, which is widespread on the South Island. New Zealand stag beetles are threatened by habitat destruction, predation by invasive mammalian predators and illegal collection. Despite the clear need for conservation, we know little about their life history and behaviour. For instance, do males of *G. helmsi* exhibit dimorphism in body length and mandible size that would indicate alternative male morphs? By measuring specimens from entomological collections and wild populations, and using linear allometric and geometric morphometric analyses, we show that there is no clear evidence that there are any alternative morphs in *G. helmsi*. Finally, we compared intact and predated field specimens from three areas that differ in rat predator abundance. We found male beetles were predated more than females and that larger males were predated more than smaller males. We also found that the overall abundance and sex ratio differed significantly between the different sites. Overall, our findings may offer some insight into stag beetle behavioural ecology, and the knowledge gained will help with the conservation for the more threatened species of *Geodorcus*.

Nesting biology of alpine *Exoneura* bees: an important high altitude pollinator

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Documenting bee natural history is crucial for understanding their evolutionary ecology and provides informative comparative data for a wide array of biological investigations. Allodapine bees (Apidae: Xylocopinae: Allodapini) offer valuable insights on the intrinsic and extrinsic factors influencing the evolution of social behaviour because of their: (i) ability to facultatively switch between solitary and group living; (ii) complex social recognition systems; and (iii) multiple origins of inquiline social parasitism. Allodapines are common pollinators of berry and pome fruit in south-eastern Australia, where they often transport and deposit more pollen than introduced managed pollinators. However, their role as pollinators in natural ecosystems is less well documented, which presents considerable opportunity to better understand macroevolutionary mutualisms with native flora given their ancient origin (at least 45 Mya) and broad distribution throughout the Global South (Africa, Madagascar, Middle East, Australia, southern Asia). Allodapines are referred to as "stem nesting" bees because they excavate nests from dead or decaying wooden substrates. They are unusual among bees in their habit of progressively rearing immatures in linear tunnels that lack brood-cell partitions – in this sense they are more similar to ants. Durability of nesting substrate is purportedly linked with morphological caste development and eusocial organisation in the sister genus *Exoneurella*. In Australian alpine environments (above 1,600m), *Exoneura* nest in trunks of the snow gum (*Eucalyptus pauciflora*) and the expansive substrate diameter permits the formation of linear galleries – a novel nest architecture for this tribe of bees. Native wood-boring longicorn beetles (*Phoracanthus*) infest and essentially ring-bark these trees, and subsequently are often portrayed in a negative light. The silver lining is that the death and decay of the tree creates an abundance of nesting substrates for an important native pollinator, insulating the bees during an environmentally harsh and extended snowbound winter diapause.

The tyranny of distance: bee pollination services in the Australasian realm

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Australasia is colloquially known to suffer from the 'tyranny of distance' *vis-à-vis* the rest of the world. The same parallel can be drawn for pollinator-dependent food crops, particularly when there is a mismatch between native pollinators and introduced foreign plants. Native bees provide considerable pollination services to crops in the northern hemisphere, but less is known about the situation in the southern hemisphere. Foraging behaviour of visitors to apple orchard flowers was recorded to assess the efficacy of pollinator service (P_{eff}) in NSW apple orchards. Introduced honey bees (*Apis* $P_{eff} = 13.02$) and native stingless bees (*Tetragonula* $P_{eff} = 6.16$) were the most abundant and efficacious pollinators, with important contributions from *Tetragonula* at 22-28°C in the Blue Mountains. Visitation abundances of these tree-nesting native bees declined with distance from native forest (<200m) and they do not occur naturally in most Australian apple growing regions. Meanwhile, native allodapine and halictine bees transferred the most pollen per-visit, but their low abundances reduce their overall efficacies (*Exoneura* $P_{eff} = 0.03$; *Lasioglossum* $P_{eff} = 0.06$). These results reveal a heavy reliance on introduced Western honey bees, since bees (*Andrena*, *Apis*, *Bombus*, *Osmia*) that are key global pollinators of apple do not naturally occur in Australasia – where there is only 15% generic overlap with bees from Central Asia - the geographic origin of wild apple (*cf.* Palaearctic-66% and Nearctic-46% generic overlaps). The historical biogeography of bees (Apoidea) therefore drives a national dependence on one introduced species for apple pollination.

An integrative approach to uncovering the distribution of the pest nitidulid *Carpophilus truncatus* in Australia

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Within a decade, the nitidulid beetle *Carpophilus truncatus* has become a major pest of nut crops around the world. In Australia, *C. truncatus* is the leading invertebrate pest of almonds, first appearing in almond orchards in Victoria, South Australia and New South Wales in 2013-14, with no records of the species outside of nut orchards until now. Uncovering the distribution of *C. truncatus* outside of almonds may help reveal the invasion history and ecology of the insect, and in doing so provide new insights for pest management strategies targeting *C. truncatus*.

We utilised four complimentary approaches to explore the historical, current and potential distribution of *C. truncatus* in Australia. First, literature and database observations were investigated to establish what is known about the ecology and distribution of the species worldwide. Second, *Carpophilus* specimens from invertebrate collections based in Victoria, NSW and Queensland were morphologically re-examined to reveal historical records of *C. truncatus*. Third, a trapping system that utilises the newly identified insect pheromone was used to survey the current distribution of *C. truncatus* in parkland habitat around Victoria, as well as sites around Cairns and Brisbane in Queensland. Finally, a laboratory study was conducted to define the thermal limits of *C. truncatus* and estimate areas of relative thermal suitability for the insect in Australia. The combination of these approaches has established the historical presence of *C. truncatus* in Queensland a century before the species became a pest in almonds further south, its presence in Victoria in habitats remote from nut crops, as well as potential thermal constraints for this species and an estimate of relative thermal suitability across Australia. An integrative approach to understanding the distribution of *C. truncatus* in Australia facilitates further research into other aspects of the ecology of the insect, including host range, habitat use and behaviour.

Response of carrion-associated flies (Diptera) to mass mortality events in an Australian alpine ecosystem

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Influxes of large amounts of carrion from human activity, natural disasters or disease can create mass mortality events (MMEs), which are increasing in frequency across the globe. While the response of scavenger communities is well understood for single carcasses, patterns of species succession and progression through the stages of decomposition may not apply under the conditions of an MME. Although studying the scavenger response to natural MMEs poses challenges, simulation studies can offer valuable insights into the potential outcomes.

This study focuses on the response of flies (Diptera) to simulated MMEs and explores their reactions when competitors from different scavenger guilds are excluded. The study was conducted in alpine areas of Kosciuszko National Park, New South Wales, and utilised deer (*Dama dama* and *Rusa unicolor*) and Eastern grey kangaroo (*Macropus giganteus*) carcasses, species which are culled due to their threat to native ecosystems. The study design involved three sites with nine plots representing control, single carcass, and MME scenarios. Pitfall traps were placed at each carcass and collected at weeks 1, 2 and 4.

22 Dipteran families were identified, of which six (*Calliphoridae*, *Muscidae, Periscelididae, Phoridae, Sepsidae* and *Sphaeroceridae*) accounted for 92% of the total fly abundance. Most families peaked in abundance in samples from week two. Average fly abundance was higher at carcasses with vertebrate scavenger exclusion, and higher at single carcasses than MME treatments. The results from this study indicate that scavenging flies respond differently to MMEs and single carcasses and that these patterns vary by family. In the absence of vertebrate competitiors, flies are able to reach higher abundances and may be dominant contributors to decomposition in this ecosystem. Further studies investigating the Dipteran responses to MMEs will help inform the role they can play as consumers of large carcass loads and in maintaining ecosystem health.

The native Australian spittlebug, *Bathyllus albicinctus*, a potential vector of exotic *Xylella fastidiosa*

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The movement of plant material across national borders enhances the rapid spread of pests and diseases worldwide. The occurrence of devastating disease outbreaks caused by plant pathogens has been on the increase. *Xylella fastidiosa*, is one of the most harmful plant pathogenic bacteria worldwide and is at the top of Australia's National Priority Plant Pests list. *Xylella fastidiosa* is transmitted by xylem-feeding insects, and accordingly any xylem feeder can act as a potential vector. Notably, *Xylella fastidiosa,* as well as documented exotic insect vectors are not present in Australia.

Our objectives were to understand feeding physiology of a native Australian spittlebug, *Bathyllus albicinctus,* and its and ability to serve as a potential *Xylella* vector. We monitored the feeding behaviour of *B. albicinctus* on grapevines, olives and oranges using the electrical penetration graph. We performed 4h continuous recordings on the three host plants and we identified feeding patterns e.g.: np (nonprobing), C (pathway), R (resting), Xc (xylem contact), Xi (xylem ingestion), Xe (xylem egestion, related with *X. fastidiosa* transmission) and N (interruption within xylem phase) previously described for spittlebugs.

Our results showed that *B. albicinctus* continuously feed on the three plant species tested and the feeding patterns obtained match those previously described for exotic xylem feeding spittlebugs known to vector *Xylella*. In addition, Xe patterns were observed in insects feeding on all of the susceptible plants. Our results suggest that *B. albicinctus* could be considered as potential vector of *X. fastidiosa* if this devastating bacterial disease is introduced in Australia.

Molecular methods for the other 95% of animal diversity

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Around 95% of all animals in Australia are invertebrates and insects contribute to 57% of known Australian animal diversity. Apart from focal or economically important species, the state and the effect of climate change and human activities on most invertebrate species remains unknown. This is partly due to difficulties in recognising the known species and taxonomic uncertainty among many taxonomic groups. Combination of traditional and molecular methods presents efficient and cost-effective options for species detection, discovery and taxonomic investigations.

Here we present two case studies:

(1) results of surveys of the critically endangered Mt Donna Buang wingless stonefly, (*Riekoperla darlingtoni*) and a flightless Kallista stonefly (*Leptoperla kallistae*) using environmental DNA.

(2) preliminary results of a taxonomic study of critically endangered Dandenong amphipod (Austrogammarus australis) and endangered Sherbrooke amphipod (*Austrogammarus haasei*) based on DNA barcoding.

The results of the survey of Mt Donna Buang wingless stonefly contributed to the alteration of development of the mountain bike trails through its primary habitat, Cool Temperate Rainforest and provided data for the species listing under the EPBC act.

The results of the Mt Donna Buang stonefly study helped to preserve their habitat and created an opportunity to test the Critical Habitat determination law in Victoria. The resolving of the amphipod taxonomy allows for further studies of their distribution, natural history, and conservation status. And the new knowledge on the distribution of flightless stonefly will be used by Melbourne Water and the local council to direct their management actions and to set local environmental standards for the local waterways.

Identifying and filling the gaps in the conservation of island endemic insects: a case study from Norfolk Island

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Given their relatively small total land area, oceanic islands house a large proportion of global biodiversity and display high rates of endemism. Island endemics are also disproportionately represented on lists of both threatened and extinct taxa.

The Norfolk Island group is a small, isolated archipelago in the southwest Pacific Ocean. Since colonisation by Europeans in 1788, most of the islands' indigenous vegetation has been cleared and many invasive species have been introduced. This has led to high numbers of species being listed as threatened, as well as numerous documented extinctions of endemic birds, plants, and land snails.

Norfolk Island's insect fauna is relatively poorly known. The island's isolation (>700 km to the nearest landmass) and its position within a biogeographic crossroad has led to the evolution of a diverse and unique endemic insect fauna yet almost no attention has been paid to their conservation needs. Considering the ecological devastation that has befallen the island, and the rates of extinction among other endemic taxa, such work is highly overdue if we are to prevent insect extinctions.

Here we provide an overview of the state of knowledge of Norfolk Island's insect fauna, with particular emphasis on the endemic taxa. We compiled an updated catalogue of insect taxa recorded from Norfolk Island and quantified the biostatus for each (endemic, native, introduced). Based on this catalogue, and a review of the associated references, we then identified key knowledge gaps relating to the conservation of the insect fauna. We discuss actions needed to fill those gaps and provide preliminary lists of priority species and sites. We present the framework used to compile this information and discuss how it can be applied elsewhere. This work lays the foundation on which future Norfolk Island insect conservation efforts can be built.

Beekeeper experience and training are associated with beneficial practices that prevent the spread of American foulbrood (*Paenibacillus larvae*)

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Western honey bees (*Apis mellifera*) are essential for global agricultural and horticultural productivity, yet bee populations are threatened by pests and disease. American foulbrood (*Paenibacillus larvae*) is an incurable and fatal bacterial disease of the honey bee larvae and is considered to be one of the worst threats to the Australian beekeeping industry. The only way to limit the occurrence of the disease is to stop its spread through the adoption of good management practices such as limiting the movement of equipment, tools and honey between hives as well as implementing regular hive inspections, honey culture testing, and the use of a barrier management system. A survey of 514 Australian beekeepers was undertaken to investigate to what extent beekeepers are adopting these practices and what factors influence their adoption. It was found that overall, beekeepers in Australia exhibit good biosecurity practices, with several associated factors influencing this, including training and experience. Formal online training was associated with improved biosecurity practices and a higher ability to identify American foulbrood. A majority of beekeepers had a high ability to identify AFB. The self-reported and tested ability of beekeepers to recognise AFB was similar. This study provides evidence to demonstrate that the mandated beneficial biosecurity practices are associated with an improvement in biosecurity outcomes, highlighting the importance of policy enforcement.

Development of a day degree model for the Northern Territory fruit fly - *Bactrocera aquilonis* (May)

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Rate of development of insects are significantly related to temperature. Within a range of temperatures that are suitable for their development, that relationship tends to follow a linear pattern. Mathematical model based on temperature are developed and used to predict insect population. This study aimed to develop a mathematical model for the Northern Territory fruit fly *Bactrocera aquilonis* (May). Laboratory reared flies (at least F_5 generation) were used to estimate lower developmental thresholds (DZ), and degree days (DDs) for each of the different life stages of the fly using carrot media as a substrate. The development time and survival of eggs, larvae, pupae and adults until egg laying in controlled environment cabinets (Climaton-520-DL) under 7 different constant temperatures: 16, 20, 24, 26, 28, 30 and 32 ^{0}C at constant RH of 70 ± 5% was studied. Data was analysed using simple linear model.

The estimated lowest temperature threshold for egg hatching was 11.6°C, development of larvae to pupae was 9.6 °C and pupae into adult was 9.5°C. The day degree (DD) required to complete each life stage was 26, 153 and 338. Approximately 209 DD was required for a teneral female to become reproductive. These day-degree data were based on DZs estimated through a mathematical linear model which do not necessarily imply the real temperatures at which development of these life stage stops. However, it provides valuable basic information that could assist in predicting population dynamics, thus in developing in-field control.

Fluffy bums and their aliens: The distribution and abundance of passionvine hopper, *Scolypopa australis* (Walker) (Hemiptera: Ricaniidae), parasitoids in Victoria

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The passionvine hopper *Scolypopa australis* (Walker) (Hemiptera: Ricaniidae) (henceforth referred to as PVH) is an Australian endemic species accidentally introduced to New Zealand in the 1800s, where it has become a major pest of kiwifruit. Due to the coevolution of parasitoids with PVH in Australia, it is believed that these natural enemies play a key role in suppressing PVH populations, resulting in minimal crop damage. Understanding the ecology of PVH parasitoids in their native range is therefore a critical step in identifying potential biological control agents that could be used in New Zealand.

Targeted collections were undertaken in greenspaces around Melbourne – from small residential gardens to peri-urban national parks – from December 2021 to May 2023 at sites where PVH were known to be present. Host plants were recorded, relative rates of parasitism were estimated, and parasitoids were identified to species level, where possible. We found that the egg parasitoid community was more diverse than the nymphal parasitoid one and that parasitism and emergence rates of adult parasitoids were relatively low, particularly for nymphs. To complement these findings, we present a network model of the tri-trophic interactions between plants, PVH and parasitoids and provide biological control management recommendations for PVH. This is the first study of PVH parasitoids to have been undertaken in Australia since the 1960s, and the results show many more species of parasitoids to be associated with PVH than previously thought.

Parental control of offspring microbiota in *Aedes aegypti* mosquitoes

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The composition of the gut microbiome can have substantial effects on the fitness of animals. The gut microbiota of mosquito larvae is acquired horizontally from the aquatic environments in which they hatch. The presence of beneficial bacteria in larval habitats is therefore crucial for successful development to adulthood. We hypothesise that female mosquitoes exert a degree of control over the gut microbiota of their juvenile offspring via oviposition site selection. We test this hypothesis by i) culturing and identifying bacteria associated with a lab colony of *Aedes aegypti* (Culicidae, Diptera) ii) rearing gnotobiotic *A. aegypti* larvae in substrates containing different strains of bacteria to determine which strains and communities best promote larval development iii) conducting a choice experiment where the same substrates are offered to gravid females to determine oviposition site choice preferences. We anticipate that gravid female mosquitoes preferentially lay their eggs in substrates containing the bacterial communities which promote the developmental success of their offspring. We successfully cultured 11 strains of bacteria associated with *A. aegypti* and found a significant effect of strain on the hatching success and time taken for larvae to pupate. Results for the choice experiment will be presented and discussed at the conference. The outcome of these experiments will contribute to a general understanding of the interactions between insects and environmental microbiota.

The role and acquisition of gut bacteria in an Australian native bee

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Melittology, the study of bees, has recently shown a surge of interest in gut bacteria. Honey bees have quickly become a model organism in microbiome research, as they harbor complex bacterial communities in their gut that play vital roles in their health and wellbeing. While most research on bee microbiota has focused on social bees, the majority of the 20,000 global bee species (approximately 90-95%) are solitary. Like their social counterparts, solitary bees provide crucial pollination and ecosystem services, but concerningly, there are growing reports of declining wild bee populations. While the primary cause is habitat loss, another potential threat that is gaining focus is agrochemical pollution. In honey bees it has been shown that exposure to such chemicals can cause gut dysbiosis that results in several negative health effects. However, very little is known about solitary bees and their associations with microbial communities.

My research investigates the bacterial associations of the widespread Australian native solitary resin bee, *Megachile tosticauda*. Using 16S sequencing, I characterized the bacterial sequences found within the food and brood and described the changes in 16S signals throughout the bee's metamorphosis. Additionally, I experimentally assessed how these bacteria are acquired and whether the bacteria in the food provide live metabolic functions that influence brood development. Finally, I verified using scanning election microscopy (SEM) whether 16S sequences provide sufficient evidence to support the notion that this bee harbors gut bacteria. My findings suggest that some bacteria may function as food, while others may be acquired through contact with the nest lumen or with pollen, at different stages of the lifecycle. However, the presence of a species-specific gut microbiome seems unlikely.

A streamlined sampling approach to quantify the invertebrates associated with the Yellow Canopy Syndrome of sugarcane

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In 2012, Yellow Canopy Syndrome (YCS) was first observed on sugarcane (*Saccharum* spp. hybrids) in Cairns, Queensland. After a decade of YCS aetiology research, the evidence for a definitive causal agent remains inconclusive. However, a previous study presented at the Australian Entomological Society conference in 2022 suggested invertebrates may play a role. The current research hypothesis is that sap-sucking invertebrates, which feed on both roots and leaves, may be associated with YCS expression. This research aimed to conducted consecutive season-long, in-field invertebrate sample collections to understand target invertebrate population dynamics concomitant with YCS development. This approach was used to identify correlations between seasonal abundance and YCS incidence. A YCS-affected field site was sampled fortnightly using existing and modified trapping methods, including yellow sticky traps, yellow pan traps, yellow stem traps, sweep-nets, a vacuum sampler as well as, whole leaf and whole plant collections. Trap height was also modified to differentiate between canopy-feeding and root-feeding invertebrates. Preliminary results showed several YCS-associated invertebrates, including two known sugarcane pests: sugarcane whitefly (*Neomaskellia bergii*) and spider mite (*Oligonychus* sp), and two novel pests to sugarcane: pasture mealybug (*Heliococcus summervillei*) and rice whitefly (*Vasdavidus indicus*). Future studies will use Koch's postulates to confirm the likelihood of one or more invertebrate candidates being the causative agent(s). In addition, novel YCS detection methods are being developed using remote sensing and DNA-based pest detection. These methods are expected to result in an improved surveillance system for pre-visual early YCS detection, allowing rapid and timely management intervention.

Functional characterization of moth sensory neuron membrane proteins (SNMPs)

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Sensory neuron membrane proteins (SNMPs) play a critical role in the insect smell system but there is a deficit of functional studies beyond *Drosophila*. Here, we use a combination of available genome sequences, manual curation, genome and transcriptome data, phylogenetics, expression profiling and gene knockdown to investigate SNMP superfamily in various insect species with a focus on Lepidoptera. We curated 81 genes from 36 insect species and identified a novel lepidopteran SNMP gene family, SNMP3. Phylogenetic analysis shows that lepidopteran SNMP3, but not the previously annotated lepidopteran SNMP2, is the true homologue of the dipteran SNMP2. Digital expression, microarray and qPCR analyses show that the lepidopteran SNMP1 is specifically expressed in adult antennae. SNMP2 is widely expressed in multiple tissues while SNMP3 is specifically expressed in the larval midgut. Microarray analysis suggest SNMP3 may be involved in the silkworm immunity response to virus and bacterial infections. We functionally characterized SNMP1 in the silkworm using RNA interference (RNAi) and behavioral assays. Our results suggested that *Bombyx mori* SNMP1 is a functional orthologue of the *Drosophila melanogaster* SNMP1 and plays a critical role in pheromone detection. Split-ubiquitin yeast hybridization study shows that BmorSNMP1 has a protein-protein interaction with the pheromone receptor (BmorOR1), and the co-receptor (BmorOrco). Concluding, we propose a novel molecular model in which BmorOrco, BmorSNMP1 and BmorOR1 form a heteromer in the detection of the silkworm sex pheromone bombykol.

Restoring declining species through translocations: A test case using flightless grasshoppers in an urban setting

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Population translocations are used increasingly as a conservation strategy for vertebrates. However, relatively few attempts have been made to translocate invertebrates despite their potential benefits for food webs, and despite the practicality of undertaking such translocations in small areas including urban environments where space is limited. We conducted 36 translocations of 1851 individuals of the generalist flightless grasshopper *Vandiemenella viatica* across urban Melbourne, where 93% of its original habitat has been lost. We aimed to understand characteristics essential for grasshopper persistence and to investigate detection, occupancy, dispersal, and habitat suitability throughout its active period to improve insect translocation success in urban settings using revegetated sites and small remnant habitats. We also measured movement and detection probability after one week in short-term trials. The one-week trial indicated that grasshopper sex and colour morph did not influence the probability of detection, and there was no evidence of directional movement by females and males. One year after translocation, *V. viatica* were found in 28 out of 36 translocation sites. These surveys showed that detection probability changed across survey seasons and was influenced by soil temperature. Also, soil temperature positively affected detection in the winter surveys. Occupancy probability was influenced by graminoid cover, plant species richness and weed cover. We found no evidence of directional movement by females and males in the F1 generation. Abundance and presence/absence data were best explained by graminoid cover and plant species richness. Our findings suggest that wingless grasshopper translocations are feasible in small urban patches of suitable habitat, helping to restore invertebrate biodiversity and ecological services.

Diversification, cospeciation and host-use evolution in Australian *Fergusonina* (Diptera: Fergusoninidae) galling flies feeding on Myrtaceae

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A unique obligate mutualism occurs between species of *Fergusonina* Malloch flies (Diptera: Fergusoninidae) and nematodes of the genus *Fergusobia* Currie (Nematoda: Neotylenchidae). These mutualists together form different types of galls on Myrtaceae, mainly in Australia. The galling association is species-specific, and each mutualism in turn displays host specificity. This tritrophic system represents a compelling arena to test hypotheses about coevolution between the host plants, parasitic nematodes and the fergusoninid flies, and the evolution of these mutualisms. Recently derived phylogenies and divergence time estimation studies of the Diptera and the Myrtaceae show that the fly family Fergusoninidae is less than half the age of the Myrtaceae, discounting the hypothesis of cospeciation and coradiation of the fly/nematode mutualism and the plants at the broadest levels. However, cospeciation may have occurred at shallower levels in the phylogeny, following the establishment of the fly/nematode mutualism on the Myrtaceae.

High-throughput collection genomics: Generating DNA reference sequences at scale

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Primary type specimens and taxonomist-identified reference specimens in natural history collections are often the best if not only source of accurate information for named species identification. Generating DNA reference sequences from these specimens at scale is crucial for both the continued relevance of the collections and for modern molecular tools to realise their full potential. Methods such as metabarcoding of trap catches, eDNA surveys and mobile DNA sequencing all require reference sequences that link their anonymous sequence data to scientific names, which in turn are keys to our collective knowledge of organisms.

We developed novel platform technology that enables the mass-generation of mitochondrial, plastid and ribosomal DNA sequences from collection specimens, largely irrespective of organism, specimen age and preservation method. Our approach miniaturises genome skimming with an acoustic liquid handler on a robotic platform, thereby greatly reducing cost and providing high-throughput processing capacity.

In this presentation, we will provide an overview of our lab development, resulting data and application examples, including primary type sequencing at the Australian National Insect Collection (ANIC), the targeted generation of reference sequence collections through the National Biodiversity DNA Library (NBDL), and taxonomic and phylogenetic research on insects.

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4	**Daniel Farrell** Department of Agriculture and Fisheries (QLD)	Insect sanctuaries for beneficial predators and parasites in tropical banana
5	**Madalaine Giannotta** Australian National Insect Collection (CSIRO), Australian National University	UCE Phylogenomics of the Australasian Sphaeropthalminae (Hymenoptera: Mutillidae)
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12	**Pia Scanlon** Department of Primary Industries & Regional Development (WA)	Advances in macro and micro photography to improve biosecurity capabilities for invertebrates
13	**Isarena Schneider** Northern Australia Quarantine Strategy, Department of Agriculture, Fisheries and Forestry	It’s so cute! Réunion planthopper detected in Australia
14	**Linda Semeraro** Royal Belgian Institute of Natural Sciences	A myriad of new species of the Tartessini (Hemiptera, Cicadellidae, Tartessinae) leafhoppers from Queensland
15	**Andras Szitos** Department of Primary Industries & Regional Development (WA)	Unidentified weevil causing crop damage in the Dongara and Mingenew region of Western Australia
16	**Amandip Kaur Virdi** Department of Primary Industries & Regional Development (WA)	Development of a day degree model for the Northern Territory fruit fly - *Bactrocera aquilonis* (May)

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