QMB Abstracts
He taonga tuku iho – Bioprotection Aotearoa Satellite

B1: Partnering with Māori to improve conservation outcomes: reflections of a non-Māori researcher

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My research team are privileged to engage in conservation genetics and genomics research for threatened taonga (treasured) species that involves te ao Māori (Māori worldview) and, when appropriate, applies kaupapa Māori (Māori centred) principles. In this talk, I will provide an overview of this research, with an emphasis on two overlapping topics. The first, is conservation research on the genetic/genomic consequences of small population size in threatened taonga species endemic to Aotearoa, especially birds. The second, is conservation genetics/genomics research on taonga species–like freshwater fish and invertebrates found nowhere else in the world–that is responsive to the needs and aspirations of iwi (tribes) and hapū (subtribes). In the former, my research team generally builds relationships with relevant iwi and hapū representatives, in parallel to te Tiriti o Waitangi (Treaty of Waitangi) partner relationships between them and the Crown. In the latter, enabled by partnerships with iwi and hapū built on mutual trust and respect, research is co-created–from start to finish–and seeks to grow capability and capacity among all partners. From there, I will briefly share some ideas for non-Māori, like me, who wish to engage with Māori as a critical first step towards co-created research that includes Western knowledge systems and mātauranga Māori (Māori knowledge systems).

B2: Restoration genetics of a critically threatened New Zealand Myrtaceae, *Syzygium maire*

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The global decline of biodiversity is among the most pressing issues facing humanity. With over 90% habitat loss, Aotearoa's swamp forests are a prime example. Wetlands are essential to ecosystem service and habitat provision, and are taonga for Māori who have been disproportionately affected by declining biological heritage. The restoration of swampland is therefore vital to the recovery of both biodiversity and cultural values. *Syzygium maire* (swamp maire, maire tawake, waiwaka), is an endemic, critically endangered canopy tree species of Aotearoa's swamp forests. Formerly widespread, extant populations are small, fragmented and under pressure from myrtle rust. Information of the geographic and environmentally structured distribution of maire tawake's genetic diversity would support conservation and restoration strategies aimed at facilitating future resilience of the species. Genomic data for tree species is lacking, however, and often neglected in conservation and restoration efforts.

Given this substantial gap in understanding, I am exploring the landscape level and environmental processes affecting *S. maire*'s genetic structure and adaptive variation. In order to achieve this, I use a novel long read, high accuracy sequencing technology to enable rapid, cost effective assembly of reference genomes for Aotearoa's endemic species. I then explore a genotyping-by-sequencing approach to assess the genetic diversity, population structure and potential local adaptation of *S. maire* as a function of climate across New Zealand. Future work will aim to describe fine-scale genetic structure and interbreeding of maire tawake populations, followed by simulation-based approaches aimed at informing integrative restoration strategies for wetland habitats.

B3: Species-wide genomics of kākāpō provides transformational tools to accelerate recovery

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The Kākāpō are one of the most beloved species in Aotearoa, but they are critically endangered, with only 248 living individuals living on tightly managed, predator-free islands. All living individuals were sequenced in 2018, capturing the entire remaining genetic variation of this species. In order to bring genomics to applied conservation practices, we have analyzed both genotypes and phenotypes using cutting-edge technologies and techniques to work properly with small sample sizes.

Genotypes were discovered via a machine-learning method, DeepVariant, which reduced Mendelian inheritance errors over more traditional methods by half. Phenotypes were processed using probabilistic programming, a form of Bayesian statistics using variational inference, allowing rapid iteration and high confidence in our outputs. This further allowed us to predict the effect of various factors and ascertain the uncertainty of our predictions, which can then be provided to the conservation management team. This data was then compared with the genotypes via genome-wide association studies, with confirmation by cross-species comparison to other studies finding the same genes for the same or similar phenotypes.

Further, we calculated this population's estimated "Breeding Values" as additional information for conservation practitioners. This method was successful for several phenotypes, including growth rate, body weight, clutch size, egg fertility, and aspergillosis susceptibility. Over the past five decades, we find that activate management has maintained both genome-wide and phenotypic diversity and, thus, evolutionary potential. By explicitly addressing and rising to the challenge of small sample sizes, we provide a path for future studies for species of conservation concern.

B4: Giving effect to Te Tiriti o Waitangi in the emerging field of chromosomics

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The critically endangered kākāpō is a nocturnal, flightless parrot endemic to Aotearoa-New Zealand, and is considered a taonga (treasure) of Ngāi Tahu, a Māori iwi (tribe) of Te Wai Pounamu (the South Island of Aotearoa-New Zealand). Once widely distributed across the North and South Islands, kākāpō populations rapidly declined as a result of human disturbance and introduced mammalian predators. Kākāpō recovery is limited by low productivity–including early hatching failure–but intensive conservation management has grown the population from 51 birds in 1995 to 248 birds alive today.

In an effort to determine the chromosomic basis of early hatching failure, we are part of a larger team combining new and existing genomic and cytogenetic resources for kākāpō. Whereas national and international publicly available scholarship regarding the genomics of culturally significant species is growing, no such scholarship exists for the emerging field of chromosomics. Here, we explore cultural perspectives and considerations associated with the creation and care of two primary cell lines made from tracheal tissue of two deceased kākāpō chicks, one female and one male. Beyond providing important context to our research, we are eager to advance early dialogue regarding the *in vitro* culture, use and storage of cells and tissues from culturally significant species to enhance conservation, both here in Aotearoa-New Zealand and beyond.

B5: Indigenous ethics in research: the protection and correct treatment of Taonga species

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Over the last 10 years, many advances have been made in our understanding of the Māori view of Aotearoa's native flora and fauna and the significant mātauranga Māori that exists within our iwi, hapū and whānau throughout the country. In this time, many claims, frameworks and guidelines have been developed to aid in the transition for carrying out genomic research with taonga species in an appropriate and respectful way. This includes the preservation and protection of the mātauranga Māori associated with a taonga species when it is used in research e.g. collection, storage and disposal of native flora and fauna. This also encompasses the mātauranga Māori (traditional Māori knowledge) surrounding these species, and the protection of any extension of that mātauranga. This presentation will speak about our recognised taonga species, how they are categorized, why they are significant and finally, what you can do in your research to ensure this significance is acknowledged. These points will be supported by Pūrakau (Māori traditional narratives) that contain mātauranga related to taonga species. The resources related to treatment of taonga species that I will be discussing are included in the references below.

1. Mead, Aroha., Waitai, Sheridan., Hutchings, Jessica., Foster, Meika., Shadbolt, Melanie., Harris, Paulina., *A Wai262 Best Practice guide,* (June 2022).
2. Murray, Haana., Witana, Hemi Nui a Tawhaki., McMath, Te Witi., Poata, Tama., Rimene, Kataraina., Hippolite, John., *Waitangi Tribunal Claim WAI262,* (October 1991).
3. The Waitangi Tribunal. *Ko Aotearoa Tenei: Report on the WAI 262 Claim,* (2011).
4. Husdon, Maui., Thompson, Ariane., Wilcox, Phillip., Mika, Jason., Battershill, Chris., Stot, Matthew., Brooks, Robert Tūrongo., Warbrick, Lisa. *Te Nononga Kaitiaki: Guidelines for Genomic Research on Taonga Species*, (2021).

B6: Standing in Both Worlds: Exploring Hapū-led bioprotection at Whareponga

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This abstract presents a research journey that explores Māori-led efforts to address biosecurity threats and conserve taonga species. The research focusses on the impacts of invasive predators and myrtle rust within the local context of Whareponga, a remote coastal marae on the East Coast of the North Island, Aotearoa. Initially, my research set out to investigate the role of marae and hapū in managing biosecurity threats, such as myrtle rust and invasive predators. However, as I progressed my focus shifted from examining their practices to exploring my own whakapapa and the extent of my responsibility in supporting marae, hapū and iwi in managing biosecurity threats on whenua Māori.

Working with tangata whenua provides a unique opportunity to integrate the values, perspectives, and knowledge embedded in the whakapapa of the whenua. By combining western scientific methods and mātauranga Māori, the research aimed to generate holistic and context-specific insights into biosecurity challenges and solutions. Using my personal experience, I explore how kaupapa Māori research can be conducted to support biosecurity management at a marae/hapū level. I will discuss the pathway I used to conduct this research and share key learnings from my personal journey, with a vision to inspire others to also work closely with Māori communities and be enriched by their teachings.

B7: How might we refresh biocontrol agents?

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Aotearoa- New Zealand's unique geography, biology and history have left us with unique and difficult biological questions. We struggle to control the introduced and damaging pests we already have in the country, and we have a constant need to be vigilant to keep out new pests and diseases. The problem is only going to get worse with climate change due to changes in the migration of people, changes in our environment, and even increased frequency of extreme weather events more likely to cause breaches in our biosecurity.

This increased threat comes at a time when we are withdrawing tools to control pests already here.

One current tool in our toolbox is Biocontrol. In its most simple form, this involves using a predator or parasite that targets the pest species. This is hugely important in New Zealand, where two tiny parasitic wasps are used to hold back an army of weevils that munch through the pasture that supports our meat and dairy industries.

Biocontrol is problematic as it usually involves the introduction of a new species into the country to attack the pest. Only about 10% of these introductions work, and recent studies have shown that initially effective biocontrol can fail. Because of this, we need to make the most of the biocontrol agents we have and find ways to better predict if biocontrol releases will be effective.

In this presentation, I will discuss new genomic and genetic approaches to improving biocontrol as a way to deal with our invasive pest problem. I will present data on trying to understand the biology of biocontrol agents, and ways this information might help us control the pests that challenge us.

B8: Predicting successful biocontrol; what we can learn from *Microctonus hyperodae* genomics

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The insect pasture pest, the Argentine stem weevil (*Listronotus bonariensis*, ASW), causes an estimated NZD$200M of damage to New Zealand pasture annually. In the 1990's the endoparasitoid wasp, *Microctonus hyperodae,* was collected from eight South American locations and released throughout NZ as a biocontrol agent against ASW. Initially, parasitism rates of ASW by *M. hyperodae* were as high as 80%, effectively reducing ASW population sizes and resultant pasture damage. Despite this initial success, parasitism rates have now declined by over 50% in multiple locations, resulting in increased ASW populations and return of pasture damage. This biocontrol decline may be a result of ASW evolving parasitism resistance, against which the asexual *M. hyperodae* was unable to coevolve. Alternatively, *M. hyperodae* may have become less parasitic of ASW by way of adaptation to novel New Zealand environments.

Here, for the first time, we were able to understand the population relatedness of the eight ecotypes of *M. hyperodae* at the time of deployment throughout New Zealand. Our data suggests that, despite their differing geographical origins and previous identified phenotypic variation, there is very little genetic difference amongst and between the eight ecotypes. This lack of genetic diversity may be due to the asexual reproduction of *M. hyperodae,* or the need for tight regulation of genomes in a species which occupies niche environments.

We next compared these eight historical populations to recent collections of *M. hyperodae* in New Zealand, in order to understand how *M. hyperodae* have been selected for and evolved under the pressures of novel New Zealand environments. Again, preliminary results indicate little genetic differences between the historical and recently collected *M. hyperodae* genomes. This work critically informs upon the population structure of a declining New Zealand biocontrol agent and provides insights for considerations of future biocontrol efforts in New Zealand.

B9: Transmission of a novel virus in a declining insect biocontrol system

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The Argentine stem weevil (*Listronotus bonariensis*, ASW) is an economically significant pasture pest in New Zealand, primarily controlled by the biocontrol agent *Microctonus hyperodae*, an endoparasitoid wasp. Initial parasitism rates of ASW in the 1990's were up to 80%, indicating very effective control, but these rates have now declined by 50% or more, resulting in severe pasture damage costing an estimated NZD$200M per annum. This decline may be a result of ASW evolving a parasitism resistance mechanism in response to the historically high selective pressure imposed by *M. hyperodae*, with which the asexual wasp was unable to coevolve.

As population genomic analyses of ASW have not yet identified a cause of biocontrol decline, we are now investigating the influence that the microbiome may have had on both the initial success or eventual failure of this biocontrol system. Bacterial endosymbionts have been linked to parasitism resistance in aphid hosts, while viruses infecting wasps can play critical roles in parasitism success or manipulate parasitoid behaviour reducing parasitism rates. 16S rRNA sequencing in ASW detected significant changes in the microbiome in response to different diets, but not between parasitised and unparasitised ASW. Metagenomic analysis of M. hyperodae revealed a novel viral infection, which is transmitted to ASW during parasitism. Sequencing of historical and contemporary *M. hyperodae* specimens indicates this viral infection was present in *M. hyperodae* prior to biocontrol release and provides preliminary evidence that the viral load in M*. hyperodae* may have decreased since release.

B10: A whole genome perspective on genetic variation and rapid adaptation in invasive species

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Evolutionary theory tells us that the immense diversity that exists on this planet does so through a complex combination of factors, in which genetic variation plays a central role. It is on this genetic variation that selection may act, enabling adaptation. Ongoing developments in sequencing and analytical tools are enabling more comprehensive characterization of diverse components of genomic variation present in the natural world. Invasive species are often used as eco-evolutionary model species, as the rapid evolutionary shifts they undergo post introduction bottleneck allows study of how molecular mechanisms and genomic variation underly adaptive processes.

Here, we use whole genome resequencing of a globally invasive avian, the common myna (*Acridotheres tristis*), to examine the impacts of successive bottlenecks on genomics variation, comparing patterns in single nucleotide polymorphisms, structural variants, and transposable elements. We further interrogate this data to determine which of these genetic components may have played a disproportionate role in the rapid adaptation each population has undergone within their new invaded ranges. In particular, we focus on transposable elements, a specific type of genetic variation that is capable of rapidly changing a genome's sequence through relocation or altered copy number. Further, we utilise cross species comparison by contrasting some of these findings with those from a second, closely related invasive avian the common starling (*Sturnus vulgaris*).

This is a first step towards allowing us to identify which patterns are more stochastic, and which are common across independently evolving invasive species, and thus may play a key role in their invasion success. Broadly, understanding how components of genetic variation contribute to adaptive potential in an invasive population has important implications not just in invasive species management and forecasting, but also in conservation efforts focused on vulnerable and managed native species.

B11: Quantifying microbial endemism through eDNA

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Microbial ecosystems are crucial for maintaining a healthy environment. As our understanding of ecosystem function improves, it becomes increasingly clear that a healthy microbial ecosystem is characterized by diversity and resilience to invasion. This suggests that the establishment of seemingly harmless invasive microbiota in an ecosystem may facilitate the subsequent colonization of more detrimental species. Unfortunately, our ability to differentiate between endemic and invasive microbiota is limited by our capacity to identify them as such. Metagenomic analysis of environmental DNA (eDNA) provides a comprehensive approach to assessing the diversity and genetic potential of microbial communities.

This presentation demonstrates how metagenomic data derived from eDNA can be utilized to quantify endemicity using examples from Aotearoa-New Zealand and Antarctica. This methodology does not rely on previously observed reference genomes, making it applicable to a wide range of environments. The methodology can be adapted to detect both genome-wide sweeps as well as gene-specific sweeps, leaving open the question as to whether endemicity and invasion is best understood from an organism-based or a gene-based concept. Given the significance of endemic organisms in maintaining ecosystem health, bioprotection efforts would greatly benefit from the preservation and enhancement of endemic microbial communities. Though these microscopic guardians may remain invisible to the naked eye, they serve as our first and best line of defense.

B12: Exploring outcomes of genetic pest control in multi-species models

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Established relationships between multiple invasive species present a challenge to predicting the outcomes of single-species management technology like gene drives. In Aotearoa New Zealand (NZ), invasive mustelid predators (e.g. stoats) are primarily dependent on invasive rodent populations. Competitive relationships also exist between rodent species and other introduced mammals like the brushtail possum. These relationships are an important consideration when predicting gene drive outcomes as they present additional sources of mortality that can strongly influence the dynamics of populations. Empirical data also suggest that these inter-species relationships may generate unintended consequences at the ecosystem level where there is potential for both competitive and predatory release of species.

To address these complexities, our research uses the newly developed SLiM4 framework to theoretically explore the feasibility of co-ordinating gene drives across four important invasive mammalian species in NZ: stoats, rats, mice and possums. We first develop an individual-based version of a published analytical model representing our target invasive species community. This multi-species model will further be used to investigate the effect of inter-species relationships on drive outcomes and assess the potential for unintended ecological impact. Our study aims to provide essential insights into the dynamics of gene drives in more biologically realistic simulations and additionally provide a valuable tool for simulating a variety of eco-evolutionary questions.

B13: Rodent Romance Gone Awry: Infertility as the Key to Rat Retreat

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The introduction of Norway (*Rattus norvegicus*) and ship rats (*Rattus rattus*) to Aotearoa by European vessels during the 1800s has had devastating consequences for native vertebrate and invertebrate populations. These opportunistic invasive mammals pose a significant threat to indigenous bird species, that are taonga to NZ Māori. Current methods for rodent elimination, primarily relying on poison and traps, face limitations in scalability on the mainland, where refuge populations facilitate survivors and re-establishment. To address this pressing issue, gene-drive technology offers a promising alternative, where infertility genes can be introduced and spread throughout target populations. However, successfully applying such technology necessitates a meticulous understanding of the target genes within the respective populations.

Prior investigations on *Mus musculus* have utilized the t-haplotype, a naturally occurring haplotype exhibiting super-Mendelian inheritance, as a means to transmit infertility genes like the female fertility gene (Prl). Simulations have demonstrated the potential efficacy of this approach in eliminating invasive *M. musculus* populations. Nonetheless, a comparable gene-drive system is yet to be developed for *R. rattus or R. norvegicus*. Therefore, this study assesses the genetic diversity and evolutionary structure of gene targets in *R. rattus* and *R. norvegicus* using whole genome resequencing data of 64 and 56 individuals respectively, across Aotearoa. Doing so describes the genetic architecture to inform the design of a gene-drive system that might effectively counteract the majority of the target population while minimizing the susceptibility to resistance development prior to eradication. Investigating the standing genetic diversity and evolution of gene targets in *R. rattus* and *R. norvegicus* significantly contributes to understanding the underlying genetic architecture. It paves the way for developing a robust and efficient gene-drive system. The findings will be important for the conservation of bird species, aiding in mitigating the ecological and cultural impact caused by these invasive mammals in Aotearoa.

B14: A relational framework guides best practices in microbiome research with Indigenous communities

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Ethical practices in microbiome research have failed to keep pace with scientific advancements in the field. As microbiome research has expanded to include Indigenous communities, a lack of oversight or guiding principles on best practices for engagement has led to ethical missteps and community exploitation. As a result, researchers seeking to "preserve" microbial species associated with Indigenous groups, but missing in industrialized populations, have failed to include Indigenous people in knowledge co-production or benefit, perpetuating a legacy of intellectual and material extraction. Here, we propose a framework centred on relationality among Indigenous peoples, researchers, and microbes to guide ethical microbiome research. Accountability underlies the foundation of these relationships and seeks to flatten historical power imbalances that favour researcher perspectives and interests to provide space for Indigenous worldviews in pursuit of Indigenous research sovereignty. Ethical inclusion of Indigenous communities in microbiome research can provide health benefits for all populations and reinforce mutually beneficial partnerships between researchers and the broader public.

B15: Impacts of plant-soil feedbacks and fire on arbuscular mycorrhizal fungi associated with invasive plants

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Climate change is causing increases in invasive species and fire activity. How these factors impact soil fungi, particularly mutualistic arbuscular mycorrhizal (AM) fungi, may determine future invasions. Positive plant-soil feedback is where plants accumulate beneficial AM fungi in the soil over time. Because mycorrhizal taxa have different abilities to survive heat from fires, fires may either disrupt positive plant-soil feedbacks to reduce plant invasion, or alternatively lead to an increase in particular mycorrhizal taxa that favour growth of invasive plant species.

We aimed to determine the role of plant-soil feedbacks and simulated heat from fire on AM fungal communities and growth of invasive plants from New Zealand's native grasslands. We first collected soil from under one native grass (*Chionochloa macra*) and two highly invasive hawkweeds (*Hieracium lepidulum*, *Pilosella officinarum*). In the lab, soils were heated to 30°C, 45°C and 60°C to simulate grassland fires, and then DNA was extracted and sequenced to measure AM fungal community structure (18S rDNA, Illumina MiSeq). In the glasshouse, we grew hawkweeds in each soil type and measured biomass. We show hawkweed biomass was influenced by soils from under different plants but not heat. Additionally, biomass of both hawkweeds was always greater in *P. officinarum* soils, suggesting potential for these soils to facilitate invasion of *H. lepidulum*. Our study empirically demonstrates the impacts of both fire and plant-soil feedbacks on AM fungal communities in plant invasions, two factors that are increasing due to climate change.

B16: Characterising soil microbial communities across the agricultural mosaic landscape of Te Kaha

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Land management can have profound impacts on soil microbial communities, which in turn may affect soil quality and the capacity of soil to respond to perturbations. Te Kaha, rohe of Te Whānau-ā-Apanui, is a predominately agricultural area, featuring a mosaic landscape of maize and expanding kiwifruit. This study sought to provide a seasonal baseline for soil microbial communities across eight, paired maize and kiwifruit sites in Te Kaha.

Maize and kiwifruit soils differed in their physicochemical characteristics, driven predominantly by higher carbon and nitrogen related properties in kiwifruit orchards. Microbial activity, via dehydrogenase enzyme analysis, was significantly higher in kiwifruit orchards. There was a significant seasonal effect on microbial activity in kiwifruit orchards, with higher activity occurring in summer compared to winter, which was not observed in maize soils. Microbial biomass, as measured by total phospholipid fatty acid (PLFA) analysis, was significantly higher in kiwifruit orchards with no seasonal effects observed. Non-metric multidimensional scaling (NMDS) and analysis of similarities (ANOSIM) of the 50 PLFA biomarkers present found that PLFA composition differed across both land use and season. Multi-level pattern analysis further revealed that 16:1ω5 and 18:1ω9, biomarkers associated with arbuscular mycorrhiza and Zygomycota, respectively[1], were two of the drivers of differences based on land use, with a higher proportion of these biomarkers found in soils from kiwifruit orchards.

These findings can help Te Kaha land managers better understand their current soil quality status and will provide insight into how soil microbial population and physicochemical properties may shift as maize fields are converted into kiwifruit orchards in the coming years.

1. Joergensen, R. G., *Phospholipid fatty acids in soil—drawbacks and future prospects*. Biology and Fertility of Soils. 58:1-6.

B17: Exploring the diversity of secondary metabolite biosynthetic gene clusters in kauri (*Agathis australis*) forest soils

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Phytophthora agathidicida is a virulent pathogen of Aotearoa New Zealand's iconic kauri (*Agathis australis*) and the causal agent of kauri dieback. Considering the irreplaceable cultural and ecological role of kauri forests, we need to identify methods to control the spread of dieback. For endemic and ecologically unique native forests, it is important to develop disease control measures with no detrimental or non-target impacts on the forest ecosystem. Therefore, in respect of preserving native biodiversity we sought to identify control solutions that exist within the indigenous soil microbiome. Previous research has identified microbial strains that displayed antagonism towards *P. agathidicida* (1). Follow-up whole genome sequencing identified various secondary metabolite biosynthetic gene clusters (SM-BGCs) in the microbial genomes, including polyketide synthases (PKSs) and non-ribosomal peptide synthetases (NRPSs). To accelerate bio-discovery efforts, this current research aimed to perform genomic sequencing directly on soil gDNA to explore the diversity of SM-BGCs that occur naturally in kauri soils.

We sampled soils associated with healthy and diseased kauri across various forests including Waipoua, Waitākere Ranges, and Puketi Forest. The kauri forests targeted for sampling varied in their degree of disturbance, fragmentation, and dieback disease expression. Following the extraction of soil gDNA, we targeted the NRPS and PKS gene regions for amplicon sequencing using long-read PacBio® HiFi sequencing. Subsequent bioinformatics analysis identified a diverse array of NRPS and PKS SM-BGCs in the kauri soil samples. Furthermore, we detected differences in the diversity, abundance, and type of SM-BGCs that naturally occur in kauri soils according to their geographic location, degree of anthropogenic disturbance, and disease outbreak.

1. Byers AK, Condron L, O'Callaghan M, et al.; *Whole genome sequencing of Penicillium and Burkholderia strains antagonistic to the causal agent of kauri dieback disease (Phytophthora agathidicida) reveals biosynthetic gene clusters related to antimicrobial secondary metabolites.* Molecular Ecology Resources 2023.

B18: Biocontrol agent *w*Mel *Wolbachia* genome remains stable in *Aedes aegypti* mosquitoes

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Wolbachia-introgression methods are increasingly being utilised as biocontrol interventions against the spread of arboviruses such as dengue and Zika. The World Mosquito Program predominantly utilises *w*Mel *Wolbachia*, an endosymbiont bacteria found natively in *Drosophila melanogaster.* When transinfected into *Ae. aegypti, w*Mel significantly reduces the potential for the mosquito to transmit arboviruses. Long-term effectiveness of a successful *w*Mel intervention method relies upon several critical features. First, *w*Mel must remain at high prevalence in field populations. Second, *w*Mel must not evolve to lose the desired *w*Mel-induced phenotypes which enable its application for biocontrol. These include cytoplasmic incompatibility which aids *w*Mel introgression into naive populations, and the reduction of virus replication within *w*Mel-infected mosquitoes. Thus, the success of the *w*Mel intervention method will in part depend on the evolutionary trajectory of *w*Mel itself, of the viruses *w*Mel inhibits, and the *Ae.aegypti* host.

Here, we investigated *w*Mel genomic evolution after its transinfection from its native host *D. melanogaster* into *Ae. aegypti*. We then assessed *w*Mel genomic evolution after its introgression into field populations up to seven years post release in four countries: Australia, Vietnam, Colombia, and Indonesia. We show *w*Mel genomic stability in terms of sequence, synteny, and structure, independent of country origin and despite transinfection into a novel host. This work suggests *w*Mel is stable in its new *Ae. aegypti* host, and supports the application of *w*Mel for biocontrol of *Ae. aegypti* transmitted arboviruses to deliver long-term public-health benefits.

B19: Bacteria and their enemies: an armoury for Aotearoa's bioprotection battle?

Birkholz, N.[1,2,3,4], de Roode, S.[1,5], Kamata, K.[1], Fagerlund, R.D.[1,2,3,4], Jackson, S.A.[1,2,3,4], Fineran, P.C.[1,2,3,4]

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Bacterial pathogens infecting humans or plants have enormous impact on our lives, be it directly by causing disease or indirectly by leading to losses in agriculture and jeopardizing our food supply. Traditionally, such pathogens have been targeted using, for example, antibiotics or bactericidal agrichemicals. However, the development of resistance can hinder the efficacy of such treatments. Possible alternatives to these approaches may be found by studying how bacteria interact with and fight against their natural enemies, including competing microbes and viral invaders (phages). Therefore, a deep understanding of the interplay between these protagonists is of interest both from a fundamental and from an application-oriented perspective.

Here, I will focus on the plant pathogen *Pectobacterium* and some aspects of the warfare it is involved in. We have extensively characterized defence systems that this bacterium uses to fend off invading phages, as well as phage strategies to mount a counter-defence response. Furthermore, we have recently examined a large collection of *Pectobacterium* strains sampled from across Aotearoa New Zealand and found that many of these produce bacteriocins, macromolecules exported from the cell to kill closely related bacteria. These examples from our research provide insight into the multiple weapons deployed in the interactions among bacteria and between bacteria and phages. We envision that our findings provide a potential strategy to target pathogens in Aotearoa New Zealand and globally.

B20: The role of soil-borne disease in the poor persistence of pastures in northern Aotearoa/New Zealand - Identification of causal agents

van Amsterdam, S. A. M.[1,3], Templeton, M. D.[2,3], Lear, G.[3] & Bell, N. L.[1]

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Globally, soil-borne plant diseases negatively impact the productivity and persistence of agricultural systems and pastures in Aotearoa/New Zealand (AoNZ) are no exception. In recent decades, there have been repeated observations of poor persistence of sown pastures in northern AoNZ(1). Economic modelling suggests that soil disease of the dominant pasture plants in this country, *Lolium perenne* (perennial ryegrass) and *Trifolium repens* (white clover), is responsible for a \$909 ha^{-1} $year^{-1}$ reduction in Waikato pasture-based farm profitability(2). Research into possible causative agents of soil disease in pastures was primarily conducted in the 1980s to early 2000s(3) when pasture management and climate were much different to the present day. Common plant pathogenic fungi including *Fusarium spp., Pythium spp.,* and *Rhizoctonia solani* are regularly detected in the roots of pasture plant species(2,3). Up-to-date research is now needed to understand the distribution and abundance of causative agents of disease in modern pasture systems. Ongoing advances in molecular biology allow us to further our understanding of this area.

My PhD project will identify and understand the distribution of fungal soil-borne pathogens in pasture soils of northern AoNZ. Putative pathogenic fungi have been isolated and are being screened using *in-vitro* and *in-planta* pathogenicity tests. I will develop molecular diagnostics (qPCR/ddPCR) to screen historical soil samples for confirmed pathogenic isolates. Additionally, I will search available soil microbiome datasets for the presence and abundance of these pathogens. Combined, this information can be used to develop cultural, biological, and chemical methods to mitigate against the impact of soil-borne disease in pastures, helping to improve their persistence in modern farming systems under a changing climate.

1. Beukes *et al.,* (2021). *Resilient Pastures: Grassland Research and Practice Series.* 17:297-306.
2. Dignam *et al*., (2022). *Journal of Sustainable Agriculture and Environment*. 1:16-29.
3. Wakelin *et al.,* (2016). *Australasian Plant Pathology.* 45:289-296.

B21: *Phytophthora agathidicida* alters its repertoire of secreted proteins in the presence of *Phytophthora cinnamomi* and *Phytophthora multivora*

Dagg, T.J.[1], Bradley, E.L.[1], Loo, T.S.[2], Tu, Y.-H.[2], Heslop, S.[3], Tarallo M.[3], Cauldron, N.C.[4], Bradshaw, R.E.[3], Mesarich, C.H.[1]

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Kauri dieback is a devastating disease of New Zealand kauri (*Agathis australis*) caused by the oomycete *Phytophthora agathidicida* (*Pa*). Alongside this pathogen, two broad-host-range *Phytophthora* pathogens, *P. cinnamomi* (*Pc*) and *P. multivora* (*Pm*), often co-occur in the soil surrounding affected trees, with glasshouse trials showing that they are capable of causing disease lesions on seedling leaves. Whether all three *Phytophthora* species cooperate to cause disease or are antagonistic towards each other remains unknown. Such knowledge is crucial for the preservation of kauri, as it may mean that disease control strategies need to target all three species. If the three species do indeed interact, it is anticipated that this interaction occurs at the molecular level through secreted proteins, since oomycetes have a limited capacity to produce secondary metabolites.

To determine whether the repertoire of secreted proteins from *Pa* changes in the presence of *Pc* and *Pm*, a proteomic analysis of secreted proteins produced by *Pa* during co-culture in clarified V8 broth, relative to growth alone, was performed at seven days post-inoculation using liquid chromatography-mass spectrometry. In total, out of 154 secreted *Pa* proteins identified, nine were produced in all species combinations tested (*Pa*+*Pc*, *Pa*+*Pm*, *Pa*+*Pc*+*Pm*), but not when *Pa* was cultured alone. A further 10 were identified that displayed a significant increase in abundance. For all but two of the proteins, an enzymatic function was predicted, with most encoded by genes that are upregulated during infection of kauri leaves and/or roots, relative to growth in culture, suggesting that they may be important during host colonization. To determine whether the 19 secreted proteins of *Pa* enhance or antagonise the growth of *Pc* and *Pm in planta*, each will now be expressed in leaves of the model host plant *Nicotiana benthamiana* and the growth of the three *Phytophthora* species on these leaves assessed.

B22: Integrated approach for understanding *Phytophthora* biology

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Phytophthora species are notorious plant pathogens that cause devastating diseases in a wide range of crops and natural ecosystems. Their invasion and spread have become increasingly concerning in the face of a changing climate, as these pathogens exhibit heightened adaptability and resilience. *Phytophthora* species associated crop damage has severe impacts in diverse disciplines, ranging from environmental, economic, social, and cultural impact. In recent years our focus has been on *Phytophthora cinnamomi,* a highly destructive plant pathogen causing root rot and significant damage to an impressively wide range of plant species (e.g., avocado, pine, lettuce). Presently, we aim to understand the principles underlying *P. cinnamomi* infection, in particular its ability to infect a broad variety of hosts (>5000 species confirmed) and its ability to survive great temperature and drought gradients.

For this, we use a combination of tools reaching from systems biology, computing, biochemistry, and cell biology, which allow us to elucidate aspects from the molecular to the ecology level. Current work is focussed on the comparative genomics of 12 *P.cinnamomi* isolates from New Zealand using a combination of long and short read sequencing approaches. Furthermore, we use RNA sequencing and proteomics to study the effect of osmotic stress on *P. cinnamomi* and its pathogen–host interaction. The assembled 'Omics' data form the basis for further phylogenetic and evolution analysis with a particular focus on effector proteins due to their key function in the infection of the host.

The systems biology approach is complimented by targeted approaches on effector proteins of interest (Crinklers and RXLR effectors), which are analysed for host targets, 3-D structures, cellular localization and function. This knowledge will impact effective control strategies urgently needed to mitigate the impact of *P. cinnamomi* and other *Phytophthora* species, safeguarding agriculture, forestry, and ecological balance in a rapidly changing environment.

B23: Effector proteins required for virulence of the fungal pathogen *Neonectria ditissima* in New Zealand apple

Florez, L.[1], Arshed, S.[1], Scheper, R.[2], Fisher, B.[2], Templeton, M.[1], Bowen, J[1]

[1]Plant & Food Research, Mount Albert, New Zealand, [2]Plant & Food Research, Hawke's Bay, New Zealand.

European canker, caused by the necrotrophic fungal pathogen *Neonectria ditissima*, is one of the most damaging apple diseases in New Zealand and north-western European countries. During plant colonization, *N. ditissima* secretes virulence factors, also known as effectors that can be recognised by plant susceptibility proteins to activate a hypersensitive response (HR). The HR-generated dead tissue serves as an ideal nutrition source for this necrotrophic pathogen and allows for extensive plant colonization. Understanding the molecular basis of *N. ditissima* virulence may ultimately lead to the formulation of novel control strategies against this necrotroph pathogen.

This study reports the first transcriptome profile of *N. ditissima* during colonization of apple fruit and twigs. Analysis of this transcriptome revealed temporal waves and host-specific gene clusters during early and late stages of infection. The most upregulated genes in planta were selected for their effector features using bioinformatics tools such as SignalP 5.0, SecretomeP 2.0, WoLFPSORT and EffectorP – fungi 3.0. To further gain insights into their function, the tertiary structures of the candidate effectors (CEs) were predicted using AlphaFold2 and then investigated for similar protein structures using the Dali server.

Unique predicted functions were identified for three CEs (*g7343*, *g2092* and *g11625*) with similarity to virulence proteins in other plant necrotroph fungi. Similarly, these CEs were knocked out of *N. ditissima*, through CRISPR-Cas9 gene editing, and a reduction of the virulence phenotype in apple fruit and twigs was observed for *g7343* KO and *g2092* KO. *g11625* KO only showed a reduction of virulence in apple twigs which aligns with g11625 transcriptomic profile of being highly upregulated during twig infection but not expressed during fruit infection. Our study reveals novel effectors in the necrotroph pathogen *N. ditissima*, their predicted function and the potential interplay of their virulence role in different host tissues.

B24: What role do spiders play in pest suppression for future food production systems? | Tō te pūngāwerewere tūranga i te tāmoe riha mō ngā punaha whakaputa kai ā mua?

Sullivan, N.J.[1,2,3], Vink, C.[2], Stringer, L.[1], Black, A.[3], Waipara, N.[3,4]

[1]Plant and Food Research, Lincoln, NZ, [2]Pest Management and Conservation, Lincoln University, Lincoln, NZ, [3]Bioprotection Aotearoa, Lincoln, NZ, [4]Plant and Food Research, Auckland, NZ.

Spiders contribute economically to crop protection by reducing pest invertebrate numbers both by direct consumption, and non-consumptive effects. Despite this, the ecosystem service they provide is poorly understood and massively undervalued.

By conducting research in the rohe of Te Whānau-ā-Apanui, alongside Te Kaha Group Ltd – an Ahuwhenua Trust, we will elevate the value of indigenous and non-indigenous spider species through the generation and sharing of knowledge with Te Rūnanga o Te Whānau-ā-Apanui and globally.

We will investigate: 1) What spider species are present in Aotearoa New Zealand kiwifruit orchard and adjacent native bush systems 2) Whether the orchard/native bush interface acts as a hard boundary, hindering spider diversity flow between the two systems 3) The contribution spiders provide to insect pest management via consumptive and non-consumptive attributes 4) Determine if vibration-based insect pest management affect spiders' ability to capture/consume prey in Aotearoa New Zealand orchard systems.

These studies will provide valuable knowledge to show how spider populations can contribute to biological control in Aotearoa New Zealand productive systems. This knowledge aligns with kaupapa Māori, and contributes to low-residue, low synthetic input production in Aotearoa. Preliminary results will be discussed.

Summary of Abstracts for the Poster Session

No.	Title	Presenter	Institutions
B25	Advancing aquacultural aspirations through genomic sequencing	Bailie, M.[1], Elliot, A.[2], Stephens, J.[2,3], Eason, C.[2-5], Kenny, N.J.[1]	[1]Department of Biochemistry Te Tari Matū Koiora, University of Otago, Dunedin, NZ, [2]Wakatū Incorporation, Nelson, NZ, [3]AuOra Ltd, Nelson, NZ, [4]CE Research Associates, Nelson NZ, [5]Faculty of Agricultural and Life Sciences, Lincoln University, Lincoln, NZ
B26	(Dis-)Incentives for Adaptation Intentions in Farming	Buelow, F.A.[1], Brower, A.[1], Cradock-Henry, N.A.[2]	[1]School of Earth and Environment, University of Canterbury, Christchurch, NZ, [2] GNS Science, Christchurch, NZ
B27	Insights into the pathogenicity of Aotearoa *Phytophthora cinnamomi* through comparative genomics	Cox, A.E.U[1]., Flanagan, S.,[1] Meisrimler C. N[1,2].,	[1]School of Biological Sciences, University of Canterbury, Christchurch, NZ, [2]Biomolecular Interaction Centre, University of Canterbury, Christchurch, NZ.
B28	“It all depends on what you value”: Value hierarchies as barriers to native plantings on dairy farms	Elliot Noe, E.[1], Stolte, O.[2], Wreford, A.[1], Buelow, F.[3]	[1]AERU, Lincoln University, Lincoln, NZ, [2]School of Psychology, University of Waikato, Hamilton, NZ, [3]University of Canterbury, Christchurch, NZ.
B29	Genomic biosurveillance of *Pseudomonas syringae* pv. *actinidiae* reveals adaptation to selective pressures in New Zealand kiwifruit orchards	Hemara, L.M.[1,2], Arshed, S.[2], Patterson, H.[1,2], Andersen, M.[2], Jayaraman, J. [2], Templeton, M.D.[1,2]	[1] School of Biological Sciences, The University of Auckland, Auckland, NZ [2] The New Zealand Institute for Plant and Food Research Limited,

			Mount Albert Research Centre, NZ
B30	Collective effector contributions to Psa fitness from susceptible to resistant kiwifruit hosts	Hemara, L.M.[1,2], Templeton, M.D.[1,2], Jayaraman, J.[1]	[1]New Zealand Institute for Plant and Food Research, Auckland, NZ; [2]University of Auckland, Auckland, NZ.
B31	Surveillance of wallaby pest species in New Zealand using environmental DNA	Kroos, G.C.[1], Fernandes, K.[1], Ashcroft, T.[2], Gemmell, N.[1]	[1]Department of Anatomy, University of Otago, Dunedin, NZ, [2]Ministry for Primary Industries, Hamilton, NZ.
B32	Characterising the Microbiome of Diverse *Actinidia* Species	Patterson, H.[1, 2], Jayaraman, J.[1], Hemara, L.[1, 2], Templeton, M.[1, 2]	[1]The New Zealand Institute for Plant and Food Research Limited, New Zealand, [2]School of Biological Sciences, University of Auckland, New Zealand.
B33	Impacts of ecological disturbance on Kauri forest health	Scott, S.M.E. Black, A., Byers, A., Waipara, N., Condron, L.	[1]Bioprotection Aotearoa, Ōtautahi/Christchurch, New Zealand, [2]Lincoln University , Ōtautahi Christchurch, Aotearoa New Zealand