Genetics Society of AustralAsia CONFERENCE

7-10 July 2025 | Auckland, New Zealand

Conference Handbook

Platinum Partners

genomics aotearoa

Waipapa Taumata Rau University of Auckland

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Event Partners

On behalf of all participants, we would like to extend heartfelt thanks to our Event Partners for their generous support to make this event possible.

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Contents

Kei ngā nui, kei ngā rahi, kei ngā taumata rau,
nau mai, haere mai, tēnā koutou katoa!
To our esteemed collegues,
a warm welcome to you all!

GSA 2025
AUCKLAND

It is our great pleasure to host you for the 72nd Annual Meeting of the Genetics Society of AustralAsia here in Tamaki Makaurau – Auckland in Aotearoa – New Zealand in July 2025.

We are here to help - please reach out if we can offer any assistance during the conference.

Local Organising Committee


Assoc Prof Anna Santure (Chair)


Dr Kimiora Henare


Dr Jessie Jacobsen


Dr Nathan Kenny


Prof Joanna Putterill


Dr Suzanne Reid


Dr Annabel Whibley

Conference Planner


Donna Rhyse Dacuno
University of Auckland
Event Services

Conference Assistants


Jamie Hyde


Eric Marshall


Patricia Pillay


Jenny Ann Sweatman


Hui Zhen Tan
(& logo designer)


Fang Fei Tham

Webmaster

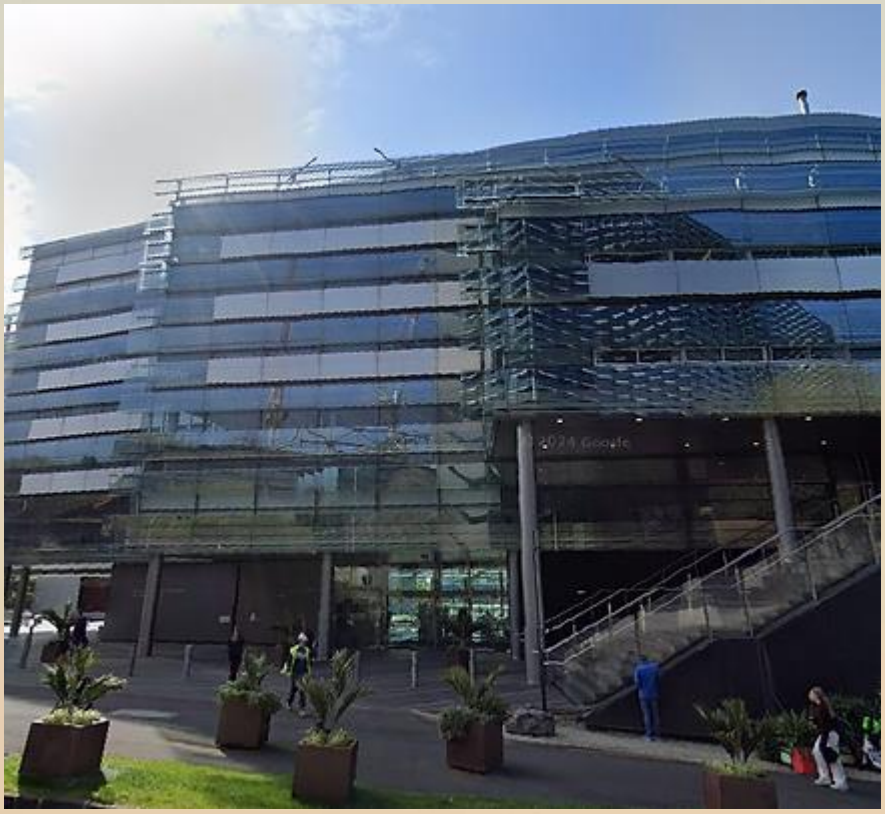

Martin Cheng
(& designer
& Chair assistant)

Venue

The Annual Conference will take place at the University of Auckland in the Owen G Glenn building, located in the heart of the city campus. All teabreak and lunch sessions will be held in the poster and exhibitor hall outside the lecture rooms.

Location: Level 0, Sir Owen G Glenn Building (OGGB), B260, Business School,12 Grafton Road, Auckland 1010

Enter the building from street level (shown below) to level 1, and head to your right to take the main stairs down to level 0. Turn left at the bottom of the main stairs, the registration desk will be down a further small set of stairs straight ahead of you. The lift is next to the stairs.



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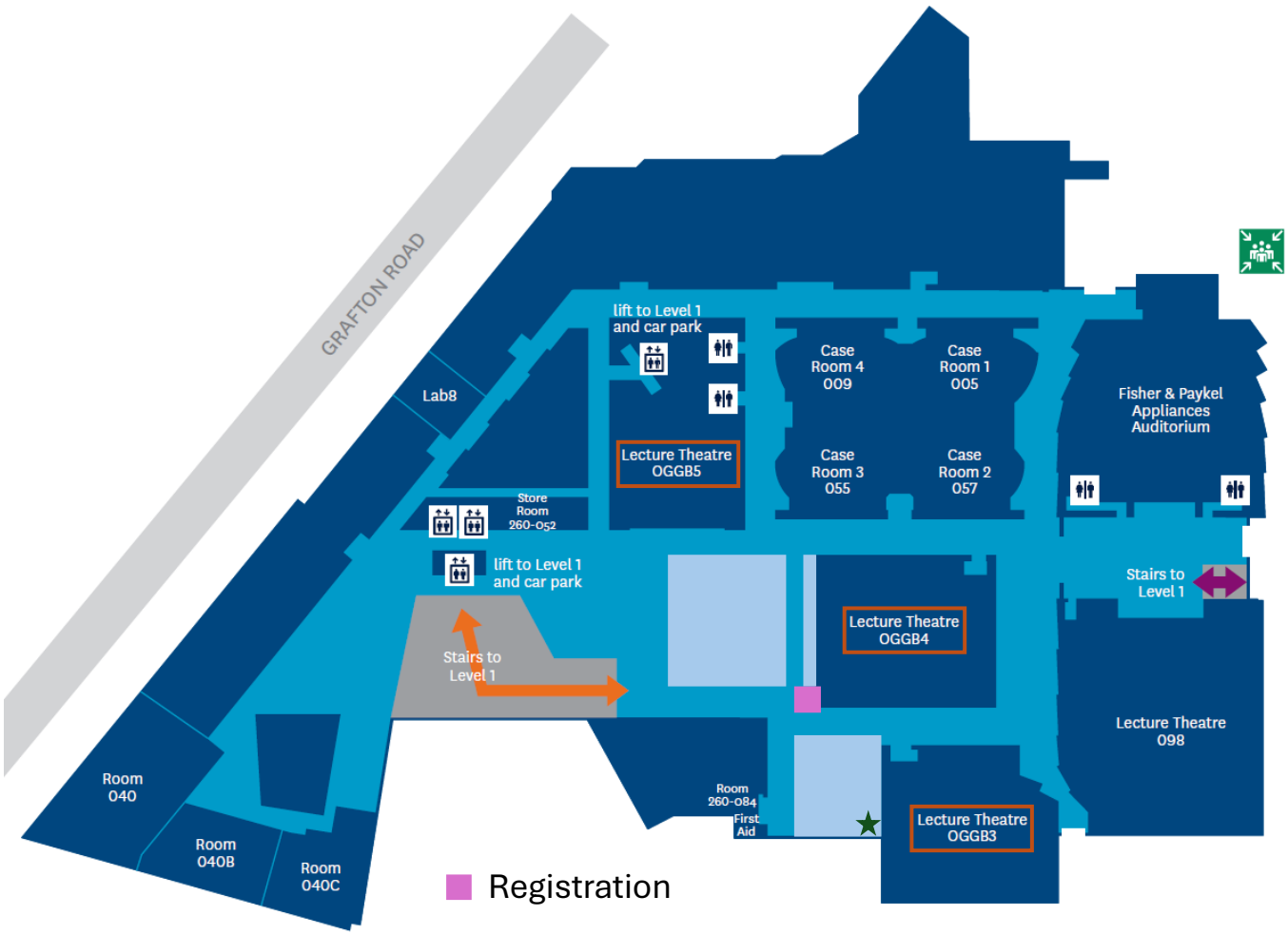
Floorplan



- Registration
- Lecture Rooms
- Partner Exhibition Tables, Posters, Food
- Special diets

General information

Registration
The registration desk is situated on Level 0 of the Owen G Glenn building. Event Services, led by our amazing conference planner Donna Rhyse Dacuno, welcome any enquiries on the conference or local information. The registration desk will be open:

Monday	2:30-5:00pm
Tuesday	8:00am-5:00pm
Wednesday	8:00am-6:00pm
Thursday	8:00am-6:00pm

Internet access
Wifi access is most reliable via Eduroam, but a username and password for the 'UoA Guest wifi' will also be available at the Registration desk.

Name badges
All conference delegates and Partner representatives are required to wear their name badges at all times during the conference and social functions. Your badge is your official entrance pass to the conference sessions and conference catering. Please leave your name badge at Registration as you leave – lanyards and plastic pouches will be reused, and the printed card recycled.

General information

Conference food

To be more sustainable, we have a very heavily vegetarian (and very yummy!) menu during conference sessions. The welcome function is 80% vegetarian. Morning and afternoon teas are 100% vegetarian. The buffet lunches on Tuesday, Wednesday and Thursday have all sides vegetarian plus 50% vegan / 50% meat main choices – please 'lean to the green' and choose the vegan main option instead of the meat! Lamb, beef and chicken are certified Halal and produced locally.

Further dietary restrictions and allergies* indicated during registration will be catered individually and available at the special diets table.

Crockery will be provided, but cannot be taken into the lecture rooms, so you are encouraged to bring your own reusable water bottles and coffee cups (with lids) that you can take with you into the sessions.

*menu items are made with ingredients stored, produced and served with safe procedures to minimise and mitigate the risk of allergen cross contamination. However, meals are produced in a kitchen that handles Gluten, Dairy, Egg, Soy, Fish, Shellfish, Tree Nuts, Peanuts, Sesame, Sulphites and Lupin and the caterer cannot guarantee that any item is 100% free from trace amount of allergen residues.

General information

Parking
Parking is available downstairs in the conference venue, with easy access from the carpark to Level 0. Pre-ordered parking tokens can be collected at the Registration Desk.

For parents
Children are most welcome at our conference and on campus but must be accompanied by whānau (a family member) at all times. A private breastfeeding room (including a fridge and sink) is available on the fourth floor of the Owen G Glenn Building. A key can be obtained from OGGB reception (on the road entrance level, level 1, one floor up from the conference location). The room is accessible via elevator.

Alternative breastfeeding spaces are available in the nearby Building 201 and a block away in the Science Centre Building 302.

In addition to the breastfeeding room, we can also offer a seminar room as an additional family space for your tamariki (children) if you want to take a break from the conference and connect with other mātua (parents / caregivers).

Please reach out to Local Organising committee members Jessie, Nathan or Anna, or check in at Registration, if you'd like access to the family room or some assistance to find the breastfeeding room.

Smoking and vaping
The University of Auckland campus is completely smoke- and vape-free, this includes the conference venue and all surrounding campus property.

Presenter information

Oral Presenters

You must load your presentation **on the morning of the day you are presenting** and onto the lectern computer **in the room** you are presenting. Our conference assistants will be in the lecture rooms at the following times:

Tuesday, Wednesday and Thursday 8:00-9:00am
Tuesday 10:00-10:30am
Wednesday and Thursday 10:20-11:00am

Please bring your file on a USB and name your file with the day and time you are presenting and your surname (e.g. Tue10:45Smith). Due to time constraints, only Keynote Presenters will be able to use their own laptop.

The lecture room computers are Windows-based and will load Powerpoint or PDF presentations. Projections are wide-screen (16:9), but Standard (4:3) will also display without distortion. Note that projections mirror the lectern monitor, so it is not possible to display speaker notes. Please feel free to have your own laptop alongside or print speaker notes if required.

Please go to the room in which you are presenting to meet the session chair and assistant **15 minutes before your session commences**. Note that full presentations are 12 minutes with 3 minutes for Q&A. Lightning presentations are 3 minutes with no Q&A.

Poster Presenters

Poster presenters are asked to put their posters up when they register. Velcro dots will be provided to mount your poster on the posterboards. Posters may be up to A0 size if portrait (841mm x 1189mm), and up to A1 size in landscape (594mm x 841mm); note that larger posters will not fit on the poster board.

Please refer to the poster list on Pages 22-25 to find your poster number and the day for your poster session (**Wednesday 12:45-1:45pm** or **Thursday 12:35-1:35pm**). Odd numbered posters will be displayed on Wednesday, and even numbered on Thursday. On your presentation day, please be available at your poster at the session time above. We will award a prize to the best student poster, and students should be with their posters during the poster sessions when judges will view their posters.

Posters will be on display for the whole conference. Poster tubes can be stored at the Registration Desk - authors must take their own posters down before 3:45pm Thursday.

Social events

Welcome reception
Generously supported by Kiwifruit Breeding Centre™

Owen G Glenn building level 1 foyer
Monday 7 July 5:10-6:30pm

Please proceed upstairs to level 1 following our Mihi Whakatau and Keynote talks from Prof Amanda Black and Dawn Lewis.
We will serve drinks and light nibbles accompanied by the Music School's Jazz Trio.

Conference dinner
Wynyard Pavilion, 17 Jellicoe Street, Auckland Central
Wednesday 9 July 7:00-10.30 pm

We encourage you to take a walk to the waterfront (30-40 minutes) to refresh after a full day at conference – but we will have some limited bus seats available. Buses will depart at 6:15pm from the Grafton Road bus stop outside the Owen G Glenn Building.

Enjoy an evening on the waterfront with our genetics community. The 3-course seated dinner will include shared entrées and a shared dessert board along with your selection of main. The food style is gastropub. There will be time afterwards to mix and mingle in the main dining room, dancefloor or outside on the waterfront (though, bring a jacket!). A drink selection will include beer, wine and nonalcoholic options. A cash/eftpos bar will be available after the bar tab is exhausted, and for non-menu drinks.

Please remember to bring your name badge and dinner wristband (indicating your selection of main) with you.

Schedule overview

	Monday 7 July 2025		Tuesday 8 July 2025		Wednesday 9 July 2025		Thursday 10 July 2025
		8:00	Registration desk open	8:00	Registration desk open	8:00	Registration desk open
			Indigenous Early Career Leaders	9:00	Keynote - Miloš Tanurdžić	9:00	Keynote - Alexei Drummond
		9:00	Keynote - Alana Alexander	9:40	Keynote - Erika Varkonyi-Gasic	9:40	Keynote - Cris Print
		9:20	Keynote - Jordon Lima	10:20	Morning tea	10:20	Morning tea
		9:40	Keynote - Conor Watene O'Sullivan	11:00	3x concurrent sessions		Precision Medicine
		10:00	Morning tea		Molecular, cellular and developmental genetics	11:00	Keynote - Lynsey Cree
			Indigenous Early Career Leaders		Genomics of taonga and under-rep species	11:20	Keynote - Emma Scotter
		10:30	Keynote - Catherine Collins		Comparative genomics	11:50	Keynote - Andrew Shelling
		10:50	Keynote - Megan Leask	12:30	Lunch + Posters	12:20	Lunch + Posters
		11:15	2x concurrent sessions		Posters 12:45-13:45		Posters 12:35-13:35
			Human genetics	14:00	3x concurrent sessions	13:45	3x concurrent sessions
			Ecological and Evolutionary Genetics		Bioinformatics and genomics		Precision medicine
		12:15	Lunch + AGM		Adaptation genomics		Ecological and population genetics
			AGM 12:30-13:00		Population genetics and phylogenetics		Evolutionary and comparative genetics
14:30	Registration desk opens	13:15	3x concurrent sessions	15:30	Afternoon tea	15:15	Afternoon tea
15:30	Mihi whakatau (welcome)		Human genetics / Genetics in primary industries	16:00	GSA Award talks	15:40	Keynote - Matt Littlejohn
15:50	Keynote - Amanda Black		Microbial, environmental and ancient genetics		Keynote - Catherine Grueber	16:20	Keynote - Phil Wilcox
16:30	Indigenous Early Career Leader		Genetics education		Keynote - Ashley Jones	17:00	GSA Awards and closing
	Keynote - Dawn Lewis	15:15	Afternoon tea		Keynote - Stephanie Waller	17:30	End of conference
17:10	Welcome reception (to ~6:30pm)	15:45	3x concurrent sessions		Keynote - Margaret Byrne		
			Molecular, cellular and developmental genetics	18:00	End of talks		
			Viral, bacterial and environmental genetics	18:00	Walk/bus to conference dinner		
			Connectivity and adaptation genomics	19:00	Conference dinner (to ~10:30pm)		
		17:30	End of day				

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Full schedule

Please note:

- an asterisk (*) indicates a student speaker eligible for our student awards;
- underlined are our GSA student award winners;
- watch out for posters from many of the lightning talk speakers!

Monday 7 July 2025	
14:30	Registration desk opens
15:30	Mihi whakatau - Welcome and open: Kaiarataki Michael Steedman
	Plenary session *Chair - Nathan Kenny, Assistant - Fang Fei Tham; Room - OGGB4*
15:50	Keynote - Amanda Black: Understanding what resilience looks like to better support Aotearoa New Zealand's most iconic and threatened kauri forests
	Indigenous Early Career Leaders Supported by Conference Partner Genomics Aotearoa genomics aotearoa
16:30	Keynote - Dawn Lewis: Environmental DNA is Indigenous DNA - considerations for ancient and contemporary metagenomics in Australia
17:10	Mixer (to 6:30pm) *Location: Level 1 foyer* Supported by Conference Partner Kiwifruit Breeding Centre
	Kiwifruit Breeding Centre™

Tuesday 8 July 2025		
8:00	Registration desk open	
	Indigenous Early Career Leaders Session Supported by Conference Partner Genomics Aotearoa  *Chair - Kimiora Henare, Assistant - Eric Marshall; Room - OGGB4*	
9:00	Keynote - Alana Alexander: Ko te tū hei waharoa: standing as a gateway between worlds	
9:20	Keynote - Jordon Lima: A Doctorate in Kaupapa Māori Research and Biomedicine: An Unexpected Journey	
9:40	Keynote - Conor Watene O'Sullivan: Ethics and applications of molecular biology in Indigenous contexts: A case study of a collaborative deep phenotyping research project within a rural Māori community	
10:00	Morning tea	
	Indigenous Early Career Leaders Session continues	
10:30	Keynote - Catherine Collins: Genomic history of tupuna from an early 14th century Te Waipounamu site	
10:50	Keynote - Megan Leask: Omics and molecular pipelines for precision medicine for and by Māori	
	Human genetics *Chair - Suzanne Reid, Assistant - Eric Marshall; Room - OGGB5*	**Ecological and evolutionary genetics** *Chair - Peter Dearden, Assistant - Patricia Pillay; Room - OGGB4*
11:15	Isabelly de Lima*: Splicing testing of crystallin gene variants in paediatric cataract	Emma Carroll: Past and future of genetic monitoring highlighted with the case study of the Aotearoa New Zealand southern right whales tohorā
11:30	Amara Shaukat: The genetic and phenotypic correlates of mitochondrial DNA copy number in the Mexican Biobank	Graham McCulloch: Evolution in action: how human-driven deforestation is driving rapid adaptation in our endemic insects
11:45	**Lightning talks**: Oyedele Olaoye*, Helen Fitzsimons, Suzanne Musgrave* and Chantel van Wyk	Kathleen McLay*: Chromosomal inversions facilitate adaptive divergence with gene flow
12:00	Lunch	**Lightning talks**: Shanshan Shen*, Ashleigh Iwikau*, Kate Moloney* and Sarah Bailey
12:15		Lunch
12:30	AGM - *room OGGB4*	
13:00	Lunch continues	

Tuesday 8 July 2025			
	Human genetics *Chair - Jessie Jacobsen, Assistant - Eric Marshall; Room - OGGB5*	**Microbial, environmental and ancient genetics** *Chair - Lisa Matisoo-Smith, Assistant - Hui Zhen Tan; Room - OGGB4*	**Genetics education** *Chair - Miloš Tanurdžić, Assistant - Fang Fei Tham; Room - OGGB3*
13:15	Sarah Jackson*: Local pangenomes of structurally complex and medically relevant loci for health and disease studies	Philipp Schiffer: Hierarchical patterns of soil biodiversity in extreme environments: Insights across biological scales	Gigi Lim: Bridging the gap: Translating genomic knowledge to the grassroots level – challenges and opportunities for Registered Nurses
13:30	Keri Multerer: Using novel approaches to incorporate higher order interactions into polygenic risk score calculations for use in a clinical setting	Rebecca French: Microbial drivers of disease in the critically endangered Kākāpō: Insights from total RNA sequencing	Georgina Dawson: Empowering future Māori scientists: ESR Genomics Bootcamp
13:45	Alix Coysh: Developing large-animal models and gene therapies for Retinitis Pigmentosa	Meriam van Os*: A comparative metagenomic study of ancient kurī (dog) palaeofaeces from Aotearoa New Zealand	Simon Baxter: Inspiring the next generation of geneticists - how hard could it be?
	Genetics in primary industries *Chair - Jo Putterill, Assistant - Eric Marshall; Room - OGGB5*		
14:00	Nathan Kenny: Tracing the genetic basis of resilience to climate change in green-lipped mussels (kuku)	Amali Thrimawithana*: Decoding the mānuka microbiome: A multiscale approach to taxonomic and functional diversity	Suzanne Reid: CHATting with students – my reflections on the use of chat bots within undergraduate biology courses
14:15	Glenn Thorlby: Biotech solutions to New Zealand's forestry challenges	Teremoana Porter-Rawiri*: Exploring fungal diversity: The Puāwaitanga of restored Wairarapa wetlands	Emily Remnant: Embedding an interdisciplinary experience into genetics education
14:30	Sihini Waidyaratne*: From Genome to Orchard: Exploring functional genomics approaches to accelerate mango breeding	Patricia Pillay*: Bones, Barcodes, and Biodiversity – optimising aDNA analyses on tropical sub-fossil collections from the Marquesas Islands	Katarina Stuart: Embracing the mess: Real learner data in bioinformatics training
14:45	Seyed Eisa Abdollahimousavi*: Identification of genetic loci affecting survival in rainbow trout (*Oncorhynchus mykiss*) infected with VHS	William Pearman: Joint consideration of selection and microbial generation count provides unique insights into evolutionary and ecological dynamics of holobionts	Jordon Lima: Pītau Error: A resource for teaching genetics and Te Reo Māori
15:00	**Lightning talks**: Conor Tumulty*, Min Zhao*, Lachlan Taylor* and Storm Voyce*	**Lightning talks**: Kristina Hames*, Richard O'Rorke, Olivia Janes* and Jessica Darnley*	Douglas Walker: DNADRV's school run: the educational benefits of integrating eDNA-based projects into the school curriculum
15:15	Afternoon tea		

Tuesday 8 July 2025			
	Molecular, cellular and developmental genetics *Chair - Nathan Kenny, Assistant - Jamie Hyde; Room - OGGB5*	**Viral, bacterial and environmental genetics** *Chair - Manpreet Dhami, Assistant - Jenny Ann Sweatman; Room - OGGB4*	**Connectivity and adaptation genomics** *Chair - Katarina Stuart, Assistant - Patricia Pillay; Room - OGGB3*
15:45	Joanna Putterill: Mutagenesis of candidate HAT complex genes INHIBITOR of GROWTH in the model legume Medicago implicates them as growth, development and flowering time regulators	Jemma Geoghegan: Exploring Aotearoa's virosphere	Shane Lavery: Concordance and drivers of New Zealand marine coastal connectivity
16:00	Sureshkumar Balasubramanian: A unifying framework for thermosensing in plants	Sarah Inwood: Viral spillover during biocontrol agent mass-rearing: an overlooked influence on biocontrol efficacy?	Sebastian Alvarez-Costes*: From Ice Age to isolation: Historical demography and inbreeding depression in New Zealand's endemic Hector's and Māui dolphins
16:15	Carlotta Wills*: (2024 Sidney James Prize for best student poster): LOTR-2: a LOTUS & Tudor domain protein with unexpected features	Emily Remnant: Change in honey bee virome due to the arrival of a novel vector	Hui Zhen Tan*: Inbreeding load in a small and managed population: two decades of Hihi/Stitchbird genomics
16:30	Shelley Grace Young (2025 Batterham Award): The role of small RNAs in honey bee immune regulation	Chandan Kumar Pradhan*: Can changes in gene expression and splicing explain host specificity of pathogens?	Catherine Meyer*: Evaluating the genetic connectivity of false killer whales (*Pseudorca crassidens*) in Aotearoa New Zealand
16:45	Rebecca McKee* (2025 Smith-White travel award): Sex-specific expression of miRNA clusters in the honey bee parasite, *Varroa destructor*	Allyson Malpartida*: Development of eDNA sampling detection methods for early detection of pathogens from on-farm water sources	Dineth Pathirana* (2025 Smith-White travel award): Genetic connectivity in a skink with geographic variation in reproductive mode
17:00	Victoria Sugrue: Building the androgen clock: An epigenetic predictor of long term male hormone exposure	Jigmidmaa Boldbaatar*: Diversity of fungi and bacteria in infected and uninfected wing tissues within natural sexual and asexual populations of a facultatively parthenogenetic stick insect, *Megacrania batesii*	Jaehwan Lee*: A Salinity Gradient Drives Local Adaptation in Baltic Pipefish Despite Gene Flow
17:15	End of day		Mark de Bruyn: Postglacial recolonization of the Southern Ocean by elephant seals occurred from multiple glacial refugia
17:30			End of day

Wednesday 9 July 2025			
8:00	Registration desk open		
	Plenary session *Chair - Joanna Putterill, Assistant - Patricia Pillay; Room - OGGB4*		
9:00	Keynote - Miloš Tanurdžić: Gene regulatory mechanisms in control of plant architecture		
9:40	Keynote - Erika Varkonyi-Gasic: Genetic Control of Flowering and Sex Determination in Kiwifruit		
10:20	Morning tea		
	Molecular, cellular and developmental genetics *Chair - Jo Putterill, Assistant - Jamie Hyde; Room - OGGB5*	**Genomics of taonga and under-represented species** *Chair - Emma Carroll, Assistant - Hui Zhen Tan; Room - OGGB4*	**Comparative genomics** *Chair - Oliver Griffith, Assistant - Patricia Pillay; Room - OGGB3*
11:00	Lynette Brownfield: The identification novel molecular mechanisms for self-incompatibility in ryegrass and clover	Tammy Steeves: Towards a more holistic assessment of genomic diversity in Aotearoa New Zealand's rarest breeding bird	Paul Waters: Sex chromosome evolution: insights from skinks
11:15	Helen Fitzsimons: HDAC4 oligomerisation drives nuclear condensate formation and impairs neuronal development	Joseph Guhlin: Genomic signatures of isolation and disease in the World's Best Penguin	Genevieve Law* (2024 Sidney James Prize): Mutation rate and selection in the unusual duplicated mitogenomes of Australasian stingless bees
11:30	Shannon Taylor*: Evolving vertebral counts without evolving the segmentation clock	Libby Liggins and Claire Rye: Building a genomic data repository for taonga species in Aotearoa New Zealand	Zahra Chew*: Conservation and diversity of ribosomal DNA in chordates
11:45	Soleille Miller: The effects of maternal age on offspring global gene expression	Roseanna Gamlen-Greene: Working with communities in Aotearoa-New Zealand to build climate resilience in kaimoana (seafood) using transcriptomics	Phoebe Keddell* Why does eusociality evolve so often in the Hymenoptera?
12:00	Erin Delargy*: Molecular mechanisms of honeybee segmentation using HCR and spatial transcriptomics	Melissa Nehmens*: Diploid near-gapless reference genome assembly of the Longspine sea urchin, *Centrostephanus rodgersii*	Taylor Gallagher*: Genomic insights from Onychophorans into the diversification of panarthropods
12:15	**Lightning talks**: Katarina Stuart, Madison Hall* and Michelle Kim*	Gemma Collins: Assembled genomes of New Zealand's endemic stick insect hybrids	**Lightning talks**: Marc Bailie, Xin Yi Sophie Huang*, FangFei Tham* and Tyla Hill-Moana*
12:30	Lunch		
12:45	Posters		
13:45	Lunch continues		

Wednesday 9 July 2025			
	Bioinformatics and genomics *Chair - Nathan Kenny, Assistant - Jamie Hyde; Room - OGGB5*	**Adaptation genomics** *Chair – Graham McCulloch, Assistant - Fang Fei Tham; Room - OGGB4*	**Population genetics and phylogenetics** *Chair - Shane Lavery, Assistant - Hui Zhen Tan; Room - OGGB3*
14:00	Chen Wu: Enhancing breeding programs with high-resolution pangraphs	Manpreet Dhami: Investigating the pathways of Fall Armyworm invasion in Aotearoa New Zealand	Bruce Weir: Allelic association analyses: Avoiding the use of allele frequencies
14:15	Astra Heywood: Unravelling inheritance patterns in polyploid hybrid crosses through haplotype tracking	Adi Nugroho* (2025 Smith-White travel award): Genetic adaptation of introduced rusa deer to highly variable climatic environments in Oceania	Tram Vi: Assessing imputation methods in populations with differing relatedness and inbreeding levels for low-coverage sequencing data
14:30	Roan Zaied: Integrating polygenic risk scores and quantitative CT metrics for machine learning-based prediction and clustering of chronic obstructive pulmonary disease	Zoe Broad*: Expression QTL divergence between ecotypes of an Australian wildflower	Cinthy Lorena Jimenez Silva: Validating calibrations in phylogenomics with FossValidation: A case study on marsupials
14:45	Benjamin Halliday: Detection and mitigation of microbiome DNA presence in saliva-derived whole genome sequence data	Kelton Cheung*: Do cane toads in Australia exhibit repeated local adaptation to different environments?	Leo Featherstone: Fitting local molecular clocks: a new tool and challenges
15:00	Endeshaw Chekol Abebe*: Depression-linked plasma protein biomarkers: Insights from differential abundance analysis and Mendelian randomization	Kamolphat Atsawawaranunt: Missing or mis-telling the story? Trade-offs for reduced representation compared to whole genome resequencing	Matthew Fullmer: Interaction range of common goods shapes Black Queen dynamics beyond the cheater-cooperator narrative
15:15	Catriona Miller*: Sex-dependent prediction of autism	Ang McGaughran: Evolution experiments in invasive blowflies: genetic bottlenecks and fitness outcomes	Arlie Macdonald*: PhyloG2P: Expanding genotype to phenotype maps in the age of genomics
15:30	Afternoon tea		
	GSA Award talks *Chair - Anna Santure, Assistant - Jenny Ann Sweatman; Room - OGGB4*		
16:00	Keynote - Ross Crozier Medal - Catherine Grueber: Monitoring and maintaining genetic biodiversity: from local to global and back again		
16:40	Keynote - Alan Wilton Award - Ashley Jones: Structural variations drive genome evolution and divergence in Eucalyptus trees		
17:00	Keynote - DG Catcheside Prize - Stephanie Waller: Exploring New Zealand's virosphere		
17:20	Keynote - MJD White Medal - Margaret Byrne: Genetics is integral to biodiversity knowledge for plant and animal conservation		
18:00	Award talks end		
18:00	Walk to conference dinner (some limited bus seats available)		
19:00	Conference dinner (to ~10:30pm)		

Thursday 10 July 2025	
8:00	Registration desk open
	Plenary session *Chair - Anna Santure, Assistant - Hui Zhen Tan; Room - OGGB4*
9:00	Keynote - Alexei Drummond: Bayesian phylogenetics and population genetics: from models to cancer genomics
	Chair - Jessie Jacobsen, Assistant - Jenny Ann Sweatman; Room - OGGB4
9:40	Keynote - Cris Print: Moving at breakneck speed – the rapidly expanding opportunities of genomic precision medicine for New Zealand
10:20	Morning tea
	Precision Medicine session Supported by Conference Partner Waipapa Taumata Rau - University of Auckland Waipapa Taumata Rau University of Auckland *Chair - Jessie Jacobsen, Assistant - Jamie Hyde; Room - OGGB4*
11:00	Keynote - Lynsey Cree: Non-invasive embryo selection: Bridging technology and ethics in reproductive science
11:20	Keynote - Emma Scotter: NZ-relevant genetic variants in motor neuron disease and their therapeutic approaches
11:50	Keynote - Andrew Shelling: Genomics and discrimination in New Zealand health and life insurance
12:20	Lunch
12:35	Poster
13:35	Lunch continues

Thursday 10 July 2025			
	Precision medicine Supported by Conference Partner Waipapa Taumata Rau - University of Auckland Waipapa Taumata Rau University of Auckland *Chair - Jessie Jacobsen, Assistant - Jamie Hyde; Room - OGGB5*	**Ecological and population genetics** *Chair - Tammy Steeves, Assistant - Fang Fei Tham; Room - OGGB4*	**Evolutionary and comparative genetics** *Chair - Paul Waters, Assistant - Jenny Ann Sweatman; Room - OGGB3*
13:45	Martin Kennedy: CYP2D6*71 is a poor metaboliser allele common in Polynesian and Māori people and absent from Europeans	Jeanne Jacobs: Genetic diversity of Coconut Rhinoceros Beetle (Oryctes rhinoceros) and its biocontrol agent Oryctes rhinoceros nudivirus	Oliver Griffith: Disentangling the paradoxical role of inflammation in mammalian pregnancy
14:00	Evelyn Jade*: Genetics of *NOTCH2NLC*-related repeat expansion disorders in NZ Māori families	Antonio L. Rayos, Jr.*: Taxonomic and biogeographic insights into the Australasian fingerworts in the Lepidozia ulothrix clade	Audald Lloret-Villas: Investigating crossover and non-crossover recombination rates in aye-ayes (Daubentonia madagascariensis)
14:15	Hao-Han George Chang: A gene variant in CALCRL, encoding a G-protein coupled receptor, is highly enriched in individuals with Māori and Pacific ancestry and associates with a higher risk of kidney failure	Mark Clifton*: Hybridisation and clonality within the endangered shrub *Callistemon forresterae* (Myrtaceae) of East Gippsland, Australia	Melanie Laird: Transcriptomic analysis of prostate plasticity in a seasonal breeding marsupial (Trichosurus vulpecula; brushtail possum)
14:30	Denis Nyaga: Benchmarking and quality control for clinical nanopore sequencing facility for acute care in New Zealand	Kahu Hema*: Can reforestation reverse the evolutionary effects of deforestation? Genetic evidence from Aotearoa's native insects	Kimberley Dainty: Identifying germline-specific promoters for gene drives in invasive wasps
14:45	Hardip Patel: Australian Indigenous pangenome to improve genomics research and clinical applications	Taoho Patuawa and Sarah Wells: Population genomics analysis of ngā roimata ō Tohe (Pimelea eremitica) to inform the conservation strategy for this taonga plant species	Pierre Ibri*: Assisted evolution of toad toxin resistance in a marsupial
15:00	Natasha Mckean: Sheep models of Alzheimer's disease	Prudence Gowo*: The diversity and phylogenetic placement of groundwater fauna, amphipods, in Australasia and in a global context	Richard Newcomb: The evolution of olfaction in whales: A genomics approach
15:15	Afternoon tea		
	Plenary session *Chair - Anna Santure, Assistant - Hui Zhen Tan; Room - OGGB4*		
15:40	Keynote - Matt Littlejohn: How the Holstein got its spots		
	Chair - Kimiora Henare, Assistant - Eric Marshall; Room - OGGB4		
16:20	Keynote - Phil Wilcox: Development of genomic resources for Māori health		
17:00	GSA Awards and closing		
17:30	End of conference		

Posters

Please note:

- odd-numbered posters are on Wednesday, even numbered on Thursday
- all posters will be displayed throughout the conference
- posters will be presented by authors during lunchtime of the indicated day
- an asterisk (*) indicates is a student speaker eligible for our student awards
- underlined are our GSA student award winners
- watch out for lightning talks from many of these poster presenters!

Day to present poster	Poster number	Theme	Presenter name	Poster title
Wed	1	Ecological, evolutionary and comparative genetics	Julia Allwood	Development of targeted meta-barcoding methods for conservation management and biodiversity support
Thu	2	Ecological, evolutionary and comparative genetics	Hamish Clarke*	Genomics and Evolution of Mimicry in a Colour-polymorphic New Zealand Stonefly
Wed	3	Ecological, evolutionary and comparative genetics	Jessica Darnley*	A genomics-informed investigation into Lamprey Reddening Syndrome
Thu	4	Ecological, evolutionary and comparative genetics	Anran Fan*	Environmental DNA reveals the biological effects of reforestation in New Zealand
Wed	5	Ecological, evolutionary and comparative genetics	Tithi Gandhi*	Haplotype-resolved genome assemblies and hybridization histories of asexual New Zealand stick insects
Thu	6	Ecological, evolutionary and comparative genetics	Kristina Hames*	Exploring the potential of virus transmission among birds in a spatially restricted ecological niche
Wed	7	Ecological, evolutionary and comparative genetics	Dorothea Heimeier	Advances in Cetacean Immunogenetics: The Cetacean IPD-MHC Database
Thu	8	Ecological, evolutionary and comparative genetics	Lia Heremia* (2025 SING Award)	Uncovering virus diversity in urban waterfowl
Wed	9	Ecological, evolutionary and comparative genetics	Xin Yi Sophie Huang*	Investigating the genetic diversity of the endangered subpopulation of humpback whales (*Megaptera novaeangliae*) in New Caledonia, Oceania
Thu	10	Ecological, evolutionary and comparative genetics	Olivia Janes*	Unpacking genetic incompatibility and early reproductive failure in threatened species
Wed	11	Ecological, evolutionary and comparative genetics	Avneet Kaur	Unraveling colour variation in Kangaroo Paws
Thu	12	Ecological, evolutionary and comparative genetics	Nina Knowles*	Untangling Australian *Ficopomatus*, a genus of notorious biofouling and invasive estuarine calcareous tubeworms
Wed	13	Ecological, evolutionary and comparative genetics	Aymee Lewis*	Genomic characterisation of bioluminescent bacteria isolated from marine fish in Aotearoa, New Zealand.
Thu	14	Ecological, evolutionary and comparative genetics	Jasmin Li*	Fungal communities in brood food and pollen of Australian Stingless Bees (*Tetragonula carbonaria*)
Wed	15	Ecological, evolutionary and comparative genetics	Kate Moloney*	Genetics to the rescue? Developing high-quality genomic resources for a critically endangered bird.

Day to present poster	Poster number	Theme	Presenter name	Poster title
Thu	16	Ecological, evolutionary and comparative genetics	Richard O'Rorke	DNADRV: getting baseline insect distribution data from eDNA splattered on your car
Wed	17	Ecological, evolutionary and comparative genetics	Niamh Ryan*	The phylogenetics and population structure of a species complex of deep-sea Scale Worms
Thu	18	Ecological, evolutionary and comparative genetics	Xuezhi Ethan Seow*	Resolving the phylogeny of a taxonomically ambiguous genus of South Pacific Lamiinae (Order: Cerambycidae; Genus: *Xylotoles*)
Wed	19	Ecological, evolutionary and comparative genetics	FangFei Tham*	National collaboration provides insight into patterns of strandings of enigmatic beaked whales
Thu	20	Genetics in primary industries	Marc Bailie	From fragments to futures: Ultra-long reads empowering invertebrate genomics in New Zealand
Wed	21	Genetics in primary industries	Madison Hall*	Towards greener pastures: Understanding the role of CONSTANS variants in perennial ryegrass flowering time
Thu	22	Genetics in primary industries	Katarina Stuart	From Genes to Green: The role of genomics in native seed production
Wed	23	Genetics in primary industries	Lachlan Taylor*	Investigating the genetics underlying late flowering in Perennial Ryegrass
Thu	24	Genetics in primary industries	Storm Voyce*	Swipe left on self-pollen: Uncovering the molecular basis for self-incompatibility in clover
Wed	25	Molecular, cellular and developmental genetics	Jacob Grupp	Optimising *In Vitro* rearing of *Nasonia* for gene editing
Thu	26	Molecular, cellular and developmental genetics	Hannah Hawley	HDAC4 biomolecular condensates: dynamics, disruption, and effects on neuronal development
Wed	27	Molecular, cellular and developmental genetics	Michelle Kim*	Functional validation of three candidate causal variants in the *xanthine dehydrogenase* gene associated with feline xanthinuria
Thu	28	Molecular, cellular and developmental genetics	Hamish Salvesen	Expanding the toolkit for genome engineering in wasps
Wed	29	Molecular, cellular and developmental genetics	Baeli Spedding-Devereux* (2025 SING Award)	CasRx as a suitable tool for plant biology research
Thu	30	Molecular, cellular and developmental genetics	Conor Tumulty*	Alternative ribosomal RNAs and their unsuspected link to sex determination in zebrafish.

Day to present poster	Poster number	Theme	Presenter name	Poster title
Wed	31	Molecular, cellular and developmental genetics	Eric Marshall*	Determining the regulatory controls of desiccation tolerance in plants
Thu	32	Human genetics and precision medicine	Clare Adams	Deriving correlations for inter-trait genetic scores in metabolic conditions affecting Pacific populations
Wed	33	Human genetics and precision medicine	Travis Johnson	Dual model nutriphenomics to identify precision dietary therapies for inherited metabolic disorders
Thu	34	Human genetics and precision medicine	Alastair Lamont	Population simulation to optimise study designs and estimate polygenic disease risk/resilience in Aotearoa Māori populations
Wed	35	Human genetics and precision medicine	Suzanne Musgrave*	The power of reanalysis for neurodevelopmental conditions; identifying new variants and reinterpreting old findings
Thu	36	Human genetics and precision medicine	Oyedele Olaoye*	Dissecting the regulatory landscape of rs4698413: a causal variant for Parkinson's disease
Wed	37	Human genetics and precision medicine	Emily Swasbrook*	Assessing pathogenicity of variants in TAB2
Thu	38	Human genetics and precision medicine	Chantel van Wyk	Evaluating the role of on-call genetic counselling service in a Prostate Cancer Clinic: A study of uptake and family risk screening
Wed	39	Human genetics and precision medicine	Emma Wade	Using a genetic lens to treat pelvic organ prolapse

Abstracts

Abstracts are arranged alphabetically by surname in the following order:

- Keynote talks (blue background)
- Concurrent session talks, including full talks and lightning talks (pink background)
- Posters (orange background)

Note that abstracts for delegates who are presenting both a lightning talk and a poster appear in both sections for convenience

Keynote talks

Ko te tū hei waharoa: standing as a gateway between worlds

Indigenous Early Career Leaders Session

Alana Alexander[1]

[1]*Department of Anatomy, School of Biomedical Sciences, University of Otago, Dunedin, New Zealand*

Abstract: Māori geneticists navigate two deeply interconnected yet distinct worlds: a world where the physical manifestation of whakapapa is investigated through lab work and bioinformatics, and Te Ao Māori, where knowledge is ordered by broader concepts of whakapapa and a deep connection to place. For Māori geneticists, especially EMCRs, standing as a gateway, waharoa, between these worlds is both a privilege and a challenge.

In this talk, I will explore some of the beautiful aspects of being a conduit between these realms, as well as some of the challenges, including upholding data sovereignty, rebuilding trust of science, and the responsibility we have for how our colleagues interact with our communities.

By sharing my experiences (and mistakes!), I aim to highlight spaces where Pākehā and tauiwi colleagues can support Māori EMCRs in their unique role as waharoa, to ultimately ensure genetics can uphold the mana of communities.

Biography: Alana uses genetics to learn how challenges of the past and present have impacted on species, and what the impact of threats might be in the future, focussing mostly on whales and dolphins. As a Māori scientist (Te Hikutū: Ngāpuhi) Alana also maintains a strong interest in ensuring that her research can be used to support kaitiakitanga and rangatiratanga of iwi, hapū and papatipu rūnaka.

Understanding what resilience looks like to better support Aotearoa New Zealand's most iconic and threatened kauri forests

Amanda Black[1], Alexa Byers[1], Leo Condron[2], Nick Waipara[3]

[1]Bioprotection Aotearoa, Lincoln University, [2]Faculty of Agriculture and Life Sciences, Lincoln University, [3]Plant and Food Research Ltd

Abstract: Globally, large-scale forest disease and dieback are increasing at alarming rates because of biological invasions, fragmentation through clearance, and changing climate regimes. The implications are dire, as these forests are essential for human survival and have a critical role in maintaining biodiversity and climate regulation.

In Aotearoa New Zealand, over 80% of our 2,500 species of native plants are found nowhere else. This endemism is threatened by invasive pathogens such as *Phytophthora agathidicida* and combined with the fragmentation of forest ecosystems and disrupted ecological feedback processes, such as localised extinction of seabird populations and their contribution of nutrients to ecosystems. These disturbances are known to affect soil microbial functional responses including the ability of old growth forest to store carbon. This is effect is critical and detrimental as forests and their soil ecosystems are recognised as major contributors to balancing the global carbon budget. These issues are complex and interconnected and the impact on northern kauri forests from successive disturbance events can give insight into ecological mechanisms that underpin forest resilience.

I'll discuss our two-phase approach to understand what resilience looks like and what we can do to support and rebuild parts of these ancient multiscale ecosystems.

Biography: Amanda is of *Tūhoe, Whakatōhea, Te Whānau-ā-Apanui* decent and is a Director of Bioprotection Aotearoa, a national centre of research excellence. Her research interests are a combination of investigative work on ecosystem processes that influence landscape resilience against biological invasions and directing research platforms towards authentic Indigenous inclusive practices for impact.

Genetics is integral to biodiversity knowledge for plant and animal conservation

GSA Awards Session – MJD White Medal

Margaret Byrne[1]

[1]*Adjunct, School of Biological Sciences, The University of Western Australia, Perth, Australia*

Abstract: The integration of genetics into conservation to address the three tiers of biodiversity, i.e. ecosystems, species and genes, is critical to effective conservation and ecological management, particularly under changing climates. As genetic techniques in population and ecological genetics, phylogeography, and phylogeny have been developed and refined, they became more readily applicable to native species and are now widely used in plant, animal and ecosystem conservation across rare and threatened species management, invasive species, restoration, forest management, climate adaptation, phylogeography, phylogeny and systematics. Genomics has revolutionised current applications in conservation genetics, particularly for assessing and understanding adaptive variation, building on previous population genetics and understanding of evolutionary history. Genomics enables assaying greater amounts of genomes that provides more power for population genetics and development of reference genomes, and phylogeny and resolution of species complexes. Collaborations are important for building larger initiatives to foster advances in applications of genetics in conservation, and for multidisciplinary synthesis that harnesses collective wisdom to take targeted genetics research and translate it into a wider context. I will highlight the application of genetics for improved knowledge informing evidence-based conservation strategies for plants and animals.

Biography: Over the 34 years of her scientific career, Professor Byrne has established strong international leadership in conservation genetics and has pioneered application of the discipline to conservation management in Australia. Her key areas of research have been in population and ecological genetics, mating systems and pollen dispersal, phylogeography, phylogeny, and climate adaptation. She is also a leader in the integration of scientific excellence into policy and management. Margaret completed her PhD at the University of Western Australia in 1991 and held Research Scientist, Principal Research Scientist and Director roles in the Department of Environment and Conservation and Department of Parks and Wildlife. She is currently the Executive Director of Biodiversity and Conservation Science in the Department of Biodiversity, Conservation and Attractions, and holds an Adjunct Professorship at the University of Western Australia.

Genomic history of tupuna from an early 14th century Te Waipounamu site

Indigenous Early Career Leaders Session

Catherine J. Collins[1], Hallie R. Buckley[1], Richard K. Walter[2], Elizabeth A. Matisoo-Smith[1]

[1]Department of Anatomy, School of Biomedical Sciences, University of Otago, Dunedin, New Zealand, [2]Archaeology, School of Social Sciences, University of Otago, Dunedin, Otago, New Zealand

Abstract: Te Pokohiwi o Kupe, or Wairau Bar, is an early archaeological site on the north-eastern coast of Te Waipounamu (the South Island) of Aotearoa (New Zealand), dated to early 14th Century and thought to be representative of the founding population of Māori in Aotearoa. Rangitāne o Wairau have upheld ahi kā and kaitiakitanga at Te Pokohiwi o Kupe for generations. This research supports iwi-led efforts to understand ancestral origins and reaffirms the site's cultural and genealogical significance. Here, in addition to 11 complete mitogenomes, we present whole genome data from six tupuna (ancestors) with >1% endogenous DNA from Wairau Bar, the first ancient genomes from tupuna Māori. Shotgun sequencing resulted in genome-wide data representing ~20k-400k SNPs from each tupuna. These data were analysed alongside previously published modern and ancient SNP data from populations across the Pacific, and screened for the presence of SNPs associated with metabolic disease. Together, these datasets assess the population history, genetic ancestry and relatedness of an early Māori population.

Biography: Catherine Collins (Kāi Tahu, Pākehā) is a Lecturer in the Department of Anatomy at Ōtākou Whakaihu Waka (University of Otago). Her current research projects apply genomic techniques, using modern and ancient DNA, to study the history of animals transported to Aotearoa by humans, both intentionally and unintentionally.

Non-Invasive Embryo Selection: Bridging Technology and Ethics in Reproductive Science

Precision Medicine Session

Lynsey M. Cree[1,2], G. Donaldson[1], H. Misaghi[1], N. Knowlton[1,3]

[1]Department of Obstetrics, Gynecology and Reproductive Sciences, School of Medicine, University of Auckland, Auckland, New Zealand, [2]Fertility Associates, Auckland, New Zealand, [3]Department of Statistics, School of Mathematical and Computational Sciences, Massey University, Auckland, New Zealand

Abstract: Non-invasive embryo selection is emerging as a technically and ethically preferable alternative to invasive procedures such as trophectoderm biopsy, in both assisted reproductive technology (ART) and livestock breeding. These approaches aim to infer an embryo viability and genomic integrity without breaching the zona pellucida.

In human ART, analysis of cell-free DNA from spent culture media avoids the potential mechanical and developmental risks associated with embryo biopsy, particularly in morphologically suboptimal embryos. However, these methods face limitations in sensitivity, reproducibility, and technical robustness due to low DNA yield and variability in culture conditions. Concurrently, morphological grading remains a cornerstone of embryo selection but suffers from inter-observer variability and low predictive power. Recent developments in AI-based assessment offer a path toward quantitative, reproducible evaluations, though their integration into clinical workflows demands rigorous external validation, standardisation across imaging platforms, and clinician interpretability.

This presentation outlines the findings from our ongoing research in non-invasive embryo assessment across human, bovine, and equine models. We focus on comparative performance, methodological challenges, and the translational implications of deploying these technologies in clinical and agricultural contexts.

Biography: Dr Cree is a biomedical scientist who's vision is to improve the health and wellbeing of individuals with infertility through understanding how mitochondrial dysfunction contributes to ovarian ageing and exploring novel means to improve IVF success rates. Her research has applications in fertility treatments in humans, and developing and optimising animal breeding strategies. She is a Senior Lecturer within the Department of Obstetrics, Gynaecology and Reproductive Sciences at the University of Auckland. Lynsey is a current member of the Advisory Committee for

Assisted Reproductive Technologies (ACART) and an Associate Editor for Human Reproduction Updates.

Bayesian phylogenetics and population genetics: from models to cancer genomics

Alexei Drumond[1]

[1]School of Biological Sciences, University of Auckland, Auckland, New Zealand

Abstract: Recent advances in Bayesian methods have significantly improved our ability to model evolutionary and population genetic processes. In this seminar, I will outline recent developments in domain-specific modeling languages, designed to simplify and enhance model specification in phylogenetics and population genetics. Additionally, I will introduce new approaches to posterior analysis in phylogenetic tree space, providing clearer interpretation and visualization of complex posterior distributions. To illustrate these methods, I will discuss their application to single-cell sequencing data from cancer, enabling joint inference of genotypes and cell lineage trees, thus revealing detailed insights into tumour evolution.

Biography: Professor Alexei Drummond, Founding Director of the University of Auckland's Centre for Computational Evolution, leads an international team revolutionizing how we study evolution through computational approaches. With joint appointments in the School of Biological Sciences and School of Computer Science, he co-developed BEAST (Bayesian Evolutionary Analysis by Sampling Trees), scientific software that has become fundamental infrastructure for evolutionary biology research worldwide. Since 2004, BEAST and its successor BEAST 2 have been used by thousands of scientists globally, with the main papers receiving over 40,000 citations, making it one of the most influential computational phylogenetics tools ever developed. Professor Drummond's mathematical models and software have transformed scientific practice by providing open-source tools for analyzing genetic and evolutionary data across disciplines—from tracking infectious disease spread to understanding linguistic origins and conservation genomics. His recent honors include the prestigious James Cook Research Fellowship (2019-2021) from the Royal Society of New Zealand Te Apārangi and recognition as a Clarivate Highly Cited Researcher (2021).

Monitoring and maintaining genetic biodiversity: from local to global and back again

GSA Awards Session – Ross Crozier Medal for a mid career researcher

Catherine E. Grueber[1]

[1]School of Life and Environmental Sciences, The University of Sydney, Australia

Abstract: For decades, conservation scientists have advocated protecting three levels of biodiversity: ecosystem, species and genetic. Regarding the latter, new genetic and genomic tools in the molecular laboratory, combined with long-standing and emerging population genetic theory, provide answers to management problems in the wild. Intensive global efforts have seen these advances converted to a range of assessment frameworks, to ensure biodiversity protection actions have the desired impact for genetic diversity. Using recent examples of empirical studies, advocacy works, and engagement with stakeholders, I show how local-scale conservation genetic success stories have fed through to the global stage and to the UN Convention for Biological Diversity. Via multistakeholder collaboration here in Australia and internationally, my team and I have developed and tested genetic biodiversity indicators, and led major synthesis of global evidence for population genetic change in nature. Using data from thousands of studies and hundreds of species across the tree of life, we found that genetic diversity losses are widespread. But, from international policy, to simple actions in our own backyards, genetically informed conservation actions can help.

Biography: Associate Professor Catherine Grueber, at the University of Sydney, investigates the population genetic impacts of conservation strategy by combining empirical studies with conservation policy and data synthesis. Her research focuses on applying population genetic theory to inform conservation action, based on molecular data, computational simulations, and meta-analysis, to generate evidence-based policy recommendations. Working with conservation practitioners and policymakers, Catherine's genetic research has advanced biodiversity management via bespoke solutions for a variety of threatened mammal and bird species, and via the development and testing of genetic indicators of biodiversity loss. Catherine completed her PhD at the University of Otago in 2010, followed by postdoctoral research at the University of Otago, and then joined the University of Sydney in 2014 as a San Diego Zoo Global research fellow. In 2019, Catherine was awarded a University of Sydney Robinson Fellowship in the School of Life and Environmental Sciences, and now leads a dynamic research team in conservation genetics.

Asia-Pacific Genetics Seminar Series

Monitoring and maintaining genetic biodiversity: from local to global and back again

Catherine Grueber
Associate Professor
University of Sydney

- University of Sydney Robinson Fellowship
- San Diego Zoo Global Postdoctoral Fellowship
- Recipient of the 2025 GSA Ross Crozier Medal, the 2015 GSA Alan Wilton Prize, and the 2011 D.G. Catcheside Prize

Moderator: A/Professor Anna Santure
University of Auckland

Wednesday July 9th, 2025 (Online)

New Delhi: 9:30 - 10:10 am
Beijing: 12:00 - 12:40 pm
Tokyo: 1:00 - 1:40 pm
Sydney: 2:00 - 2:40 pm
New Zealand: 4:00 – 4:40pm

This talk will be given in-person during the GSA Awards session and also live-streamed. Feel free to share the link with colleagues not attending GSA 2025!

Register here: https://tinyurl.com/5f8ydfv3

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Genetics Society of Thailand
iGF

Structural variations drive genome evolution and divergence in *Eucalyptus* trees

GSA Awards Session – Alan Wilton Award for an early career researcher

Zixiong Zhuang[1], Scott Ferguson[1], Justin Borevitz[1], **Ashley Jones**[1]

[1]Research School of Biology, Australian National University, Canberra

Abstract: *Eucalyptus* trees are widespread across Australia, providing habitat to a rich biodiversity of marsupials, birds and insects, being key foundation species in natural ecosystems. Using long-read sequencing, we investigated how *Eucalyptus* genome architecture has changed over time to unveil their adaption to the environment. We investigated a key species, *E. viminalis*, which is experiencing high mortality and dieback in NSW. Long-read sequencing of 50 wild *E. viminalis* trees across three populations identified thousands of genome structural variations (SVs) segregating within the populations, potentially influencing adaptation. These SVs had influenced genes in multiple ways, including deleting gene exons, disrupting gene order, translocation of genes, and complete deletion of genes. This included phenotypically important genes such as the terpene synthase gene family. We further extended this work by assembling the genomes of 33 diverse *Eucalyptus* species, which span millions of years of evolution. We observed a dramatic increase in genome SVs as species diverged, suggesting these play a key role in early architectural divergence. Further divergence led to mutations obscuring rearrangements and a loss of syntenic regions (gene order conservation). Insertions, deletions, duplications, inversions and translocations were observed as major contributors to genome structural divergence. Our pioneering research on SVs in *Eucalyptus* provides insights into understanding their role in genome evolution and adaptive traits for this ecologically important genus.

Biography: Ash is a postdoctoral fellow at the Australian National University conducting genome research on a wide variety of Australian native plants, and invasive fungi that threaten plant biodiversity. He has been developing innovative approaches to apply Oxford Nanopore sequencing to drive scientific breakthroughs in genome evolution of trees and understanding plant-pathogen interactions. His current research investigates genome structural rearrangements within *Eucalyptus* trees to unveil critical insights into adaptive traits, novel phenotypes, and evolutionary mechanisms. His collaboration with government agencies has enhanced biosecurity practices and conservation outcomes, while partnerships with public health organisations have contributed to addressing pressing issues, including the COVID-19 pandemic. Ash's innovative nature and expertise has garnered him the nickname "DNA Whisperer", and he continues to push the boundaries of plant and fungal genomics.

Omics and molecular pipelines for precision medicine for and by Māori

Indigenous Early Career Leaders Session

Hannah Darroch[1], Oluwatobi Eboda[1], Calvin Young[1], Christian Mosimann[2], Robert Lalonde[2], Caleb Calhoun[1], Emily Morice[1], Daniel Lyth[1], Clare Adams[1], Alastair Lamont[1], Ben Rangihuna[1], Elizabeth Ledgerwood[1], Alan Davidson[3], Nicola Dalbeth[3], Rinki Murphy[3], Tristan Pascart[4], Janak de Zoysa[3], Lisa Stamp[4], Tony Merriman[5], Julia Horsfield[1], Phil Wilcox[1], **Megan Leask**[1]

[1]University of Otago, Dunedin, New Zealand, [2]University of Colorado, Aurora, Colorado, USA, [3]University of Auckland, Auckland, New Zealand, [4]University of Otago, Christchurch, New Zealand, [5]University of Alabama at Birmingham, Birmingham, Alabama, USA

Abstract: Precision medicine that uses genetic signatures of cardiometabolic disease is poised to revolutionise healthcare. However, the genetic studies driving these advances lack Māori and Pacific data, threatening to exacerbate the health inequities these populations already face. We have begun identifying genetic signals that are unique to these populations and influence metabolic traits. Included in our analyses we have metabolite and expression data so we can assign function to the non-coding genetic signals we identify. To assay the functional effect of these non-coding variants we have pioneered an alternative approach to the usual cell-based assays by testing enhancer activity in vivo using zebrafish. This allows us to test the function and tissue-specificity of DNA variants in regulatory/enhancer elements in the full complement of cell types that exist in vivo. Our showcase T2D-associated variant near JAZF1 drives gene expression with tissue specificity in the brain and the kidney. Using CRISPR/Cas9 for JAZF1 in zebrafish we have begun to unravel the role that JAZF1 plays in these tissues that leads to metabolic dysfunction. We can also apply the same molecular pipeline to various other non-coding variants that we identify in our analyses while training the next generation of Māori researchers!

Biography: Megan's research focuses on understanding the genetics of complex disease, with particular expertise in gout, chronic kidney disease, and serum urate regulation. I am also internationally recognized for my work in Indigenous genomics, with a strong commitment to addressing the underrepresentation of Māori and Pacific peoples in genetic research. I use bioinformatics, zebrafish and cell-based assays to explore the function of non-coding and coding genetic variants implicated in complex disease, aiming to identify clinically relevant genetic factors unique to Māori and Pacific populations. My long-term research goals are to reduce health disparities by advancing precision medicine tailored to these communities and increasing Māori capability and capacity in precision genomics.

Environmental DNA is Indigenous DNA - considerations for ancient and contemporary metagenomics in Australia

Indigenous Early Career Leaders Session

Dawn Lewis[1,2,3], Vilma Pérez[1,3,4], Bastien Llamas[1,3,4]

[1]Australian Centre for Ancient DNA, University of Adelaide, Australia, [2]Summer Internship for Indigenous Peoples in Genomics (SING Australia), Australia, [3]ARC Centre of Excellence for Australian Biodiversity and Heritage (CABAH), University of Adelaide, Australia, [4]ARC Centre of Excellence for Indigenous and Environmental Histories and Futures (CIEHF), Australian National University, Australia

Abstract: Environmental DNA is increasingly being utilised in metagenomic studies for conservation and archaeological research. In particular, the application of sedimentary ancient DNA (sedaDNA) has enormous potential to unlock a unique temporal archive of environmental and ecological change into the past and even track human presence where archaeological remains are lacking. The use, storage and sovereignty of environmental data, however, has very limited oversight outside anthropocentric research studies. From an Indigenous perspective, this could lead to neo-colonial harm and mistrust. Here, we consider sedaDNA, and environmental DNA more broadly, through the lens of Aboriginal Peoples' deep connection with *Country*, as an inseparable embodiment of the seas, skies, waters, lands, and spirits of Indigenous Australia. Because sedaDNA touches on all aspects of *Country*, including human and non-human kin, its use requires approaches that go beyond consultation and/or engagement with Indigenous stakeholders. We argue that co-designed research is the future of these collaborations—with Indigenous-led research projects being the ideal goal. We offer insights into the future of productive collaborations between Indigenous stakeholders and researchers. We address the potential pitfalls of proposing—or often imposing—new scientific techniques, such as sedaDNA, without comprehensive engagement with Traditional Knowledge holders and how two-way learnings can improve study design and results interpretation. Through research case studies at Aboriginal archaeological sites in Australia, we explore the benefits of using sedaDNA in collaboration with Traditional Knowledge holders to strengthen results interpretation, as well as the lessons learned throughout this process. Further, we highlight the need for upskilling Indigenous communities in academic sciences and the importance of building capacity for Indigenous scientists, while also addressing the challenges involved, to ensure a truly holistic understanding of ancient and contemporary environmental research.

Biography: Dawn is a Woolwonga (Aboriginal) woman and great-grandaughter of "Shotgun" Nellie Flynn of Rum Jungle in the Northern Territory of Australia. She is currently completing her PhD in Applied Indigenous Genomics at the Australian Centre for Ancient DNA (University of Adelaide) where she undertakes human repatriation and archaeological metagenomic research within Indigenous community-lead projects. Dawn previously completed her MSc. at the University of Oxford and is currently a joint coordinator for SING Australia.

A Doctorate in Kaupapa Māori Research and Biomedicine: An Unexpected Journey

Indigenous Early Career Leaders Session

Jordon S. Lima[1]

[1]*Te Aho Matatū (Cancer Genetics Laboratory), Department of Biochemistry, Ōtākou Whakaihu Waka (University of Otago), Ōtepoti (Dunedin), Aotearoa New Zealand*

Abstract: With no intention to pursue a career in academia, I ended up writing a doctorate that ultimately challenged the colonial narrative in biomedical sciences that typically represented my people and those of Indigenous populations globally. I was hooked by the chance to contribute meaningfulness to the clinical protocols for circulating tumour DNA (ctDNA) testing; a blood-based cancer screening and surveillance tool that could be used to improve access to and engagement with cancer screening, particularly for the Māori, remote, and rural communities in Te Tairāwhiti that I call home. I used a mix methods approach to determine community priorities for an analysis of the utility and social acceptability of ctDNA testing and established long-term goals promoting longevity beyond the scope of my doctoral research.

In this presentation, I will discuss the key findings and experiences I had throughout this tumultuous journey by (1) defining the kaupapa Māori and translational biomedical research methodologies that underpinned my research, (2) describing the methods by which these two methodologies were combined to address a research question relevant to the priorities of the communities involved, and (3) summarising how these can be used as a guide for the next generation of kaupapa Māori biomedical researchers.

Biography: Ko Hikurangi me Titirangi ngā maunga.
Ko Waiapu me Ūawanuiaruamatua ngā awa.
He uri ahau nā Ngāti Porou, nā Te Aitanga-a-Hauiti, nā Ngā Puhi hoki.
Ko Jordon Lima tōku ingoa.
My PhD research focus was to work with my communities across Te Tairāwhiti to explore the regional tikanga and kawa for circulating tumour DNA (ctDNA) testing. My vision is to (re)-design innovative laboratory workflows, clinical protocols, and science outreach resources for biomedical technologies that meet the needs and priorities of Māori, remote, and rural communities to improve the experiences of cancer patients, their whānau, and their cancer care providers.

How the Holstein got its spots

Matt D. Littlejohn [1,2], R. Spelman [1], Y. Yamanaka [3], R. Mort [4], S. Jivanji[1,2]

[1]Livestock Improvement Corporation; Newstead, Hamilton, New Zealand, [2]School of Agriculture and Environment, Massey University; Palmerston North, New Zealand [3]McGill Integrated Core of Animal Modeling, McGill University; Montreal, Canada [4]School of Biomedical and Life Sciences, Lancaster University; Lancaster, UK

Abstract: Coat patterning traits represent some of the oldest selected phenotypes in domestic animals. Many of these traits have come to define modern breeds, with the white-spotted coats of Holstein-Friesians being one of the most striking examples in cattle. Unlike the majority of other hallmark coat patterns, however, white spotting represents one of the last coat pattern traits yet to be characterized at the molecular level. Here, we detail two major-effect variants responsible for this trait, comprising intronic and long-distance acting regulatory variants. We demonstrate causality through gene edited cell and animal models, and show these variants are likely responsible for patterning traits in other bovine breeds. These effects include interactions with other patterning loci, including speckles, 'black socks', and reversion of the 'white face' pattern emblematic of Hereford cattle.

Biography: Matt Littlejohn is a geneticist who applies a range of bioinformatic, molecular, and statistical genetics techniques to investigate trait variation in animals. Matt's work focusses on identification of causative variation, and he has discovered major-effect variants in cattle, sheep, and dogs. Matt leads the Variant Discovery Team at LIC, and has a joint appointment with Massey University where he is Co-director of the AL Rae Centre for Genetics & Breeding.

Moving at breakneck speed – the rapidly expanding opportunities of genomic precision medicine for New Zealand

Cristin G. Print[1]

[1]*Department of Molecular Medicine and Pathology, University of Auckland*

Abstract: When I qualified in medicine in 1989 I was fascinated by genes and genomes, however at that time the fields of genomics and computational science had relatively little to offer the majority of patients. Fast forward to today, the advances in what we can achieve using genomic technologies and AI in medical care and medical research are astounding, with technological developments still accelerating. Cris' keynote will discuss current examples of genomic precision medicine at various stages of development, from research to the clinic. He will look at both the opportunities and risks currently facing NZ in this field, including what genomic precision medicine may mean for equity in health outcomes. Cris will end by raising for discussion several future scenarios for genomic precision medicine in New Zealand, and how we may be able to shape where we land.

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NZ-relevant genetic variants in motor neuron disease and their therapeutic approaches

Precision Medicine Session

Miran Mrkela[1,2], Miriam Rodrigues[3,7], Serey Naidoo[1,2], David Gordon[1,2], May Aung-Htut[3], Rita Mejzini[3], Steve Wilton[3], Anthony Akkari[3], Marv Caruthers[4], Jannai McCracken[1,2], Jules Devaux[1,2], Siobhan Kirk[1,2], Chitra Vinnakota[1,2], Christina Buchanan[5], Dympna Mulroy[5], Harry Fraser[5], Hannah Wyatt[6], Kylie Drake[6], Elsa Parker[6], Howard Potter[6], Kelly Williams[7], Marina Kennerson[8], Nicole Edwards[1,2], Anjali Henders[9], Jessie Jacobsen[1,2], Igor Stevanovski[10], Ira Deveson[10], Klaus Lehnert[1,2], James Cleland[11], Richard Roxburgh[2,3,12], **Emma Scotter**[1,2]

[1]School of Biological Sciences, University of Auckland, Auckland, New Zealand [2]Centre for Brain Research, University of Auckland, Auckland, New Zealand, [3]Centre for Molecular Medicine and Innovative Therapeutics, Health Futures Institute, Murdoch University, Murdoch, WA, Australia [4]Department of Biochemistry, University of Colorado, Boulder, Colorado, USA, [5]Neurology Department, Auckland City Hospital, Auckland, New Zealand, [6]Canterbury Health Laboratories, Christchurch, New Zealand, [7]Macquarie University Motor Neuron Disease Research Centre, Faculty of Medicine, Health and Human Sciences, Macquarie University, Sydney, NSW, Australia, [8]Molecular Medicine Laboratory and Neurology Department, Concord Repatriation General Hospital, Concord, New South Wales, Australia, [9]Queensland Brain Institute, The University of Queensland, Brisbane, Queensland, Australia, [10]Genomics and Inherited Disease Program, Garvan Institute of Medical Research, Sydney, New South Wales, Australia, [11]Tauranga Hospital, New Zealand Te Whatu Ora Hauora a Toi, Bay of Plenty, New Zealand, [12]Neurogenetic Clinic, School of Medicine, Faculty of Medical and Health Sciences, University of Auckland, Auckland, New Zealand

Abstract: New Zealand has one of the highest mortality and incidence rates of motor neuron disease (MND) globally. Our national genetics study indicates New Zealanders with familial MND carry pathogenic variants that are common in other populations (*C9orf72* repeat expansions, *SOD1* missense mutations) or rarer variants of less certain pathogenic significance. A diagnostic gene panel (Blueprint) identified a variant of uncertain significance at a 5' splice site in *DCTN1*, while whole-genome sequencing identified a 4-bp insertion in *NEK1* and a repeat expansion in *NOTCH2NLC*. RNA sequencing of patient fibroblasts indicated that the *DCTN1* variant causes partial exclusion of an exon crucial for *DCTN1* function, while an *in vitro* reporter assay showed the *NEK1* insertion causes a frameshift and premature

truncation, with heterozygous loss-of-function a known pathomechanism. The *NOTCH2NLC* repeat expansion, confirmed by long-read Oxford nanopore sequencing, was causative not of MND but of the phenocopy disorder neuronal intranuclear inclusion disease, which appears to disproportionately affect East Asian and Māori people. Our programme of antisense oligonucleotide and CRISPR-suppression strategies, successfully applied to a rare variant in *UBQLN2*, offers a precision approach to model these variants for further pathogenicity classification and to target them for therapy.

Biography: Associate Professor Emma Scotter is the head of the Motor Neuron Disease (MND) Research Lab based at the School of Biological Sciences, University of Auckland and affiliated with the Centre for Brain Research. Her team runs a national study of the genetics of MND, currently focused on familial MND. Her team investigates the consequences of, and potential interventions for, identified variants using neuropathology, IPSC and other cell models, transcriptomics, and molecular medicines such as antisense oligonucleotides and CRISPR-Cas. Associate Professor Scotter was made a member of the NZ order of merit (MNZM) in 2024 for services to MND research.

Genomics and discrimination in New Zealand health and life insurance

Precision Medicine Session

Andrew N. Shelling[1]

[1]*Centre for Cancer Research/Te Aka Mātauranga Matepukupuku and Department of Obstetrics, Gynaecology and Reproductive Sciences*

Abstract: The use of genomics offers substantial benefits to society by revolutionising approaches to healthcare and personalised medicine. It enables early detection of genetic predispositions to various diseases, allowing for proactive and tailored treatment plans, access to clinical trials and improved health outcomes. Currently, the insurance industry in New Zealand, are legally allowed to ask for and use applicants' genetic test results in underwriting decision, which is genomic discrimination. There is considerable evidence, both nationally and internationally, that individuals frequently decline medical genetic testing or participation in genomic research studies because of fears of genomic discrimination. By failing to address genomic discrimination in insurance, New Zealand is falling behind a host of countries against which it would normally benchmark itself with. As a result, a group of over 100 New Zealand clinicians, academics, scientists, lawyers, and representatives from Māori, Pacifica, medical charities, privacy, patient groups and individuals have formed a collaborative alliance, known as "Against Genomic Discrimination Aoteoroa", or AGenDA. AGenDA has recently made written and oral submissions to the Contracts of Insurance Bill to address this critical issue.

Biography: Professor Andrew Shelling is Director of Research for the Centre for Cancer Research/Te Aka Mātauranga Matepukupuku and Department of Obstetrics, Gynaecology and Reproductive Sciences. His research is primarily interested in understanding the molecular changes that occur during the development of genetic disorders, focusing on breast and gynaecological cancer, and reproductive disorders.

Gene regulatory mechanisms in control of plant architecture

Miloš Tanurdžić[1]

[1]*School of Chemistry and Molecular Biosciences, The University of Queensland, St. Lucia, QLD 4072, Australia*

Abstract: The exceptional range of plant phenotypic and developmental plasticity is best seen in the unique form and shape each plant takes: its potential is genetic, but its ultimate phenotype is adapted through interactions with the environment. A great example of this plasticity is shown by the unique architecture of plant shoots, from the branchless maize or wheat cultivars to intricately and uniquely branched trees. Axillary buds that form in axils of leaves determine the branching potential of a plant, but it is the dormancy status of each bud that determines the actual shoot architecture. We have been studying gene regulatory processes in control of initiation of axillary bud dormancy in the model plant Arabidopsis as well as in perennial tree crops. Using transcriptomics, epigenomics and systems biology tools, we have identified early transcriptomic changes in response to dormancy-inducing signals and some of the key components of the bud dormancy gene regulatory networks, including regulation of chromatin accessibility and histone modifications. We discovered chromatin remodellers, epigenetic modifiers and transitive RNAi components as some of the early targets of strigolactone signaling and dormancy initiation and maintenance, which prompted us to look at changes to chromatin accessibility and chromatin modifications in response to the dormancy-inducing plant hormone strigolactone in axillary buds as well as in protoplasts. We identified hundreds of putative cis-regulatory components and several novel trans-acting transcription factors of the dormancy gene regulatory network and discovered molecular pathways including hormone metabolism, cell cycle regulation, RNAi, translation, proteostasis and autophagy pathways that underly the induction and maintenance of cellular stasis during bud dormancy. Focusing on the early epigenomic reprograming using CUT&Tag in wild type and strigolactone-deficient buds we identified specific changes in the distribution of H3K4me3, H3K27me3 and H3K27ac marks correlated with strigolactone-induced transcriptional changes. Additionally, we identified branching phenotypes in Arabidopsis mutants of several strigolactone-regulated histone modifiers, including the H3K27 demethylase JMJ30. Together, these results show that changes in chromatin states and accessibility at defined genomic locations act to control plant architecture through the regulation of axillary bud dormancy Similar approaches in tree crops allowed us to identify evolutionarily conserved components of bud dormancy gene regulatory networks and their integration with flowering time gene regulatory networks.

Biography: After a misguided adventure in medicine, Miloš got his first degree in Biology with a minor in Endocrinology in Serbia before he moved to the US for his doctoral training in Genetics at Purdue University (Thesis work in plant comparative

and functional genomics). In 2004, he moved to Cold Spring Harbor Laboratory where he did postdoctoral work on plant epigenomics with Rob Martienssen. In 2012 Miloš moved from NY to Brisbane and started his first independent position at UQ, first with the School of Biological Sciences and now with the School of Chemistry and Molecular Biosciences. His research interests are many, and currently focus on the molecular genetic mechanisms responsible for the fascinating phenotypic plasticity in plants. The research efforts in the Tanurdžić lab are focused on harnessing transformative genomics technology to understand the genetics of plant development, and to discover regulatory mechanisms coordinating plant growth and development in a variety of plant species, from the model plant organism Arabidopsis to grain and horticultural crops like wheat, mango, avocado and macadamia.

Genetic Control of Flowering and Sex Determination in Kiwifruit

Erika Varkonyi-Gasic[1]

[1]*Plant and Food Research, Auckland, New Zealand*

Abstract: Flower development in fruit trees and vines is controlled by complex gene regulatory networks, and understanding these genetic mechanisms is essential for improving fruit yield and accelerating the development of new cultivars. Central to the regulation of flowering and reproductive maturity are PEBP (phosphatidylethanolamine-binding protein) genes including *FLOWERING LOCUS T* (*FT*) and *CENTRORADIALIS* (*CEN*). In *Actinidia chinensis* (kiwifruit), targeted editing of *CEN* genes leads to premature flowering and reduced plant size, significantly shortening generation time and enabling faster crop improvement. Modulating the balance between specific FT and CEN further impacts plant growth cycles and the timing of flowering, demonstrating the role of the PEBP family in shaping plant architecture and seasonal development. In addition, our research explores the genetic basis of sex determination in kiwifruit. We reveal that the *SHY GIRL* (*SyGl*) gene plays a dual role in determining both sex identity and sexually dimorphic traits. Through its pleiotropic effects, SyGl promotes more prolific flowering in male plants compared to females and hermaphrodites. This facilitates transposon-mediated relocation of male-determining chromosomal loci across different *Actinidia* species, offering new insights into the dynamic evolution of plant sex chromosomes and highlighting the genetic flexibility underlying dioecy in plants.

Biography: Dr Erika Varkonyi-Gasic is a Science Team Leader at Plant & Food Research, where she directs cutting-edge work in plant developmental biology, specializing in small RNA and flowering control. Her work has informed crop improvement and climate resilience strategies, especially in kiwifruit, apple, and pear.

Exploring New Zealand's Virosphere

GSA Awards Session – DG Catcheside Award for the top doctoral student

Stephanie J. Waller[1], Jemma L. Geoghegan [1]

[1]*Department of Microbiology and Immunology, University of Otago, Dunedin, New Zealand*

Abstract: The emergence of new viruses often is the result of viral host-jumping, yet we know little about the ecological and evolutionary forces driving this process. Advances in metatranscriptomics have revolutionised virus discovery, but past research has focused heavily on species of medical or economic concern, leaving vast portions of the virosphere unexplored. To truly understand viral diversity and emergence, we must look beyond traditional hosts. New Zealand's native species—isolated for millions of years—offer a rare opportunity to study viral evolution in a unique setting. Nevertheless, almost nothing is known about the viruses harboured by New Zealand's fauna. This work explores the viromes of tuatara, bats, eels, skinks, and geckos, uncovering over 130 viruses, including highly divergent ones representing novel viral families. These findings reveal how location, host specificity, adaptive radiation, and New Zealand's geological history shape viral communities. None of the detected viruses were linked to disease, reinforcing the idea that most viruses exist harmlessly within their hosts. This work provides a crucial baseline for tracking virome changes over time and lays the foundation for future studies, deepening our understanding of viral evolution and emergence on a global scale.

Biography: Dr. Stephanie Waller is a postdoctoral researcher at the University of Otago, specializing in viral evolution and biodiversity. Her research focuses on uncovering hidden viral diversity using metatranscriptomics, particularly in New Zealand's unique wildlife. She now works on avian influenza research, investigating viral evolution and transmission dynamics. Her work aims to enhance our understanding of viral emergence, host-virus interactions, and the broader virosphere.

Ethics and Applications of Molecular Biology in Indigenous Contexts: A case study of a collaborative deep phenotyping research project within a rural Māori community

Indigenous Early Career Leaders Session

Conor Watene O'Sullivan[1]

[1]*The Moko Foundation*

Abstract: This presentation details the journey of a Māori health organisation (The Moko Foundation) in a ground-breaking deep phenotyping genomic research project conducted in rural Northland, New Zealand, highlighting the fruitful collaboration between a flax roots Māori organization and multi-disciplinary world-class research teams. The project aimed to harness the synergies between Kaupapa Māori research methodologies, community based participatory research and advanced genomic science to uncover novel insights into health and disease and build health resilience in an indigenous community. This project acted as a gateway for the Moko Foundation to capitalise further on the range of opportunities within the system of biomolecular research.

Conor will share how community engagement and ethical practices were central to the project, aiming to build trust and mutual respect. The project highlighted ongoing gaps in how research groups respond to Māori needs, pointing to areas for improvement. A key outcome was the educational impact on Māori communities, especially in encouraging rangatahi into science. The project also established a model for two-way capability sharing—boosting scientific literacy in communities while enhancing cultural competency among researchers through Kaupapa Māori approaches.

Biography: Conor Watene O'Sullivan (Te Rarawa, Ngāti Maru, Te Arawa) was raised in Te Hiku o te Ika and educated through Kura Kaupapa Māori before completing a Bachelor of Health Science at the University of Auckland. With a background in health science, he has spent the past eight years serving his community through a range of kaupapa Māori health initiatives under the Moko Foundation. Playing a major role in the Moko Foundation's partnership with the Maurice Wilkins Centre—combining cutting-edge biomedical science with kaupapa Māori values—Conor now serves as the Centre's Kaiārahi Māori. In this role, he is leading the implementation of a much-needed Māori Strategic Framework to enhance the responsiveness of research to Māori needs—an essential step in transforming Aotearoa New Zealand's research landscape.

Development of genomic resources for Māori health

Phillip L. Wilcox[1], Stephen Robertson[1], Benjamin Halliday[1], David Markie[1], Ben Iwikau Te Aika[1], Cris Print[2], Claire E Rye[2], Andrew Sporle[2], Huti Puketapu-Watson[3], Helen Wihongi[4,5], Donia Macartney-Coxson[6], Joep de Ligt[6], Polona Le Quesne Stabej[2], Ben Curran[2], Nick Jones[2], Jun Huh[2] , Elizabeth Goodin[1], Alastair Lamont[1], Kimiora Henare[2], Irene Kereama-Royal[7], Anna Rolleston[8], Jennie Harre-Hindmarsh[3], Wyeth Wasserman[9], Karen Miga[10]

[1]University of Otago, Dunedin, New Zealand, [2]University of Auckland, Auckland, New Zealand, [3]Ngāti Porou Oranga, Gisborne, Aotearoa New Zealand, [4]Te Whatu Ora Waitematā, New Zealand, [5]Te Whatu Ora Te Toka Tumai Auckland, New Zealand, [6]Institute of Environmental Science and Research. Porirua, Wellington, [7]Ira Tātai Whakeke Charitable Trust, [8]The Centre for Health, Tauranga, New Zealand, [9]University of British Columbia, Vancouver, Canada, [10]University of California Santa Cruz

Abstract: Over the past five years multiple bespoke genomic resources for Māori health in Aotearoa have been developed. These resources have applications in precision medicine. They have been developed using mātauranga Māori and tikanga-based research methodologies, and have been co-led and overseen by multiple Māori with backgrounds in health and/or community leadership. These resources include: a variome database ('He Kākano'), consisting of summary level information on gene variant frequencies; a preliminary pangenome; and a computational platform ('Rakeiora') for accessing and analysing genomic and whakapapa (genealogical) data, and health information. In this talk I will provide brief descriptions of these resources, the tikanga Māori-based study design methods used to construct them and some of the applications that they have or could be used for.

Biography: Associate Professor Phillip Wilcox's Māori tribal affiliations are Ngāti Rakaipaaka, Ngāti Kahungunu ki te Wairoa, Rongomaiwahine and Te Aitanga a Mahaki. He is based in the University of Otago's Department of Mathematics and Statistics, and has experience in applied genomics and statistical genetics, as well as engagement with indigenous communities regarding gene technologies. He is also an Affiliate of the University of Otago's Bioethics Centre, and is the current convenor of MapNet, a NZ-wide collective of gene mapping scientists, and led the Virtual Institute for Statistical Genetics from 2008 to 2013. He is also a Deputy Director of the Maurice Wilkins Centre. For over 20 years he has worked in the interface of genetic sciences and Te Ao Māori, and co-leads four genomics-based projects focussing on Māori health. A/Prof Wilcox has also worked on genetics of plant species (particularly forest trees) and Māori health. He also co-initiated the Summer Internship of iNdigenous peoples in Genomics Aotearoa (SING-Aotearoa), and was a member of the Health Research Council of New Zealand's Ethics Committee which oversees New Zealand's institutional and regional ethics committees.

Concurrent session talks

Identification of genetic loci affecting survival in rainbow trout (*Oncorhynchus mykiss*) infected with VHS

Seyed Eisa Abdollahi-Mousavi[1,2], Iraj Hashemzadeh Segherloo[2], Amaal Gh. Yasser[4], Louis Bernatchez[3]

[1]Khorramshahr University of Marine Science and Technology, Khorramshahr, Iran, [2]Shahrekord University · Fisheries and Environmental Sciences, Shahrecord, Iran, [3]University Laval · Department of Biology, [4]Griffith University · Australian River Institute

In this study VHS infected rainbow trout *Oncorhynchus mykiss* were kept under consistent environmental conditions to minimize environmental variance in a commercial fish farm to assess genetic differences between VHS sensitive and resistant individuals. To confirm VHS infection, along with clinical symptoms, real-time PCR was also used. To analyze genetic differences between disease susceptible and resistant individuals next-generation-sequencing was used. Data pertaining to 10124 loci were produced and compared between resistant and sensitive fish. In 37 loci an allele frequency difference of ± 50 percent or more was detected between resistant and sensitive fish groups. The majority of genes related to these loci bear roles in immunity system. Overall, a fairly clear clustering pattern was observed between resistant and sensitive fish groups in principal components analysis (PCA). As in this study environmental conditions during all stages of fish rearing were similar for all individuals, it is probable that the different resistance of fish to VHS had a genetic basis and it may be possible to use these data in marker assisted selection (MSA) programs to produce VHS resistant populations of rainbow trout.

Depression-linked plasma protein biomarkers: Insights from differential abundance analysis and Mendelian randomization

Endeshaw Abebe[1,2], Anwar Mulugeta[1,3], Iqbal Madakkattel[1], David Stacey[1], Elina Hyppönen[1]

[1]Australian Centre for Precision Health, Clinical and Health Sciences, University of South Australia, Adelaide, South Australia, Australia, [2]Department of Biomedical

Sciences, College of Health Sciences, Debre Tabor University, Debre Tabor, Ethiopia, [3]Department of Pharmacology, College of Health Sciences, Addis Ababa University, Addis Ababa, Ethiopia

Plasma proteins are potential biomarkers and drug targets for depression, yet evidence linking them to the disorder is scarce. To identify proteins associated with depression, we conducted differential protein abundance analysis (DPAA) on 2,920 plasma proteins from over 48,000 UK Biobank participants. For DPAA-identified proteins, we performed enrichment analysis and protein-protein interaction analysis, followed by Mendelian randomization (MR) using genetic summary data for proteins (N=34,557) and depression (166,773 cases, 507,679 controls), and assessed potential drug targets. Through DPAA, we identified 22 proteins associated with depression (Padjusted < 1.71×10^{-5}), with risk changes of 11%-27% per SD difference in protein levels. Most proteins were linked to increased risk, except for LRRN1, CNTN5, and ADAMTS8, which were protective. Many of these proteins were enriched in immune and inflammation pathways, underscoring their role in inflammation-driven depression. MR analysis provided strong genetic evidence for BTN3A2 and suggestive evidence for LGALS4 and TNFRSF10B as causal candidates for depression ($p<0.05$), albeit with modest effect sizes (3%-11%, per SD). BTN3A2 and LGALS4 exhibited consistent differential expression in depression, while TNFRSF10B displayed a discordant direction between DPAA and MR findings. Our findings highlight drug targets with potential for novel and repurposed therapies for depression.

From Ice Age to Isolation: Historical Demography and Inbreeding Depression in New Zealand's Endemic Hector's and Māui Dolphins

Sebastian Alvarez-Costes[1], Scott C. Baker[2], Rochelle Constantine[3], Emma L. Carroll[3], Isabella M. Reeves[4], Ludovic Dutoit[5], Sara Ferreira [1], Dorothea Heimeier[3], Neil J. Gemmell[1], Joanne Gillum[1], Rebecca M. Hamner[2], Will Rayment[6], Wendi Roe[7], Ben Te Aikā[8], Alana Alexander[1]

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Hector's and Māui dolphins, endemic to Aotearoa, New Zealand, are small coastal dolphins facing significant anthropogenic threats. The IUCN lists the ~15,000 Hector's dolphins (South Island) as endangered, while the Māui dolphin (North Island), with only ~54 individuals, is critically endangered. We assessed the demographic history and population structure of both subspecies using whole genome data from 48 individuals. Paleoceanographic trends have shaped contemporary admixture patterns and population structure, with the closure of the Cook Strait separating the Māui and Hector's dolphins during the LGM, and with productive regions (East/West Coast) acting as sources for less favourable habitats (South Coast). Māui dolphins diverged from Hector's dolphins ~12–16 kya and exhibit reduced genetic diversity, inbreeding depression, and higher genetic load, confirming the genetic decline in the Māui dolphin, which could severely impact its survival given their critically low population size. Similarly, the South Coast Hector's population shows elevated inbreeding compared to the larger, more diverse East and West Coast populations. Admixed individuals at population edges display higher genetic diversity, emphasizing the importance of protecting migratory corridors. Conservation strategies must prioritize migratory corridors while assessing adaptive variation and deleterious alleles in local populations to ensure the recovery of these subspecies.

Missing or mis-telling the story? Trade-offs for reduced representation compared to whole genome resequencing

Kamolphat Atsawawaranunt[1], Katarina C. Stuart[1,2], Annabel Whibley[1,3], Kyle M. Ewart[4,5], Richard E. Major[5], Rebecca N. Johnson[5,6], Anna W. Santure[1]

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Researchers must navigate several trade-offs when deciding which population sequencing method to use. The decision between reduced representation approaches and whole genome resequencing (WGS) impacts marker density, sequencing depth, and multiplexing capabilities, which will in turn affect the power to accurately characterize certain genomic features, such as regions of the genome exhibiting signals of selection. To investigate the effect of sequencing method on the detection of putatively adaptive regions, we compared selection scan analyses of a

set of restriction site-associated DNA sequencing (RADseq) datasets for the common myna (*Acridotheres tristis*) with a smaller WGS dataset. Although selection scan statistics were found to be correlated between datasets, no common outliers were found. We compared allele frequencies and genotypes across datasets and found that discordances were due to missing markers, different individuals sampled, or erroneous genotype calls. Most importantly, two regions with strong signals of selection were missed in the lower-density dataset, and population-specific allelic dropout created false signals of selection in the RADseq datasets. Our results highlight the advantages of WGS over RADseq when used for selection scan analyses, especially on highly structured populations such as those observed in invasive or endangered species.

Unravelling the Genomic Landscape of Wide Crosses in Actinidia Species

Sarah Bailey[1], Chen Wu[1], Ting-Hsuan Chen[2], Astra Heywood[2], Ignacio Carvajal[1], Elena Hilario[1], Usman Rashid[1], Amardeep Nath[3], Susan Thomson[2]

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One way to increase genetic diversity and resilience within a breeding programme is through introgression with wild relatives or species. Hybridization between diverse plant species can be difficult due to hybrid incompatibility which can result in seed abnormalities, reduced fitness and sterility. We are investigating wide hybrid crosses between tetraploids *Actinidia chinensis* and *Actinidia melanandra*, belonging to the chinensis and distant arguta clades respectively. The resulting F1 hybrid progeny display signs of hybrid incompatibility including seed abnormalities and low vigour. Despite having good macro-synteny, clear evolutionary events have contributed to the speciation of the chinensis and arguta clades. One example is the male sex-determining region (SDR), which is present on Chromosome 25 in *A. chinensis* but found on Chromosome 3 in *A. arguta*[1]. Using a trio-binning method, we assembled a phased genome of a male F1 hybrid. We have explored the repeat content and CpG methylation of Chromosome 3, which also contains the SDR of *A. melanandra*. A deeper understanding of the differences between chinensis and arguta clades may provide insights for improving the efficiency and success of hybrid crosses between Actinidia clades.

[1] Akagi, T et al. 2023. Nature Plants, 9:393-402.

From Fragments to Futures: Ultra-Long Reads Empowering Invertebrate Genomics in New Zealand

Marc Bailie[1], Nicolás Zúñiga-Soto[2 3], Leo Zamora[4], Josh Gilligan[1], Natalí Delorme[4], Jackie Stephens[5], Charles Eason[6 7], Miriana Stephens[5], Nathan Kenny[1]

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Ultra-long read sequencing has revolutionised genomics by simplifying the analysis of large DNA fragments, allowing researchers to resolve complex genomic regions and detect structural variants with high accuracy. Technologies like Oxford Nanopore can now produce reads over two megabases long, vastly improving genome assembly continuity, especially across repetitive or rearranged regions.

Applying these methods to non-model invertebrates reveals genomic diversity often hidden from short-read approaches. High-quality assemblies uncover novel genes, structural variation, and lineage-specific adaptations, key to understanding evolutionary and ecological dynamics.

In Aotearoa New Zealand, this technology is advancing aquaculture by decoding the genomes of endemic species such as *Aulacomya maoriana* (Kopakopa) and *Panopea zelandica* (geoduck). These insights will inform sustainable breeding, disease resilience, and conservation. The work supports kaitiakitanga, the Māori principle of guardianship, by providing a genomic foundation for protecting taonga (treasured) species.

Our journey to achieving ultra-long read sequencing reflects a commitment to integrating cutting-edge science with mātauranga and tikanga Māori (Māori knowledge and practices). In partnership with enterprises like Wakatū Incorporation, this approach ensures New Zealand's aquaculture sector can thrive while honouring cultural values and safeguarding natural resources for future generations

A unifying framework for thermosensing in plants

Sureshkumar Balasubramanian[1]

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Increasing temperatures coupled with a growing population present a significant challenge for global food security. Plants are highly sensitive to temperature and even 1ºC increase is predicted to have a significant negative impact on agricultural productivity. Therefore, there is a need to understand how plants sense and respond to changes in ambient growth temperature. We have discovered a key role for POWERDRESS (PWR), which acts in a complex with HISTONE DEACETYLASE 9 to confer thermal responses. Mutations in PWR leads to reduced temeprature sensitivity. I will present the results of a genetic suppressor screen, which reveals additional players governing thermal responses in plants and suggests that temperature cues are perhaps integrated into pre-existing signalling cascades and this distinguishes thermosensing from other classing sensor-response relationship mechanisms. I will present our current thoughts and an overview of the field.

Inspiring the next generation of geneticists - how hard could it be?

Simon W. Baxter[1], Hayley Bugeja[1]

[1]*School of BioSciences, University of Melbourne, Melbourne, Australia*

Genetics is core topic of biology electives in the final years of high school. So, how much content overlap should there be between high school and first year biology at university when it comes to genetics? How much genetics knowledge should bachelor of science students have, if they are not planning to complete a genetics major? Can we still support students that have not studied biology since year 9 or 10? Here we will provide an overview of the educational approach to teaching first year genetics at University of Melbourne, as part of the first-year biology curriculum, which has experienced mixed reactions from students. We aim to create an opportunity to identify and discuss some of the core areas and concepts of genetics for all students, and areas that may be best left to specialist second or third year courses. Furthermore, our approaches to assessment in an evolving era of AI will be discussed.

Diversity of fungi and bacteria in infected and uninfected wing tissues within natural sexual and asexual populations of a facultatively parthenogenetic stick insect, *Megacrania batesii*

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The potential pathogens and susceptibility of natural insect populations are poorly known. In facultatively parthenogenetic animals, susceptibility to fungal and bacterial pathogens might vary depending on whether hosts were produced asexually or sexually, since the higher heterozygosity and greater genetic diversity enabled by sexual reproduction could promote resistance to infection. The facultatively parthenogenetic stick insect *Megacrania batesii* can flexibly switch from asexual to sexual reproductive modes depending on whether mating takes place and form sexual and asexual populations in the wild. *M. batesii* also occur in two major types of habitats characterised by different species of host-plants. Natural populations of *M. batesii* harbour unknown infections that manifest as dark spots on the wings or body. We collected infected and uninfected wing tissue samples from several natural populations of *M. batesii* to identify pathogens by targeted DNA sequencing of bacterial (16S) and fungal (ITS2) genomic regions. We found that both fungal and bacterial communities differed significantly between infected and uninfected wings. We also observed differences in pathogen community composition between sexual and asexual populations and between habitat types. Our results contribute to knowledge of factors that influence pathogen diversity in natural insect populations.

Expression QTL divergence between ecotypes of an Australian Wildflower

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Plants adapt to their local environment through complex interactions between genes, gene networks, and hormones. Gene expression plays an intermediary role between the genotype and phenotype and thus is vital to understand how expression is regulated. Variants that regulate gene expression i.e. expression quantitative trait loci

(eQTL) are known to contribute to differences in traits both within species and between. As regulatory elements, they can have widespread, pleiotropic effects, thus affecting the evolution of many traits. However, little is known about the different roles of regulatory elements in adaptive evolution, particularly when populations adapt in parallel to the same environment. To gain insight into the regulatory elements involved in adaptive evolution, we identified eQTLs associated to an adaptive trait (gravitropism) that has evolved in parallel in the Australian Wildflower, *Senecio lautus*. We used one population of *S. lautus* to look at gene expression from 60 pools of individuals with contrasting degrees of gravitropic expression and being exposed to control or rotation conditions. We found eQTLs regulating the expression of 790 genes interacting across various hormonal pathways, indicating that pleiotropism driven by hormonal function divergence can have important implications for the divergence of adaptive traits in nature.

The identification novel molecular mechanisms for self-incompatibility in ryegrass and clover

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Plant reproduction relies on a pollen grain landing on the female stigma of a flower, germinating and growing a pollen tube to deliver sperm cells to the ovule for fertilization. In some plants the pollen tube can only grow through the female tissues if it comes from a genetically distinct individual, preventing self fertilization. This self-incompatibility has evolved independently within flowering plant families and generally relies upon a receptor on one tissue (male or female) recognizing a specific ligand secreted from the other tissue. While self-incompatibility prevents inbreeding, it limits breeding strategies in self-incompatible crops.

Self-incompatibility impacts the breeding of two key forage crops in New Zealand, ryegrass (*Lolium* spp.) and white clover (*Trifolium repens*). Here, we will report on our discovery of the molecular mechanisms underlying self-incompatibility in these two plant families. We used a range of genomic tools and key features of self-incompatibly genes to identify candidate loci, followed by expression analyses and protein modelling to develop working models for both self-incompatibility systems. We propose that both mechanisms evolved from plant defense and stress signalling pathways, with the receptor in the ryegrass system representing a new class of plant receptor.

Past and future of genetic monitoring highlighted with the case study of the Aotearoa New Zealand southern right whales tohorā

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The field of genetic monitoring has used molecular tools to provide insights into the ecology and population dynamics of natural populations, particularly those of conservation concern, for several decades. Here we highlight how this field has grown and can continue to innovate using the examples of the New Zealand southern right whale (*Eubalaena australis*, Tohorā nō Aotearoa). Genetic monitoring of this species began three decades ago in Aotearoa New Zealand, providing a remarkable archive from which to develop knowledge on the species and innovate techniques in molecular ecology. Here we reflect on the power of genetic monitoring to provide insight into population structure, genetic diversity and the changes in census population sizes of this species, as well as the conservation implications of the findings. We also explore the future of genetic monitoring by describing how this archive being is, or could be used, to develop or apply newer methods including epigenetic markers for age, reproductive status, understand functional genomic markers, and reconstructing kinship.

A gene variant in CALCRL, encoding a G-protein coupled receptor, is highly enriched in individuals with Māori and Pacific ancestry and associates with a higher risk of kidney failure

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We have identified a coding variant in the hormone receptor gene *CALCRL*, implicated in blood pressure regulation, that is common in people with Māori and Pacific Island ancestry but virtually absent in other ethnicities. The *CALCRL* variant correlates with reduced kidney function and altered blood pressure and increases the risk of kidney failure. Functional analyses *in vitro* show that the variant increases the sensitivity of CALCRL to the ligand adrenomedullin. Knock-in rats with the orthologous gene variant

show decreased systolic blood pressure and increased nitric oxide signalling (NO; a potent vasodilator) but high levels of Angiotensin II (a vasoconstrictor). As NO antagonises the effects of Angiotensin II on vascular tone, we hypothesise that the *CALCRL* variant perturbs the homeostatic balance of these vasoactive agents and this may play a role in driving the severity of kidney injury in diabetes.

Do cane toads in Australia exhibit repeated local adaptation to different environments?

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Knowledge about a species' native range is important for understanding the underlying evolutionary processes that occur following their introduction to a novel environment. Cane toads (*Rhinella marina*) were introduced to Australia in 1935 and are still expanding their range across the Kimberley region of Western Australia. Despite low genetic diversity, cane toads appear to have adapted to novel, arid environments as they travelled westward across Australia, and differ to their eastern Australian conspecifics in morphology, physiology and behaviour. The recent discovery of two ecomorphs in the native range (rainforest and coastal areas) raises the question of whether repeated and parallel adaptation occurred after introduction. It is possible that what appears to be novel adaptation may be sorting of native range ecomorph alleles into the environments to which they are pre-adapted. We leveraged whole-genome and reduced representation sequence data to 1) investigate if native range ecomorphs are genetically distinct, 2) detect signals of selection in native and invasive populations and 3) evaluate the genetic composition of the outlier SNPs in the toads across the invasion trajectory. This study will provide insights into rapid evolution and resources for future management of this species.

Conservation and diversity of ribosomal DNA in chordates

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Ribosomal RNA sequences are highly conserved across eukaryotes. Three of the four ribosomal RNAs (18S, 28S and 5.8S) are encoded by ribosomal DNA (rDNA) units, with internal transcribed spacers (ITS1 and ITS2) separating the genes. While the conservation of rRNAs is well documented, the full diversity of rDNA sequences remains underexplored. To address this, we developed ribocop, a novel bioinformatic workflow to accurately detect rDNA sequences in genome assemblies. We used ribocop to examine rDNA sequence and structure in over 700 chordate species. Our results confirm the remarkable conservation of 18S, 28S and 5.8S sequences across the phylum, reflecting strong functional constraints on rRNA.

As expected, mammalian rDNA units are larger than those in other lineages at ~35Kbp. In contrast, rDNA unit sizes across fish, amphibians, turtles, lizards, snakes, birds and sharks are consistently smaller suggesting that rare expansions in these groups likely arose through random events. To better understand how unit size evolves we also examined the composition of rDNA units. We observed distinct lineage-specific patterns, including striking ITS1 enlargement in birds and expansions in the mammalian ITS2 and intergenic spacer. These results provide new insight into rDNA unit diversity and the evolutionary dynamics shaping rDNA architecture across chordates.

Hybridisation and clonality within the endangered shrub *Callistemon forresterae* (Myrtaceae) of East Gippsland, Australia

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Hybridisation is known both to be a driver of evolution but also potentially a threatening process for narrow range endemic (NRE) species. Determining the

genealogy of a NRE species where hybridisation is suspected is integral to its conservation management. We used DArTseq SNPs to explore hybridisation and clonality in the endangered NRE *Callistemon forresterae* from East Gippsland, Victoria, Australia. *Callistemon forresterae* is part of a complex of East Gippsland callistemons that have been previously hypothesised as separate hybrid swarms resulting from mating between two common co-occurring species, *C. citrinus* and *C. subulatus*. The genomic results provided support for the hybrid hypothesis, as well as strong evidence of clonality and, consequently, extremely low genotypic diversity. Genotypically different maternal lines had variably intermediate morphologies supporting the existence of a hybrid swarm. However, seed-grown progeny shared identical genotypes with source plants, indicating apomixis also occurs within the species. Collectively, our results suggest that sexual reproduction in this hybrid taxon is extremely limited and apomixis-derived clonality may be maintaining stable morphology in progeny at an individual genotype level. The impact of our results on the conservation listing of *C. forresterae* will be discussed.

Assembled genomes of New Zealand's endemic stick insect hybrids

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Some stick insects possess the remarkable ability to reproduce asexually in the absence of males, and in New Zealand, two genera have hybridized to form female-only populations. This adaptation has resulted in four known hybrid species, providing a unique opportunity to study the effects of hybridization on genome structure and function. However, assembling high-quality genomes for these species is challenging due to their triploid nature and large genome size. Therefore, we are employing a combination of Oxford Nanopore (long-read), Illumina (short-read), and Omni-C (Hi-C–based proximity ligation) sequencing technologies to assemble haplotype-phased reference genomes. Our approach involves adjusting bioinformatic pipelines to accommodate these complex genomes which require high coverage, in the absence of PacBio HiFi reads. By annotating repetitive regions with custom libraries and analyzing RNA sequences from various tissues, we aim to investigate chromosomal rearrangements, allelic expression in polyploids, and transposable element suppression. This study will reveal how hybrid parthenogenesis persists after the loss of sex and diploid-to-triploid transitions. New Zealand stick insects offer an excellent

model to explore variation in reproductive modes, ploidy, heterozygosity, and genome evolution.

Developing large-animal models and gene therapies for Retinitis Pigmentosa

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Retinitis pigmentosa (RP) is a group of inherited retinal degenerative diseases causing progressive vision loss and blindness. With no cures, treatment development is limited by rodent models that lack translational relevance. Large animal models, particularly sheep, offer more genetically, physiologically and clinically relevant systems, with human-like eye size, retinal structure, visual processing, and importantly, naturally occurring RP-like phenotypes.

To address this need, we are developing two genetically modified RP sheep models: one carrying a heterozygous RP1 R677X mutation (dominant) and another with homozygous CERKL deletions (recessive). Using CRISPR/Cas9, we have achieved high-efficiency editing in ovine cell lines (90% for RP1 R677X, 70% for CERKL) and are generating gene-edited embryos to establish founder sheep lines. In parallel, we are designing adeno-associated virus (AAV)-based gene editing and augmentation therapies for these mutations, laying the groundwork for preclinical testing aiming to halt and reverse vision loss.

This multidisciplinary project at the University of Auckland, in collaboration with the South Australian Research and Development Institute (SARDI), integrates genetics, disease modelling, ophthalmology and gene therapy expertise. By developing dominant and recessive RP models, we aim to bridge the gap between small animal studies and human trials, advancing gene therapy development for inherited retinal diseases.

Identifying Germline-Specific Promoters for Gene Drives in Invasive Wasps

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Invasive wasps cost New Zealand more than $330 million annually. Current control methods have failed to limit the spread of these damaging species, resulting in the biomass of invasive wasps in the Nelson Lakes beech forest surpassing that of birds, rodents, and stoats combined. As a result, alternate biocontrol methods, namely gene drives, are being investigated as population suppression techniques.

Essential for a successful gene drive strategy is the identification of a germline specific regulatory element to drive transgene expression with precise spatial and temporal control. Known examples of such promoters, however, is limited to a few model species, and previous attempts to translate these promoters to other species has given rise to inefficient gene drives. As such, methods to identify meiosis-specific promoters in non-model species such as invasive wasps are critical for generation of successful gene drives.

In this study, we combine spatial transcriptomics, HCR, and life-stage and caste RNAseq analysis to identifying potential promoters for use in hymenopteran gene drives. By combining these techniques, candidate promoters can be assessed for both spatial and temporal expression, reducing the likelihood of generating gene drives with inefficient or leaky promoters.

A genomics-informed investigation into Lamprey Reddening Syndrome

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Pouched lamprey (*Geotria australis*, also known as kanakana or piharau) are ancient jawless fish found in the Southern Hemisphere. They are culturally and ecologically important to Aotearoa, New Zealand, yet relatively little is known about their ecology. Lamprey reddening syndrome (LRS) is a recently emerged disease in Southland, New Zealand, and causes significant mortality of afflicted lamprey. Despite numerous attempts, a definitive cause of LRS has not been found. Guided by iwi collaboration to ensure tikanga, a metatranscriptomic dataset of 28 lampreys, from both Australia and New Zealand, 11 of which were diseased, was recently established. Using these rich data, we will uncover the microbial composition, with particular focus on viral communities, for each individual matched with their disease status. This approach allows for novel viruses to be discovered, which is often a major limitation in traditional approaches to disease investigations. This research project will reveal the causative agent of LRS and illustrate the potential of genomics-informed diagnostics for taonga species. By determining the cause of LRS, we can protect culturally, ecologically and economically important fish within New Zealand and beyond.

Empowering Future Māori Scientists: ESR Genomics Bootcamp

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During COVID-19, the Māori Impact Group observed how limited Māori expertise in infectious diseases delayed the ability to make an impact for Māori. As a response the ESR Genomics Bootcamp was developed in partnership with Pūhoro STEMM Academy and ONT. The bootcamp centred around a mock outbreak scenario, designed to showcase the leadership role of genomics in maintaining the safety of Aotearoa. With kōrero from Māori Impact group Kaupapa Māori scientists, Te Ao Māori concepts and the vital connection between genomics and mātauranga Māori highlighted the importance of integrating cultural perspectives into scientific practices. The bootcamp demonstrated to rangatahi and tauira Māori how genomics and bioinformatics can be an applied solution for hauora and taiao issues, how the two can create a positive impact for Māori when applying a kaupapa Māori lens, and study and employment pathways in Aotearoa. To create a generation of informed and inspired scientists, applied science and research should be presented and connected as a solution to relevant issues facing communities. A for Māori, by Māori, with kaupapa Māori approach is central to providing a relatable and relevant offering that connects learners and community to create positive impact, as platformed by the ESR Genomics Bootcamp.

Postglacial recolonization of the Southern Ocean by elephant seals occurred from multiple glacial refugia

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The Southern Ocean is warming more rapidly than other parts of our planet. How this region's endemic biodiversity will respond to such changes can be illuminated by studying past events, through genetic analyses of time-series data sets including historic and fossil remains. Archaeological and subfossil remains show that the southern elephant seal (*Mirounga leonina*) was common along the coasts of Australia and New Zealand in the recent past. This species is now mostly confined to sub-Antarctic islands and the southern tip of South America. We analysed ancient seal samples from Australia (Tasmania), New Zealand, and the Antarctic mainland to examine how southern elephant seals have responded to a changing climate and anthropogenic pressures during the Holocene. Our analyses show that these seals formed part of a broader Australasian lineage, comprising seals from all sampled locations from the south Pacific sector of the Southern Ocean. Our study demonstrates that southern elephant seal populations have dynamically altered both range and population sizes under climatic and human pressures, over surprisingly short evolutionary timeframes for such a large, long-lived mammal.

Splicing testing of crystallin gene variants in paediatric cataract

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Paediatric cataract, an opacification of the crystalline lens, is a leading cause of childhood blindness. Genetic variants in 13 genes encoding crystallin proteins are a common cause of this rare disease. Lens tissues are unavailable for RNA extraction and crystallins are not expressed in the blood, which complicates testing of splicing

variants in these genes. This study evaluated the utility of a functional assay to reclassify variants of uncertain significance (VUS) in crystallin genes. Classification followed the American College of Medical Genetics (ACMG) guidelines. Variants around donor (-10/+10bp) and acceptor (-25/+10bp) splice sites of crystallin genes were selected for testing (ClinVar, Cat-Map) based on their low allele frequency (gnomAD) and high predicted splice impact (SpliceAI). Using the pSpliceExpress plasmid, the mini-gene assay observed wildtype and variant splicing in human lens epithelial cells (HLE-B3). A total of 148 splicing variants were identified, 66 of which are currently classified as VUS, with 11 selected for testing. 3 variants were reclassified as Likely Pathogenic (*CRYBA1* c.215+2 T>C, *CRYBB1* c.432+5 G>C, *CRYBB2* c.173+1 G>T), and 2 as Likely Benign (*CRYBA1* c.500+1 G>T, *CRYBB3* c.327+3 G>C). Although not all tested variants met criteria for reclassification, the assay's strength lies in its ability to reclassify variants near the threshold according to ACMG guidelines.

Molecular mechanisms of honeybee segmentation using HCR and spatial transcriptomics

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Segmentation is very well understood in species such as *Drosophila melanogaster* and *Tribolium castaneum*. These two species have very different forms of segmentation, *Drosophila melanogaster* is a long germ band insect, producing all its segments at once, and *Tribolium castaneum* is a short germ band species, generating segments in anterior-posterior sequence. Many species, however, exist in between these extremes of segmentation mechanism. The honeybee *Apis mellifera* is a worldwide pollinator, responsible for over 5 billion dollars worth of apicultural services in New Zealand annually, as well as being a fantastic emerging model organism in which to study segmentation.

Here, though next generation FISH (HCR), we show the mode of segmentation in honeybees to be progressive, as they pattern all segments before gastrulation which is a strictly long germ trait but do so in an anterior posterior fashion akin to short germ. Next, using the spatial transcriptomics platform StereoSeq we have mapped gene expression in whole embryos to a single cell resolution. This allows not only for the mapping of known segmentation genes, but also the discovery of novel genes with roles in segmentation. This allows us to expand our understanding of the evolution of segmentation mechanisms.

Investigating the pathways of Fall Armyworm invasion in Aotearoa New Zealand

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Fall armyworm (*Spodoptera frugiperda*) is a globally invading, highly destructive pest insect. Its arrival in Aotearoa New Zealand, and rapid spread shortly thereafter, has caused concerns amongst the primary sector. Particularly in the North Island, where the combination of warmer climate and suitable crops are facilitating multiple generations and yield losses.

Here, we compare the genomes of the first wave of fall armyworm introductions from 2022-2023 season with populations from Asia, Africa and Australia to estimate the gene flow, known markers of resistance and signals of local adaptations that could be carried along the invasion front. We find that the globally invasive lineage of fall armyworm is indeed the pervasive lineage in Aotearoa New Zealand. We also identify previously characterised pesticide resistance alleles and geneflow from the African lineage. Finally, we estimate whether a single or multiple introductions likely via Australia underpin the genomic diversity of the New Zealand population.

Together, our results will inform the understanding of invasion pathways of fall armyworm in New Zealand and support the management plan for this new to New Zealand pest.

Fitting local molecular clocks: a new tool and challenges

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Molecular clock rates are the key parameter enabling phylodynamic inference in units of time. Phylodynamic datasets have grown in recent years, with datasets of hundreds

to tens-of-thousands of samples replacing those on the order of tens to hundreds. As these datasets span increasing ecological and epidemiological complexity, local molecular clocks will be essential to accommodate their heterogeneity, such as when sampling across pathogen variants of concern or host-species. With this goal in mind, I introduce a novel and accessible client-side application, Clockor2 (https://clockor2.github.io/), designed to help genomic epidemiologists explore local clock hypotheses using root-to-tip regression. It lowers the barrier to fitting local clocks, which is a combinatorially expensive task that often presents convergence issues in larger Bayesian phylodynamic analyses. Clockor2 paris ease of use and scalability, now handling trees of at least ten-thousand samples and prioritises data-security as a client-side only application. I further discuss statistical and computational challenges to fitting local clocks in a regression framework, including non-independence due to phylogenetic structure, and current work to improve the inbuilt clock-search algorithm and reduce over-fitting.

HDAC4 oligomerisation drives nuclear condensate formation and impairs neuronal development

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Dysregulation of histone deacetylase four (HDAC4) is linked to various neurodevelopmental and neurodegenerative diseases, including Alzheimer's disease and Parkinson's disease, both of which are associated with increased nuclear accumulation of HDAC4. In our Drosophila model, elevated HDAC4 levels lead to the formation of punctate nuclear foci that display features of biomolecular condensates. The presence of condensates correlates with neurodevelopmental defects, impaired long-term memory, and reduced longevity. Condensate formation depends on HDAC4 oligomerisation. The N-terminus of HDAC4 contains a glutamine-rich region forming an alpha-helix, which self-oligomerises through a hydrophobic core stabilised by glutamine-dominated polar interaction networks. Both the hydrophobic core and polar interaction networks are essential for oligomerisation and condensate formation. Genetic disruption of these elements reduces condensate number and mitigates HDAC4 overexpression-induced neurodevelopmental defects. In contrast, HDAC4-induced phenotypes are exacerbated by the presence of the transcription factor MEF2, which facilitates nuclear import of HDAC4 and stabilises condensates. Our findings suggest that HDAC4 dysregulation contributes to neuronal dysfunction, potentially mediating disease onset and progression in neuronal disease, and

highlight that targeting oligomerisation of HDAC4 or MEF2 binding could offer therapeutic benefits.

Microbial Drivers of Disease in the Critically Endangered Kākāpō: Insights from Total RNA Sequencing

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When a disease emerges, determining the causative pathogen (if one exists), can be challenging. Total RNA sequencing can identify the 'infectome'—viruses, bacteria, fungi, and eukaryotic parasites—making it an ideal tool for pathogen investigation, particularly in endangered host species where samples are limited and challenge studies are not possible. The kākāpō (*Strigops habroptilus*) is a critically endangered parrot which suffers from exudative cloacitis, a debilitating disease causing cloacal inflammation. Despite this disease emerging >20 years ago, the cause remains elusive. We characterised the infectome of lesions and cloacal swabs from nine affected kākāpō, and compared this to cloacal swabs from 45 non-diseased kākāpō. Three bacterial species - *Streptococcus gallolyticus*, *Enterococcus faecalis* and *Escherichia coli* - were significantly more abundant in diseased compared to healthy kākāpō. The genetic diversity observed in *S. gallolyticus* and *E. faecalis* suggests these bacteria originate from exogenous sources rather than kākāpō-to-kākāpō transmission. The presence of extraintestinal pathogenic *E. coli* (ExPEC)-associated virulence factors in diseased kākāpō suggests *E. coli* may play a critical role in disease progression. These results, combined with the consistent presence of one *E. coli gnd* sequence type across multiple diseased birds, suggests this species may be the primary cause of exudative cloacitis.

Interaction range of common goods shapes Black Queen dynamics beyond the cheater-cooperator narrative

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Dependencies among microorganisms often appear mutualistic in the lab, as microbes grow faster together than alone. However, according to the Black Queen (BQ) hypothesis, these dependencies are underpinned by benefits from loss-of-function mutations when others in the community can supply necessary common goods. BQ dynamics often describe cheater-cooperator scenarios, where "cheaters" produce nothing and rely on "cooperators". We have previously proposed that in systems with multiple goods an alternative endpoint can emerge where an ecosystem of interdependent ecotypes engage in "mutual cheating" and production is distributed; in contrast to centralization, with one ecotype providing all goods for the ecosystem. Here, we present an eco-evolutionary model that reveals that BQ dynamics can result in both distributed- or centralized production. The number of beneficiaries a producer can support distinguishes between these two endpoints. While many ecosystems evolve to be minimally- or maximally-centralized, we also find intermediates where apparently redundant ecotypes coexist for long durations. Due to non-producers occupying space, producers are unable to distribute the production of goods. Despite this stalling of division of labor, we observe that sudden structural shifts can occur that purge the non-producers from the ecosystem. Overall, our findings unveil complex interactions beyond the simple cheater-cooperator narrative.

Genomic Insights from Onychophorans into the Diversification of Panarthropods

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Onychophorans occupy an early branching position in *Panarthropoda*, a super-phylum containing *Arthropoda* and *Tardigrada*. Despite diversity within these groups, modern Onychophorans retain morphological similarities to their Cambrian ancestors. Although their body plan remains largely unchanged, Onychophorans exhibit remarkable physiological diversity. Not only do Onychophorans utilize three reproductive modes, but they also capture prey in a matrix of slime proteins that solidify into one of the hardest biological substances. These adaptations distinguish

Onychophorans from all other Metazoans. Ultimately, these conserved ancestral morphologies and unique physiological adaptations raise a fundamental question: how did the extraordinary diversity in animal form and function emerge in *Panarthropoda*?

Recent sequencing of an Onychophoran genome provides novel understanding of Onychophoran biology and evolution. Here, we leverage Omni-C to understand how a highly repetitive Onychophoran genome folds in three dimensions. Interestingly, highly conserved Hox genes have been found to be unconventionally organized compared to well-studied Panarthropod species. For the first time in an Onychophoran, we also present RNA-seq analysis of Onychophoran tissues, and *in situ* gene expression associated with Hox gene regulation and slime production. Ultimately, this work begins to highlight molecular aspects of physiology in a non-model organism whilst providing fundamental insights into diversification in *Panarthropoda*.

Working With Communities in Aotearoa-New Zealand to Build Climate Resilience in Kaimoana (Seafood) Using Transcriptomics

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Climate change threatens marine ecosystems through marine heatwaves and ocean acidification, worsening declines in taonga (treasured) species. Species used for kaimoana (seafood) and mahinga kai (customary food gathering) are of special concern. In Aotearoa-New Zealand, Māori communities and commercial and recreational fishers have observed shifts in kaimoana distribution and health as ocean temperatures rise and marine heatwaves become more frequent and severe.

The effects of marine heatwaves on kaimoana remain poorly understood. Identifying whether some populations are more resilient than others is important for management. We focus on two taonga: pāua (*Haliotis iris*) and kōura (*Jasus edwardsii*). We'll present preliminary data from an experiment and the 2025 marine heatwave in Aotearoa.

This project is co-designed with Māori and other local community members to establish a baseline for the resilience and vulnerability of taonga species to marine heatwaves. Communities include Kāti Huirapa ki Puketeraki and the East Otago Taiāpure (Otago), Ōnuku Rūnanga and the Akaroa Taiāpure (Canterbury), and Te Rūnanga o Makaawhio and the Makaawhio Mātaitai (Westland). Using transcriptomic analysis to measure heat stress responses, we aim to understand species responses and identify genetic mechanisms supporting resilience, informing future management strategies.

Exploring Aotearoa's virosphere

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Aotearoa is a unique place to study the evolution of viruses. Separated from Gondwana over 80 million years ago, many of our native hosts have lived in isolation, likely harbouring novel and highly divergent viruses. Our fauna therefore provides a powerful natural experiment to evaluate the key genetic and ecological parameters that affect viral evolution. Specifically, the unusual amalgam of native and invasive species, with well-documented history of invasive introduction, provide a unique opportunity to determine the factors that contribute to viral host-jumping over ecological timescales. We sample animal hosts such as birds, fish, reptiles and mammals to uncover what viruses they harbour, determine how their viruses have evolved over time and how their ecology and life history may promote viral host-jumping and disease outbreaks. Overall, we aim to reveal more of the unexplored virosphere, uncover potential disease-causing viruses, and identify factors that shape the virome.

The diversity and phylogenetic placement of groundwater fauna, amphipods, in Australasia and in a global context

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This study aims to characterize amphipods across different aquifers and chemically distinct groundwater ecosystems using full-length 18S rRNA sequencing in New

Zealand, Australia, and within a global context. There has been a significant increase in investigations using molecular techniques to identify the types of fauna present in groundwater ecosystems. However, species identification in these novel studies is often hindered by the absence of detailed reference sequences. Here, we report the use of both morphological and molecular techniques to construct phylogenies and investigate evolutionary relationships in groundwater fauna, specifically amphipods. Amphipod specimens were collected from various aquifers across the North and South Islands of New Zealand, as well as from New South Wales, Australia. These specimens were morphologically characterized, and their DNA was extracted for the amplification of the full-length 18S gene. Long-read sequencing was performed using Oxford Nanopore Technology. The diversity and phylogeny of these specimens were analyzed. We present results on the phylogenetic analysis of Australasian amphipods and their placement within the regional and global amphipod context. Additionally, we discuss protocol optimization and methods for obtaining high-quality DNA from amphipods for long-read amplicon sequencing.

Disentangling the paradoxical role of inflammation in mammalian pregnancy

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While the first mammals laid eggs, live-birth evolved in a common ancestor of marsupial and eutherians more than 170 mya. In the common ancestor, pregnancy was short, with mothers giving birth to small under-developed young. This mode of reproduction has been retained in most marsupials. In eutherians, pregnancy occurs over an extended period with more developed young at birth. Interestingly, in eutherians and marsupials, the immune system is coopted at stages of pregnancy in a coordinated fashion. I examined the role of inflammatory signalling in pregnancy for a suite of mammals to better understand how and why inflammation is used to support placentation. By studying gene expression and exploring the impacts of manipulating inflammatory signalling I explore the role of inflammation in pregnancy. These results suggest that inflammation is the result of novel interaction of maternal and fetal tissues that occurred when pregnancy first evolved. In most marsupials, inflammation has been retained likely to support the timing of pregnancy and parturition. In eutherian mammals and macropods where placentation extends beyond attachment, inflammation has been modulated using different mechanisms. Our results highlight the importance of thinking about inflammation as a powerful regulator of pregnancy, rather than a cause of infertility.

Genomic Signatures of Isolation and Disease in the World's Best Penguin

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Historical population dynamics shape modern genetic diversity, affecting susceptibility to disease threats. By understanding these patterns, we can improve conservation success. Hoiho (Yellow-eyed penguin, Megadyptes antipodes), one of the rarest species of penguin in the world and native to Aotearoa, provides an unparalleled opportunity to study how independent populations, disease risk, and population genetics, both historical and contemporary, intertwine. Our analyses of 251 hoiho genomes reveal a coalescent event dating to approximately 120,000-140,000 years ago, suggesting a severe population bottleneck during a previous glacial period. Meanwhile, phylogenetic analyses predict likely colonisation and isolation of the northern hoiho population (i.e., mainland New Zealand and Rakiura) from the subantarctic Campbell and Enderby islands around 1,400 - 7,000 years ago. Despite ~200 generations of largely isolated evolution, genetic diversity remains surprisingly similar between populations, suggesting moderate founding populations. Today, the northern population faces an urgent threat of extinction from a DNA virus, while the subantarctic populations seem unaffected. We identify candidate genomic regions linked to this disease with a genome-wide association study. By linking historical population dynamics and more recent isolation events and incorporating the dimension of disease risk, we show the power of genomics to guide conservation management.

Towards greener pastures: Understanding the role of CONSTANS variants in perennial ryegrass flowering time

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Perennial ryegrass (*Lolium perenne* L.) is New Zealand's primary forage and the foundation of its pasture systems. Each spring, ryegrass undergoes a seasonal shift to flowering that reduces pasture quality and livestock performance. To mitigate this, we aim to develop ryegrasses that remain vegetative under field conditions by increasing their daylength requirements for flowering. Previous research identified a variant of the flowering gene *CONSTANS* (*CO*) as a target for increasing ryegrass daylength requirements. *CO* is a transcription factor that promotes expression of the key floral inducer *VRN3* during the day; at night, it is degraded by the COP1/SPA complex. The balance of these two activities determines a plant's daylength requirements for flowering. Targeted sequencing of *CO* uncovered a SNP encoding a serine-to-arginine substitution in a putative transactivation domain. We hypothesise this change may reduce the transactivation ability of *CO*, and aim to test this using yeast- and tobacco-based assays. Interestingly, the SNP is also located close to a degradation motif recognised by COP1/SPA, suggesting it may affect *CO* stability. We aim to test this hypothesis in a tobacco-based expression system. Insights gained from this study will support the development of non-flowering ryegrass to improve spring pasture quality and livestock performance.

Detection and Mitigation of Microbiome DNA Presence in Saliva-Derived Whole Genome Sequence Data

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Saliva-derived DNA is frequently used for sequencing studies when blood collection is impractical or inappropriate. However, saliva samples contain oral microbiome contamination, compromising downstream applications. The He Kākano project aims

to generate a population-specific genomic catalogue for Māori using primarily saliva-derived sequencing data (n=809) to assist genomic health care in Aotearoa. The presence of microbial sequences resulted in false positive variation, complicating accurate variant calling of the cohort. To quantify this issue, sequencing data from matched blood and saliva (n=5) were used to test different mitigation strategies for this problem. On-target effects were assessed through a reduction of unique saliva sequence, misalignment, and spurious variation. Optimised mitigation was achieved using a combination of sequence pre-screening using the taxonomic classification tool Kraken2 and increased aligner seed length of 24 (Burrows-Wheeler Aligner). Validation in a saliva-derived sequence cohort of unrelated individuals (n=22), showed a significant reduction in saliva-derived false positive variants (Wilcoxon test, $p < 0.001$), which otherwise appear as strong candidates for rare disease, being both extremely rare when compared to population datasets and biased towards loss-of-function variation. This approach is theoretically applicable to any target species to mitigate contamination from taxonomically distant organisms.

Exploring the potential of virus transmission among birds in a spatially restricted ecological niche

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Wild birds are important viral reservoirs, harboring pathogens like influenza viruses, flaviviruses, and coronaviruses, which can also affect humans and other animals. Their unique immune system often allows them to remain asymptomatic despite being infected with multiple viruses at once. Birds' ability to fly and act as viral reservoirs makes them critical vectors for viral spread, yet little is understood about the factors driving virus diversity and their ability to cross host barriers. This project explores the transmission dynamics of viruses between both native and introduced passerine bird species in Aotearoa, New Zealand. With limited knowledge of the viruses affecting New Zealand's bird species, this study aims to investigate the virome of passerines and identify the prevalence of cross-species transmission. Passerines, due to their diversity and wide habitat distribution, make an ideal model for understanding viral risks to conservation, agriculture, and public health. Using data collected over three years and encompassing 453 samples, we will employ a metatranscriptomics approach where viral genomes will be recovered and cross-referenced with public databases, followed by phylogenetic analysis to identify both known and novel viruses, assess cross-species transmission, and track virus diversity across time, providing crucial insights into potential viral risks to New Zealand's ecosystems and public health.

HDAC4 biomolecular condensates: dynamics, disruption, and effects on neuronal development

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Histone deacetylase four (HDAC4) forms punctate nuclear foci when its abundance increases. Our previous work demonstrated that increased HDAC4 foci correlate with neurodevelopmental and memory impairments in a Drosophila model. Similar accumulations of nuclear HDAC4 have been observed in neuronal disease, including Alzheimer's disease. Contrary to the previous belief that these foci were static, denatured aggregates of HDAC4 protein, our live imaging and FRAP studies revealed that these foci are instead highly dynamic, resembling liquid-liquid phase separated droplets termed biomolecular condensates. These condensates undergo fusion events, where coalescence increases their size and mobility. Their dynamic nature suggests the feasibility of targeted strategies to disrupt their formation and reduce severity of neuronal impairment. We designed short peptides to interfere with binding of HDAC4 to MEF2, which is required for both nuclear import of HDAC4 and the stabilisation of condensation. Expression the M1-L285 peptide significantly reduced condensate formation and mitigated the severity of defects in brain development associated with their presence. These data provide a novel perspective on the role of HDAC4 in neuronal disease and potential therapeutic targets.

Can reforestation reverse the evolutionary effects of deforestation? Genetic evidence from Aotearoa's native insects

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Recent research across the globe has highlighted the evolutionary impacts of human-driven environmental change. However, questions remain concerning the potential for environmental restoration to reverse such evolutionary shifts. As a case in point, the loss of endemic forest since human arrival to Aotearoa has driven rapid adaptive shifts in native insect phenotypes, including reductions in *Zelandoperla* stonefly wing length and melanism. In this study, we tested whether reforestation has the potential to reverse such anthropogenic shifts by selecting for flighted and melanic phenotypes. We used phenotypic and genetic screening of wing-reduction (*AGGF1*) and colouration (*ebony*) loci to compare populations from neighbouring deforested versus

recently reforested streams within two major catchments: the Clutha and Mataura rivers. Preliminary data revealed a shift in the full-wing phenotype from 4.5% in deforested populations to 11.8% in reforested (p=0.004), supporting the hypothesis that reforestation reverses the evolutionary impacts of deforestation. By contrast, we identified no substantive shifts in the frequency of melanic individuals between populations, suggesting that selection pressures on insect colour may be subtle, and potentially dependent on ecological interactions. Regardless, the preliminary evidence for reacquisition of flight following reforestation lays the foundation for further research on the evolutionary response to ecological restoration.

Unravelling Inheritance Patterns in Polyploid Hybrid Crosses Through Haplotype Tracking

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In commercial breeding programs, interspecific hybridisation introduces genetic diversity by combining desirable traits from different species, producing hybrid plants. Polyploid speciation allows for the rapid formation of new species, promoting biodiversity. This process can lead to introgression, where genetic material from one species is introduced into the hybrid genome. While introgression can bring in beneficial traits through recombination, it may also introduce undesirable traits, complicating inheritance patterns and reducing vigour. Understanding inheritance patterns is crucial for identifying vigour loss and examining the impact of chromosome structure on pairing and recombination. Recombination between species can be inhibited, so successful integration of beneficial traits is key to selecting stable, productive plants.

A proposed method tracks inheritance patterns by mapping haplotypes and reads of offspring in unitig and phased haplotype genome assemblies of parent plants. Using reduced representation sequencing, this approach is cost-effective for large-scale breeding programs. Pangraph assemblies confirm the method's accuracy in identifying inheritance patterns. A key challenge is accurately assembling haplotypes,

especially in polyploids. This method will be tested in second-generation hybrids with whole-genome sequencing and is expected to apply to mixed-ploidy species crosses, leading to the release of a haplotype tracker tool and pipeline for polyploid amplicon data processing.

Investigating the direct and indirect effects of rising CO_2 levels on kākahi (freshwater mussels)

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This project will investigate the impacts of freshwater acidification, driven by rising atmospheric CO2, on kākahi (freshwater mussels, *Echyridella* sp.) in Aotearoa New Zealand. By using cutting-edge molecular tools, including genome, transcriptomic and single-cell sequencing, alongside histological techniques, this study will examine the genetic, phenotypic and molecular differences within and across kākahi populations in Te Awa o Waikato (Waikato River). This work will proceed in concert with a wider programme of investigation examining the response of this ecosystem to climate change-related stressors, and be performed alongside multiple stakeholders and community groups. Specifically, this study will explore the cellular-level patterns and differentiation across key life stages including the larval (glochidia) and newly-settled adult phases. The findings from this study will provide critical insights into the broader implications of climate change for freshwater ecosystems in Aotearoa NZ, with a focus on protecting our taonga species from the effects of CO2-induced acidification.

Investigating the genetic diversity of the endangered subpopulation of humpback whales (*Megaptera novaeangliae*) in New Caledonia, Oceania

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Functional genetic diversity plays a crucial role in determining the fitness and viability of wild populations. The major histocompatibility complex (MHC), a commonly studied functional genomic marker, is essential for immune defence against diseases and parasites. Maintaining high MHC diversity is therefore vital for sustaining an effective immune response and may influence the long-term survival of exploited populations. Humpback whales (*Megaptera novaeangliae*) in Oceania underwent a demographic bottleneck due to whaling deep into the twentieth century. Today the abundance of 6,404 whales remains low relative to the presumed historical numbers, leading to their IUCN status as 'endangered'. Here, we focus on the key Oceania winter breeding ground of New Caledonia using previously generated population age structure derived from an epigenetic ageing assay and cetacean-specific MHC panel to investigate whether functional genetic diversity has changed with generations since whaling. Using data from 1996–2020, we will categorise individuals into age cohorts and evaluate genetic and functional diversity at class I and class II MHC loci in each cohort, and compare with neutral genetic diversity from matched microsatellite loci. This will provide insight into how the demographic bottleneck caused by whaling has impacted functional and neutral markers in Oceania humpback whales.

Assisted evolution of toad toxin resistance in a marsupial

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The introduction of the bufotoxin-secreting cane toad (*Rhinella marina*) to Australia in 1935, had a huge impact on many of Australia's native predators due to their vulnerability to bufotoxin. There has been limited success in controlling the spread of cane toads, which managed to invade most of tropical Australia, driving some of its native predators to the brink of extinction. One such species, the northern quoll (*Dasyurus hallucatus*), is now listed as endangered primarily due to cane toad ingestion. Resistance to cardiac steroid toxins, such as bufotoxins, is linked to modifications in the alpha subunit of the sodium/potassium ATPase enzyme and has naturally evolved in many animal groups that adapted to preying on species secreting these toxins.

Here, we used CRISPR prime editing to introduce bufotoxin resistance-associated modifications to the endogenous *ATP1A1* gene of cells derived from fat-tailed dunnart, a closely related marsupial to the northern quoll. These genetic modifications significantly increased the bufotoxin tolerance of CRISPR-edited cells compared to wildtype. Our study establishes a proof of principle of engineering heritable bufotoxin resistance in a marsupial species and shows that assisted evolution can be a viable strategy to aid the recovery of northern quoll populations.

Viral spillover during biocontrol agent mass-rearing: an overlooked influence on biocontrol efficacy?

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Biological control, which uses natural enemies to manage pests, has been practiced for over a century. Despite improvements in establishment success and mitigation of off-target effects, the traits that drive biocontrol efficacy remain poorly understood. This is because long-term studies of established biocontrol programs are rare. We are addressing this gap using a unique sample collection of a parasitoid wasp used for biocontrol in Aotearoa, New Zealand, sequencing wasps from throughout an eight-year mass-rearing process and the subsequent decades post-release.

While large-scale rearing and release have been shown to affect the diversity and fitness of biocontrol agents, impacts on the microbiome and virome are often overlooked. We recently discovered a DNA virus carried by the wasp and transmitted to its target host during parasitism. While initially restricted to some sub-populations, the viral infection spilled over into all other sub-populations during mass-rearing and has subsequently been detected in all post-release samples tested to date. We are investigating the evolutionary impacts of this spillover on the virus and wasp to understand its potential influence on biocontrol efficacy and to provide fundamental knowledge about complex interactions between viruses, parasitoids, and hosts.

The galaxiid fish genome: testing for molecular signatures of repeated freshwater adaptation

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Galaxiids are a dominant component of the Southern Hemisphere fish fauna. While several *Galaxias* species retain the ancestral marine 'whitebait' phase, they readily lose this migratory ability to form landlocked populations and species. The kōaro (*Galaxias brevipinnis*) is a widespread freshwater galaxiid that possesses exceptional climbing ability, having colonised myriad upland lakes in both Aotearoa and southern Australia. Despite its ancestral migratory state, multiple kōaro landlocking events have occurred across Te Waipounamu, with repeated and rapid adaptive shifts. The highly parallel nature of this system allows comparison of multiple landlocked populations to identify loci involved in adaptation repeatedly and at a population-specific level using GWAS methodology. Here I present the first high-quality galaxiid genome, and test for genomic signatures of repeated landlocking. The kōaro genome assembly (604 Mb; N50 = 7.8 Mb) sheds new light on the genetic basis for repeated adaptive shifts in this climbing species.

Local pangenomes of structurally complex and medically relevant loci for health and disease studies

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A significant number of medically relevant loci (e.g. MHC, RHD, KIR and pharmacogenes) are highly divergent between human populations. Many of these loci have adaptively evolved in response to local environmental differences with diversity driven by structural variations (SVs). Combinations of tandem repeats, indels, inversions and other rearrangements can significantly alter gene function. These variations can impact infection response, drug efficacy and transfusion compatibility. Short-read sequencing methods have failed to resolve these complexities, creating gaps in our understanding of the mechanism and rates of SV change. For example, SVs in individuals of diverse ancestries are frequently misinterpreted due to reference biases and lack of clarity around common vs rare variations.

We have developed a local assembly workflow that leverages long-read sequencing to generate haplotype-phased assembles. SVs are then presented using locus-specific pangenome graphs. This approach enables comprehensive SV characterisation, improving the resolution of complex loci across large datasets. This method was employed to show continent-specific structural diversity of blood group genes, particularly complexities at the RHD and RHCE loci. Moving forward, this method will facilitate rapid construction of haplotypic variation databases for MHC, KIR, PGx, blood group genes and other medically relevant loci for disease association studies and clinical functional assessments.

Genetic diversity of Coconut Rhinoceros Beetle (*Oryctes rhinoceros*) and its biocontrol agent *Oryctes rhinoceros* nudivirus

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The coconut rhinoceros beetle (CRB, *Oryctes rhinoceros*) is a pest species of coconut palms. CRB was accidentally introduced in the Pacific from its native range in Asia. To limit the damage and control the spread of CRB, Oryctes rhinoceros nudivirus (OrNV) was successfully introduced as a biocontrol agent. Following a period of effective biocontrol by OrNV there are now variants of CRB that are no longer managed by some OrNV isolates. This study aims to identify CRB genotypes less susceptible to OrNV and/or more successful in establishing and spreading. We have used Genotyping-by-Sequencing to explore the genetic diversity of CRB populations. In parallel we have studied a collection of OrNV isolates, to determine the efficacy of different variants. Using OrNV genome sequencing data, we developed a rapid assay to perform isolate identification using nanopore sequencing. This assay allows detection and identification of OrNV isolates in field-collected CRB samples from across the Pacific. This also allows us to follow the presence and spread of biocontrol virus isolates across the region and pair this with improved knowledge of the CRB populations. The combined understanding of the diversity of CRB and OrNV contributes to improved management of CRB.

Genetics of *NOTCH2NLC*-related repeat expansion disorders in NZ Māori families

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NOTCH2NLC-related repeat expansion disorders (NREDs) are a range of neurodegenerative phenotypes caused by GGC repeat expansion in the 5' UTR of *NOTCH2NLC*. They include oculopharyngodistal myopathy (OPDM) and dementia-dominant and neuromuscular-dominant phenotypes of neuronal intranuclear inclusion disease (NIID), but *NOTCH2NLC* expansion has also been linked to amyotrophic lateral sclerosis and Parkinson's disease. *NOTCH2NLC* expansion is almost exclusively reported in East Asia but has recently been detected in multiple Māori families – total prevalence is unknown but could represent a meaningful proportion of neurodegenerative/neuromuscular disease in Māori people. Using Nanopore long-read sequencing, we bioinformatically profiled the structure and methylation of the repeat expansion and created consensus sequences for 9 expansion-positive Māori participants and 7 controls. Expanded consensuses were compared to previously published consensuses of 54 Asian individuals, finding significant differences in repeat length and proportion of GGA interruptions between NRED phenotypes in both novel Māori and published Asian participants. Methylation profiling revealed hypermethylation of very long "hyperexpansions" in unaffected carriers, hypothesised to be protective against gain-of-toxic-function by epigenetically silencing *NOTCH2NLC* expression. Understanding the relationship between repeat structure, methylation, and disease phenotype is important for prognostic predictions for current patients, and for determining cellular pathomechanisms and eventually progressing to therapeutic development.

Unpacking genetic incompatibility and early reproductive failure in threatened species

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Understanding the genetic causes of early reproductive failure for intensively managed threatened species is essential for making informed management decisions. Early reproductive failure may be due to either infertility or embryo death, yet the genetic causes attributed to each differ. Infertility is generally attributed to highly inbred individuals, while early embryo death is generally attributed to genetically incompatible pairings. However, it is often unclear what it means to be

"genetically incompatible" or how "genetic incompatibility" is best measured, especially in a conservation context.

Here, we present a systematic review to demonstrate that genetic incompatibility remains poorly defined and underexplored, and to recommend more explicit descriptions and measurements of genetic incompatibility. For example, we suggest that overlapping and identical runs of homozygosity (ROH) between mates can be used as a proxy for genetic incompatibility.

We demonstrate the utility of this approach using a uniquely rich empirical dataset, namely the extensive genomic and phenotypic data available for kākāpō (*Strigops habroptilus*), a Nationally Critical parrot endemic to Aotearoa New Zealand. In particular, we update existing research with ROH data to investigate the link between genetic incompatibility and early embryo death, to guide conservation actions and improve reproductive outcomes in kākāpō and beyond.

Validating Calibrations in Phylogenomics with FossValidation: A Case Study on Marsupials

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Bayesian molecular dating relies on calibration densities, yet the use of multiple time constraints often introduces biases that can compromise divergence time estimates. To address this, we present FossValidation, a Bayesian cross-validation framework that assesses the internal consistency of fossil calibrations by comparing posterior divergence time estimates with their prior densities. Our approach builds on the multi-species coalescent (MSC) model, which accounts for incomplete lineage sorting across loci, and is implemented in the StarBeast3 package. We demonstrate the utility of FossValidation through a phylogenomic analysis of marsupials. By applying our method to a set of ten calibrations, we identify and exclude inconsistent calibration points. Using the consistent subset, we reconstruct a calibrated phylogeny, revealing that the diversification of key marsupial lineages likely occurred near the Cretaceous–Paleogene boundary. This supports previous findings and highlights the evolutionary and conservation significance of deep marsupial clades. Our results also show that removing a single outlier calibration can substantially reduce discordance in divergence time estimation. This framework provides a practical tool for evaluating calibration reliability in large, multi-gene phylogenomic datasets.

Why does eusociality evolve so often in the Hymenoptera?

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The order Hymenoptera (ants, bees, and wasps), is widely recognized for the repeated evolution of complex societies. These societies are termed eusocial and are formally defined by three life-history traits: co-operative brood-care, reproductive division of labour, and overlapping generations. In nature, hymenopterans present a diverse range of social organisations across the continuum from solitary living to advanced eusociality. Eusociality has independently evolved at least 12 times across the Hymenoptera, a frequency proposed to derive from a repeatedly co-opted ancestral molecular toolkit. Identification of toolkit genes may provide candidates to address the diverse economic and ecological effects of advanced eusocial Hymenopterans such as honeybees, fire ants, and yellowjacket wasps.

Previously, a paucity of genomic resources and inconsistent methods of classifying social organization prevented a comprehensive comparison across most independent eusocial lineages to identify toolkit components. Over 400 unique hymenopteran species now have publicly available genomes on NCBI, and when combined with an additional genome generated from this study, these species span at least 10 independent evolutions of eusociality. We use a consistent social classification method in combination with the ortholog identification program OrthoFinder to identify eusociality-associated genomic patterns, comparing the most eusocial lineages in relation to the toolkit theory to date.

CYP2D6*71 is a poor metaboliser allele common in Polynesian and Māori people and absent from Europeans

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CYP2D6 is an important liver protein that metabolises many drugs. The *CYP2D6* gene is extremely polymorphic, which can lead to variable activity of *CYP2D6*, and risks of adverse drug reactions. However, the full extent of variability in *CYP2D6* is unknown, particularly for understudied populations. In prior work we showed that an allele called CYP2D6*71 which is not observed in Europeans, constitutes close to 10% of alleles in Māori and Pasifika people. Understanding the functional impact of the CYP2D6*71 allele is crucial to allow accurate inference of drug metabolizer phenotypes.

The key CYP2D6*71 variant (rs118203758) is a G42E substitution in the N-terminal membrane insertion region of CYP2D6. We tested the functional impact of this variant by identifying several individuals with CYP2D6*71 homozygote or heterozygous with a known null allele, then using mass spectrometry to detect the metabolic products of solanidine, a recently described biomarker for CYP2D6 activity, in stored plasma samples. In these cases, evidence for negligible metabolism of solanidine could be seen, which indicates that CYP2D6*71 is most probably a non-functional, poor metabolizer allele. Given the prevalence of this allele in Aotearoa-New Zealand *CYP2D6* testing in this country must include CYP2D6*71 to ensure phenotypes are correctly inferred.

Tracing the genetic basis of resilience to climate change in green-lipped mussels (kuku)

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Molluscs such as the green-lipped mussel or kuku *Perna canaliculus* are vital to our ecosystems and taonga (treasured species) of cultural and economic importance. Climate changes, including temperature extremes and ocean acidification, threaten this species, but some lineages are more resilient to these issues than others. The source of this resilience is unknown, but differences in early development are well implicated, and a degree of heritability has been noted for this trait. It is thought that slight heterochronic shifts and changes in gene expression allow differences in phenotype, conferring some individuals with an ability to survive in these conditions.

Using cutting-edge approaches, we aim to pinpoint the key differences exhibited by resilient kuku. We have assembled the genome of this species to an excellent standard. We are now leveraging this resource to determine the molecular mechanisms underlying resilience, using a range of approaches including single cell

RNA sequencing (SPLiT-seq), WGBS, and more traditional genotyping techniques. These novel genetic and molecular tools have the potential to be transformative in industry, while allowing significant scientific breakthroughs in our understanding of mollusc growth, development and genetics.

Functional validation of three candidate causal variants in the *xanthine dehydrogenase* gene associated with feline xanthinuria

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Xanthinuria is an autosomal recessive disorder caused by variants in *xanthine dehydrogenase* (*XDH*) or *molybdenum sulfurase* (*MOCOS*) genes in humans. In feline xanthinuria, three candidate causal variants in the *XDH* gene have been identified to date. *XDH* is a key enzyme in the metabolism of purines to uric acid, and disruptions in the normal purine metabolism result in the accumulation of xanthine in the urine. Due to its poor solubility, xanthine precipitates to form crystals within the urinary tract, potentially resulting in life-threatening blockages. Affected cats present with symptoms commonly associated with feline lower urinary tract disorder (FLUTD). The aim of this study is to assess the functional relevance of identified feline variants. Wild type and variant *XDH* cDNA will be constructed, cloned into a mammalian expression vector, and transfected into a mammalian cell line. Protein expression will be determined prior to combining wild-type and variant proteins with xanthine. The resulting metabolites will be analysed using High-Performance Liquid Chromatography (HPLC) to evaluate *XDH* activity. Identifying causal variants will not only aid veterinarians to diagnose and manage feline xanthinuria but enable the potential for genetic testing to assist with breeding programs and identify at risk cats.

Transcriptomic analysis of prostate plasticity in a seasonal breeding marsupial (*Trichosurus vulpecula*; brushtail possum)

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Seasonal breeding in male brushtail possums (*Trichosurus vulpecula*) triggers massive changes in prostate size and activity—including a four-fold increase in size in preparation for breeding followed by rapid regression. Despite these extreme seasonal changes and their link to reproductive fitness via seminal fluid production, the genetic mechanisms involved in turning the possum prostate 'on' and 'off' are unknown.

Here I used RNAseq to profile global gene expression patterns of possum prostates throughout the year (n=38). Using DESeq2, I found that active (breeding) and inactive (non-breeding) prostates exhibit different profiles of differentially expressed genes (DEGs). Compared to inactive prostates, those at peak activity show enrichment for GO terms associated with lipid and polysaccharide secretion, as well as cell death, suggesting genetic preparation for regression occurs well ahead of morphological changes. Different prostate regions also show significantly different gene expression patterns (>7000 DEGs) indicating different roles in seminal fluid production.

As the first transcriptome of the marsupial prostate, this work reveals core genetic processes underpinning seasonal reproduction in mammals. Given that possum prostates resemble those of humans, and that their seasonal growth mimics benign prostatic hyperplasia in men, genes involved in prostate regression could also make useful therapeutic targets.

Concordance and drivers of New Zealand marine coastal connectivity

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In recent years there have been great strides made in the sophistication and detail of the collection and analysis of marine genetic connectivity within single species, However, the methods of comparing connectivity across species, and linking this with biophysical dispersal models, have been much slower to develop. This is problematic, as it is becoming clear that an understanding of the patterns of concordance in connectivity across multiple species is necessary to better comprehend community-level patterns, and integration with predicted dispersal patterns provides insights into the common drivers of those community patterns. Here, a novel approach, "genogeographic clustering", was used to determine concordance of spatial population structure in a community of 21 species of coastal marine organism in New

Zealand waters. These results were then integrated with predicted patterns of larval dispersal derived from Lagrangian tracking with a nationwide circulation model. This approach shows promise in helping us determine both the concordance in spatial patterns among species in a community, and the potential physical and biological processes driving those patterns.

Mutation rate and selection in the unusual duplicated mitogenomes of Australasian stingless bees

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The overall architecture of the mitochondrial genome (mitogenome) is highly conserved, particularly in animals. However, there are exceptions: the mitogenomes of the Indo-Malay/Australasian (IM/AA) clade of stingless bees (Apidae: Meliponini) were recently discovered to exhibit long inverted repeats. Depending on the species, these mitogenomes contain two identical copies of either all, or some, mitochondrial genes. Here, we investigated the ratio of mitochondrial to nuclear mutation rate and selection pressures experienced by the amphimeric mitogenomes found in the IM/AA clade, in comparison to related stingless bees, in order to investigate links between mutation rate and the amphimeric mitogenome structure. This analysis was conducted in silico using assembled mitochondrial and nuclear genes from species taken from across the three main clades of Meliponini, with the use of several newly sequenced mitogenomes. Given the potential for mitogenome structure and mutation rate to impact co-evolved nuclear genes, we examined the possibility of mito-nuclear co-evolution in the stingless bees and the role it may have played in divergence within the IM/AA clade. Through this comparative examination of stingless bee genomes (both mitochondrial and nuclear), we contribute to an increased understanding of mito-nuclear co-evolution and speciation of the Australasian stingless bees and beyond.

A Salinity Gradient Drives Local Adaptation in Baltic Pipefish Despite Gene Flow

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While environmental factors can drive genetic differentiation in marine species, their influence along environmental gradients remains poorly understood. The Baltic Sea, with its pronounced salinity gradient (1–25 Practical salinity unit), provides an opportunity to examine salinity-driven genetic patterns in marine populations. Here, we test the hypothesis that salinity gradients contribute to population structuring in *N. ophidion*, potentially driving ecological isolation. To this end, we collected 233 individuals from six locations within the Baltic Sea that differed in salinity. To assess population structure and migration events between populations, we conducted FST, PCA, STRUCTURE, and TREEMIX analyses. Additionally, we identified alleles associated with different salinities at loci detected by FST, RDA, LFMM. Despite low overall genetic differentiation and ongoing gene flow, our findings revealed a clear spatial genetic structure among populations. Importantly, we detected 24 outlier SNPs associated with selective pressures, consistently identified across all three independent methods. Moreover, Mantel test results indicated that these outlier SNPs were more strongly associated with salinity than with geographic distance. One of the outliers, lrrc8da, is known to play a role in osmoregulation during notochord development in teleost, suggesting a potential mechanism by which environmental gradients may shape population structure through early developmental adaptation.

Building a genomic data repository for taonga species in Aotearoa New Zealand

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The Aotearoa Genomic Data Repository (AGDR) is an Aotearoa-based resource that enables researchers and Māori communities to fulfil their obligations relating to the guardianship, management, sharing and use of genomic data from biological samples that are *taonga* (precious or treasured). The AGDR was jointly developed by Genomics Aotearoa and the New Zealand eScience Infrastructure, with funding from the Ministry of Business Innovation and Employment. Its design is based on the principles of Māori data sovereignty, enabling *kaitiaki*- (Māori guardianship) centric control over who can access genomic data, and for what purposes. The AGDR has been developed in line with the globally-relevant CARE Principles and FAIR Principles, ensuring data is

findable, interoperable, and re-usable in cases where there is prior and informed consent, and access is provided by kaitiaki. Four years since the initial launch, we will provide an update on the current state of the AGDR, including metadata dictionary development and evolution, the use of Biocultural Notices and Labels and the role of the AGDR Advisory Board. We will also present some potential future directions of the repository over the next five years.

Bridging the Gap: Translating Genomic Knowledge to the Grassroots Level – Challenges and Opportunities for Registered Nurses

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The rapid advancements in genomics offer unprecedented opportunities for personalized and precision medicine, promising improved patient outcomes. However, translating genomic knowledge to the grassroots level—specifically registered nurses (RNs), who form the largest healthcare workforce globally—remains a critical challenge.

Research examining genomic literacy among RNs, including comparative studies conducted across three countries with similar educational systems, consistently highlights both low overall knowledge and commonly held misconceptions. Despite the increasing relevance of genomics to clinical practice, gaps in foundational knowledge persist due to inadequate incorporation of genomics into nursing education and continuing professional development.

The lack of structured educational frameworks, resource constraints, and minimal emphasis on genomics within nursing curricula contribute to the disconnect between scientific discovery and practical application. These barriers hinder the ability of RNs to effectively integrate genomic knowledge into their practice, compromising their capacity to participate meaningfully in precision healthcare.

This presentation will discuss strategies to address these challenges, including the development of accessible and relevant educational programs, fostering interdisciplinary collaboration, and leveraging technology to enhance knowledge translation. Drawing upon recent research, including an international study on nursing students' genomic literacy, we will outline a pathway toward enhancing genomic literacy at the grassroots level.

Pītau Error: A Resource for Teaching Genetics and Te Reo Māori

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Pītau Error® is a game I invented in 2022 to teach a Genetics module for Science Wānanga – an initiative held on marae (traditional meeting houses) to engage tauira Māori (students) with sciences. I designed Pītau Error® to (1) encourage tauira to draw upon familiar knowledge systems to comprehend complex genetics concepts, (2) accommodate for tauira aged 4-17 with varying levels of prior understanding, (3) reduce the knowledge burden on science teachers, and (4) capitalise on the passion of outreach scientists for improving science literacy nationally.

In this presentation, I will use the physical Pītau Error® cards to demonstrate how they can be used to (1) illustrate genetics concepts of increasing complexity in English-medium, bilingual-, and Māori-immersion classes using simple and familiar language, (2) dissect elements of English and te reo Māori grammar, and (3) teach reo Māori to English-speaking classes. I will also briefly discuss the vision I have for an equitable rollout of Pītau Error® to schools across Aotearoa, further development of accompanying resources such as tutorial videos filmed with outreach scientists, and an establishment of a Charitable Trust for providing copies of the game to low-income schools.

Investigating crossover and non-crossover recombination rates in aye-ayes (*Daubentonia madagascariensis*)

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Meiotic recombination consists of the genetic exchange between homologous chromosomes and, coupled with mutation, is a primary source of variation. It is driven by the repair of DNA double-strand breaks which are resolved either as crossovers or non-crossovers (*i.e.*, with or without an exchange of flanking markers). Crossovers often span multiple kilobases and, due to their relatively easy detection, have been studied in a variety of species. In contrast, non-crossover tract lengths are short (several base pairs) and thus, despite accounting for the majority of recombination events, they remain less frequently explored. However, several studies have recently

begun to describe the non-crossover landscape in a small set of primates, including humans (as a representative of hominoids) as well as baboons and rhesus macaques (as additional representatives of catarrhines). To expand upon this previous work, we here use a pedigree-based approach to infer both the crossover and non-crossover recombination landscape of aye-ayes (*Daubentonia madagascariensis*) – a strepsirrhine representative and one of the world's most endangered primate species. Additionally, comparative analyses allow us to address similarities and differences in the rates and patterns of recombination across the primate order.

PhyloG2P: Expanding genotype to phenotype maps in the age of genomics

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Genotype to phenotype mapping has long been expected to be revolutionised by the growing abundance of fully sequenced genomes from across the tree of life. However, a mountain of genomic data alone will not produce this revolution, and rigorous statistical approaches are required to make sense of large-scale genomic data. One such statistical approach are so-called PhyloG2P methods. These methods take advantage of convergent evolution across phylogenies to map genotype to phenotype, and they offer a compelling framework through which to take advantage of the wealth of genomes now available. Of particular interest, PhyloG2P methods can uncover the genetic basis of trait variation between species, which may be beyond the reach of standard population genetics approaches.

In this presentation, based on a review paper we have recently written, I will introduce the concepts of PhyloG2P analysis with examples of their application. I will also discuss recent developments that allow for these methods to be applied to quantitative traits.

Development of eDNA sampling detection methods for early detection of pathogens from on-farm water sources

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Early detection of livestock pathogens is essential for mitigating risks and implementing effective control or eradication strategies. However, current pathogen surveillance methods rely on host sampling, which limits spatiotemporal coverage. Environmental nucleic acid (eNA) sampling is a promising method for pathogenic surveillance of microbial and viral communities relevant to livestock health and may assist in early detection and monitoring of livestock disease. On-farm water points offer a promising alternative source for detecting pathogenic eNAs, but effective field sampling protocols remain underdeveloped. In this study, we evaluate optimal eNA sampling protocols to support surveillance that may assist in the early detection and monitoring of livestock disease. We evaluated the performance of four water sampling approaches – syringe, cartridge, funnel and passive filters – to detect and capture eNA bacterial and viral communities from livestock troughs. Our results showed that all tested sampling methods were effective at capturing bacterial and viral eNA. Filter pore size had the greatest influence on filtered volume, with larger pores allowing greater water throughput, however, total DNA concentrations were lower when using syringe filters. Despite this, syringe filters were the most cost-effective and are recommended for large-scale sampling by industry and landholders. As eNA provides occurrence data (presence/absence), there is a risk of false positives and we do not recommend replacing current surveillance methods, but rather using eNA detection as a complementary tool to enhance early warning and support pathogen risk identification.

Evolution in action: how human-driven deforestation is driving rapid adaptation in our endemic insects

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Under the fast-changing conditions of the Anthropocene, species must either disperse, adapt, or face extinction. However, the extent to which wild populations can adapt to rapidly shifting environmental conditions remains controversial, as evolution is typically considered to be a slow, incremental process. While the biological effects

of some anthropogenic pressures – such as pollution and overfishing – have been well studied, the evolutionary consequences of human-driven forest loss are largely unknown. In this study, we used broad-scale ecological sampling to show how recent deforestation across Aotearoa has driven rapid and repeated shifts in wing length in the polymorphic stonefly *Zelandoperla fenestrata*. Through whole-genome re-sequencing, we identified key genetic variants in the *AGGF1* gene underpinning wing loss, and show how selection on standing genetic variation has driven rapid evolution in this species. Our results highlight the capacity of our endemic species to respond to environmental change, providing an exciting new "textbook example" of anthropogenic evolution.

Evolution experiments in invasive blowflies: genetic bottlenecks and fitness outcomes

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A fundamental question in invasion biology is why some invasions fail, and others succeed. In fact, we often cannot even ask this question, because we typically lack data from failed invasions. In the Invasomics Lab, we work on a suite of invasive blowfly species that enable us to test key predictors of invasion success in a tractable experimental model.

In this talk, I will discuss our recent findings around the effects of genetic bottlenecks on fitness outcomes in the invasive blowfly, *Calliphora vicina*. We first investigated standard population genomic metrics for wild-caught samples (20,501 SNPs) and found low overall genetic diversity consistent with recent invasion to Aotearoa New Zealand. Next, we created inbred and outbred lines of *C. vicina* in the laboratory and found significant reductions in fitness for the inbred relative to the outbred lines. Interestingly, fitness effects differed across the phenotypic traits we measured, and none were high enough to cause population collapse – suggesting some potential for compensatory effects in *C. vicina*, even when highly inbred.

Following this pilot study, we are now in the midst of a major longer-term experimental evolution study that will track the genotypic and phenotypic changes that occur in inbred versus outbred lines over the course of multiple generations. I'll wrap up the talk by describing this exciting new experiment and the insights we expect to gain about how successful biological invasion proceeds at a mechanistic level.

Sheep models of Alzheimer's Disease

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Alzheimer's disease (AD) is a devastating neurodegenerative disease. The prevalence is rapidly increasing due to an ageing population worldwide, creating a looming population health crisis. Many rodent models of AD have been created, but none capture the full symptomatology without massively overexpressing multiple human mutations in transgenes, which creates problems for preclinical therapeutic testing. Here we present two large animal sheep models of AD with a single mutation in either the native *APP* or *PSEN1* gene. The gene edited sheep were produced by injection of CRISPR-Cas9 RNP complexes, including a single strand donor DNA carrying the *PSEN1* E280A or *APP* Swedish mutation, into single cell zygotes, which were then implanted. The founder lambs were whole genome sequenced to confirm zygosity. The *PSEN1* founders including a homozygous, two heterozygous and two hemizygous sheep. The *APP* founders were both heterozygous. No off-target editing was detected. All animals are outwardly healthy and growing normally. F1 offspring have been bred from both lines. Both lines have a consistent CSF and plasma biomarker phenotype which corresponds to human carriers. The *PSEN1* line has an Aβ1–42:Aβ1–40 ratio skewed in favour of Aβ1–42 and the *APP* line shows massive overproduction of both Aβ peptides.

Sex-specific expression of miRNA clusters in the honey bee parasite, *Varroa destructor*

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The honey bee mite, *Varroa destructor*, is one of the biggest threats to the western honey bee, *Apis mellifera*. Yet, little is known about microRNA (miRNA) expression throughout the mite lifecycle, or how miRNAs are involved in development and sex differentiation. Here we identify the complete set of miRNAs in *V. destructor* by sequencing the small RNAs of male and female *V. destructor* throughout its lifecycle. We identify 171 precursor miRNAs, including 88 novel miRNAs specific to mites. miRNA expression varies significantly between life stages, revealing miRNAs specific to developmental stage and sex. Reproductive adult females (foundresses) show an expression pattern distinct from other adult females, which is largely driven by three significantly upregulated miRNA clusters, indicating a role for miRNA regulation in reproduction. Additionally, a cluster of three miRNAs from a novel miRNA family (vde-miR-nov-1) are significantly upregulated in all females compared to males, which may indicate the role of miRNAs in sex determination and differentiation. Our results demonstrate that miRNA regulation has a critical role in the biology and development of *V. destructor*. Characterising the downstream impacts of miRNAome expression will enable a better understanding of mite development and reproductive processes, providing targets for future control methods.

Chromosomal Inversions Facilitate Adaptive Divergence with Gene Flow

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How the evolution of new ecotypes or species proceeds in the face of ongoing gene flow remains a fundamental question in evolutionary biology. Through comprehensive population genetic analyses of parapatric population pairs of *Senecio lautus* wildflowers at six locations, we identify chromosomal inversions that play a critical role in the independent and repeated evolution of distinct populations of headland ecotypes, from adjacent dune populations. By employing genotype-environment association analyses and gene functional enrichment approaches, we demonstrate how inversions contain genes associated with adaptation to divergent soil conditions in dune and headland environments at multiple locations, suggesting inversions are under selection. Furthermore, we show that inversions exhibit greater divergence between ecotypes as gene flow increases, suggesting a direct role for chromosomal inversions in overcoming the homogenizing effects of gene flow. By utilising a unique

system of replicated evolution, these findings progress our understanding of the genomic architecture underlying local adaptation and speciation with gene flow.

Evaluating the genetic connectivity of false killer whales (*Pseudorca crassidens*) in Aotearoa New Zealand

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In group-living animals, social behaviours influence gene flow and can shape population-level genetic variation. The false killer whale (*Pseudorca crassidens*, FKW) is a highly social, elusive cetacean with complex societal organisation. Social groups, defined as individuals in constant close association, typically have low mitochondrial DNA (mtDNA) haplotype diversity and may have restricted gene flow between them, despite overlapping ranges. Stranding records suggest FKWs are widely distributed around Aotearoa New Zealand (NZ) waters, yet only two social groups of approximately 50 and 80 individuals have been identified through long-term research. These social groups inhabit the northeastern coast of Te-Ika-a-Māui, the North Island, during austral summers, however their population status and kinship patterns remain unclear. Remote biopsy skin samples from the two well-studied social groups (n1 = 29, n2 = 57) are used in combination with country-wide strandings samples (n = 52) to assess genetic connectivity among NZ FKWs. We will use mtDNA control region and ddRAD sequencing to determine population structure, genetic diversity and kinship of known social groups and stranded whales, grouped by region. mtDNA analyses has revealed important connections between regions, with nine haplotypes across all samples, including five new haplotypes, and moderate haplotype diversity (0.498, SD ± 0.001).

Sex-dependent Prediction of Autism

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Several models have been developed to predict autism using genetic information. Autism has a male-to-female diagnosis ratio of 4:1; however, the influence of biological sex on prediction outcomes remains underexplored. We present an ensemble model to predict autism, integrating polygenic risk scores (PRSs), common genetic variants, and autism associated genes with the MSSNG whole genome sequencing dataset. Following training, our model achieved an accuracy of 0.68, an area under the curve (AUC) of 0.72, and a recall of 0.77 on the test dataset. Common variants contributed more significantly to autism prediction in males than females ($p < 0.001$). The 16p11 locus was particularly predictive for females ($p < 0.001$). Gene enrichment analysis using the Allen Brain Atlas revealed that expression of female autism associated genes was enriched (FWER < 0.05) in the primary somatosensory cortex, inferior parietal cortex, and parietal neocortex during fetal development. Male autism associated gene expression was enriched (FWER < 0.05) in the dorsolateral prefrontal cortex and anterior cingulate cortex across development (fetal to adult). These findings underscore a sex-dependent role for common genetic variants in autism development. They highlight the utility of ensemble models incorporating common variation and biological sex for autism prediction.

The effects of maternal age on offspring global gene expression

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Ageing and senescence are ubiquitous phenomena across the natural world, profoundly impacting humans and other animals. The functional decline brought about by aging can significantly impair reproductive performance in parents and can result in reduced viability and lifespan in their offspring. Currently, the genetic and epigenetic mechanisms by which parental age affects offspring remain largely unknown. These effects could represent an important, yet underexplored, source of variation in offspring fitness, lifespan, and species-specific reproductive strategies in nature and they may also directly impact human health. Here, we utilized the clonal system of F. candida to test the effect of parental age on offspring global gene expression. We begin by comparing transcriptomic profiles between old mothers and young mothers to look for global epigenetic signatures of senescence. Then, we compare gene expression differences between the offspring of those old and young mothers to see if these epigenetic signatures are translated to the next generation.

This study presents itself as a starting point for understanding the molecular underpinnings for reduced fitness in offspring resulting from older parents.

Genetics to the rescue? Developing high-quality genomic resources for a critically endangered bird

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The Chatham Island black robin (*Petroica traversi*) is a Nationally Critical bird species restricted to two offshore islands (Rangatira and Mangere) in the Chatham Islands archipelago. To reduce the high extinction probability of the smaller of the two populations, ten females were translocated from Rangatira to Mangere in 2022. We are combining extensive genomic and ecological data to investigate the relative influence of genetic factors (i.e., reduced inbreeding and increased genetic diversity following admixture) and demographic factors (i.e., the reduction of a male-biased sex ratio and addition of breeding females) on improved vital rates and population persistence following genetic rescue. Here, we share the development of foundational genomic resources for the Chatham Island black robin, including a long-read reference genome and a short-read whole genome resequencing dataset for the entire study population over four generations. We demonstrate the utility of these resources for precisely estimating genome-wide diversity and admixture in a highly inbred bird. In addition to directly aiding the conservation management for an iconic species endemic to Aotearoa New Zealand, this unique dataset opens the door to an in-depth elucidation of the mechanisms behind genetic rescue as a conservation strategy.

Using Novel Approaches to Incorporate Higher Order Interactions into Polygenic Risk Score Calculations for Use in a Clinical Setting

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A polygenic risk score (PRS), important to the advancement of personalised "precision" medicine, quantifies an individual's genetic predisposition to disease. While PRS can help identify individuals at higher risk before disease onset, they currently explain only a small portion of heritability, limiting their accuracy and clinical utility. Current PRS calculations use only "G" SNPs summary statistics from Genome

Wide Association Studies (GWAS) and do not account for epistatic gene-gene ("GxG") and gene-environment ("GxE") interactions. My recently completed PhD research improved PRS calculations to include non-additive effects of higher order GxG and GxGxE interactions (where "E" comprises data from electronic health records). These methods utilized machine learning and Shapley values for G and GxG feature selection in addition to novel methods developed for GxGxE feature discovery. I used these methods to predict type 2 diabetes (T2D) risk in 67,402 UK Biobank individuals, identifying distinct risk cohorts—traditional G, GxG, and GxGxE—and capturing 47% more T2D cases otherwise missed by PRS based on single-SNP effect sizes. These findings helped define T2D subtypes and postulate cellular mechanisms and lead to the development of a clinically relevant "PRScr-mult" model integrating multiple epistatic interactions into risk assessments validated against commonly used clinical measures.

The power of reanalysis for neurodevelopmental conditions; identifying new variants and reinterpreting old findings

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Variants of uncertain significance (VUS) for rare conditions pose a significant challenge in human genetics, with most VUS lacking functional evidence or population-level recurrence to improve the accuracy of clinical classification. With the rapid development of genetic testing in healthcare and research, reinterpretation of previously identified VUS is critical. Here we present two cases, which following reanalysis led to variant reclassification/identification and downstream functional evaluation. For one participant, reanalysis of clinical exome sequencing revealed a heterozygous missense variant in *CHD3* (p.Arg579Gln), a gene with a recently characterised neurodevelopmental condition that aligned with the participant's phenotype allowing the return of the result to the family. For another participant, a p.Pro106Leu variation in the *PPP1R3F* gene (a brain-expressed glycogen-targeting subunit of protein phosphatase-1) had previously been classified as a VUS. *PPP1R3F* has recently been implicated in an X-linked neurodevelopmental condition, but with limited understanding of the functional impact of variants on brain glycogen metabolism regulation. Using CRISPR-Cas9, we have edited our candidate variant into the U87-MG glioblastoma cell line to ascertain its impact on glycogen metabolism and thus its clinical relevance for this family. These two cases are clear examples of the importance of VUS reanalysis when previous genome-wide testing was uninformative.

Diploid near-gapless reference genome assembly of the Longspine sea urchin, *Centrostephanus rodgersii*

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Despite the utility of reference genomes across taxonomic groups, many species with important ecosystem roles, such as sea urchins, trail behind more charismatic or economically important species in their genomic resource availability. The longspine sea urchin, *Centrostephanus rodgersii*, is a subtropical-temperate species that is extending its range and increasing in abundance under current climate change conditions. This positive climate change response creates negative social, economic, and ecological impacts due to their voracious consumption of kelp forest assemblages. To add a genomic resource for an underrepresented class of organisms and to inform management of *C. rodgersii*, we created a diploid high-quality reference genome using Oxford Nanopore Technology long reads, Illumina short reads, and Hi-C data. The two haplotypes each contain 23 scaffolds, representing 22 chromosomes and the mitochondrial genome, have 99.48% and 99.37% completeness, and are lengths of 914.4 Mb and 912.9 Mb, respectively, with high (2.3%) heterozygosity between them. Additionally, syntenic comparisons were made with other sea urchin genomes to identify conserved regions across large evolutionary distances within class Echinoidea. This genome can be used to further understand climate change responses within this class of organisms and to understand population genomics for *C. rodgersii*.

The evolution of olfaction in whales: A genomics approach

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Major evolutionary transitions, such as the shift of cetaceans from terrestrial to marine life, can put pressure on sensory systems to change. Relatively little is known about the role of smell in the evolution of mysticetes (baleen whales). While their toothed cousins, the odontocetes, lack the anatomical features to smell, it is less

clear whether baleen whales have retained this sense. To address this question, we mined the olfactory genes from available cetacean genomes. For the signal transduction and chaperone genes we examined, all were intact in mysticetes, compared with inactivating mutations observed in many odontocete homologues. We analysed genome quality assessment methods (BUSCO vs N50) and developed an automated pipeline for identifying odorant receptor (OR) genes (GMPipe). Using this novel pipeline, over 700 OR genes were recovered from eight mysticete genomes. While many OR groups had been lost or showed signs of random drift, others exhibited evidence of evolving under purifying or positive selection. One orthologous group in particular from the OR10 family showed signs of relative expansion and purifying selection. Overall, our results support baleen whales having the ability to smell, with evidence of specialisation to a new olfactory landscape.

Genetic adaptation of introduced rusa deer to highly variable climatic environments in Oceania

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Rusa deer (*Cervus timorensis*), native to Indonesia, have been introduced and are established across Oceania region. These populations were formed from independent and serial introductions, as well as admixture events, making rusa deer an excellent model for studying how introduction patterns and differing environments affect evolutionary trajectories. This project aims to test the hypothesis that genetic variation within introductions will be related to introduction regime and environment gradients and to investigate adaptive genetic variation across rusa deer populations in Oceania. We used samples from introduced rusa deer populations in New Caledonia, New Zealand and Australia to generate comprehensive panels of SNPs using DArTseq. We measured genetic differentiation among these introduced populations, identified associations between genetic variation and environmental variables and detected putative loci under selection. We found a significant positive correlation between genetic distance and environmental distance ($p = 0.001$, $r = 0.665$), indicating that populations exposed to more distinct environmental conditions exhibit greater genetic differentiation. Using three different methods to detect SNPs putatively under selection, we identified a total of 349 SNPs. PCAdapt, Bayescan, and Redundancy Analysis (RDA) detected 10, 41, and 298 outlier loci, respectively. This project provides insights into the genetic basis of adaptation.

Benchmarking and quality control for clinical nanopore sequencing facility for acute care in New Zealand

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There are ~200 children in high-dependency neonatal/paediatric acute care in New Zealand at any time, necessitating a scalable distributed solution for acute care genomics. We have established an expandable clinical pipeline using the PromethION 2 solo system connected to Fabric GEM™ AI-based clinical decision support. During establishment, we performed benchmarking using Global Alliance for Genomics and Health (GA4GH) benchmarking tools and Genome in a Bottle samples HG002 - HG007. Evaluation of ~3.3x10^6 truth single nucleotide variants (SNVs) and ~500x10^3 small insertions and deletion (indels) at between 20-40x coverage identified SNV recalls = 0.992 ± 0.001, precision = 0.997 ± 0.0006, and F1 = 0.995 ± 0.0008 across multiple sequencing runs. Small indels yielded recalls = 0.838 ± 0.043, precision = 0.922 ± 0.019, and F1 = 0.874 ± 0.032. Analysis of the Coriell Copy Number Variation Reference Panel demonstrated reliable large-scale genomic variation detection after only ~2M reads, equivalent to ~2hr sequencing time. Finally, in the validation phase, we identified concordant genetic results across all 22 families processed through our pipeline, conducted in parallel with a clinically accredited facility available to New Zealand clinicians. This demonstrates the feasibility of rapid precision medicine for critically sick children using long-read technology.

Dissecting the regulatory landscape of rs4698413: a causal variant for Parkinson's disease

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Background: Two-sample Mendelian randomization and genome-wide association studies (GWAS) have identified rs4698413 as a non-coding variant associated with Parkinson's disease (PD). However, its functional mechanism remains unclear.

Methods & Results: Using CRISPR-Cas9 genome editing, we introduced a heterozygous (C|T) genotype in KOLF2.1J iPSCs and subsequently reverted it to homozygous (T|T) to assess its regulatory effects. RNA-seq analysis revealed allele-specific reciprocal regulation of *FGF4* and *NT5E*, genes implicated in stem cell differentiation and neuroinflammation. Contrary to initial hypotheses, Micro-C analysis showed that rs4698413 does not physically interact with these differentially expressed genes (DEGs), ruling out chromatin looping as the primary regulatory mechanism. Similarly, DNA methylation analysis identified allele-specific 5mC changes, but these modifications were restricted to non-DEG loci, excluding epigenetic regulation as the main driver.

Instead, bioinformatics analysis (FABIAN, motifbreakR) identified rs4698413 as a SOX transcription factor (TF) binding site, where the T-allele facilitates SOX-dependent activation of *FGF4*, while the C-allele disrupts enhancer function, leading to downstream transcriptional changes. These findings position rs4698413 as a transcriptional regulator in PD, emphasizing the critical role of (TF) binding over chromatin interaction or methylation in regulating disease-associated genes.

Conclusion: This study underscores the importance of integrating genome editing, functional genomics, and epigenetics to decipher non-coding variant function in PD and highlights rs4698413 as a SOX-dependent regulatory element.

DNADRV: getting baseline insect distribution data from eDNA splattered on your car

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Insects underpin many ecosystem processes, from pollination to waste disposal, but are increasingly threatened by climate change altering their habitats, disrupting their life cycles, and intensifying pressures from invasive species, diseases, and extreme weather events. Three climate change application areas requiring urgent research are:
(1) identifying habitats that support insect diversity,
(2) restricting spread of heat-tolerant insect pests/disease-vectors,
(3) climate-induced asynchronies arising between insects and their environment.
Addressing these requires datasets that span large spatial transects, but insect sampling presently tends to use trap data (i.e. point-samples). However, as you travel by car, an incredible diversity of insects fly past you and recede into the distance as you continue along the road. What if the car itself was the sampling tool? Car license plates are a standardized size, gather insects, and we propose them as the novel basis for collecting baseline insect distribution data.

We have optimized and piloted methods to inexpensively identify insects and their commensals (bacteria, fungi, plants) from eDNA traces left on car license plates. Importantly, our project engages with a car using public who might not always consider the impact of climate change on invertebrates and how the demise of insect diversity would alter our world.

Australian Indigenous pangenome to improve genomics research and clinical applications

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The human reference genome is a cornerstone of biomedical research and clinical genomics, providing a coordinate system for functional annotations and a substrate for DNA sequence alignments. However, the current reference genome has diversity representation biases, inaccuracies and it is incomplete. These shortcomings introduce errors in genomics applications, particularly for ancestrally diverse Indigenous populations. In partnerships with Indigenous communities, the National Centre for Indigenous Genomics is developing reference genomes. We have generated 18 high-quality haplotype assemblies with more than 25% chromosomes as T2T. We show variations in chromosome sizes indicative of large-scale genomic

rearrangement and deletion tolerance across human populations. We created pangenome to uncover complex structural variations in medically relevant blood group genes, immune loci, and pharmacogenes that are specific to Indigenous communities suggestive of their adaptive evolution. This genomic resource can transform genetic testing and diagnosis, paving the way for precise, personalized medicine for Indigenous Australians. Through the nationally collaborative Australian Alliance for Indigenous Genomics (ALIGN) program, we aim to influence clinical genomic services and research practices in the use of pangenome resources.

Genetic connectivity in a skink with geographic variation in reproductive mode

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The skink *Saiphos equalis* is only one of three vertebrates in the world to display oviparity (egg-laying), viviparity (live birth), and a "transitional" intermediate reproductive mode within the species. We analysed population structure, divergence, and gene flow dynamics between populations of different reproductive modes to investigate how these reproductive modes might be maintained within *S. equalis*, and whether there is evidence of admixture between egg-laying and live-bearing populations. Our initial population structure analysis found potential admixture between an oviparous and transitional population, which we explored further with more fine-scale analyses of populations along a viviparous-transitional-oviparous continuum, within a 100 km transect in central NSW. Analysis of this transect found no evidence of admixture; populations were highly structured. We suspect the initial apparent admixture observation was a result of isolation by distance patterns at the whole-species level. Additionally, we found relatively high divergence among populations and limited gene flow, even between populations of the same reproductive mode. We predict that gene flow may be limited by potentially low dispersal ability in *S. equalis* and landscape features acting as barriers, resulting in rapid divergence and local adaptation driving the evolution of multiple reproductive modes within the species.

Population genomics analysis of ngā roimata ō Tohe (*Pimelea eremitica*) to inform the conservation strategy for this taonga plant species

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Ngā roimata ō Tohe (*Pimelea eremitica*) is an endemic, low sprawling shrub which is listed as a nationally critical threatened plant species in Aotearoa New Zealand. The only known wild population occurs on Maringinoa, which is an exposed summit of a large basaltic outcrop of Maunganui, located on the west coast of Te Taitokerau (Northland). Despite an extensive conservation effort over the last 20 years, the wild population has declined to severe critical levels. With approximately 140 individual clone plants currently held in nursery, all with a known origin to a wild or nursery-raised parent plant, individuals from different family lines were selected and sampled. We performed a population genomic analysis using 2,314 SNPs generated de novo. As predicted, analyses revealed the presence of many clones from previous propagation events within the population, with the extant population consisting of 11 to 12 unique plants from a total of 24 sampled. Estimates of relatedness were high with many plants being either first- or second-degree relatives, indicative of inbreeding within a closed population. Estimates of self-relatedness were congruent with this assessment and revealed that heterozygosity has been lost in the Maringinoa population over time, with plants sampled most recently being the most inbred. In contrast, plants sampled in the 1990's which are now mostly extinct in the wild not only demonstrated the highest levels of individual heterozygosity but also represent some of the most differentiated genotypes. Thus, plants propagated from these early sampling events will be vital to future cross breeding attempts aiming to maintaining genetic diversity in the population.

NOTE: This presentation will be co-presented by Taoho Patuawa (Te Roroa) and Dr Sarah Wells (Unitec).

Joint consideration of selection and microbial generation count provides unique insights into evolutionary and ecological dynamics of holobionts

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The relationship between, and joint selection on, a host and its microbes – the holobiont – can impact evolutionary and ecological outcomes of the host and its microbial community. Here we present a novel agent-based modelling framework for understanding the ecological dynamics of hosts and their microbiomes. Our model explicitly incorporates numerous microbial generations per host generation allowing

for selection on both host and microbe. We apply our model to explore community fitness and diversity in the face of rapid environmental change. We demonstrate that multiple microbial generations can buffer changes experienced across host lifetimes by smoothing environmental transitions. Our simulations reveal that microbial fitness and host fitness may be at odds with each other when considering the impact of vertical inheritance of microbial communities from a host to its offspring – where high values favour microbial fitness, while low values favour host fitness – these tradeoffs are minimized when microbial generation count per host generation is high. We suggest that these results arise from 'cross-generational priority effects' which maintain diversity within the community and can subsequently be acted upon by selection. Our model is readily extensible into new areas of holobiont research and provides novel insights into holobiont evolution under variable environmental conditions.

Bones, Barcodes, and Biodiversity – optimising aDNA analyses on tropical sub-fossil collections from the Marquesas Islands

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Molecular techniques offer powerful complementary tools for determining the taxonomic identity of fragmented and morphologically non-diagnostic bone from archaeological and palaeontological contexts. This study focuses on recovery and identification of ancient DNA (aDNA) from tropical bone assemblages, using collections from the central East Polynesian island of Nuku Hiva (Marquesas Islands) as a case study. We illustrate how aDNA sampling strategies, laboratory protocols, primer selection, and sequencing methods can be optimised to improve the recovery and identification of samples from tropical sites and legacy collections. We developed laboratory protocols to optimise aDNA recovery from bone fragments. We then used a combination of Sanger sequencing on larger bone fragments and high-throughput sequencing via bulk-bone metabarcoding (BBM) for pooled smaller bone fragments to amplify and sequence taxonomically diagnostic barcoding regions. To ensure robust identifications, we constructed a custom reference database, tailored to our specific primers, and developed a novel decision tree framework to assign each aDNA sequence to an appropriately supported taxonomic level. We focus on seabirds to illustrate the efficacy of BBM and our protocols to improve aDNA recovery and

taxonomic classification. Our findings demonstrate successful DNA extraction and identifications are possible for bone fragments from tropical sub-fossil collections.

Exploring Fungal Diversity: The Puāwaitanga of Restored Wairarapa Wetlands

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My master's project worked at the interface between mātauranga Māori and science to investigate Māori understandings of fungi in their ecological roles and how fungal community composition in responds to restoration. I interviewed seven Māori who share a connection to Wairarapa and have a passion for nurturing the environment. These interviews revealed that fungi support local environmental aspirations by enriching wetland soils and enhancing ecological functions. To complement these qualitative insights, I used molecular methods to characterise fungal communities, collecting soil samples from 19 sites that represented wetlands in three ecosystem states; pasture, restored, or remnant. Using PCR and sequencing fungal ITS genes, I explored fungal diversity and found no significant effect of wetland state on community composition. By aligning mātauranga Māori with scientific methods, I used a ranked abundance analysis and species-level identification in non-metric multidimensional scaling to highlight endemic and macrofungal species of particular interest to Māori, providing a more holistic understanding of fungal community responses to land use and ecological restoration in Wairarapa wetlands. This rangahau reaffirms the close relationship Māori continue to have with fungi, with the hope that articulating these unrepresented connections will contribute to improved wetland restoration outcomes for Māori.

Can changes in gene expression and splicing explain host specificity of pathogens?

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Blast diseases cause around 40% of crop losses in the world, presenting a significant threat to global food security. Fungal pathogen *Magnaporthe oryzae* can cause blast disease in fifty-odd grasses including the economically important cereal crops like rice. There is substantial host specificity with different isolates of the fungal pathogens being specific to cereal hosts. However, the molecular mechanisms underlying such host adaptation/specificity remains unclear. Here, we compared the transcriptomes resulting from compatible and incompatible interactions between the blast fungal pathogen and specific cereal hosts to assess whether changes in gene expression and splicing could explain host/pathogen specificity. RNA from multiple combinations of compatible/incompatible interactions were isolated and sequenced. Using custom-made computational approaches, integrated with transcriptomics, we are attempting to identify potential regulatory elements governing these interactions. Our preliminary findings have been promising with transcriptomes from compatible interactions being distinct from incompatible interactions, which allow us to get a better insight in to the transcriptional regulation at the host-pathogen interface. Overall, the research findings from this study would shed light on the determinants of host-pathogen interaction. Further, the findings would help us contribute in developing new strategies to reduce the yield losses due to the blast disease.

Mutagenesis of candidate HAT complex genes INHIBITOR of GROWTH in the model legume Medicago implicates them as growth, development and flowering time regulators

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Optimal flowering time is key to productivity, but flowering control in the important legume family is not fully understood. For example, key Arabidopsis regulators, FLC and CO, do not regulate flowering in the temperate legume Medicago. Most plants have two *INHIBITOR OF GROWTH* (*ING*) genes encoding proteins with conserved ING and PHD finger domains. INGs are predicted to function as epigenetic readers in chromatin modifying complexes like HAT. We showed that Medicago MtING2 promotes flowering and growth, but MtING1 did not regulate flowering. The *MtING* double knockout mutants displayed a striking, non-flowering, highly dwarfed phenotype. But interestingly, *MtING* double PHD finger mutants showed only mild

dwarfing and weak delays to flowering, raising questions as to the importance of the PHD finger. Large changes to gene expression were seen in the *Mting2-2* single mutant and the double knockout mutant, with key flowering genes downregulated and predicted floral repressors elevated. MtINGs promoted the expression of Medicago homologs of target genes of the Arabidopsis NuA4 HAT complex. Our findings demonstrate the key combined function the *MtING* genes play in regulation of global gene expression, flowering time and wider development and implicate an important role in epigenetic regulation via HAT complexes.

Taxonomic and biogeographic insights into the Australasian fingerworts in the *Lepidozia ulothrix* clade

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The floras of Australia and New Zealand are characterised by very high endemism of bryophytes. The large genus *Lepidozia* (fingerworts; family Lepidoziaceae) is represented by more than 20 mostly endemic species in these countries. The genus has been monographed in New Zealand, but issues surrounding species circumscription remain. This study focused on the *Lepidozia ulothrix* clade, with members shared between Australia and New Zealand. We performed phylogenetic analyses of multilocus data set and applied several methods for molecular species delimitation. Our results support the conspecificity of *L. serrulate* and *L. ulothrix*, which is compatible with patterns of morphological variation observed in Tasmanian and New Zealand populations. The distribution of *L. septemfida* extends to the Wet Tropics Bioregion of north-east Queensland where the species is represented by a distinct subspecies rather than a completely different species as supported by morphology and species delimitation results. Tasmanian and Victorian specimens previously attributed to the New Zealand endemic *L. hirta* belong to a distinct and unnamed lineage. Our study shows that integrative taxonomic approaches can uncover overlooked diversity and refine existing species circumscriptions, even in relatively well-studied Australasian lineages such as *Lepidozia*.

CHATting with students – my reflections on the use of chat bots within undergraduate biology courses

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Students appreciate rapid responses to course related queries. This can be challenging in large courses or when students are studying asynchronously. In Semester Two 2024, I piloted the use of a Watson RAGbot Virtual Assistant in a large Stage Two Genetics course to explore its potential as a student-facing information resource. I will share my experiences in its use as a course-specific housekeeping tool as well as a content resource for learning. Implementation was straightforward but required consideration to course design and LMS resources. These observations informed the subsequent use of a Cogniti bot, developed for and by educators at the University of Sydney (https://cogniti.ai/). Cogniti is designed to let teachers build custom chatbot agents that can be given specific instructions, and specific resources, to assist student learning in context-sensitive ways. I have implemented a Cogniti Socratic tutor bot in a very large Stage One Cell Biology course during Semester One 2025. Students can have private conversations at their own pace, resolving course concepts problematic to them at that time. I will present data on its use and ability to assist my students in becoming self-regulated learners.

Embedding an interdisciplinary experience into genetics education

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By the third year of an undergraduate degree, students majoring in Genetics are expected to have achieved a level of disciplinary prowess that they can take into their future careers. However, complex global challenges and ‘wicked’ problems rarely align with an individual discipline.

Here I discuss the impacts of integrating a faculty-based interdisciplinary project unit into the Genetics and Genomics major. Genetics students come together with two alternative disciplines to focus on the very relevant and timely complex topic of Survival. Our program involves a combination of disciplinary and interdisciplinary content, with individual and group tasks throughout the semester. Students reinforce knowledge, understanding and application of their discipline while exploring the theme of Survival from their own specialist background, as well as from a wider perspective in interdisciplinary teams, addressing key problems of interest to stakeholders in government.

By actively teaching group work strategies with a focus on collaborative, group project work and monitoring group dynamic over semester, I outline how students learn the

critical ‘soft skills’ that set them up to solve hard problems and work across the disciplinary divide.

Change in honey bee virome due to the arrival of a novel vector

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The arrival of the honeybee parasitic mite *Varroa destructor* in Australia poses significant challenges to the bee industry, given its known role as a viral vector. Current evidence indicates that viruses of concern globally, such as Deformed wing virus, are absent from Australia and did not enter with the varroa incursion. However, Australian bees have several viruses and it is not yet clear whether the impact of these viruses will increase in the presence of varroa.

In this study, we characterised the viral landscape of honeybees as Varroa spread, analysing viral prevalence and load in over 150 samples in Australia’s mite-infested region before, during and after mite establishment. We find a strong correlation between mite presence and two novel rhabdoviruses, Apis Rhabdovirus 1 and 2, which show significantly increased prevalence and viral loads post-varroa infestation. These findings suggest a spillover of these rhabdoviruses into Australian honeybee populations due to the Varroa incursion.

Our work now aims to define the relationship between *Varroa* and the viruses present in Australia to uncover whether *Varroa* is capable of vectoring novel Australian viruses, and discover the impact of these novel viruses on bee health.

Hierarchical Patterns of Soil Biodiversity in Extreme Environments: Insights Across Biological Scales

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Information about geographical patterns of biota, species diversity and distribution, is scarce for soils, despite their pivotal role as ecosystem service providers. The Atacama is the driest non-polar desert on earth and it is believed that only specialized taxa can survive there. Accordingly, only some microbial life-forms and few plants, and vertebrates are present. Above ground invertebrates have been reported in the Atacana Desert but its soils have not been comprehensively analyzed. By studying different areas across the Atacama, we aimed to better understand resilience of soil organisms in times of global aridification. We investigated diversity of soil nematodes at the genomic, genetic, taxonomic, community and life-cycle levels. We found distinct patterns and assemblages along the different habitats in the desert: dune systems, high altitude mountains, saline lakes, river valleys and fog oases. We also observed that distribution of asexual taxa is more likely to occur at higher altitudes, and that the distribution of genera richness in the Atacama follows a latitudinal diversity gradient and is influenced by (rare) precipitation. Our work shows that even under extreme environmental conditions stable, healthy soil communities can persist, but we do see indicators of poor soil food webs.

The genetic and phenotypic correlates of mitochondrial DNA copy number in the Mexican Biobank

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Mitochondria are important components of the cell and mitochondrial dysfunction can be involved in complex disease through alteration in mitochondrial copy number. We analyzed ~4400 individuals from the Mexican Biobank (MXB) to investigate the genetic and phenotypic correlates of mtDNA copy number (mtCN). We computed mtCN using array data and investigated the role of blood cell type variation in mtCN

variation. We performed a genome-wide association study on mtCN and identified three variants rs533353962, rs372129830 and rs867763743 significantly associated with mtCN that are low-frequency variants in MXB (MAF ~0.01) and are rare or absent elsewhere in the world. These fall in *SNAPIN* shown to regulate mitochondrial homeostasis at synapses, *INF2* shown to be involved in stimulating mitochondrial division through mechanisms leading to mitochondrial membrane constriction, and *PKD1*, mutations in which have been implicated in polycystic kidney disease likely through mitochondrial abnormalities. Further, we performed a pheWAS for mtCN with 20 complex traits and observed mtCN to be significantly associated with Creatinine, Triglycerides, Cholesterol, HDL and LDL levels, Diastolic blood pressure and Rheumatoid arthritis (FDR < 0.05). Overall, these results indicate a significant role of the mitochondrial genome through copy number influencing various complex diseases in a population-specific manner.

Swimming in the clouds: novel colour morphs of New Zealand's *Leucocarbo* shags are explained by MC1R polymorphism

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Avian plumage polymorphism provides an ideal model for exploring the ecological and genetic bases of phenotypic diversity, shedding light on adaptive evolution. The Otago (*Leucocarbo chalconotus*) and Foveaux (*Leucocarbo stewarti*) shags are closely related seabird taxa endemic to southern New Zealand. In contrast to their Southern Ocean island sister taxa, which all have pied (black/white) colouration, these 'mainland' taxa each comprise two distinct adult plumage colour morphs: pied and bronze (dark brown). The frequencies of these colour morphs vary with latitude, and they appear to be fully interbreeding. My research aims to discover the evolutionary and genetic bases of this colour polymorphism by employing candidate gene and genome-wide sequencing approaches in a phylogenomic context. Sequencing of the vertebrate pigmentation gene MC1R reveals a novel amino acid substitution in this New Zealand seabird clade that strongly discriminates intraspecific colour morphs. I hypothesise that the novel bronze colouration underpinned by this dominant mutation is an adaptive response to southern New Zealand's cloudy coastal freshwater plumes.

Towards a more holistic assessment of genomic diversity in Aotearoa New Zealand's rarest breeding bird

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Estimates of genomic diversity are often used to assess the 'genomic health' of threatened species. Such assessments generally focus on single nucleotide polymorphisms (SNPs) despite recent methodological advancements facilitating the incorporation of a wider breadth of genomic diversity including structural variants (SVs). We combine a long-read reference genome and short-read whole genome sequence data to provide a more holistic assessment of genomic diversity for the Nationally Critical tara iti (*Sternula nereis davisae*) using both SNPs and SVs. To contextualise these data, we compare estimates made using similar genomic resources for two close relatives, the more populous and widespread Australian fairy tern (*S. n. nereis*) and the Nationally Critical kakī (*Himantopus novaezelandiae*). Tara iti have fewer SNPs, fewer SVs, lower effective population size, lower individual heterozygosity, lower nucleotide diversity and higher inbreeding estimates than AFT or kakī. These data, combined with low reproductive rates, indicate the genomic health of tara iti is poor. Thus, a robust assessment of the risks of both inbreeding and outbreeding depression–conducted in collaboration with the Tara Iti Research Advisory Group and alongside the Tara Iti Recovery Group–is underway to determine if genetic rescue may be an effective conservation action to mitigate extinction risk.

Embracing the Mess: Real Learner Data in Bioinformatics Training

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Bioinformatics workshops are widely used to teach researchers genomic data analysis. These workshops incorporate exemplar datasets that learners work through

in pre-designed analyses. This approach makes the workshop content more accessible for those unfamiliar with coding and ensures that the dataset is thoroughly tested and validated beforehand. However, many genomic analyses rely on fairly standardized genomic data formats, making it feasible for participants to use their own data with minimal preprocessing. I provide an example of a workshop focused on genetic outlier analysis, where I gave learners the option to use their own data. This hybrid approach allows for a more authentic learning experience by enabling attendees to engage with the unique patterns in their own data. Those without their own data benefited from exposure to a diversity of real-world scenarios and collaborative discussion. I discuss some of the extra preparation steps I needed to conduct to prepare the workshop content and talk about some of the limitations that could not be overcome. While this method introduced variability and occasional troubleshooting challenges, it presented opportunities for group problem-solving, a framework for more thorough discussion of the underlying biology, and a richer, more practical learning experience.

From Genes to Green: The Role of Genomics in Native Seed Production

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Demand for native Australian seeds for horticulture and restoration is growing rapidly. Rewilding, revegetation, and carbon offset projects all rely on genetically healthy seeds capable of producing self-sustaining populations. To meet this demand, native seed production areas (SPAs) are being developed. However, SPA-grown seed faces risks, including inbreeding, accidental interspecific hybridization, and loss of genetic diversity. Despite these challenges, genetic tools are not widely implemented in SPAs. As these projects are still in their early stages, best practices for maintaining genetic health—such as careful seed sourcing and mixing to produce climate-resilient seeds—remain poorly understood. We conducted a systematic literature search and found that, despite strong research interest in SPAs, there is a striking lack of genetic resources (e.g., reference genomes, sequencing data) for most species. Furthermore, only a handful of studies have tracked multigenerational changes in genetic diversity within SPAs, and key plant trait groups are largely absent from the literature. To address these gaps, we propose a framework for future research, along with key questions that must be examined to optimize the genetic health and yield of native seeds. Our approach aims to balance ecological integrity with cost-effective management strategies, ensuring SPAs can support long-term restoration success.

Building the Androgen Clock: An Epigenetic Predictor of Long Term Male Hormone Exposure

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Aging is a complex process characterised by biological decline and a wide range of molecular alterations. Epigenetic clocks leverage age-associated changes in DNA methylation to estimate chronological age and identify factors influencing aging. Here, we utilise epigenetic clocks to explore sex differences in biological aging and the female-specific lifespan advantage commonly observed among mammals. We observe an accelerated aging rate in adult male sheep compared to females. Notably, the removal of androgens by male castration decelerates the aging rate, suggesting a causal role of androgens in the sex difference in longevity.

We identify several androgen-sensitive CpG dinucleotides that progressively lose methylation throughout the lifespan in intact males but remain stable in castrated males and females. Using these sites, we develop a novel epigenetic predictor – the Androgen Clock – capable of estimating the period of androgen exposure. Our results show that the clock's 'ticking rate' can be accelerated in female mice by dihydrotestosterone supplementation, or halted entirely in males by castration.

Finally, we explore potential applications of this tool in medicine and agriculture. Beyond this, the Androgen Clock offers a valuable model for understanding age-associated DNA methylation changes by its capacity for manipulation through small molecule intervention without compromising cell survival.

Inbreeding load in a small and managed population: two decades of Hihi/Stitchbird genomics

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The biodiversity crisis has resulted in increasingly small and isolated populations with low genetic diversity and increased inbreeding, which can impact fitness and adaptive potential. While genomics is routinely used to characterise threatened populations, more studies on the dynamics of genetic load and purging are needed to assess management strategies. Our study system is the hihi/stitchbird, *Notiomystis cincta*, a forest-dwelling songbird endemic to Aotearoa, New Zealand. The hihi underwent a prolonged bottleneck on an offshore island and has been successfully translocated to seven North Island sites. We used whole genome resequencing data across two decades from the reintroduced population of Tiritiri Matangi. Low-coverage sequences were first imputed to quantify runs of homozygosity. We tested for inbreeding depression by modelling lifetime reproductive success against genome-wide inbreeding. We calculated genetic load in lethal equivalents using longevity data and quantified the opportunity for purging using the available pedigree. We found high inbreeding levels and some evidence of inbreeding depression within the population. The genetic load detected reflects past bottlenecks and subsequent management. Purging of mildly deleterious mutations could be less effective due to drift and reduced selection. These findings contribute to understanding small population dynamics and the evolutionary mechanisms that affect adaptive potential.

Evolving vertebral counts without evolving the segmentation clock

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A major question in evolutionary developmental biology is how organismal diversity is generated. Lake Malawi cichlid fishes are a fascinating system with which to study this

problem, varying in phenotype but having extremely limited genetic diversity. In particular, Lake Malawi cichlid fish differ in somite counts. We investigated the origin of this evolvability in somite number, as the somitogenesis process is well-understood in other vertebrate species.

We studied two cichlid fish species, *Astatotilapia calliptera* and *Ramphochromis chilingali*, which form 30 and 38 somites respectively. As the rate of segment production is near-identical in both species, we focused on differences in axial morphogenesis during somitogenesis. At the onset of somitogenesis, *R. chilingali* embryos are longer than their *A. calliptera* counterparts, and the pre-somitic mesoderm (which will give rise to the somites) is larger and has more cells in *R. chilingali* than in *A. calliptera*. However, the Tbox genes, which are required for axial elongation in other vertebrates, are expressed identically between the two species, and the dynamics of morphogenesis do not differ between species. This suggests that morphogenetic differences at the onset of somitogenesis can produce phenotypic evolution in somite number, without evolving the process of somitogenesis itself.

Investigating the Genetics Underlying Late Flowering in Perennial Ryegrass

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Perennial ryegrass (*Lolium perenne*) is a critical forage in New Zealand farming systems, utilised due to its high metabolisable energy (ME) content in vegetative tillers. ME availability decreases during the transition from vegetative to reproductive tiller growth, impacting agricultural productivity. Flowering (heading) in perennial ryegrass is induced by long photoperiods after prolonged exposure to cold temperatures and naturally occurs in spring. Genetic variation in the flowering control pathways has been linked to variation in flowering times in other temperate grasses, however this has not been well characterised in ryegrass.

This project focusses on a ryegrass population which has been consistently observed to segregate for floral emergence times, from late October through to mid-December. Using extended daylength experiments we have shown that the photoperiod response plays a role in variable flowering times and genetic analyses have identified variation in Chromosome 4 that is associated with late flowering in this population. We are now exploring variants in putative photoperiod genes in this region of Chromosome 4 to

investigate the function of these genes in ryegrass and identify alleles that could be used for breeding late-flowering ryegrass.

National collaboration provides insight into patterns of strandings of enigmatic beaked whales

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Beaked whales (Ziphiidae) represent one of the most speciose groups of cetaceans, however, their cryptic behaviour and inaccessible habitat make them difficult to study. As a result, most of what is understood of most species of beaked whales has been collated from stranded individuals, and Aotearoa New Zealand in particular is a stranding hot spot. Anthropogenic threats such as naval sonar have been linked to unusual mortality events in beaked whales, raising concerns about the scarcity of knowledge on population size, structure and distribution. This lack of baseline information hinders their conservation and management, especially as many beaked whale species have a global distribution. Here, we utilise the New Zealand Cetacean Tissue Archive (NZCeTA) to provide insight into the spatial and temporal distribution of beaked whales using DNA species identification methods. NZCeTA is a national collaboration effort between mana whenua, Department of Conservation and the University of Auckland – Waipapa Taumata Rau formed in 1991 and currently holds samples from 13 of 24 beaked whale species. Using NZCeTA we aim to elucidate seasonal and sex-biased patterns of stranding mortalities of beaked whale species around Aotearoa, New Zealand. Our goal is to demonstrate the utility of a collaborative national tissue archive and opportunistic data collection to provide baseline data on elusive cetaceans.

Biotech Solutions to New Zealand's Forestry Challenges

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Forestry is New Zealand's third-largest export earner, contributing ~$6 billion annually. However, the sector faces increasing challenges from climate change, biosecurity threats, and the need for more sustainable management practices. Traditional tree breeding is slow, with long reproductive cycles delaying the delivery of improved germplasm. Biotechnology offers transformative solutions to enhance

forest resilience, sustainable increase productivity and provided forest-based biomaterials to replace petrochemical sourced products.

Since the early 1990s, Scion has applied biotechnological approaches to modify and evaluate traits in the conifer species, which constitute approximately 95% of New Zealand's planted forest estate. More recently we have developed CRISPR gene editing protocols for *Pinus radiata* and Douglas-fir, providing a platform for the rapid development of solutions to emerging challenges. Ongoing work uses gene editing to prevent invasiveness (sterile trees), address disease resistance and improve biomass/wood quality. Work will be presented that uses gene editing to modify the composition and structure of *Pinus radiata* cell walls with the aim of improving wood quality and producing woody biomass that is more easily deconstructed to provide feedstocks for a future forest biorefinery.

Decoding the mānuka Microbiome: A Multiscale Approach to Taxonomic and Functional Diversity

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Plants host diverse communities of microorganisms—bacteria, fungi, archaea, and viruses—collectively called their microbiome. These microorganisms play crucial roles in plant health and function, modulating growth, nutrient uptake, stress tolerance, and pathogen resistance. *Leptospermum scoparium* (mānuka) has an intricate relationship with microorganisms, including notable roles in growth and plant protection. We investigated the taxonomic and functional characteristics of the mānuka microbiome, using a multi-tissue, meta-omic approach from plants in our germplasm collection. We also included mānuka samples from five different locations in New Zealand. Genomic read data revealed that the beta diversity is tissue-specific, indicating compositional differences among tissues. Shannon diversity further revealed high bacterial diversity among most tissues, and lower fungal and viral diversity. Fungal diversity was highest in root tissue, and viral diversity was in mature tissue such as old stem, old leaf and root. To explore further,

metagenomic data were assembled into genomes (MAGs), and >270 MAGs were recovered. This dataset is currently being explored, together with meta-transcriptomic data, to investigate putative functional roles of microbes in these tissues. Together, the study results will further our understanding of the mānuka microbiome, emphasizing the importance of both local and spatial factors in shaping microbial communities.

Alternative ribosomal RNAs and their unsuspected link to sex determination in zebrafish

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The ribosome is a ribonucleoprotein complex that has traditionally been thought of as a universal cellular machine translating diverse messenger RNA into protein. Despite this, many vertebrate species possess distinct ribosomal RNA loci, which is suggestive of functional specialisation. For example, zebrafish (*Danio rerio*) possess at least three distinct 45S rRNA-encoding loci, including 45S-M, which lies in the only sex linked region of the genome, and is amplified in the female germline at the time of gonad differentiation[1]. Recently, we showed that targeted mutation of 45S-M ribosomal DNA (rDNA) inhibits feminisation without affecting male development - suggesting 45S-M is both a specialist ribosome locus and a primary determinant of sex[2]. To better understand the locus, we used long-read Nanopore sequencing to overcome the challenge of resolving highly repetitive rDNA. In doing so, we successfully assembled the 45S-M rDNA locus, defining a consensus of 15 full 45S-M rDNA units flanked by a terminal 18S rDNA unit, which is colocalised with the telomere on chromosome 4. Looking forward, long-read sequencing will be combined with targeted zebrafish breeding experiments to determine the minimal rDNA complement required for feminisation. Together, these approaches will clarify the functional role of alternative ribosomal RNAs in zebrafish sex determination.

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A comparative metagenomic study of ancient kurī (dog) palaeofaeces from Aotearoa New Zealand

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Kurī (the now-extinct Polynesian dog) were introduced to Aotearoa by Polynesian explorers upon their arrival about 750 years ago. Coming from the tropical Pacific, they rapidly adapted to Aotearoa's temperate climate and mastered its resources. The diverse landscape and environmental conditions across Aotearoa resulted in varying diets and lifestyles. Palaeofaecal samples from kurī in archaeological sites provide an opportunity to study such geographical and temporal differences in greater detail.

This comparative study presents findings from Next Generation Sequencing shotgun data from sixteen kurī palaeofaeces. Samples included are from Northern and Southern Aotearoa and covers various time periods: initial Māori settlement (1250-1450 AD), the Middle period (1450-1650 AD), and the European contact period (late 18-19th century AD). Included sites are the Long Bay Restaurant site (upper North Island, Early-Middle period, n=4), Kahukura (lower South Island, Middle period, n=4), and two occupation phases at Sealers Bay Camp on Codfish Island/Whenua Hou (Southern Aotearoa, Early period and European contact, n=8).

The focus of this talk will be on the diet of kurī and their gut microbiome. These results are placed in a broader context by integrating them with the archaeological and ethnographic record.

Evaluating the Role of On-Call Genetic Counselling service in a Prostate Cancer Clinic: A Study of Uptake and Family Risk Screening

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Prostate cancer is the second most common cancer in males in Oman. With the rise of precision medicine, targeted therapies and germline genetic testing for prostate cancer have become more common. This study aimed to assess the uptake and impact of an in-hospital, on-call genetic counselling service for the Genitourinary (GU) cancer programme. A retrospective file-based study was conducted using data from the genetic counselling database. A total of 120 prostate cancer patients were seen from September 2021 to March 2025. The number of patients counselled increased steadily, coinciding with the inclusion of an on-call genetic expert in the GU programme. Patients' ages ranged from 41 to 88 years. Among them, 42 had a family history of *BRCA*-associated cancers, 31 had a family history of non-*BRCA*-associated cancers, and 47 had no cancer history. A cancer panel identified pathogenic *BRCA2* variants in eight patients eligible for targeted therapies. This led to predictive counselling and testing for 56 at-risk family members, enabling early screening. Integrating an on-call genetic counselling service into the prostate cancer clinic enhanced patient engagement and helped identify hereditary cancer risks. Continued collaboration between genetic specialists and oncologists is essential for providing comprehensive care and supporting patients and their families in managing cancer risk.

Assessing imputation methods in populations with differing relatedness and inbreeding levels for low-coverage sequencing data

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Low-coverage sequencing (LCS), at 1-fold or lower, followed by genotype imputation has become a cost-efficient approach for obtaining whole-genome SNPs. Several imputation methods for LCS data have been developed over the last decade. However, comparisons of their accuracy in inferring missing genotypes and their effectiveness for downstream analysis such as population genetics have not been

comprehensively studied. In this study, we assessed imputation performance of five different tools: GLIMPSE2, GeneImp, QUILT2, STITCH, and Beagle5.4, using populations simulated by SLiM4 that represent different levels of genetic relatedness and inbreeding. Imputation accuracy was calculated at the level of variant, haplotype, and sample. The effectiveness of using imputed genotypes in recovering genetic structure, relatedness, inbreeding coefficients, and demographic history was also evaluated. The imputation accuracy of different methods was further tested in a real population of 283 hihi (stitchbird) samples. Our results suggest a high accuracy of all the tested methods on populations with high levels of genetic relatedness. Imputation accuracy of different tools and the results of downstream analysis might be affected in different ways across other scenarios of population structure, and thus we recommend applying our simulation and imputation pipeline to determine the most suitable imputation method for different population scenarios.

Swipe left on self-pollen: Uncovering the molecular basis for self-incompatibility in clover

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Clover is the most important pastoral legume to agriculture in New Zealand. Many clover species, including White clover (*Trifolium repens*), are self-incompatible, meaning for fertilisation to occur pollen must come from a genetically distinct plant. Self-incompatibility has slowed genetic gain and limited breeding in white clover as it prevents inbreeding which is needed to purge deleterious alleles and fix beneficial alleles.

Self-incompatibly has evolved in a range of plants resulting in distinct mechanisms across families. Self-incompatibility often originates from a single locus, the *S*-locus, that contains one gene expressed in the male tissue (pollen/anther) and another in the female tissue (stigma/pistil). These genes often encode a complementary set of interacting proteins, a receptor and ligand pair, that underpin the recognition of self or non-self pollen.

We have identified the putative *S*-locus genes in clover and predict that they encode a receptor and ligand. In this research, we aim to validate and characterise the predicted proteins, including their expression patterns, protein-protein interactions and cellular locations. This will uncover the molecular mechanism responsible for self-incompatibility in clover, and ultimately advance clover breeding.

From Genome to Orchard: Exploring functional genomics approaches to accelerate mango breeding

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Mango is a globally popular commercial crop and a leading horticultural industry in Australia. Conventional mango breeding is often limited by the prolonged juvenile phase of trees, which delays the screening of key developmental traits. However, functional genomics and genetic markers can significantly accelerate cultivar improvement and hybridization while reducing uncertainties in trait selection. In this study, several genomic approaches are being employed to understand the genetic regulation of juvenility and precocity (early flowering) in mango.

Preliminary *in silico* variant analysis of cultivars in the Queensland Mango Breeding Program revealed the chromosomal positions and gene-level variant distribution in selected flowering genes. These findings will be further validated through genome-wide association studies (GWAS) by integrating with phenotypic data. Ongoing work includes RNA sequencing to uncover differentially expressed genes (DEGs) governing the juvenile-to-adult phase transition, alongside quantitative trait loci (QTL) mapping in a segregating population to locate potential early flowering loci and genes. Additionally, our proof-of-concept experiments demonstrate that biomaterial-based nanocarriers can facilitate transient gene silencing through RNA interference (RNAi), with future work underway to target flowering genes. Overall, this study lays the groundwork to develop genetic markers to fast-track mango breeding and biotechnological tools for floral pathway manipulation.

DNADRV's school run: the educational benefits of integrating eDNA-based projects into the school curriculum

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Successfully teaching molecular biology to students should result in two alternative outcomes: inspiring further pursuit by some students and that others retain sufficient core concepts to make informed decisions in a future of ubiquitous genomic technologies. However, molecular biology's complexity creates strong "learning loss" effects. A passionate science teacher is not always enough, and at Saint Patrick's College (Wellington) we are exploring the insertion of a charismatic environmental DNA project into the curriculum that is naturally spaced into distinct "chunks": sample collection, lab work, receipt of results and researching the organisms sequenced. Spacing complex learning into discrete chunks can mitigate the "learning loss" effect. Furthermore, retention is improved when projects reflect student values or are unusual enough to be memorable. Our DNADRV (DNA drive) project samples biodiversity of micro- and macro-organisms around Aotearoa New Zealand by swabbing vehicle number plates. This presentation is a teacher's perspective on actively involving year 9 students in research with real benefits for understanding invertebrate biodiversity. Consideration is given to how project "chunks" can be adjusted to match any school's resources – therefore enabling concepts taught in later years (including tertiary level) to be introduced and retained by students in early stages of their education.

Sex chromosome evolution: insights from skinks

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Sex chromosomes evolve from ordinary autosomes after one of the pair gains a sex determining locus across with recombination is suppressed. After recombination is suppressed, the sex specific chromosome losses gene function and degrades. It was long thought that inversions on the Y resulted in large regions of recombination suppression with the X in single events. However, there has never been direct evidence of this due to the degraded nature of Y chromosomes.

The mechanisms leading to suppressed recombination have been debated at length. Other models include pre-existing low recombination rates, different reproductive strategies, gradual expansion rather than large stepwise expansion of recombination suppression, and there is even a neutral model of recombination suppression. Here we present the genome of two species from the skink genus Tiliqua, in which we present the first direct evidence for at least one inversion on the Y chromosome. There was Y degeneration pre-speciation, which was then followed by a Y inversion that further suppressed recombination with the X. This inverted region shares near 1 to 1 synteny with the X and, incredibly, remains conserved in both species.

Allelic Association Analyses: Avoiding the Use of Allele Frequencies

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We review common estimators of descent measures: coefficients of inbreeding, relatedness and population structure, and we show our rationale for making several recommendations. We endorse Sewall Wright's concept that descent measures should be for target sets of alleles relative to reference sets. In order to avoid the confounding effect of study dimensions, numbers of individuals sampled per population and numbers of populations sampled, however, we modify Wright's original definitions of F-statistics to make pairs of alleles in the reference sets to be from distinct individuals or populations instead of being from random pairs of alleles. We also recommend that estimators be devised from a statistical-genetic perspective rather than from a purely statistical one, and so recommend against the use of so-called standard estimators of inbreeding and relatedness. If genotypic data are available to an investigator, we recommend that they not be reduced to allelic data to avoid the implicit assumption of Hardy-Weinberg equilibrium within each population. As natural populations are finite, and in line with empirical results, we recommend that both inbreeding and relatedness be considered in estimating either quantity. This recommendation, along with use of distinct individuals and populations for reference allele pairs, leads us to recommend against the use of sample allele frequencies in estimating descent measures. Consequently, we recommend not trying to estimate unknown allele probabilities. Our recommendations are all part of our overall recommendation to join other authors in the use of allele-sharing statistics: these statistics are the proportions of pairs of alleles in a target set that are identical in state. Allele-sharing estimators preserve the rankings of descent measures when these are defined as probabilities of identity by descent. Our algebraic work shows some unexpected equalities between apparently-different estimators in common use.

LOTR-2: a LOTUS & Tudor domain protein with unexpected features

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Epigenetic regulation is mediated by a complex network of molecular signals and often facilitated by organisation of biomolecules into membraneless condensates. A class of condensates known as “germ granules” play important roles in germline gene

expression, small RNA pathways, and have functional roles in processes related to fertility and development. Some well-characterised germ granule proteins contain a specific protein domain called the LOTUS (Limkain, Oskar and TUdor domain proteinS 5/7) domain, which is conserved across kingdoms, but is highly divergent in sequence. Here we identify and investigate a novel LOTUS domain protein in *C. elegans*, LOTR-2. In line with the known association between LOTUS domains and germ granules, we observe changes in germ granule organisation and formation in *lotr-2* mutants. Correspondingly, these mutants also show differential expression of small interfering RNAs (siRNAs). However, while all known LOTUS domain proteins in *C. elegans* are germline-expressed and localise to germ granules, we found that LOTR-2 surprisingly is not expressed in the germline and is rather expressed in the somatic gonad. Furthermore, upon total RNAseq of *lotr-2* mutants we found downregulation of pathways relating to somatic development. Together, these results suggest broader functions of LOTUS domain proteins within the intersection between soma and germline.

Enhancing breeding programs with high-resolution pangraphs

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Pangraphs, which integrate variants from multiple genomes into sequence graph structures, have recently emerged as essential mapping references to mitigate single-reference bias. In breeding programs, pangraphs have great potential for tracing haplotype inheritance, identifying genomic regions linked to traits of interest, and enhancing genomic selection. We at Plant and Food Research, in collaboration with our breeding partners at the Kiwifruit Breeding Centre (KBC), are developing reference pangraphs to accelerate kiwifruit and kiwiberry breeding. Our approach includes: (1) constructing high-quality, phased, telomere-to-telomere (T2T) genome assemblies, (2) building pangraphs using cutting-edge graph-building tools, and (3) developing workflows for downstream user applications. For the quality assessment of highly accurate phased diploid assemblies, we introduce phasing quality check criteria and highlight the importance of generating mapping-back and cross-genome heterozygosity profiles, which are currently absent from standard assembly quality check pipelines. We emphasize the critical role of manual curation in enhancing

research discoveries and improving pangraph quality. We compared two state-of-the-art graph-building tools, PGGB and Minigraph-Cactus, using graphs generated from multiple manually curated assemblies. Our analysis explores their effectiveness in studying key features relevant to downstream breeding applications, including genomic selection and other trait-associated insights.

The Role of Small RNAs in Honey Bee Immune Regulation

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The RNA interference pathway is critical in innate insect immunity during viral infections. *Apis mellifera* are exposed to viral pathogens including *Iflavirus aladaformis* (Deformed wing virus) which in association with the ectoparasitic mite *Varroa destructor* is the leading cause of hive deaths globally. However, the effects of bee viruses and *Varroa* on bee health are challenging to untangle. Australia was *Varroa* free until the first hive detection in NSW, June 2022, providing a final opportunity to investigate the sRNA and transcriptional responses to viruses within the remaining *Varroa*-naïve Australian honeybees. I experimentally infected Varroa-naïve *A. mellifera* pupae with DWV or the highly pathogenic *Triatovirus nigereginacellulae* (Black queen cell virus) and collected pupae after 48 or 96 hours. I examined the immunological response to infection using sRNA and mRNA sequencing. Overall, I found that the antiviral defence response is significantly stronger within BQCV-injected vs DWV-injected pupae. qPCR and sRNA sequencing results demonstrated that the viral loads of DWV reach similar levels to BQCV-injected pupae, but unlike BQCV, the siRNA response is reduced, and the miRNA response is minimal. I further identified differentially expressed RNAi immune genes. Overall, this study increases our understanding of the *A. mellifera* immune response during DWV and BQCV infections in *Varroa*-naïve honeybees.

Integrating polygenic risk scores and quantitative CT metrics for machine learning-based prediction and clustering of chronic obstructive pulmonary disease

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Chronic obstructive pulmonary disease (COPD) was the fourth-leading global cause of death in 2021. Smoking is a major risk factor for COPD, however, genetic predisposition and environmental exposures also play significant roles. Polygenic risk scores (PRS) and quantitative computed tomography (CT) have been used independently for COPD prediction, but whether their combination improves predictive accuracy remains unclear. We analyzed genotype and CT scan data for 7024 individuals (3214 cases, 3810 controls) from the COPDGene study. PRSs for measures of lung function, which include two million single nucleotide polymorphisms (SNPs), were computed from imputed genotype data. CT scans were processed using Quadtree Decomposition (QtD) to quantify tissue heterogeneity across low-density (emphysematous tissue), medium-density (normal-appearing lung tissue), and all lung tissue combined. We trained random forest models using PRS, QtD, and clinical risk factors (CRFs), followed by an ensemble model integrating all predictors. The ensemble model achieved an AUC of 0.86 and outperformed single-modality models. QtD, particularly for medium-density tissue, emerged as the strongest predictor, followed by CRFs and PRS. Our findings indicate that integrating PRS and quantitative CT data enhances COPD prediction and stratification, offering a promising framework for early diagnosis and risk assessment of COPD.

Hormonal control and crosstalk in the molecular regulation of parthenocarpy

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Parthenocarpy, the development of fruit without pollination or fertilization, is a valuable trait in horticulture. It enables seedless fruit production, favoured by consumers, and addresses pollination challenges linked to climate change, pollinator decline, and the rise of Controlled Environment Agriculture (CEA).

In *Arabidopsis*, the *arf8* mutant induces parthenocarpy by altering auxin signalling, but the resulting fruit are only about half the size of seeded fruit. To enhance fruit growth, we screened other hormone-related mutants and found that a double mutation in cytokinin oxidase 3/5 (*ckx3/5*) also conferred parthenocarpy, though with similarly reduced fruit size. Since hormone combinations are known to improve fruit development more than single hormones, we hypothesized that combining hormonal pathway mutations would enhance parthenocarpic growth.

Indeed, the *arf8/ckx3/5* triple mutant produced larger siliques than either single mutant. Transcriptome and histological analyses of the mutants were conducted to explore the mechanisms behind this enhancement.

Building on our *Arabidopsis* findings, we are now applying this strategy to fruit crops such as tomatoes, apples, and blueberries. Our aim is to integrate parthenocarpy with other desirable traits using gene editing to develop ideal fruiting plants tailored for CEA systems.

Posters

Deriving correlations for inter-trait genetic scores in metabolic conditions affecting Pacific populations

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Genomic technologies are foundational to personalized medicine. Traditionally, genome-wide association studies (GWAS) and polygenic risk scores (PRS) have been pivotal in linking genetic variants to disease susceptibility, uncovering relevant molecular pathways, and estimating disease risk. However, the accuracy of PRS can depend on large datasets with adequate representation of the populations for which risk estimates are being applied. This poses challenges for underrepresented populations in both research and clinical settings, owing to extensive genetic heterogeneity in disease etiology. To address these limitations, alternatives to estimating genome wide disease risk may be more useful. We explore inter-trait genetic correlations to derive trait clusters among gout, chronic kidney disease, and type 2 diabetes gBLUP genetic scores in the GoGDK cohort through correlation. From these trait clusters, principal component analyses are planned to detect genetic variants affecting linked traits with potential pleiotropic affects via GWAS. This work will provide a statistical framework for understanding metabolic disease co-morbidities in Pacific peoples, potentially contribute to more accurate estimates of genome-wide disease risk for these populations and potentially identify new targets for drug repurposing and/or discovery. Furthermore, we discuss the future governance and structure of the GoGDK legacy dataset, which implement principles of Māori data sovereignty.

Development of targeted meta-barcoding methods for conservation management and biodiversity support

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Metabarcoding facilitates the sequencing of the same DNA region in many samples simultaneously. Metabarcoding is now a well-established method within molecular biology, used for variable applications, such as the earth microbiome project and other ecological assessments. Regardless of the objectives for the data or the field deployed, metabarcoding typically involves use of generic primers to amplify from conserved regions, with the region targeted often being conventional DNA barcode regions, such as 16S, ITS and COI. This method conveys many advantages with countless studies taking this approach. However, use of a single binding primer pair to amplify a DNA region across a vast breadth of species can also come with disadvantages. One disadvantage is that primer-binding efficiency can vary species to species, creating a bias that results in preferential amplification of some species compared to others, and in some cases, species may fail to be detected at all. There also may be instances where the DNA region is not sufficiently powerful for all species within a sample, resulting in some sequence data where the species cannot be confidently identified. Here we discuss different metabarcoding applications, including customised approaches developed to be deployed as tools to support conservation science and biodiversity management.

From Fragments to Futures: Ultra-Long Reads Empowering Invertebrate Genomics in New Zealand

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Ultra-long read sequencing has revolutionised genomics by simplifying the analysis of large DNA fragments, allowing researchers to resolve complex genomic regions and detect structural variants with high accuracy. Technologies like Oxford Nanopore can now produce reads over two megabases long, vastly improving genome assembly continuity, especially across repetitive or rearranged regions.

Applying these methods to non-model invertebrates reveals genomic diversity often hidden from short-read approaches. High-quality assemblies uncover novel genes, structural variation, and lineage-specific adaptations, key to understanding evolutionary and ecological dynamics.

In Aotearoa New Zealand, this technology is advancing aquaculture by decoding the genomes of endemic species such as *Aulacomya maoriana* (Kopakopa) and *Panopea zelandica* (geoduck). These insights will inform sustainable breeding, disease resilience, and conservation. The work supports kaitiakitanga, the Māori principle of guardianship, by providing a genomic foundation for protecting taonga (treasured) species.

Our journey to achieving ultra-long read sequencing reflects a commitment to integrating cutting-edge science with mātauranga and tikanga Māori (Māori knowledge and practices). In partnership with enterprises like Wakatū Incorporation, this approach ensures New Zealand's aquaculture sector can thrive while honouring cultural values and safeguarding natural resources for future generations

Genomics and Evolution of Mimicry in a Colour-polymorphic New Zealand Stonefly

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The evolutionary genetic basis of Batesian mimicry, where a harmless species evolves to resemble a toxic or unpalatable one, has long fascinated biologists. In rare cases, mimicry systems can be highly dynamic, being maintained by frequency-dependent selection, where only some individuals in a population resemble a harmful 'model'. In the New Zealand stonefly *Zelandoperla*, Batesian mimicry of an unrelated poisonous species (*Austroperla*) has been linked to an intraspecific colour-polymorphism controlled by the ebony locus. A loss-of-function mutation in this gene increases melanisation, causing normally light-coloured individuals to resemble the noxious, melanic *Austroperla*, leading to reduced predation risk. Here, I test the distribution of mimicry across the southern *Zelandoperla* clade, tracing the origin of the polymorphism using DNA sequence variation. I show that the ebony mimicry polymorphism is older than previously thought, arising early in the clade's history. I assess the impacts of historic climate change, gene flow, and human-driven environmental change on the distribution of colour morphs in this species.

A genomics-informed investigation into Lamprey Reddening Syndrome

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Pouched lamprey (*Geotria australis*, also known as kanakana or piharau) are ancient jawless fish found in the Southern Hemisphere. They are culturally and ecologically important to Aotearoa, New Zealand, yet relatively little is known about their ecology. Lamprey reddening syndrome (LRS) is a recently emerged disease in Southland, New Zealand, and causes significant mortality of afflicted lamprey. Despite numerous attempts, a definitive cause of LRS has not been found. Guided by iwi collaboration to ensure tikanga, a metatranscriptomic dataset of 28 lampreys, from both Australia and New Zealand, 11 of which were diseased, was recently established. Using these rich data, we will uncover the microbial composition, with particular focus on viral communities, for each individual matched with their disease status. This approach allows for novel viruses to be discovered, which is often a major limitation in traditional approaches to disease investigations. This research project will reveal the causative agent of LRS and illustrate the potential of genomics-informed diagnostics for taonga species. By determining the cause of LRS, we can protect culturally, ecologically and economically important fish within New Zealand and beyond.

Environmental DNA reveals the biological effects of reforestation in New Zealand

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Large-scale deforestation has driven major shifts in freshwater ecosystems globally, but the potential of reforestation to restore freshwater biodiversity remains unclear. New Zealand, which has experienced severe deforestation over recent centuries, followed by extensive planting of exotic forest, provides a powerful system for assessing the impacts of this ecosystem change. Using environmental DNA (eDNA), we compared the freshwater insect communities of native forests versus exotic plantations in southern New Zealand. Specifically, we conducted eDNA analyses of mayfly, stonefly, and caddisfly (EPT) communities across 15 native forest and 15 exotic forest streams, detecting 85 distinct taxa. Most species were shared between both forest types, with eDNA assemblages primarily differentiated by geography rather than habitat type. However, a few widespread forest EPT taxa were consistently absent from exotic plantation eDNA assemblages, suggesting they are particularly

sensitive to vegetation type. Although insect eDNA diversity in exotic forests was lower than in native forests, our findings suggest that exotic plantations may have potential to broadly restore formerly deforested communities to resemble those of native forests.

Haplotype-resolved genome assemblies and hybridization histories of asexual New Zealand stick insects

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New Zealand stick insects comprise 23 endemic species across 10 genera. Since migrating from New Caledonia ~20 million years ago, they have undergone a complex history of genome evolution, marked by shifts in reproductive modes. This is notable in the genus *Acanthoxyla*, where hybridization between sexual species has triggered transitions to parthenogenetic forms of asexuality (development of offspring from unfertilized eggs), resulting in female-only populations. To investigate how the loss of sex and hybridization influence genome evolution in these parthenogens, we are generating high-quality, haplotype-resolved genome assemblies of the *Acanthoxyla* lineages using Nanopore long reads, Illumina short reads and Hi-C data. The *Acanthoxyla* parthenogens possess large (3–5 Gb), highly repetitive, and polyploid genomes, presenting unique challenges for assembly. Using these assemblies and RNA sequencing data, we will compare allele-specific gene expression and DNA methylation patterns between the parthenogens and their sexual relatives. Additionally, using highly conserved single copy orthologs, we are reconstructing the hybridization histories of the *Acanthoxyla* parthenogens and their sexual relatives. Together, these genome assemblies, phylogenetic and gene regulation analyses will contribute to a comprehensive understanding of the evolutionary history of New Zealand stick insects, as well as the consequences of hybridization and asexuality on genome evolution.

Optimising *In Vitro* Rearing of *Nasonia* for Gene Editing

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The parasitoid wasp *Nasonia vitripennis* is a Hymenopteran parasitoid which parasitises blowfly pupae. Research on control strategies for invasive wasps in Aotearoa/New Zealand use *Nasonia* as a model as it has haplodiploid genetics similar to eusocial wasps.

N. vitripennis embryos take 14 days to develop into adults inside blowfly pupae. To shorten the time for screening for gene edited or transgenic wasps, we are developing methods to rear edited *N. vitripennis* embryos on a germ-free medium. This allows for observations during metamorphosis and improved rearing post gene-editing injections.

Previously, 1 hour old *N. vitripennis* embryos were removed from their host blowfly pupae, injected, and then placed back into host pupae. We adapted an *in vitro* rearing technique using protein extract from pressed blowfly pupae to allow visualisation of injected larvae. Injected embryos were placed onto a mesh in 24 well plates and provided with protein extract for 6 days, followed by an 8 day dry period. We varied the amount of bleach used during embryo sterilisation and the volumes of protein extract and examined survival rate.

The successful germ-free rearing of edited *N. vitripennis* will transform future genetic and developmental work on this species.

Towards greener pastures: Understanding the role of CONSTANS variants in perennial ryegrass flowering time

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Perennial ryegrass (*Lolium perenne* L.) is New Zealand's primary forage and the foundation of its pasture systems. Each spring, ryegrass undergoes a seasonal shift to flowering that reduces pasture quality and livestock performance. To mitigate this, we aim to develop ryegrasses that remain vegetative under field conditions by increasing their daylength requirements for flowering. Previous research identified a variant of the flowering gene *CONSTANS* (*CO*) as a target for increasing ryegrass daylength requirements. *CO* is a transcription factor that promotes expression of the key floral inducer *VRN3* during the day; at night, it is degraded by the COP1/SPA complex. The balance of these two activities determines a plant's daylength requirements for flowering. Targeted sequencing of *CO* uncovered a SNP encoding a serine-to-arginine

substitution in a putative transactivation domain. We hypothesise this change may reduce the transactivation ability of *CO*, and aim to test this using yeast- and tobacco-based assays. Interestingly, the SNP is also located close to a degradation motif recognised by COP1/SPA, suggesting it may affect *CO* stability. We aim to test this hypothesis in a tobacco-based expression system. Insights gained from this study will support the development of non-flowering ryegrass to improve spring pasture quality and livestock performance.

Exploring the potential of virus transmission among birds in a spatially restricted ecological niche

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Wild birds are important viral reservoirs, harboring pathogens like influenza viruses, flaviviruses, and coronaviruses, which can also affect humans and other animals. Their unique immune system often allows them to remain asymptomatic despite being infected with multiple viruses at once. Birds' ability to fly and act as viral reservoirs makes them critical vectors for viral spread, yet little is understood about the factors driving virus diversity and their ability to cross host barriers. This project explores the transmission dynamics of viruses between both native and introduced passerine bird species in Aotearoa, New Zealand. With limited knowledge of the viruses affecting New Zealand's bird species, this study aims to investigate the virome of passerines and identify the prevalence of cross-species transmission. Passerines, due to their diversity and wide habitat distribution, make an ideal model for understanding viral risks to conservation, agriculture, and public health. Using data collected over three years and encompassing 453 samples, we will employ a metatranscriptomics approach where viral genomes will be recovered and cross-referenced with public databases, followed by phylogenetic analysis to identify both known and novel viruses, assess cross-species transmission, and track virus diversity across time, providing crucial insights into potential viral risks to New Zealand's ecosystems and public health.

HDAC4 biomolecular condensates: dynamics, disruption, and effects on neuronal development

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Histone deacetylase four (HDAC4) forms punctate nuclear foci when its abundance increases. Our previous work demonstrated that increased HDAC4 foci correlate with neurodevelopmental and memory impairments in a Drosophila model. Similar accumulations of nuclear HDAC4 have been observed in neuronal disease, including Alzheimer's disease. Contrary to the previous belief that these foci were static, denatured aggregates of HDAC4 protein, our live imaging and FRAP studies revealed that these foci are instead highly dynamic, resembling liquid-liquid phase separated droplets termed biomolecular condensates. These condensates undergo fusion events, where coalescence increases their size and mobility. Their dynamic nature suggests the feasibility of targeted strategies to disrupt their formation and reduce severity of neuronal impairment. We designed short peptides to interfere with binding of HDAC4 to MEF2, which is required for both nuclear import of HDAC4 and the stabilisation of condensation. Expression the M1-L285 peptide significantly reduced condensate formation and mitigated the severity of defects in brain development associated with their presence. These data provide a novel perspective on the role of HDAC4 in neuronal disease and potential therapeutic targets.

Advances in Cetacean Immunogenetics: The Cetacean IPD-MHC Database

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The Major Histocompatibility Complex (MHC) is a cluster of highly polymorphic genes essential for immunity in jawed vertebrates, enabling the recognition of pathogens and the initiation of immune responses. The IPD-MHC database provides a comprehensive and curated repository for MHC alleles from non-human species. Recently, the Cetacea Leukocyte Antigen (CeLA) section was added, focusing on MHC genes of whales, dolphins, and porpoises. The database currently includes 103 class IIa alleles for DRA, DRB1, DQA and DQB from twenty different species of baleen and

toothed whales. These alleles consist of complete exon 2 and full-length sequences for class I, DRA, DQA and DQB, derived from genome assemblies of the Bottlenose dolphin (Tursiops truncatus) and blue whale (Balaenoptera musculus) from EMBL and NCBI data. Future updates will incorporate full-length MHC sequences from newly assembled, high-quality cetacean genomes. We present examples of demonstrating how this new data, along with the tools embedded in the IPD-MHC database, can enhance our knowledge of how cetaceans have evolved immune responses to marine pathogens. This information will support conservation efforts by providing critical insights into the health and resilience of these species, many of which remain critically endangered.

Uncovering virus diversity in urban waterfowl

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Avian species such as waterfowl serve as important viral reservoirs. Throughout history, humans have maintained a close relationship with birds, which has intensified in recent times due to factors such as agriculture and deforestation. These factors, coupled with increased human mobility, heighten the risk of viral spillover events and disease outbreaks. Despite this, we know very little about viruses in Aotearoa's waterfowl, particularly those that inhabit urban ecosystems.

This study uncovered the faecal virome harboured by waterfowl in botanical gardens and city parks across Aotearoa, where interactions between waterfowl and humans are frequent. Using a metatranscriptomic approach, we assessed the extent of human exposure to viruses carried by New Zealand's urban waterfowl to quantify zoonotic risk. To this end, we identified viruses across 9 viral families including avian influenza virus and avian coronaviruses. By doing so, we have identified viruses that may pose a potential risk for future disease outbreaks in humans and other animals. This research not only provides valuable insights into the viral diversity among New Zealand's urban waterfowl but also strengthens infectious disease surveillance efforts.

Investigating the genetic diversity of the endangered subpopulation of humpback whales (*Megaptera novaeangliae*) in New Caledonia, Oceania

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Functional genetic diversity plays a crucial role in determining the fitness and viability of wild populations. The major histocompatibility complex (MHC), a commonly studied functional genomic marker, is essential for immune defence against diseases and parasites. Maintaining high MHC diversity is therefore vital for sustaining an effective immune response and may influence the long-term survival of exploited populations. Humpback whales (*Megaptera novaeangliae*) in Oceania underwent a demographic bottleneck due to whaling deep into the twentieth century. Today the abundance of 6,404 whales remains low relative to the presumed historical numbers, leading to their IUCN status as 'endangered'. Here, we focus on the key Oceania winter breeding ground of New Caledonia using previously generated population age structure derived from an epigenetic ageing assay and cetacean-specific MHC panel to investigate whether functional genetic diversity has changed with generations since whaling. Using data from 1996 – 2020, we will categorise individuals into age cohorts and evaluate genetic and functional diversity at class I and class II MHC loci in each cohort, and compare with neutral genetic diversity from matched microsatellite loci. This will provide insight into how the demographic bottleneck caused by whaling has impacted functional and neutral markers in Oceania humpback whales.

Unpacking genetic incompatibility and early reproductive failure in threatened species

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Understanding the genetic causes of early reproductive failure for intensively managed threatened species is essential for making informed management decisions. Early reproductive failure may be due to either infertility or embryo death, yet the genetic causes attributed to each differ. Infertility is generally attributed to highly inbred individuals, while early embryo death is generally attributed to genetically incompatible pairings. However, it is often unclear what it means to be "genetically incompatible" or how "genetic incompatibility" is best measured, especially in a conservation context.

Here, we present a systematic review to demonstrate that genetic incompatibility remains poorly defined and underexplored, and to recommend more explicit descriptions and measurements of genetic incompatibility. For example, we suggest that overlapping and identical runs of homozygosity (ROH) between mates can be used as a proxy for genetic incompatibility.

We demonstrate the utility of this approach using a uniquely rich empirical dataset, namely the extensive genomic and phenotypic data available for kākāpō (*Strigops habroptilus*), a Nationally Critical parrot endemic to Aotearoa New Zealand. In particular, we update existing research with ROH data to investigate the link between genetic incompatibility and early embryo death, to guide conservation actions and improve reproductive outcomes in kākāpō and beyond.

Dual model nutriphenomics to identify precision dietary therapies for inherited metabolic disorders

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Inherited Metabolic Diseases (IMDs) are individually rare but collectively common, and often respond well to dietary interventions. However, identifying optimal diets remains challenging due to early onset and low patient numbers. To address this, we are developing a pipeline we term 'nutriphenomics'; an animal model-based platform to rapidly and cost-effectively test nutrient-disease interactions. Using *Drosophila melanogaster* for its genetic tractability and synthetic diet compatibility, we screen precision dietary interventions, followed by validation in the mouse model to assess mammalian relevance. We have developed over 40 fly models of IMDs, focusing on amino acid catabolism disorders. These models replicate human disease traits including developmental delay, neurological dysfunction, and variability in disease severity and onset. Notably, we have identified nutrient formulations that fully rescue phenotypes in flies, with translational studies in mice underway. This approach not only highlights therapeutic windows but also elucidates underlying disease mechanisms. Here, I present the strategy, current progress, and key examples, with the aim of accelerating dietary therapy development for IMDs.

Unraveling colour variation in Kangaroo Paws

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Kangaroo Paws (*Anigozanthos* spp.) are iconic Australian wildflowers known for their striking floral colour diversity, which plays a key role in pollinator attraction and horticultural appeal. Despite their ecological and economic importance, the genetic basis of colour variation and the role of hybridisation in shaping this diversity remain poorly understood. In this study, we explore the genomic landscape of colour variation using a multi-tiered sampling design across a natural hybrid zone involving two contrasting *Anigozanthos* species. We sequenced hybrids, sympatric parental individuals, and allopatric populations to dissect patterns of introgression, ancestry, and divergence. This comprehensive approach allows us to differentiate between local gene flow and long-term species divergence, while testing hypotheses about the origin and maintenance of floral colour traits. To complement this, we have generated high-coverage (~30x) whole-genome data for 21 individuals spanning species and colour morphs. These data will serve as the foundation for phylogenomic reconstruction and future trait-mapping efforts. Our integrative framework combines hybrid zone genomics, reference population comparisons, and high-resolution phylogenomics to better understand the evolutionary and genomic underpinnings of floral colour variation in *Anigozanthos*. This work lays the groundwork for genomic-assisted trait improvement and deeper insights into plant speciation processes.

Functional validation of three candidate causal variants in the *xanthine dehydrogenase* gene associated with feline xanthinuria

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Xanthinuria is an autosomal recessive disorder caused by variants in *xanthine dehydrogenase* (*XDH*) or *molybdenum sulfurase* (*MOCOS*) genes in humans. In feline xanthinuria, three candidate causal variants in the *XDH* gene have been identified to date. *XDH* is a key enzyme in the metabolism of purines to uric acid, and disruptions in the normal purine metabolism result in the accumulation of xanthine in the urine. Due

to its poor solubility, xanthine precipitates to form crystals within the urinary tract, potentially resulting in life-threatening blockages. Affected cats present with symptoms commonly associated with feline lower urinary tract disorder (FLUTD). The aim of this study is to assess the functional relevance of identified feline variants. Wild type and variant *XDH* cDNA will be constructed, cloned into a mammalian expression vector, and transfected into a mammalian cell line. Protein expression will be determined prior to combining wild-type and variant proteins with xanthine. The resulting metabolites will be analysed using High-Performance Liquid Chromatography (HPLC) to evaluate *XDH* activity. Identifying causal variants will not only aid veterinarians to diagnose and manage feline xanthinuria but enable the potential for genetic testing to assist with breeding programs and identify at risk cats.

Untangling Australian *Ficopomatus*, a genus of notorious biofouling and invasive estuarine calcareous tubeworms

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Ficopomatus is a genus of brackish-water tubeworms in the annelid family Serpulidae. The genus consists of six species. Of these species, *Ficopomatus enigmaticus* and *F. uschakovi* have been reported from Australia. While *F. enigmaticus* can be found in warm-temperate climates world-wide, the remaining five species, including *F. uschakovi*, are found in tropical localities of Southeast Asia and Americas. Both species are invasive, although the extent and patterns of these invasions remain unclear. Morphological and some limited genetic differences have also been found within *F. uschakovi*, suggesting that further studies are needed to understand whether this taxon is a complex of species. I aim to provide a morphological and molecular investigation of *F.uschakovi*. The morphological study will be done using both light and electron scanning microscopy and photography. To infer the phylogeny of the species using molecular data, I will sequence and analyse the mitochondrial cytochrome b (Cytb) gene, which has previously been used to analyse relationships within *F. enigmaticus*. These analyses will lead to a greater understanding of the morphological and molecular diversity within *F. uschakovi*, including the potential identification and description of new species.

Population simulation to optimise study designs and estimate polygenic disease risk/resilience in Aotearoa Māori populations

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For commonly occurring polygenically inherited conditions, disease risk/resilience estimates have most often been derived from GWAS (genome-wide association studies), which require large genotyped datasets. These datasets often do not include indigenous peoples, who can have important genetic differences from more commonly represented populations of predominantly European descent. Existing datasets from Māori domiciled in New Zealand are few and are underpowered for prediction due to their small size. In addition, establishing sufficiently large GWAS is unlikely in Aotearoa/NZ because of costs associated with generating genotypic data and reluctance of many Māori to participate in such studies. In order to offset further health inequities arising from a lack of Māori-specific DR prediction models, new studies are required. Such studies require both (a) optimal designs that incorporate known genetic relationships on non-genotyped as well as genotyped individuals, and (b) analytical methods that more accurately predict phenotype than GWAS-based methods such as polygenic risk scores. We have used a population simulator to model genetic structures of Māori communities, incorporating estimates historical population sizes, as well as post-colonisation admixture with Europeans. Our research uses these simulations to explore what features of study design and analytical methods lead to optimal disease risk/resilience prediction.

Genomic Characterisation of Bioluminescent Bacteria Isolated from Marine Fish in Aotearoa, New Zealand

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Bioluminescence in bacteria is a genetically encoded trait that plays key ecological roles in marine environments, such as predator avoidance, prey attraction, and host-microbe interactions. Despite extensive studies on these microbes, their presence and genomic diversity in association with marine fish in Aotearoa, New Zealand, remains largely unexplored.

This study addresses this gap by isolating and cultivating bioluminescent bacteria from multiple anatomical sites of commercially caught marine fish, including the eyes, mouth, gills, anus, gut contents, and body surface. Thirty-two visibly luminous strains were characterised using morphological, biochemical, and genomic methods, including long-read whole genome sequencing. High-resolution taxonomic

classification identified most isolates as genera Photobacterium. Genome annotation using Bakta revealed conserved lux operon genes, confirming their genetic capacity for bioluminescence. Phylogenetic analysis aims to further resolve strain-level relationships, providing insight into their evolutionary context.

These findings offer valuable genomic and evolutionary insights into the identity, diversity, and functional potential of bioluminescent bacteria in marine fish from Aotearoa, New Zealand.

Fungal Communities in Brood Food and Pollen of Australian Stingless Bees (*Tetragonula carbonaria*)

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Tetragonula carbonaria is one of the most widely managed species of stingless bees in Australia. They serve an important role as pollinators of both native plants and economically significant crops. However, these bees face increasing health threats from anthropogenic stressors, including the widespread use of pesticides and fungicides, which may have unintended impacts on beneficial members of the nest mycobiota. Stingless bee species from other parts of the world are known to rely on fungi in brood food and pollen to provide nutrients for larval development, but there is limited knowledge around this in *T. carbonaria*. Our study aimed to characterise the fungal communities present in brood food and pollen from *T. carbonaria* colonies across their natural distribution along the east coast of Australia. ITS1 amplicon sequencing was performed on brood food and pollen samples from managed colonies. Sequence data were processed using the DADA2 pipeline and analysed with the phyloseq package in RStudio. Analyses revealed *Zygosaccharomyces* as the dominant fungal genus present in both brood food and pollen. Notably, this yeast genus has been previously identified as essential to brood maturation in the Brazillian stingless bee *Scaptotrigona depilis*, suggesting a potentially similar functional role in *T. carbonaria*.

Determining the Regulatory Controls of Desiccation Tolerance in Plants

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Plants face constant challenges from diverse abiotic stressors threatening survival. As sessile organisms, they evolved sophisticated genetic and metabolic networks to

respond to detrimental environmental conditions. During stress exposure, plants modify gene expression patterns to reconfigure their cellular environment for enhanced protection and resilience. These expression patterns link to specific environmental conditions, revealing key genetic insights facilitating abiotic stress responses. As climate change intensifies, drought events are becoming more frequent and widespread, causing greater agricultural losses. Desiccation tolerance (DT), a rare adaptation across all life domains, enables survival under extreme water-deficiency. While common in plant reproductive organs, DT in vegetative tissue (VDT) is incredibly rare. VDT's emergence across diverse plant species suggests DT mechanisms potentially exist within vegetative tissue under alternative regulation compared to reproductive organs. Environmental pressures may have rewired reproductive DT mechanisms resulting in VDT capability. The genetic mechanisms underpinning VDT remain poorly understood. Extensive dehydration time-series experiments have generated comprehensive RNA-seq datasets associated with drought and DT responses. A comparative genetics approach investigates VDT's molecular mechanisms, emphasising transcription factors' regulatory role. Identifying regulatory elements conferring VDT could enable its introduction or restoration in crops, enhancing drought tolerance.

Genetics to the rescue? Developing high-quality genomic resources for a critically endangered bird

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The Chatham Island black robin (*Petroica traversi*) is a Nationally Critical bird species restricted to two offshore islands (Rangatira and Mangere) in the Chatham Islands archipelago. To reduce the high extinction probability of the smaller of the two populations, ten females were translocated from Rangatira to Mangere in 2022. We are combining extensive genomic and ecological data to investigate the relative influence of genetic factors (i.e., reduced inbreeding and increased genetic diversity following admixture) and demographic factors (i.e., the reduction of a male-biased sex ratio and addition of breeding females) on improved vital rates and population persistence following genetic rescue. Here, we share the development of foundational genomic resources for the Chatham Island black robin, including a long-read reference genome and a short-read whole genome resequencing dataset for the entire study population over four generations. We demonstrate the utility of these resources for precisely estimating genome-wide diversity and admixture in a highly inbred bird.

In addition to directly aiding the conservation management for an iconic species endemic to Aotearoa New Zealand, this unique dataset opens the door to an in-depth elucidation of the mechanisms behind genetic rescue as a conservation strategy.

The power of reanalysis for neurodevelopmental conditions; identifying new variants and reinterpreting old findings

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Variants of uncertain significance (VUS) for rare conditions pose a significant challenge in human genetics, with most VUS lacking functional evidence or population-level recurrence to improve the accuracy of clinical classification. With the rapid development of genetic testing in healthcare and research, reinterpretation of previously identified VUS is critical. Here we present two cases, which following reanalysis led to variant reclassification/identification and downstream functional evaluation. For one participant, reanalysis of clinical exome sequencing revealed a heterozygous missense variant in *CHD3* (p.Arg579Gln), a gene with a recently characterised neurodevelopmental condition that aligned with the participant's phenotype allowing the return of the result to the family. For another participant, a p.Pro106Leu variation in the *PPP1R3F* gene (a brain-expressed glycogen-targeting subunit of protein phosphatase-1) had previously been classified as a VUS. *PPP1R3F* has recently been implicated in an X-linked neurodevelopmental condition, but with limited understanding of the functional impact of variants on brain glycogen metabolism regulation. Using CRISPR-Cas9, we have edited our candidate variant into the U87-MG glioblastoma cell line to ascertain its impact on glycogen metabolism and thus its clinical relevance for this family. These two cases are clear examples of the importance of VUS reanalysis when previous genome-wide testing was uninformative.

Dissecting the regulatory landscape of rs4698413: a causal variant for Parkinson's disease

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Background: Two-sample Mendelian randomization and genome-wide association studies (GWAS) have identified rs4698413 as a non-coding variant associated with Parkinson's disease (PD). However, its functional mechanism remains unclear.

Methods & Results: Using CRISPR-Cas9 genome editing, we introduced a heterozygous (C|T) genotype in KOLF2.1J iPSCs and subsequently reverted it to homozygous (T|T) to assess its regulatory effects. RNA-seq analysis revealed allele-specific reciprocal regulation of *FGF4* and *NT5E*, genes implicated in stem cell differentiation and neuroinflammation. Contrary to initial hypotheses, Micro-C analysis showed that rs4698413 does not physically interact with these differentially expressed genes (DEGs), ruling out chromatin looping as the primary regulatory mechanism. Similarly, DNA methylation analysis identified allele-specific 5mC changes, but these modifications were restricted to non-DEG loci, excluding epigenetic regulation as the main driver.

Instead, bioinformatics analysis (FABIAN, motifbreakR) identified rs4698413 as a SOX transcription factor (TF) binding site, where the T-allele facilitates SOX-dependent activation of *FGF4*, while the C-allele disrupts enhancer function, leading to downstream transcriptional changes. These findings position rs4698413 as a transcriptional regulator in PD, emphasizing the critical role of (TF) binding over chromatin interaction or methylation in regulating disease-associated genes.

Conclusion: This study underscores the importance of integrating genome editing, functional genomics, and epigenetics to decipher non-coding variant function in PD and highlights rs4698413 as a SOX-dependent regulatory element.

DNADRV: getting baseline insect distribution data from eDNA splattered on your car

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Insects underpin many ecosystem processes, from pollination to waste disposal, but are increasingly threatened by climate change altering their habitats, disrupting their life cycles, and intensifying pressures from invasive species, diseases, and extreme weather events. Three climate change application areas requiring urgent research are:
(1) identifying habitats that support insect diversity,
(2) restricting spread of heat-tolerant insect pests/disease-vectors,
(3) climate-induced asynchronies arising between insects and their environment.
Addressing these requires datasets that span large spatial transects, but insect sampling presently tends to use trap data (i.e. point-samples). However, as you travel by car, an incredible diversity of insects fly past you and recede into the distance as you continue along the road. What if the car itself was the sampling tool? Car license plates are a standardized size, gather insects, and we propose them as the novel basis for collecting baseline insect distribution data.

We have optimized and piloted methods to inexpensively identify insects and their commensals (bacteria, fungi, plants) from eDNA traces left on car license plates. Importantly, our project engages with a car using public who might not always consider the impact of climate change on invertebrates and how the demise of insect diversity would alter our world.

The Phylogenetics and Population Structure of a Species Complex of Deep-Sea Scale Worms

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Steadily rising extinction rates highlight the need for a comprehensive understanding of marine biodiversity. Given our poor understanding of the deep sea, these studies are particularly crucial. Recent Genetic analysis shows, many marine invertebrates described with broad bathymetric ranges represent species complexes with more restricted distributions. Despite their ubiquity, the distribution of marine annelids remains poorly understood, with species' broad bathymetric ranges potentially reflecting inadequate identification. This study focuses on annelid scale worms in the genus *Laetmonice* (family *Aphroditidae*), with 32 currently recognised species. The majority of these were described solely on morphology, leaving them vulnerable to missing cryptic species. This study aims to clarify population structure and identify putative undescribed species in the genus. Research voyages in Australian waters

collected 144 specimens of *Laetmonice* at depths of 460m to 5,000m. Using mtDNA sequences (COI and 16S) I will assess whether genetically distinct lineages exist within the samples. I will evaluate population structure and estimate gene flow using an array of genomewide SNPs. This will allow me to delineate putative species, forming the basis of further morphological examination of the voucher specimens. The results will contribute to a better understanding of diversity and bathymetric distribution of the genus *Laetmonice*.

Expanding the toolkit for genome engineering in wasps

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Despite the power of genome engineering to support discovery and offer novel insight into biology, its applications in creating transgenic non-model insects has been limited. Our research is aiming to develop transgenic technologies and improve capabilities of CRISPR/Cas applications in *Nasonia vitripennis*, a parasitic wasp. Traditionally, injected eggs are placed back into host pupae until emerging as an adult, limiting the ability for developmental genes to be investigated in a dynamic manner. We have integrated the use of an *in vitro* rearing medium to support wasp larval development in an environment in which their development can be directly observed. Access to developing embryos will allow gene functions to be investigated and a more efficient method of screening for transgenic progeny. Beyond basic research, advances in genome engineering technologies in a model wasp species will support the development of tools and knowledge for evaluating genetic biocontrol strategies in pest species.

Resolving the phylogeny of a taxonomically ambiguous genus of South Pacific Lamiinae (Order: Cerambycidae; Genus: *Xylotoles*)

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The subfamily Lamiinae (Coleoptera: Cerambycidae) comprises more than 20,000 extant species globally. The internal taxonomy of this subfamily was traditionally based on 19th century morphological schemes, but recent molecular studies have demonstrated major discrepancies with morphological taxonomies. The South Pacific region has multiple genera of poorly studied and taxonomically ambiguous lamiines. We aim to resolve the phylogenetic relationships among representatives of genus *Xylotoles* which as currently defined is distributed across New Zealand, Lord Howe and Norfolk Island, and potentially northern Australia and New Guinea. The systematics of Xylotoles remain unclear partially due to a lack of molecular data and partially due to high morphological conservatism and/or convergence between different lineages of South Pacific lamiines. We will use integrative methods to assess the phylogenetic relationship of this group, as well as close relatives, using specimens obtained from the Australian Museum (Sydney), the New Zealand Arthropod Collection (Auckland) and recently collected field specimens. Our study will contribute to understanding processes of species dispersal in the South Pacific region and will have implications for conservation research in the region.

CasRx as a suitable tool for plant biology research

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To determine the roles of specific genes involved in plants, specific knockdown and mRNA localisation could be performed using the CRISPR/Cas13 system. The CRISPR/Cas13 system has been identified to be able to target single-stranded RNA for cleavage leading to gene silencing, and for mRNA localisation in animals (using an inactivated version of Cas13 fused with a fluorescent protein) (Cao *et al.*, 2021; Burmistrz *et al*, 2020). Cas13 has shown vast potential within different animal models, but its usefulness for mRNA knockdown and mRNA localisation has not been well explored in plant systems.

Due to pollen having thick cell walls, it is difficult to identify key components involved in asymmetric division and cell-fate specification involved in plants, making it difficult understanding how pollen development works in flowering plants. The CRISPR/Cas13 system could be used to understand the importance of specific genes involved in pollen development and the role they have in regulating it. It could also be used to characterise and validate potential genes thought to be involved in pollen development.

Results will be shown focusing on optimising the CRISPR/Cas13 system for stable transformation in *Arabidopsis thaliana* and transient transformation in *Nicotiana benthiana*.

From Genes to Green: The Role of Genomics in Native Seed Production

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Demand for native Australian seeds for horticulture and restoration is growing rapidly. Rewilding, revegetation, and carbon offset projects all rely on genetically healthy seeds capable of producing self-sustaining populations. To meet this demand, native seed production areas (SPAs) are being developed. However, SPA-grown seed faces risks, including inbreeding, accidental interspecific hybridization, and loss of genetic diversity. Despite these challenges, genetic tools are not widely implemented in SPAs. As these projects are still in their early stages, best practices for maintaining genetic health—such as careful seed sourcing and mixing to produce climate-resilient seeds—remain poorly understood. We conducted a systematic literature search and found that, despite strong research interest in SPAs, there is a striking lack of genetic resources (e.g., reference genomes, sequencing data) for most species. Furthermore, only a handful of studies have tracked multigenerational changes in genetic diversity within SPAs, and key plant trait groups are largely absent from the literature. To address these gaps, we propose a framework for future research, along with key questions that must be examined to optimize the genetic health and yield of native seeds. Our approach aims to balance ecological integrity with cost-effective management strategies, ensuring SPAs can support long-term restoration success.

Assessing pathogenicity of variants in TAB2

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TGF-beta-activated kinase 1 binding protein 2 (TAB2) is a key regulatory protein in inflammatory and developmental pathways. While the pathogenic role of gain-of-function (GOF) variants in *TAB2* is recognised, particularly in the context of

frontometaphyseal dysplasia (FMD), the molecular mechanisms driving this phenotype remain poorly understood. To further characterise the impact of GOF missense mutations, we combined a cell-based luciferase reporter assay with AI-driven protein structural predictions –AlphaFold– to assess their effects on transcriptional regulation. Ten *TAB2* missense variants, seven of which are from known patients with FMD, including two confirmed pathogenic positive-controls, will be analysed for their influence on activator protein-1 (AP-1) transcriptional activity. We aim to demonstrate that specific GOF variants enhance AP-1 signalling, suggesting a potential mechanism for TAB2-mediated pathology. These findings will provide insights into the molecular consequences of *TAB2* GOF variants and highlight the utility of integrative functional and structural approaches in variant characterisation.

Investigating the Genetics Underlying Late Flowering in Perennial Ryegrass

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Perennial ryegrass (*Lolium perenne*) is a critical forage in New Zealand farming systems, utilised due to its high metabolisable energy (ME) content in vegetative tillers. ME availability decreases during the transition from vegetative to reproductive tiller growth, impacting agricultural productivity. Flowering (heading) in perennial ryegrass is induced by long photoperiods after prolonged exposure to cold temperatures and naturally occurs in spring. Genetic variation in the flowering control pathways has been linked to variation in flowering times in other temperate grasses, however this has not been well characterised in ryegrass.

This project focusses on a ryegrass population which has been consistently observed to segregate for floral emergence times, from late October through to mid-December. Using extended daylength experiments we have shown that the photoperiod response plays a role in variable flowering times and genetic analyses have identified variation in Chromosome 4 that is associated with late flowering in this population. We are now exploring variants in putative photoperiod genes in this region of Chromosome 4 to investigate the function of these genes in ryegrass and identify alleles that could be used for breeding late-flowering ryegrass.

National collaboration provides insight into patterns of strandings of enigmatic beaked whales

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Beaked whales (Ziphiidae) represent one of the most speciose groups of cetaceans, however, their cryptic behaviour and inaccessible habitat make them difficult to study. As a result, most of what is understood of most species of beaked whales has been collated from stranded individuals, and Aotearoa New Zealand in particular is a stranding hot spot. Anthropogenic threats such as naval sonar have been linked to unusual mortality events in beaked whales, raising concerns about the scarcity of knowledge on population size, structure and distribution. This lack of baseline information hinders their conservation and management, especially as many beaked whale species have a global distribution. Here, we utilise the New Zealand Cetacean Tissue Archive (NZCeTA) to provide insight into the spatial and temporal distribution of beaked whales using DNA species identification methods. NZCeTA is a national collaboration effort between mana whenua, Department of Conservation and the University of Auckland – Waipapa Taumata Rau formed in 1991 and currently holds samples from 13 of 24 beaked whale species. Using NZCeTA we aim to elucidate seasonal and sex-biased patterns of stranding mortalities of beaked whale species around Aotearoa, New Zealand. Our goal is to demonstrate the utility of a collaborative national tissue archive and opportunistic data collection to provide baseline data on elusive cetaceans.

Alternative ribosomal RNAs and their unsuspected link to sex determination in zebrafish

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The ribosome is a ribonucleoprotein complex that has traditionally been thought of as a universal cellular machine translating diverse messenger RNA into protein. Despite this, many vertebrate species possess distinct ribosomal RNA loci, which is suggestive of functional specialisation. For example, zebrafish (*Danio rerio*) possess at least three distinct 45S rRNA-encoding loci, including 45S-M, which lies in the only sex linked region of the genome, and is amplified in the female germline at the time of gonad differentiation[1]. Recently, we showed that targeted mutation of 45S-M ribosomal DNA (rDNA) inhibits feminisation without affecting male development -

suggesting 45S-M is both a specialist ribosome locus and a primary determinant of sex[2]. To better understand the locus, we used long-read Nanopore sequencing to overcome the challenge of resolving highly repetitive rDNA. In doing so, we successfully assembled the 45S-M rDNA locus, defining a consensus of 15 full 45S-M rDNA units flanked by a terminal 18S rDNA unit, which is colocalised with the telomere on chromosome 4. Looking forward, long-read sequencing will be combined with targeted zebrafish breeding experiments to determine the minimal rDNA complement required for feminisation. Together, these approaches will clarify the functional role of alternative ribosomal RNAs in zebrafish sex determination.

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Evaluating the Role of On-Call Genetic Counselling service in a Prostate Cancer Clinic: A Study of Uptake and Family Risk Screening

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Prostate cancer is the second most common cancer in males in Oman. With the rise of precision medicine, targeted therapies and germline genetic testing for prostate cancer have become more common. This study aimed to assess the uptake and impact of an in-hospital, on-call genetic counselling service for the Genitourinary (GU) cancer programme. A retrospective file-based study was conducted using data from the genetic counselling database. A total of 120 prostate cancer patients were seen from September 2021 to March 2025. The number of patients counselled increased steadily, coinciding with the inclusion of an on-call genetic expert in the GU programme. Patients' ages ranged from 41 to 88 years. Among them, 42 had a family history of *BRCA*-associated cancers, 31 had a family history of non-*BRCA*-associated cancers, and 47 had no cancer history. A cancer panel identified pathogenic *BRCA2* variants in eight patients eligible for targeted therapies. This led to predictive

counselling and testing for 56 at-risk family members, enabling early screening. Integrating an on-call genetic counselling service into the prostate cancer clinic enhanced patient engagement and helped identify hereditary cancer risks. Continued collaboration between genetic specialists and oncologists is essential for providing comprehensive care and supporting patients and their families in managing cancer risk.

Swipe left on self-pollen: Uncovering the molecular basis for self-incompatibility in clover

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Clover is the most important pastoral legume to agriculture in New Zealand. Many clover species, including White clover (*Trifolium repens*), are self-incompatible, meaning for fertilisation to occur pollen must come from a genetically distinct plant. Self-incompatibility has slowed genetic gain and limited breeding in white clover as it prevents inbreeding which is needed to purge deleterious alleles and fix beneficial alleles.

Self-incompatibly has evolved in a range of plants resulting in distinct mechanisms across families. Self-incompatibility often originates from a single locus, the *S*-locus, that contains one gene expressed in the male tissue (pollen/anther) and another in the female tissue (stigma/pistil). These genes often encode a complementary set of interacting proteins, a receptor and ligand pair, that underpin the recognition of self or non-self pollen.

We have identified the putative *S*-locus genes in clover and predict that they encode a receptor and ligand. In this research, we aim to validate and characterise the predicted proteins, including their expression patterns, protein-protein interactions and cellular locations. This will uncover the molecular mechanism responsible for self-incompatibility in clover, and ultimately advance clover breeding.

Using a genetic lens to treat pelvic organ prolapse

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Pelvic organ prolapse (POP), or the herniation of the pelvic organs into the vagina, is an incredibly common condition, experienced by 6% of people with a vagina, under 30 and over 50% of those who are post-menopausal. Current treatment options are lacking and there is nothing to address the underlying connective tissue failure.

In this project we aim to find rare genetic variants that contribute to POP in young people using data from the UK BioBank and an Aotearoa cohort. Using transcriptomics and proteomics on tissue from the vaginal wall, we will link genetic variants to differences in expression of extracellular proteins in the pelvic floor.

We have shown that prolapse in young women is associated with connective tissue disorder, and that haploinsufficiency of genes causative of recessive connective tissue disorders is enough to cause severe POP.

As this project develops we aim to recruit a cohort of pre-menopausal people with prolapse, and discover rare variants that contribute to their phenotype. We aim to identify people at high risk of POP after vaginal delivery and also to discover key, extra-cellular components of pelvic floor strength that can be engineered into bio-therapeutics for prolapse treatment.

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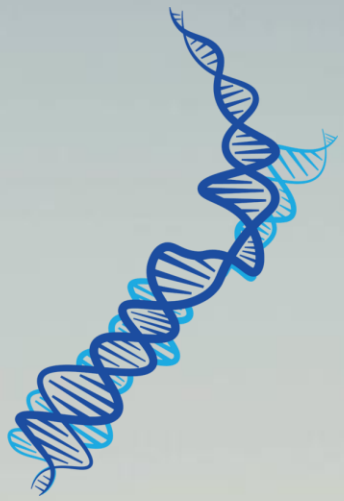

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