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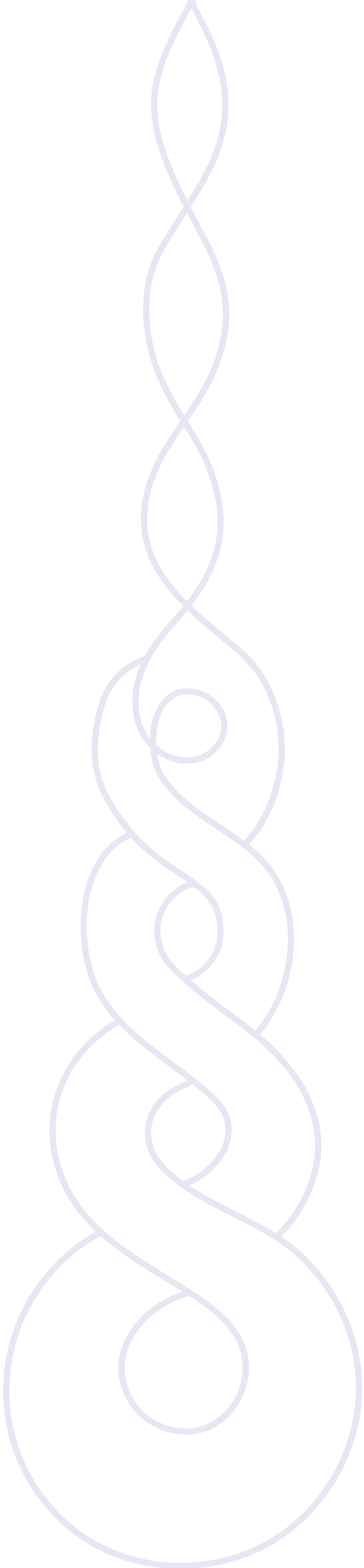
2024 Annual Report

Genomics Aotearoa dedicates this report to the memory of those team members who are no longer with us:

Dr. Warren Parker
Governance Board

Prof. Craig Cary
Science Leadership Team

Dr. Kristene Gedye
Project Lead



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Genomics Aotearoa
Annual Report

Year 7

1 July 2023 – 30 June 2024

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Report from the Directors

It has been another hugely productive year for Genomics Aotearoa, but also a sad and challenging one, with the unexpected passing of three of our team: Board member Warren Parker, Science Leadership Team member Craig Cary, and Principal Investigator Kristene Gedye. These three people made valuable and treasured contributions to the work of Genomics Aotearoa, and it is with great sadness that we note their passing and acknowledge the important roles that they each played within our organisation.

We would like to thank the entire Genomics Aotearoa team, from all our partner institutions, for their ongoing hard work, dedication, and passion for genomics. Their efforts have seen new projects funded, partnerships created and extended, groundbreaking research undertaken, and outstanding work published in the international scientific literature.

The fantastic achievements of Genomics Aotearoa researchers are evident throughout this report, but we particularly want to highlight our work in training. Our role is to build research infrastructure, and a critical component of that is the infrastructure of people. The Genomics Aotearoa training programme began in mid-2019, and by the end of 2024 we will have delivered over 100 workshops to more than 2,000 participants from dozens of organisations. We are immensely proud of this effort, much of which has been in partnership with New Zealand eScience Infrastructure (NeSI), who have provided the essential resources and support for Genomics Aotearoa's computational needs. Moreover, NeSI have been tireless supporters of our efforts to upskill the nation's researchers in genomics and bioinformatics. Many thanks to all who have contributed to our training work, and especially to those who freely give their time to help others develop their skills.

As we celebrate Genomics Aotearoa's achievements to date, we also look to the future, and are both excited and grateful that ongoing funding has been confirmed through to 2030. This is a strong endorsement for the whole Genomics Aotearoa team, as well as a clear acknowledgement that genomics and bioinformatics have critical roles to play as Aotearoa New Zealand moves through the current difficult economic times. Ongoing investment in genomics paves the way for new business opportunities, enhanced product development, improved resilience to climate change, equitable healthcare, better monitoring of biodiversity, and optimal management of our natural environment.

Looking ahead, the Genomics Aotearoa team will continue to work hard at our core business – undertaking innovative genomics and bioinformatics research and delivering critical infrastructure for the country's research community, while also planning for a future where genomics and bioinformatics are key drivers of a reinvigorated economy.

It is often hard to see progress in the day-to-day activities we carry out. But looking back over the past seven years, Genomics Aotearoa has had a substantial impact across all of the areas in which we have invested. We are proud of all that we have achieved, but also filled with ambition for what Genomics Aotearoa will become in the future. It's been a long road already, but we have so much further to go. We hope you will join us on that journey.

PETER DEARDEN

Prof Peter Dearden
Co-Director of Genomics Aotearoa

Prof Mik Black
Co-Director of Genomics Aotearoa

Report from the Chair

Genomics Aotearoa has worked hard over the last seven years to build our national capability and capacity in genomics and bioinformatics. We have funded around 250 researchers and trained nearly 2,000 people. We have accomplished what we set out to achieve.

Genomics is a dynamic field where techniques become redundant and new knowledge is integrated at a fast pace. Our board and executive have developed a vision for the future, "Genomic Futures for Aotearoa New Zealand", and ongoing funding has been confirmed, enabling GA to continue its journey in the service of science.

We can look back on many ground-breaking achievements over this first phase of our existence including:

- World leading work on the Kākāpō genome, including the use of artificial intelligence. This research has given the Department of Conservation new tools to manage and improve the prospects for the survival and recovery of our threatened species.
- Advances in Indigenous genomics, particularly *He Kākano: The Aotearoa Māori Variome* and *Rakeiora*. Together these are the foundation for better diagnosis and treatment for Māori, contribute to health equity in Aotearoa New Zealand, and provide a roadmap for precision medicine.
- Our innovative *Indigenous Genomics Platform*, which is a model for co-designed genomics projects that are Māori driven, have benefit to Māori communities, promote Māori researchers and/or benefit Māori business.

We have established and continue to maintain the *Aotearoa Genomic Data Repository*, in collaboration with NeSI. The *AGDR* is a part of our infrastructure and is a key resource that supports Indigenous data sovereignty. This approach is world leading, reflecting the unique Te Tiriti partnership. It is critical that this resource is enabled into the future.

Science is not the indulgence of rich nations, but a pathway to an improved standard of living for all, enhanced economic productivity, better environmental protections and social equity. Science provides us with pathways to understand our world, and in understanding it, make it a better place. Aotearoa New Zealand, like the rest of the world, faces huge challenges. As our climate changes, and the world's population increases, we need new ways to make a living, new ways to manage our environments and new ways to give our people the wellbeing they deserve. Genomics and computational biology are tools to discover knowledge with which we can chart a path into the future.

We sadly lost three of the Genomics Aotearoa family this year. I particularly want to acknowledge the great sense of loss of my fellow board member Warren Parker. Warren used his vast experience across agriculture, forestry, conservation and life in general to share views that were balanced and forward thinking. His contributions were always well researched, probing and insightful.

Warren was a man of conviction and action who, through logic, respect for others, and a constantly positive attitude, sought to make Aotearoa New Zealand a better place.

I will be stepping down as chair of Genomics Aotearoa at the end of 2024. It has been a pleasure and a privilege to serve such a forward-thinking organisation. We can all be proud of Genomics Aotearoa's achievements, which are a credit to the board, the directors, the executive team, our advisors and most importantly the dedicated researchers who put in the hard work and long hours, who think creatively, and who have a passion for genomics in Aotearoa New Zealand. I thank and pay tribute to every one of you.

Genomics is a powerful source of knowledge to help us navigate an uncertain future.

Genomics Aotearoa has made a palpable difference to the frontiers of science in this country. The platform is set to capitalise on the resources, the people and the capabilities we have built to create economic opportunity, to protect our environment, and enhance our health and wellbeing.

William Rolleston.

Dr William Rolleston CNZM
Chair of the Genomics Aotearoa Governance Board

Report from the Vision Mātauranga Manager

As the current Genomics Aotearoa term draws to a close and we consider advances in genomics infrastructure and research in Aotearoa, we first acknowledge the contributions of those Genomics Aotearoa whānau whom we have lost in the last year.

Genomics Aotearoa Board member Warren Parker was a man of the highest integrity. He cared deeply for his community and was passionate in his support for research that fulfilled community aspirations. Warren's presence and wisdom will be greatly missed by the Genomics Aotearoa Board and staff.

Kristene Gedye was a Principal Investigator for the Genomics Aotearoa *Distributed Sequencing* project. As a Senior Research Officer in Molecular Biology in the Massey University School of Veterinary Science, Kristene supervised many students and was respected for her depth of knowledge and technical ability. The loss of Kristene has been deeply felt beyond her whānau, and she is mourned by all her colleagues.

Craig Cary was a member of the Genomics Aotearoa Science Leadership Team. A Professor in the University of Waikato's School of Science, Craig spent four decades studying microbial life in extreme environments, including 18 seasons in Antarctica. Craig was a valued mentor, known for his inclusive, considerate and kind nature. He also maintained strong research relationships with mana whenua communities. His loss leaves a significant void in the research community and beyond.

As we acknowledge the contributions of Warren, Kristene, and Craig, we also celebrate the spirit in which they gave of their time and expertise.

Moe mai rā e ngā Rangatira.

While reflecting on the achievements of the past term, we also look forward to the next phase of Genomics Aotearoa. In this next phase Genomics Aotearoa remains committed to inclusive and collaborative research. Particularly important is our responsibility to engage meaningfully with Māori – building relationships of trust, increasing our awareness and understanding of cultural sensitivities, and importantly – engaging reciprocally and delivering benefits back to community. We endeavour to learn from past shared experiences, and remain steadfast in upholding our obligations under Te Tiriti o Waitangi.

As an organisation we value all work undertaken with hapori Māori over the last seven years. A few of the many highlights include *He Kākano: The Aotearoa Māori Variome* and *Rakeiora* projects, the support of *SING Aotearoa* (the Summer Internship for INdigenous peoples in Genomics), and development of the *Indigenous Genomics Platform* and the *Aotearoa Genomic Data Repository.*

A particular highlight, the *AGDR* provides a vital within-nation data storage facility for genetic data from Aotearoa's taonga species; this data can only be accessed with approval from the respective kaitiaki, that is the hapū or iwi who maintain mana whenua over the sample collection area. While we acknowledge the complex issues surrounding Māori and Indigenous sovereignty over genetic and genomic data, we attempt to address these challenges in partnership and with commitment to Te Tiriti.

In this spirit of partnership and collaboration we look forward to continuing our work with hapori Māori, seeking pathways to address the diverse challenges facing mana whenua communities of Aotearoa, and the challenges facing our shared planet and our shared humanity.

Tracey Godfery *(Ngāti Awa, Ngāi Tūhoe, Ngāti Tūwharetoa, Ngāti Hikairo, Ngāti Maru)*
Vision Mātauranga Manager of Genomics Aotearoa

Our Impact

OUR RESEARCH AND RESEARCHERS

Building a network of researchers and organisations to build genomics capability

45 Postdoctoral Researchers

32 PhDs, MSc, and BSc Hons students

1.7mil
hours of CPU time on NeSI over the past 12 months, across **17** different projects.

17 Ongoing Projects

21 Completed Projects

38 Total Projects

278 Researchers and Specialists
44 New in the Reporting Period

TE AO MĀORI

Increasing Māori capability and capacity in genomics.

1000+ Māori Genomes Sequenced

48 Data sets in the Aotearoa Genomic Data Repository

8 Indigenous Genomics Platform Projects

2 Funded in the Reporting Period

SING (Summer Internship for INdigenous Genomics)
14 Interns

CAPABILITY BUILDING

Bioinformatics training provided to researchers **free of charge.**

2004 Researchers Trained over the Lifetime of GA

582 Researchers Trained This Year

5 Early Career Researcher Travel Scholarships Awarded

Metagenomics summer school attendees to date: **100** from at least **15** institutions

97 Courses Delivered

28 Courses This Year

OUTPUTS

Publishing and presenting cutting-edge research

35 Publications this year

211 Peer-reviewed publications to date

3463 Citations, with **1740** within the last 2 years

YouTube Statistics
700 subscribers
59,093 views

43 Case studies demonstrating real-world impact

14 Genomics Aotearoa Friday Seminars this year

4 Asia Pacific Genetics Seminars this year

Genomics Aotearoa

A platform for collaboration

Seven years ago, Genomics Aotearoa was initiated with the goal of leading, facilitating, and promoting genomics research in Aotearoa New Zealand. As we look back, those goals have undoubtedly been achieved.

Over the years, the number of research institutions working within the Genomics Aotearoa framework has progressively increased, and now includes ten partners that largely represent the genomics expertise of the entire country. The partners are five universities: University of Auckland, Massey University, University of Otago, Waikato University, and Victoria University of Wellington; and five Crown Research Institutes, AgResearch, Environmental Science and Research (ESR), Manaaki Whenua - Landcare Research (MWLR), Plant & Food Research (PFR) and Scion.

The number of associate organisations has grown to 34 and represents researchers and end-users of genomics and bioinformatics across all sectors. 278 researchers have taken part in Genomics Aotearoa projects.

Genomics Aotearoa now has well-established avenues to support leadership and engagement by hapori Māori in genomics research. Now more than ever before, Māori researchers, communities, businesses, whānau and students are better able to participate in, and experience the benefits of, genomics research.

Our end-users include central and local government, health authorities, hospitals, clinicians, patients and their whānau, primary producers, conservation practitioners and hapori Māori. The connections among our consortium partners and end-users ensure that capabilities and discoveries have and will be translated into real-world benefits throughout the country.

The enabling infrastructure that Genomics Aotearoa has developed underpins the research outcomes that have been achieved. We have broadened out from our early focus on technical infrastructure to building an infrastructure of people. Critical to this has been the financial support, training, and development of early-career researchers.

Since 2017, the platform has supported 45 world-class early-career scientists in Aotearoa New Zealand. Genomics Aotearoa support has enabled postdoctoral fellows to become researchers and lecturers and lead their own research programmes. Doctoral candidates continue to be involved in many projects, along with undergraduate and graduate students. Extensive genomics and bioinformatics training is freely available to all. Worldwide linkages capitalise on, and contribute to, our international best practice.

Our cultural infrastructure is essential to our commitment to Te Tiriti o Waitangi. The *Aotearoa Genomic Data Repository* enables the appropriate curation and assignation of cultural rights to genomic data. This unique database is increasingly being used as a research data source. *Te Nohonga Kaitiaki Guidelines* and additional resources developed within projects represent best-practice for inclusive research involving taonga species.

Partnership with the New Zealand eScience Infrastructure (NeSI) continues to be essential to our research delivery. The *AGDR* and the bioinformatics capability that we have co-developed with NeSI remain free for all researchers to use in Aotearoa New Zealand.

Our initial seven-year programme of research ends later this year. We are grateful to the Ministry of Business, Innovation and Employment (MBIE) whose ongoing support has enabled a second tranche of funding for 5.5 years to be approved by government.

Genomics Aotearoa has developed a strategy and pathways for the future of genomics research in this country. We aim that our future work will provide continued opportunities to solve real-world problems and achieve long-term social impacts for everyone in Aotearoa New Zealand.

Partner Organisations

THE UNIVERSITY OF AUCKLAND
Te Whare Wānanga o Tāmaki Makaurau
NEW ZEALAND

agresearch
āta mātai, mātai whetū

VICTORIA UNIVERSITY OF WELLINGTON
TE HERENGA WAKA

University of Otago
ŌTĀKOU WHAKAIHU WAKA

genomics aotearoa

MASSEY UNIVERSITY
TE KUNENGA KI PŪREHUROA
UNIVERSITY OF NEW ZEALAND

Plant & Food™ Research
Rangahau Ahumāra Kai

scion™
FORESTS ▪ PRODUCTS ▪ INNOVATION

Manaaki Whenua
Landcare Research

E/S/R
Science for Communities

THE UNIVERSITY OF WAIKATO
Te Whare Wānanga o Waikato

Associate Organisations

AbacusBio

AngusPure

Applied Molecular Solutions

AsureQuality

Auckland City Hospital

Auckland University of Technology

Beef + Lamb New Zealand Genetics

Biomatters

Bioprotection Aotearoa

Bragato Research Institute

Brain Research New Zealand

Cardiac Inherited Disease Group

Cawthron Institute

Garvan Institute of Medical Research

GeneCrypt Limited

Growing Up in New Zealand

Hill Labs

LabPLUS

Livestock Improvement Corporation (LIC)

Maurice Wilkins Centre for Molecular Biodiscovery

Multi-Ethnic New Zealand Study of Acute Coronary Syndromes (MENZACS)

National Institute of Water and Atmospheric research (NIWA)

New Zealand eScience Infrastructure (NeSI)

New Zealand Merino

New Zealand's Biological Heritage National Science Challenge

Orion Health

Pastoral Genomics

Prevar

Real Time Genomics

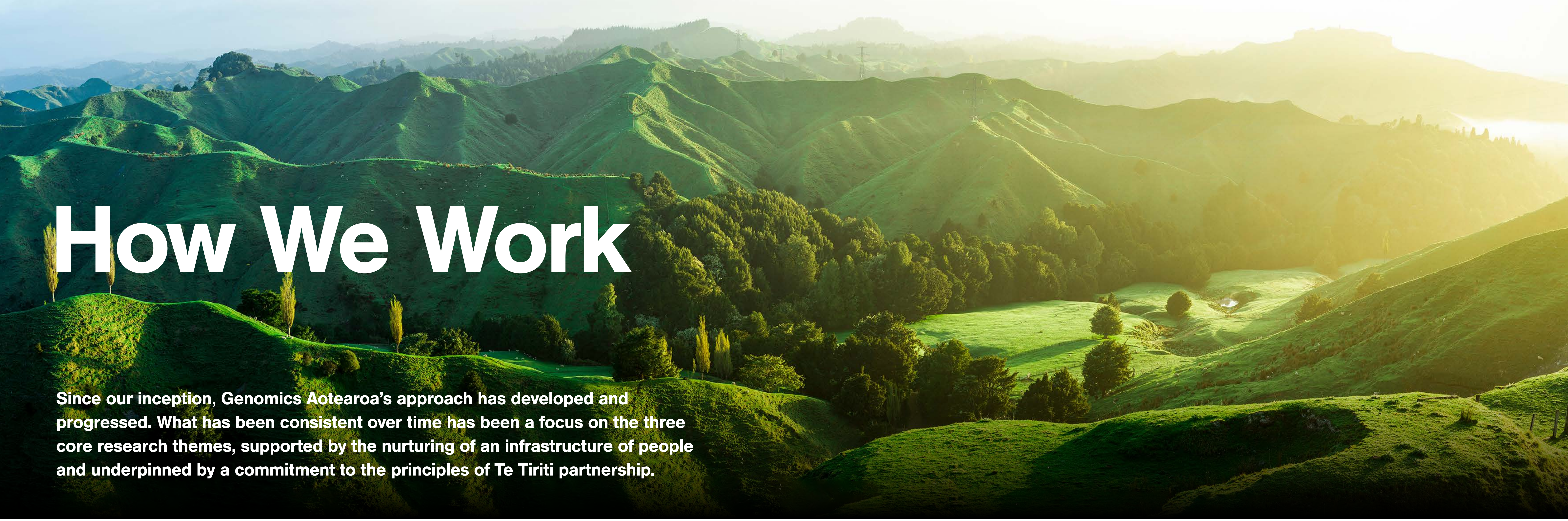
Royal College of Pathologists of Australasia

Sophia Genetics

University of Canterbury

Health New Zealand (Te Whatu Ora) Waitematā

Wilderlab



How We Work

Since our inception, Genomics Aotearoa's approach has developed and progressed. What has been consistent over time has been a focus on the three core research themes, supported by the nurturing of an infrastructure of people and underpinned by a commitment to the principles of Te Tiriti partnership.

Over the years, two important changes have improved the way we work. These are the development of a dedicated hub for Māori-led genomics research – the *Indigenous Genomics Platform* (*IGP*) – and the cross-theme *High Quality Genomes and Population Genomics* project (*HQG+PG*).

The *IGP* started life three years ago and has been nurtured by Vision Mātauranga Manager Tracey Godfery to be a model for hapori Māori leadership in genomics research. Currently the platform has eight projects underway.

The successful *HQG+PG* project led to a second iteration (*HQG+PG II*). Like its predecessor, *HQG+PG II* is a flagship for Genomics Aotearoa, spanning environment, primary production and infrastructure, and encompassing fifteen sub-projects. The *HQG+PG II* projects are presented in the applicable Environment, Primary Production and Infrastructure sections of this report.

Although this report only covers projects that have begun or continued in the last year, many completed projects have led to new endeavours, and continue to be supported by our researchers.

Indigenous Genomics Platform: Bringing Co-leadership in Genomics Research to Life

Fundamental to the *IGP* is the importance of collaborative partnerships and providing support for projects that are driven by Māori aspirations, are led (or co-led) by the community themselves, and contribute to increasing Māori capability and capacity in genomics. Projects supported by the *IGP* since its inception contribute to a growing awareness of genomics technology, enabling communities to identify beneficial genomics solutions while also supporting the discussion of any sensitive issues surrounding genomics research or technology. Also integral to the *IGP* is the knowledge sharing that takes place between researchers and communities, benefiting researchers through the valuable cultural learnings they gain from reciprocal partnerships.

Environment: Genomics for Biodiversity Discovery, Conservation, and Resilience

Some of the most complex biological puzzles in our natural environment are benefiting from the new approaches developed in Genomics Aotearoa's environment projects. These challenges include cryptic and mixed genomes from environmental samples, large and complex animal and plant genomes, and small populations of threatened species. A significant number of new tools, technologies and pipelines continue to be tested, refined, and shared among the genomics community of Aotearoa New Zealand.

Health: Genomics for Health Equity and the Wellbeing of All New Zealanders

Health is a cornerstone of wellbeing in Aotearoa New Zealand. Enabling equitable access to the most up-to-date tools is key to harnessing the power of genomics for health. The vision of health genomics is to enable personalised medicine that targets individual healthcare needs and increases equity in treatment outcomes. The successful implementation of genomics for health relies on the committed involvement of all sectors of the community, including hapori Māori and other community groups, whānau, researchers and clinicians.

Primary Production: Genomic Solutions to Increase Productivity and Investment

Genomics Aotearoa's primary production projects are developing tools, technologies and approaches for agriculture, horticulture, aquaculture and fisheries applications. These projects aim to better protect Aotearoa New Zealand from invasive species and pests, improve livestock and crop production, and develop new and diverse initiatives in primary industry.

Infrastructure: Supporting Research and Building Capability

In the last seven years Genomics Aotearoa has been building an infrastructure of high-quality computing and bioinformatics support to enable the growth of genomics research in country, and for the country. Secure, state-of-the-art computing facilities and data curation, together with a platform for training and nurturing future researchers, are essential to this infrastructure.

Genomics Aotearoa has established solid foundations for on-going support and capability building in bioinformatics. These foundations include a leadership team of experts from several institutions, working groups that progress roadmaps for bioinformatics, computing and data management support, two full-time training co-ordinators, and a key partnership with New Zealand eScience Infrastructure (NeSI).

Engagement: Promoting Understanding and Acceptance of Genomic Solutions

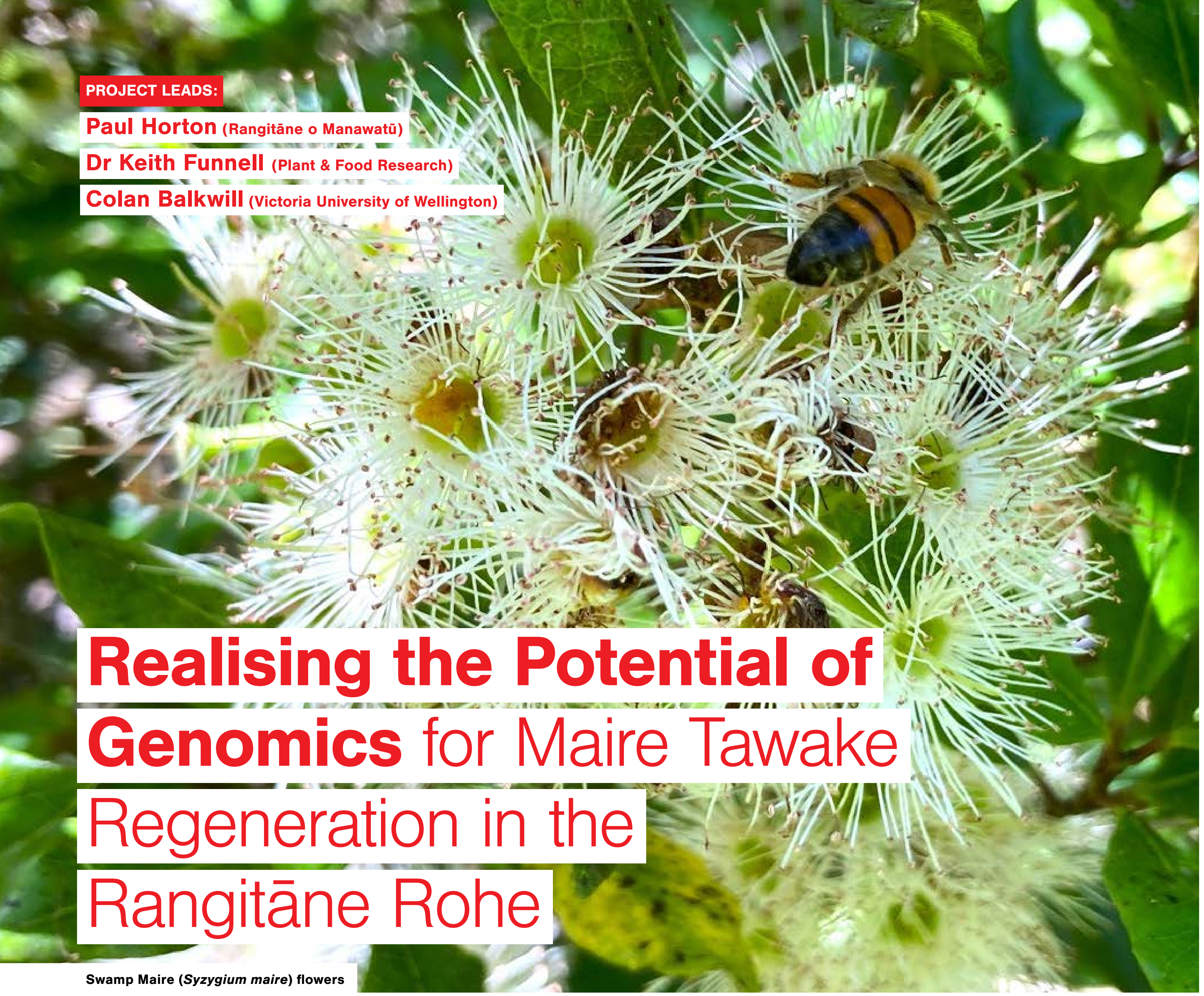
Genomics Aotearoa outreach and engagement activities continue to grow, as understanding of genomic solutions is key to social acceptance. In the past year, the *Genome: Science of Life* digital exhibition hit the road, touring various parts of the country, and our new video series "*What If...*" has gained national coverage via the RNZ website.

Indigenous Genomics Platform

Maintaining focus on opportunities for Māori-developed and Māori-led research, this past year has seen the initiation of two new *Indigenous Genomics Platform* (*IGP*) projects.

Te Iwi o Te Roroa are leading a collaborative project that utilises genetic tools to assist with the conservation of their taonga ‘Ngā roimata ō Tōhe’, an endemic shrub which is classified as a nationally critical threatened species. Likewise, Te Rarawa Iwi have initiated a collaborative project focused upon one of their most important taonga species, kauri.

Like the ongoing *IGP* projects reported this year, these new initiatives embody the purpose and aspirations of the *IGP* – Māori identified and led projects that advance mana whenua or other hapori Māori aspirations, while also engaging collaboratively with genomic science and researchers.



PROJECT LEADS:

Paul Horton (Rangitāne o Manawatū)

Dr Keith Funnell (Plant & Food Research)

Colan Balkwill (Victoria University of Wellington)

Realising the Potential of Genomics for Maire Tawake Regeneration in the Rangitāne Rohe

Swamp Maire (*Syzygium maire*) flowers

The nationally critical threatened tree maire tawake (swamp maire; *Syzygium maire*) is the subject of active restoration in the rohe of Rangitāne o Manawatū.

Populations of the tree are small, fragmented and often surrounded by farmland. With fewer than 12 mature trees remaining within each of the three remaining populations within the rohe, a lack of genetic diversity may hinder regeneration of a naturally sustainable forest. Rangitāne o Manawatū hopes to inform plans for forest restoration by integrating mātauranga Māori with genomics, for maire tawake and other species.

Last year's preliminary population genetic analysis of seedlings sourced from the Manawatū was finalised. Together with the genome data on established trees, this represents an unprecedented dataset for a threatened native tree.

In addition, kinship analysis has confirmed that seedlings sourced from the Manawatū are suitable for replanting. Inbreeding and genetic diversity estimates have highlighted priority genotypes, and this has helped develop strategies for replanting at both the individual and population level.

Suitable sites for planting were derived from mātauranga Māori and first-hand experience, complemented by an ecological analysis of the rohe of Rangitāne o Manawatū. Six suitable sites have been confirmed for replanting, with three already under Rangitāne o Manawatū management.

The project has delivered more than anticipated, enabling Rangitāne o Manawatū to use the relationships within the partnership to share resources and new learnings. This has strengthened the working partnership between Rangitāne o Manawatū and Plant & Food Research in a practical sense and created benefits in other areas of shared work.

The successful propagation of maire tawake and an understanding of the genetic relationships has helped inform a replanting programme that will enable the return of this taonga to the landscape of the Rangitāne o Manawatū rohe.

Image Credit: **Andy McKay (iNaturalist) CC BY 4.0**

Swamp Maire (*Syzygium maire*) berries

CASE STUDY:

A Mana Whenua Approach to Restoration of Maire Tawake

When the rebuild of Te Ahu a Turanga (Manawatū Tararua highway) encroached upon the last remaining patch of swamp land and indigenous forest, Rangitāne o Manawatū were concerned. Maire tawake, once widespread throughout the whenua, was threatened again.

In lands now drained for pasture, maire tawake were once at the centre of a thriving ecosystem. Now they only persist in isolated pockets and are unable to naturally regenerate due to the drainage of habitat. With the dual threat of myrtle rust and climate change looming, Rangitāne o Manawatū knew they needed to act swiftly to bring swamp maire back from the brink of extinction within their rohe.

Rangitāne o Manawatū approached researchers at Plant & Food Research and Victoria University of Wellington to develop a mātauranga and genomics informed restoration plan.

From the project's genesis, mātauranga Māori and other ways of knowing have fed into the research. This was a partnership in the true sense of the word. Genomics researchers were the conduit into the wider science system, providing access to a broad range of expertise. Iwi researchers were the conduit into Te Ao Māori, supporting the research team to develop an authentic understanding of mātauranga and kaitiakitanga. Both systems of knowledge complemented each other, in a project that the researchers believe could be a prototype for other research in Aotearoa New Zealand.

"Science doesn't have to compete with mana whenua ways of being. Making the most of each other's strengths and wisdom enables us to find the best outcome. It has been a fresh approach. Everyone was willing to listen and partner together to save maire tawake, and with it, a part of the whenua and the culture," said project co-leader Wayne Blissett of Rangitāne o Manawatū.

"Rangitāne has an active taiao team that is using both mātauranga Māori and pūtaiao-based solutions to address the many issues occurring in our rohe. The team has a strong track record of developing and applying pūtaiao with mātauranga Māori. We saw this problem with a vulnerable species in our rohe, and we wanted to find a solution," Blissett continued.

"With only a small population to restore the species from, we saw genomics as a powerful tool to assess if restoration was going to be possible, and if so, how could we give swamp maire the best chance to produce self-sustaining populations," said Dr Keith Funnell, senior scientist at Plant & Food Research.

Colan Balkwill, a PhD student from Victoria University, also worked on the project. Colan focussed on landscape and habitat level population genomics of swamp maire and explored genetic diversity to understand swamp maire's adaptive potential, and to select and propagate plants for restoration and conservation.

Rangitāne o Manawatū gifted the genome sequence of maire tawake a Māori name: *Ngā Hua o te Ia Whenua* (*The Fruits of Ia Whenua*), a global first for an Indigenous people.

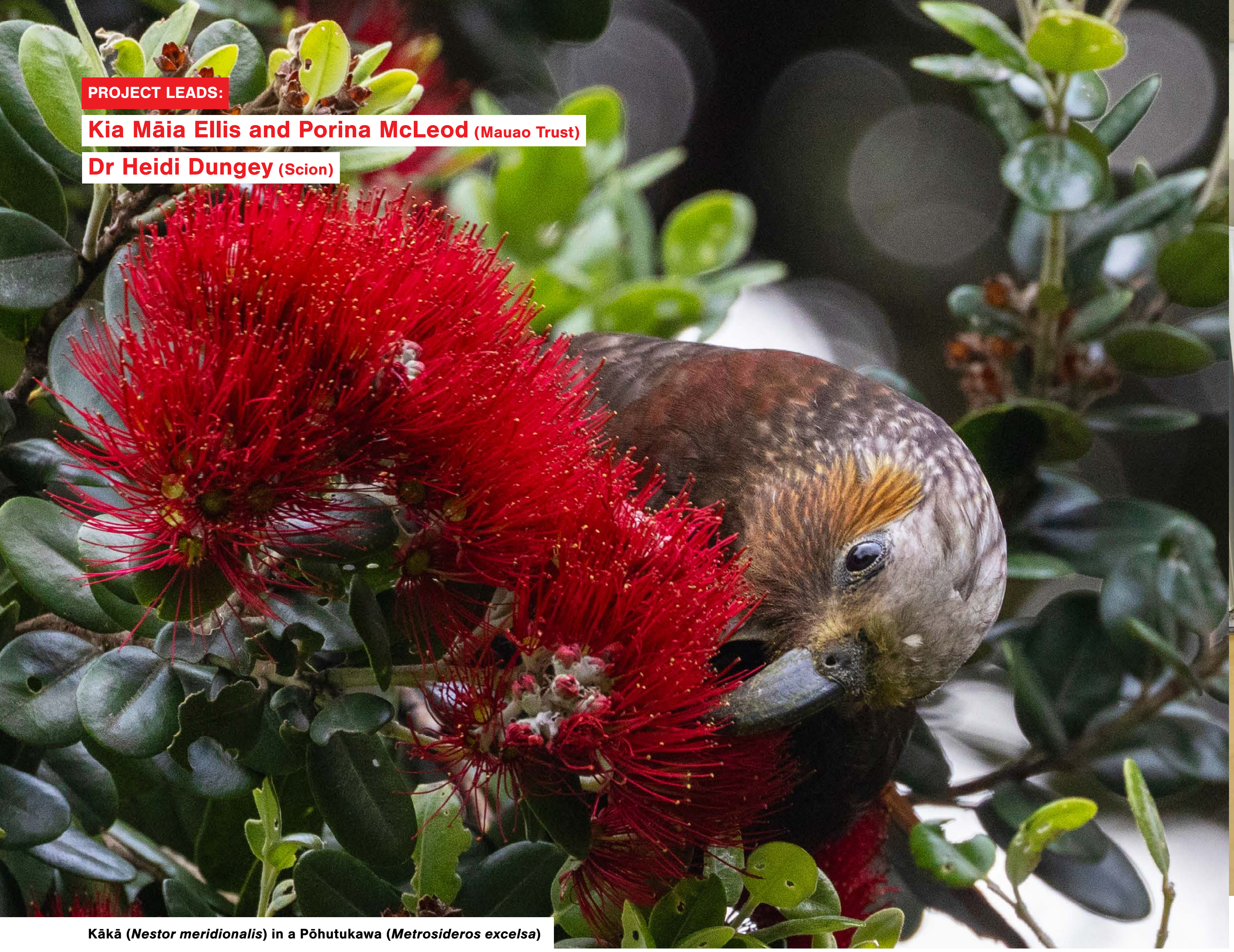
The project has been a success on many levels. In just two years, Rangitāne o Manawatū have gone from having no genetic information for maire tawake, to having an almost complete, micro-scale genetic restoration plan, and seedlings with known genetic profiles in the ground. A strategy has been developed for iwi and pūtaiao researchers to follow when partnering on projects in the future. Research that involved iwi has demystified the science. Most importantly, there is now a pathway for the return of this taonga species to the landscape.

Image Credit: **Karin Van Der Walt - Otari Native Botanic Garden**

PROJECT LEADS:

Kia Māia Ellis and Porina McLeod (Mauao Trust)

Dr Heidi Dungey (Scion)



Kākā (*Nestor meridionalis*) in a Pōhutukawa (*Metrosideros excelsa*)

Identifying the Pōhutukawa on Mauao

The Mauao Trust are working with Scion scientists to determine whether the pōhutukawa trees on Mauao (Mount Maunganui) are native or introduced, or a hybrid of the two. The research will inform iwi management decisions for pōhutukawa under attack from myrtle rust and build capability in genomics among mana whenua.

Māori principles and values are woven throughout the research in close alignment with the Mauao Trust strategy for the health and wellbeing of the maunga. This is the first research project on Mauao to be led by a Māori organisation, it provides a unique opportunity for mana whenua to grow skills in genomics and be directly involved as kaitiaki of their own trees on Mauao.

Preliminary DNA extractions using automated extraction with Azora Bioscience have resulted in good yields. Genotyping of the samples is expected to commence in July 2024, with further analysis to follow. Leaf shape data will also be collected to determine if species and hybrids are easily identifiable without the need for future genotyping.

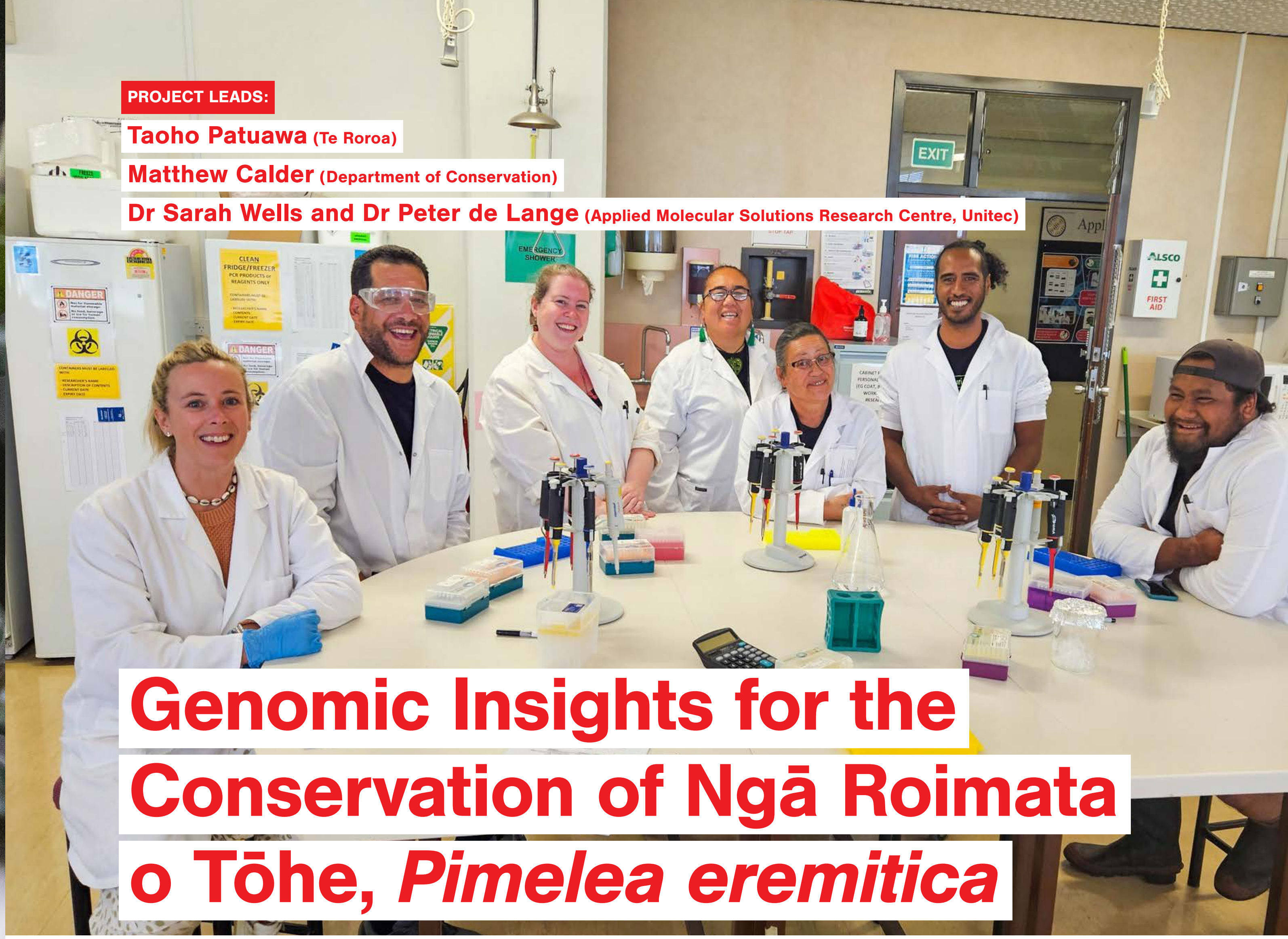
The project is also supporting the Master's study of Kawana Warahi at Te Pukenga/Toi Oho Mai. Kawana has gained considerable experience in aerial mapping using drones and is hoping to work with the Trust to gather aerial imagery of pōhutukawa and Mauao. This imagery will add another layer to the project and provide Trustees who can't easily access the steep terrain of Mauao with a three-dimensional visualisation of the maunga.

PROJECT LEADS:

Taoho Patuawa (Te Roroa)

Matthew Calder (Department of Conservation)

Dr Sarah Wells and Dr Peter de Lange (Applied Molecular Solutions Research Centre, Unitec)



Genomic Insights for the Conservation of Ngā Roimata o Tōhe, *Pimelea eremitica*

Ngā Roimata ō Tohe is a nationally critical threatened shrub with a single remaining population, at Maringinoa in Te Tai Tokerau (Northland). Te Iwi o Te Roroa are mana whenua of this rohe and wish to secure the future of this taonga.

Although new to Genomics Aotearoa, the project builds on more than 20 years of conservation work by Te Roroa, the New Zealand Department of Conservation (DOC), Auckland Botanic Gardens, Unitec, and other researchers, whānau, and contractors.

The goal of the project is to better resolve the conservation genomics and genetic diversity of the few remaining Ngā Roimata ō Tōhe.

The project has facilitated a hui that brought together the knowledge and perspectives of Te Roroa and the scientific expertise of researchers. Held in Waipoua, the hui celebrated connection, respect, and shared vision. This hui was followed by a workshop at Unitec. The workshop was dedicated to sharing knowledge, with a focus on the molecular techniques used to study Ngā Roimata ō Tohe samples collected by Te Roroa from their nursery. These samples will undergo genotyping by sequencing at AgResearch, Invermay.

Whanaungatanga among kaitiaki and research organisations will enable Te Iwi o Te Roroa to participate further in genetic research for the conservation of many taonga species within their rohe.

This kaupapa exemplifies the power of combining traditional Māori knowledge and insight with modern science to achieve common goals. Both parties are committed to the conservation and protection of Ngā Roimata ō Tohe, recognising its importance to the biodiversity of the region and to the cultural heritage of Te Roroa.

Image Credit (upper): **Unitec**
Image Credit (lower): **Pettania Hohaia (Te Roroa)**

PROJECT LEADS:

Debbie Martin (Te Rarawa)

Prof Amanda Black (Lincoln University)

Assoc Prof Michael Knapp and Prof Peter Dearden (University of Otago)

Genomic Tools to Preserve Kauri Ora in the Warawara Ngāhere

Kauri dieback* is a disease caused by the fungus-like pathogen *Phytophthora agathidicida* (PA). The pathogen infects the tree's root system, reducing the ability to take up water and nutrients and transport them through the plant. The result is referred to as kauri disease or kauri dieback and is having devastating effects on Aotearoa New Zealand's kauri forests.

In collaboration with scientists from Bioprotection Aotearoa, Lincoln and Otago Universities, and private company BioSense, Te Rarawa Kauri Ora rangers are developing real-time, point-of-need surveillance for kauri dieback in the Warawara Forest.

This new project will test a proof-of-concept diagnostic pipeline for surveillance of kauri dieback in the Warawara Ngāhere. The approach involves co-development of new environmental management techniques, designed to build and strengthen relationships among Te Rarawa and researchers. A key objective is that new diagnostic tools will help Te Rarawa Kauri Ora rangers better monitor and manage kauri dieback.

With less than six months of research conducted so far, the team have moved on from simplifying existing (soil based) PA detection to developing a new, root-based approach. If successful, the technique could significantly improve the ability to detect the presence of the PA pathogen, reducing handling time, and helping to maintain the health of kauri in the Warawara Ngāhere.

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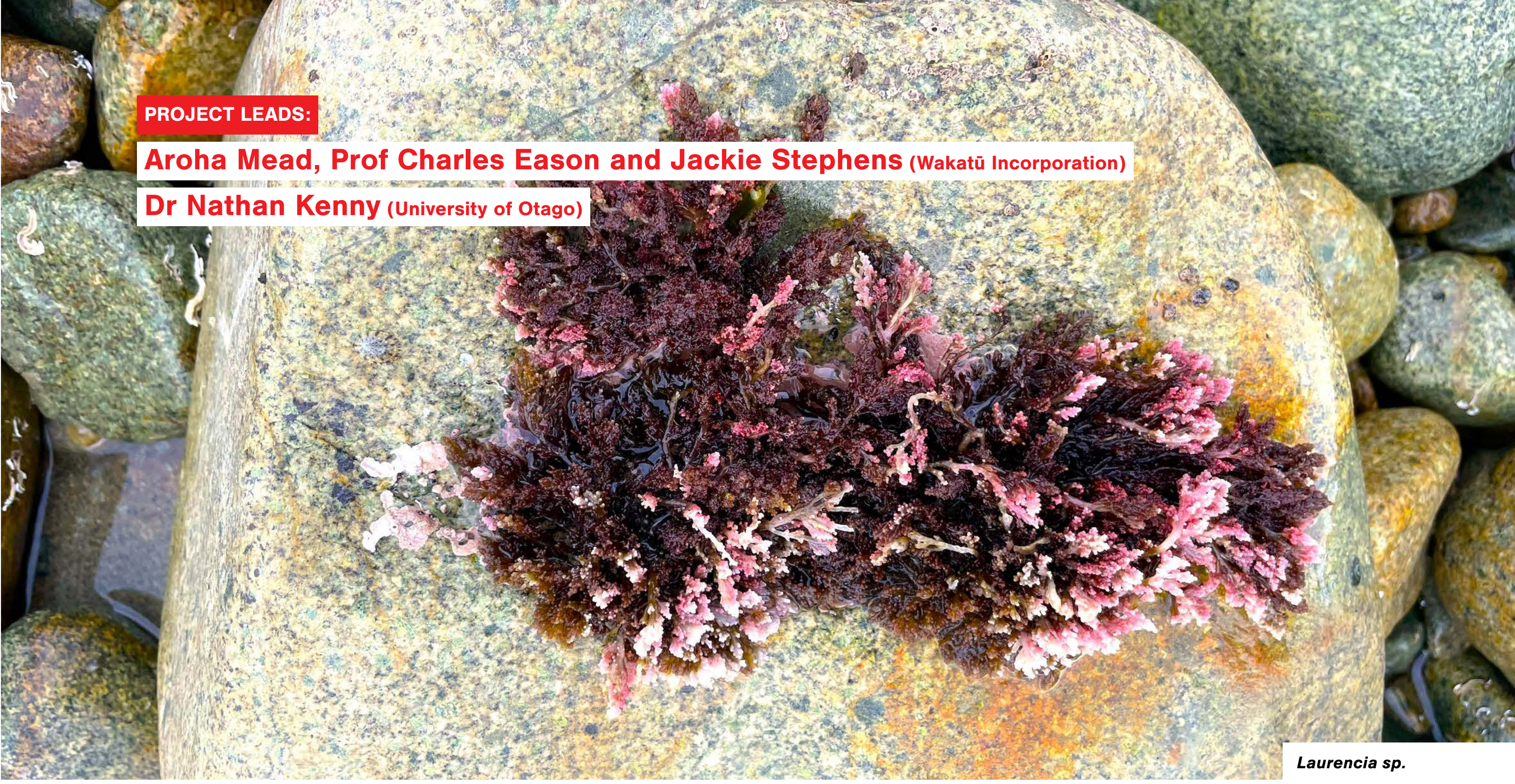
*Genomics Aotearoa researchers are aware of the sensitivity of the term kauri dieback. The term is used here as it is the prevailing term used in public discussion. We acknowledge the more appropriate term of kauri ora. Indeed, kauri ora is what we wish for all kauri of Aotearoa New Zealand.



Laurencia sp.

PROJECT LEADS:

Aroha Mead, Prof Charles Eason and Jackie Stephens (Wakatū Incorporation)

Dr Nathan Kenny (University of Otago)

Nā Tō Rourou, Nā Taku Rourou

Sharing the Benefits of Genomics

Nā Tō Rourou, Nā Taku Rourou explores the genomic basis for important traits of high-value marine species, while ensuring the research benefits are owned by the appropriate individuals, communities or institutions.

Sometimes, initiatives to sequence the genomes of native species are not sensitive to the Wai 262 Te Tiriti o Waitangi claim or the implications of the United Nations Convention on Biological Diversity and Nagoya Protocol for Access and Benefit Sharing (ABS). In response, *Nā Tō Rourou, Nā Taku Rourou* establishes a model for collaboration among Māori organisations and research institutions.

Wakatū Incorporation's strategy of cataloguing, characterising, and developing a deep understanding of the endemic species of *Te Tauihu o te Waka* is the perfect vehicle for testing this Māori-centred model.

The project is sequencing the genomes of kopakopa (the ribbed mussel *Aulacomya atra maoriana*) and karengo (a red seaweed), both species of significant interest to Wakatū and the hapū and Iwi of Te Tauihu. The project builds on collaborative work between the Cawthron Institute and Wakatū regarding the use of these species in aquaculture. The sequencing work in this project provides new avenues for the husbandry of these species, with the benefit of genome-scale data.

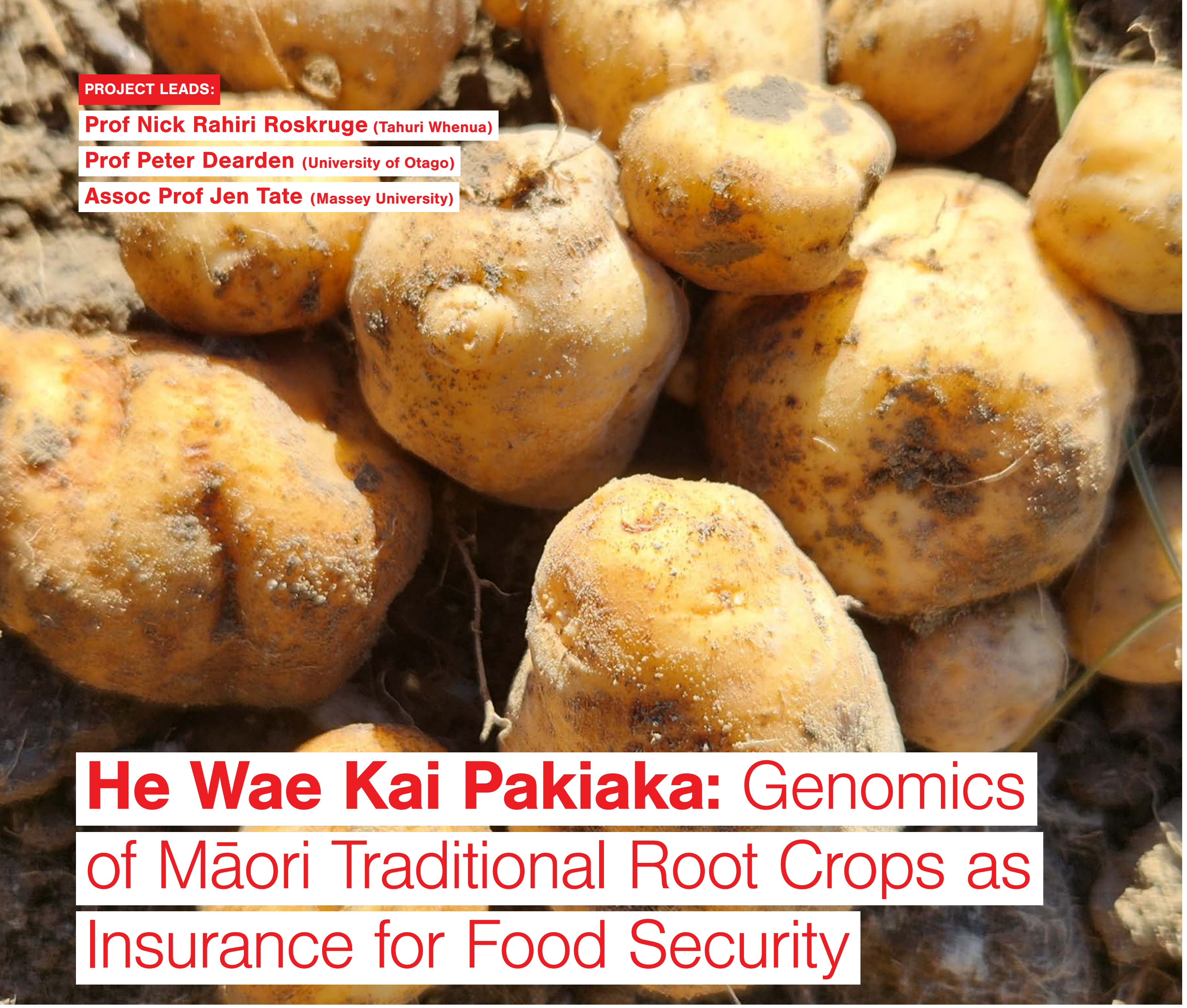
Initiated last year, the project team have now completed the genome assembly for kopakopa and a draft assembly for karengo. For DNA sequencing, the team successfully used the new PromethION 2 platform at the Otago Genomics Facility. Transcriptomic work has also begun which will aid genome annotation. Re-sequencing is also underway, which will provide the raw data for generating markers and a relationship matrix, as well as contributing to understanding productivity traits.

These data lay a foundation for embedding genomic approaches in the aquaculture of kopakopa and for the identification of useful traits in karengo, both having potential commercial benefit.

Alongside genomics research, the project team has established principles for genetic characterisation of organisms from the rohe of Te Tauihu, and documented how the ABS model is implemented. Together, these actions establish a framework for good practice and an exemplar for future work. Additional benefits have also accrued, such as training rangatahi in novel skills, and providing employment opportunities.

University of Otago scientists have benefitted from learnings related to tikanga and mātauranga, which enables them to approach this work in a well-rounded way. Science lead Dr Nathan Kenny (Te Ātiawa and Ngāi Tahu) has been promoted to Senior Lecturer this year, in recognition of his achievements in science and ongoing inclusive contributions to genomics research in Aotearoa New Zealand.

Image Credit: **Cecilia Biancacci - Cawthron Institute**



PROJECT LEADS:

Prof Nick Rahiri Roskruge **(Tahuri Whenua)**
Prof Peter Dearden **(University of Otago)**
Assoc Prof Jen Tate **(Massey University)**

He Wae Kai Pakiaka: Genomics of Māori Traditional Root Crops as Insurance for Food Security

Māori recognise a growing and urgent need for food security and food sovereignty of ‘traditional Māori’ foods. *He Wae Kai Pakiaka* (a grounded solution) offers a strategic and secure approach to gathering mātauranga Māori and plant materials, supported by science through the molecular characterisation of landraces (cultivars or varieties).

The national Māori horticulture collective, Tahuri Whenua, leads the project. The collective draws from its kaumātua rōpū and membership to collect and curate plant materials. Mātauranga together with international germplasm protocols ensure accessibility to these resources for future generations.

Māori growers across Aotearoa New Zealand have entrusted this project with a collection of 20 taewa (Māori potato; *Solanum tuberosum*) and 12 kūmara (*Ipomoea batatas*) cultivars.

In its first year, the project has seen the collection and in-field production of several taewa and kūmara cultivars. The first round of genetic analysis for seven taewa and seven kūmara cultivars has been undertaken. A further 13 taewa and five kūmara were cultivated to provide plant tissue, roots and tubers for genetic analysis and phenological characterisation.

Leaf and flower samples have been collected and prepared for nine taewa cultivars with plans to do this for several kūmara samples during the 2024/25 growing season. These samples will eventually be submitted to the Dame Ella Campbell Herbarium (Massey University, Palmerston North) and the Allan Herbarium (Manaaki Whenua Landcare Research, Christchurch) for curation.

A repository of mātauranga Māori and Māori grower experiences of taewa and kūmara is being created, through connection with Māori growers and expertise across Aotearoa New Zealand. This repository of knowledge will be shared widely with te iwi Māori.

CASE STUDY:

Bringing Traditional Food to the Forefront of Science

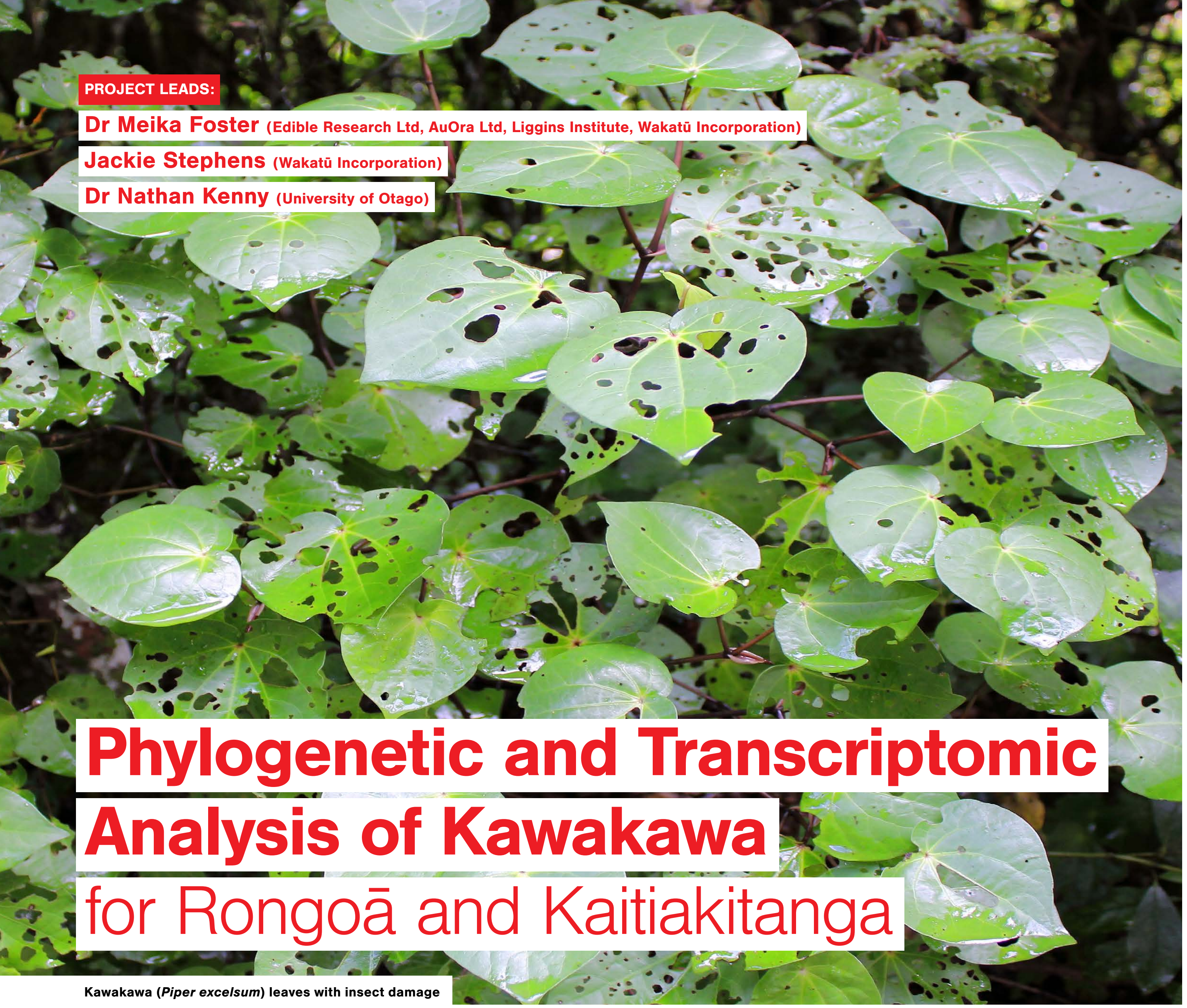
Although a staple in Māori food culture for over 200 years, until recently, taewa (other iwi might know these as parareka, peruperu, or rīwai) have not been commercially cultivated. Two decades of effort have been spent to increase the awareness, knowledge and availability of this crop. *He wae kai pakiaka* aims to create an insurance policy for this taonga against the multiple threats of climate change, potato diseases and pests.

He wae kai pakiaka is enabling science researchers to partner with, and be guided by Māori horticulturists. The project has conducted the first in-depth genetic analysis of taonga root crops, and it will be the first crop submission to an International Genetic Collection by an Indigenous people.

“We wanted to take an innovative, mana whenua-led approach to the project; bringing mātauranga Māori and science together to inform the ways in which we work and the outcomes for Māori growers. We need to ensure that taewa and kūmara are available for future generations, especially considering the changes that we expect in the environment in the coming decades and centuries,” said Dr Nick Roskruge, project lead.

The project also supports PhD candidate Saii Semese, who has connected with many growers across Aotearoa New Zealand and presented his research at several Māori and academic fora, including the Tahuri Whenua Research Symposium in September 2023 at Wharerata, Massey University and the recent International Plant Protection Congress in Athens, Greece (July 2024).

“This research is extremely valuable as it will help these taonga species survive into the future. Working with mana whenua has been a rewarding experience for me as a researcher, with new ways of thinking informing my usual scientific approach. I hope that this innovative approach can be integrated into other projects, with science and mātauranga Māori working as one to increase knowledge for the benefit of all,” said Saii.



PROJECT LEADS:

Dr Meika Foster (Edible Research Ltd, AuOra Ltd, Liggins Institute, Wakatū Incorporation)

Jackie Stephens (Wakatū Incorporation)

Dr Nathan Kenny (University of Otago)

Phylogenetic and Transcriptomic Analysis of Kawakawa for Rongoā and Kaitiakitanga

Kawakawa (*Piper excelsum*) leaves with insect damage

Kawakawa (*Piper excelsum*), is of great ecological and cultural importance. While multiple varieties of kawakawa are known from across the motu, to date there have been no investigations of the diversity, population structure and inter-relatedness of sub-populations of this species.

Within a tikanga-informed framework for sample acquisition, processing, data sovereignty and benefit-sharing, the team is using a transcriptomic approach to understand kawakawa diversity, bridging this knowledge gap and adding genomics to the rich existing mātauranga related to kawakawa.

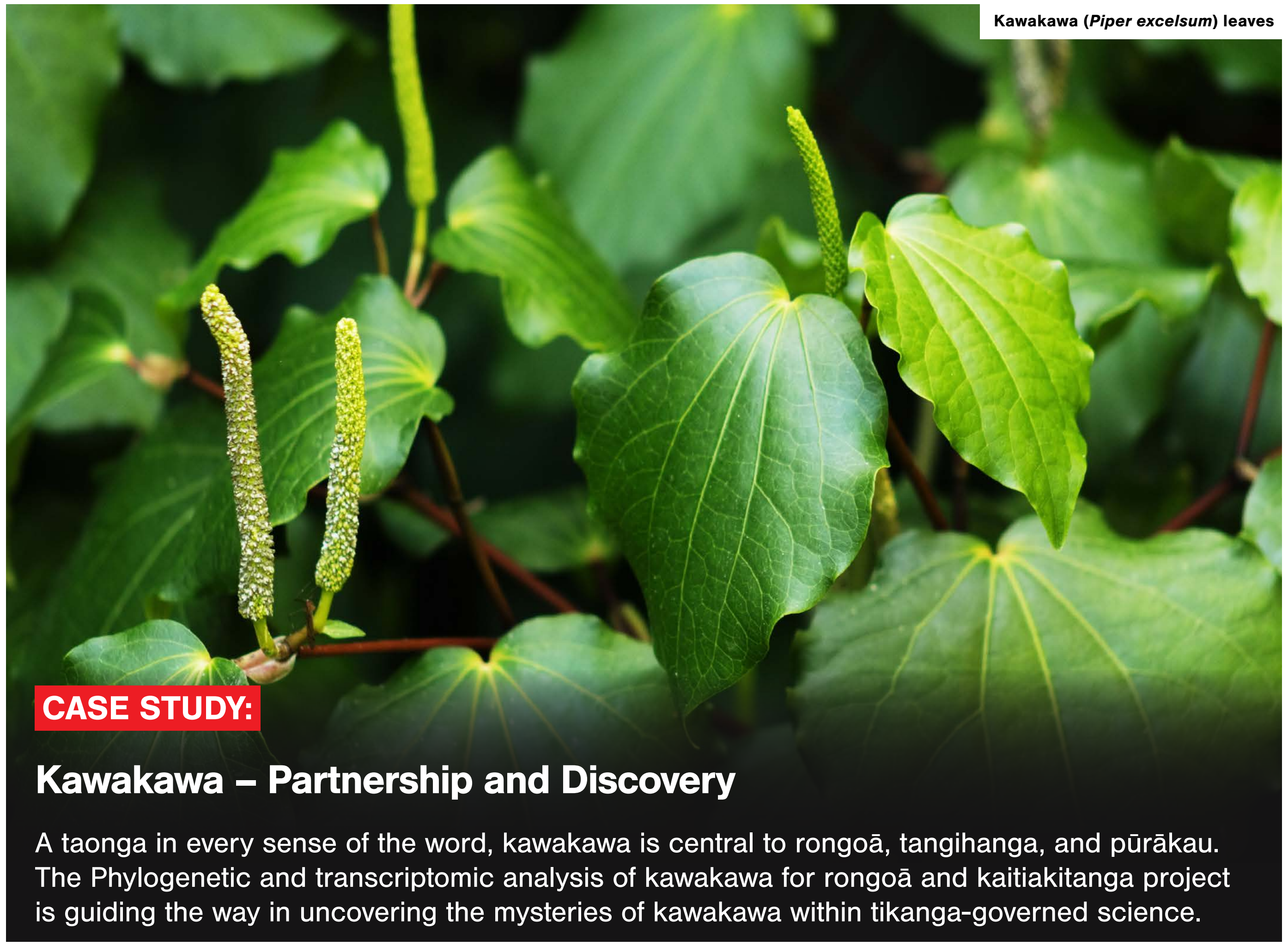
Encouraging progress has been made over the past year. Molecular work began in March 2023. Samples of kawakawa were mainly gathered from Te Tauihu, with some from further afield. These samples will be supplemented with those from other rohe as the work progresses.

Laboratory work required optimisation of protocols for RNA extraction, because of the high phenolic and secondary metabolite content of kawakawa leaves. Libraries have been made with triplicate replicates for every sample.

A "first pass" analysis pipeline has been completed. This has revealed population sub-structure even between specimens collected from similar areas. Further work continues towards publication of the results in partnership with communities.

A highlight has been the production of a professionally edited video showing the approach and initial outcomes. This will assist communication with source communities and aid as an outreach tool.

Through Wakatū, employment opportunities have arisen from this kaupapa. While not funded directly from this grant, Wakatū interns have been part of the sample collection, processing and communication of this work.



Kawakawa (*Piper excelsum*) leaves

CASE STUDY:

Kawakawa – Partnership and Discovery

A taonga in every sense of the word, kawakawa is central to rongoā, tangihanga, and pūrākau. The Phylogenetic and transcriptomic analysis of kawakawa for rongoā and kaitiakitanga project is guiding the way in uncovering the mysteries of kawakawa within tikanga-governed science.

Embodying Wakatū Incorporation's 500-year intergenerational vision, the project applies mātauranga Māori alongside western science.

The whānau owners of Wakatū Incorporation descend from families that belong to four tribes in the Nelson, Golden Bay, and Tasman areas: Ngāti Koata, Ngāti Rārua, Ngāti Tama and Te Ātiawa. The organisation initiated this project through a wish to both protect the taonga and to use the science to benefit their people.

"The project provides an opportunity for us to use our knowledge of kawakawa in rongoā, and as a food. We can then think about our future when it comes to conservation and enterprise," said Miriana Stephens (Ngāti Rārua, Ngāiterangi and Ngāti Ranginui), Tūmu Auaha (General Manager) of AuOra, Wakatū Incorporation.

"Our hope is to develop high value Indigenous ingredients underpinned by science and mātauranga, that realise economic, cultural, environmental and social benefits," Miriana continued.

Every step of the scientific process is guided by Māoritanga; from karakia while gathering plants, to whakanoa in the laboratory, all with the goal of upholding kaitiakitanga of this taonga in perpetuity.

Preliminary analysis showing population sub-structure is an exciting result, as it could enable targeted selection of kawakawa with different properties. This result aligns with mātauranga and oral histories, which suggest that specific plants were taken from one part of the country to another.

The University of Otago and Wakatū have used the results to support an MBIE Smart Ideas application to extend the research. Experience from this project also helped postdoctoral fellow Dr Roseanna Gamlen-Greene (Waikato-Tainui, Pākehā) win a prestigious Ngā Puanga Pūtaiao Fellowship.

For Dr Nathan Kenny (Te Ātiawa, Ngāi Tahu), the most exciting part of the project has been working with Wakatū to help shape tikanga and Māori-led science research.

"It's a new approach for science, doing things in direct partnership with mana whenua, so the benefits can be vested in the people who have traditionally held mātauranga. The approach benefits our organisation, the University of Otago, mana whenua, and science in Aotearoa New Zealand," said Dr Kenny.

"The work is an exemplar of the value of mātauranga Māori to inform genomics research, as a pathway for others to follow and build from. We hope that this project will benefit other Iwi and hapū wanting to manage their taonga using scientific tools in a tikanga-led way."

PROJECT LEADS:

Nicole Pakau (Te Arawa Fisheries, Smart Māori Aquaculture)

Assoc Prof Peter Ritchie (Victoria University of Wellington)

Prof Maren Wellenreuther and Dr David Chagné (Plant & Food Research)

Development of Genomic Resources for the Selective Breeding of Haku

Haku/Kingfish (*Seriola lalandi*)

Pressures on the seafood industry and fisheries continue to grow. In Aotearoa New Zealand, aquaculture programmes rely on only three species: kuku or kūtai (greenshell mussels), tio (Pacific oysters), and Chinook salmon. Increasing demand for alternative food resources is the motivation for diversification of the industry.

Haku (kingfish) have an extensive coastal distribution. Being easy to lure, it is likely that considerable numbers of the fish were caught by Māori in the past. Although an important traditional food for Māori, no quantitative data on customary catch of haku were available prior to this project.

This year a high-quality genome assembly for haku from local waters was generated, with a high level of completeness (98.60%). The local haku genome assembly is significantly different to a published kingfish genome from China. The annotation of the haku mitogenome has been completed, and the genomic architecture has been investigated. Protein annotation of the genome is in progress, which will contribute to understanding the genomic underpinnings of specific traits.

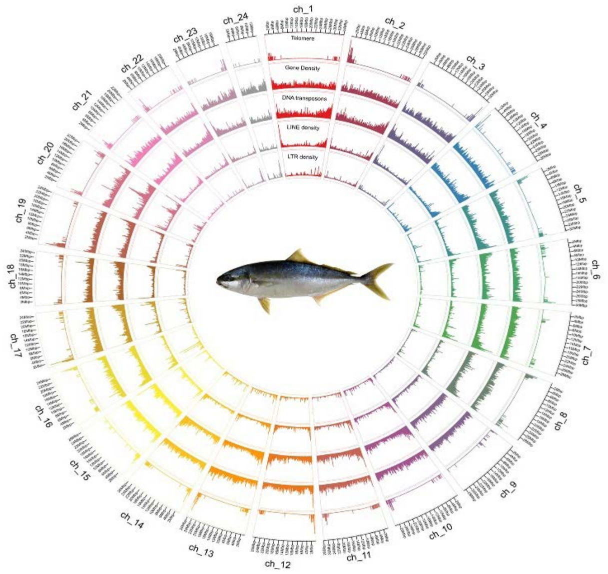
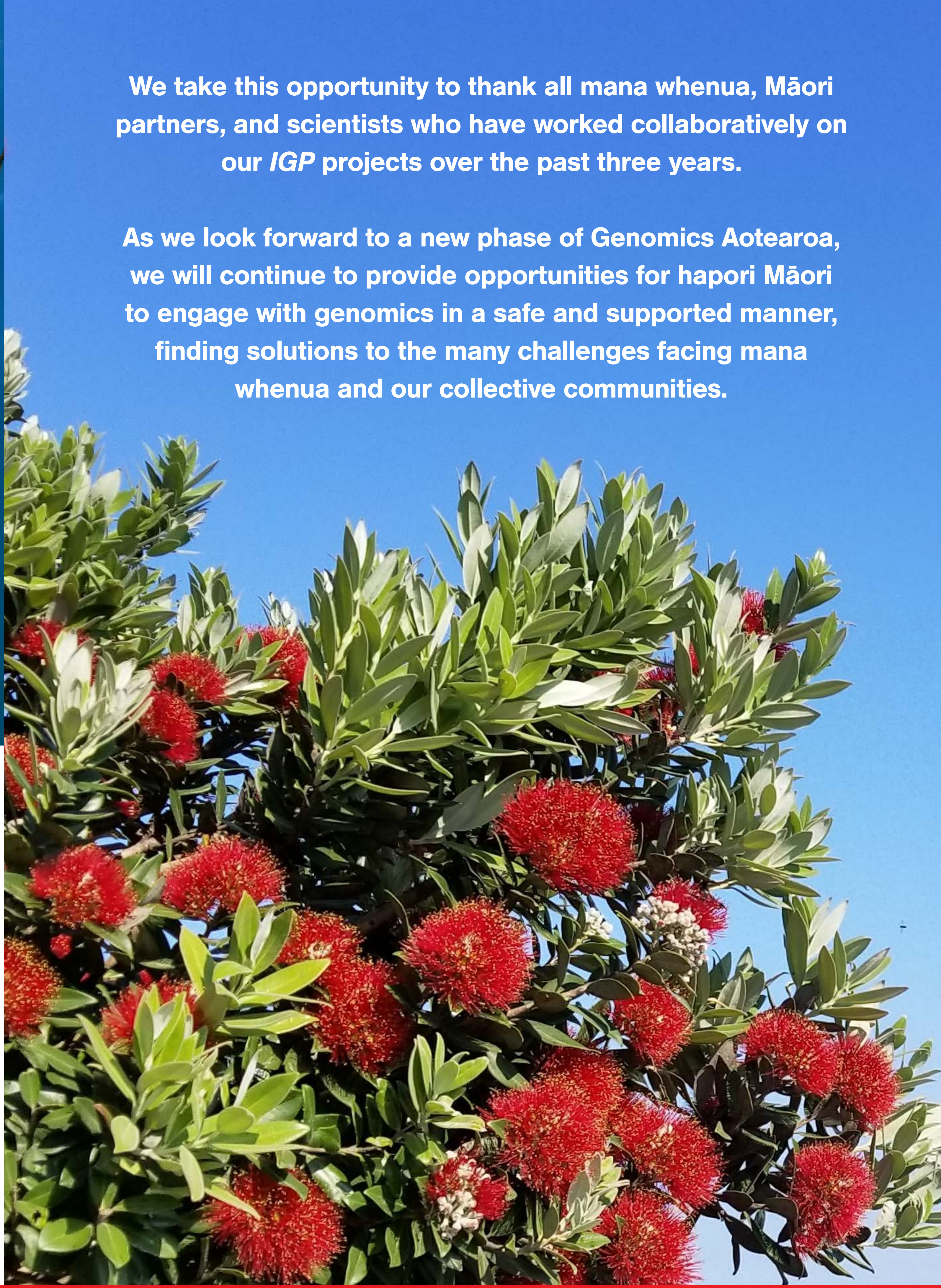


Figure: Circos plot of assembled genome for haku/ warehenga (yellowtail Kingfish, Seriola lalandi). The genome has 24 chromosomes, with each chromosome represented by a different coloured segment.

Circos Plot Haku Image Credit: **Australian National Fish Collection, CSIRO (CC By Attribution-Non-commercial)**



We take this opportunity to thank all mana whenua, Māori partners, and scientists who have worked collaboratively on our *IGP* projects over the past three years.

As we look forward to a new phase of Genomics Aotearoa, we will continue to provide opportunities for hapori Māori to engage with genomics in a safe and supported manner, finding solutions to the many challenges facing mana whenua and our collective communities.

Environment

Two environment projects are reported on this year, together with the five *HQG+PG II* sub-projects. The tools being developed are helping answer complex biological questions for a vast array of species, combining genomics with other data sources to better manage our natural environment and taonga.

As we look back, we acknowledge the other environment projects that were completed during Genomics Aotearoa's first term:

- *High Quality Genomes,*
- *Environmental Metagenomics,*
- *High Quality Genomes and Population Genomics,* and
- *Environmental Microbiomes.*

These projects laid the foundations for those reported this year, including a new project using genomics to understand disease risk in hoiho, our precious and endangered taonga, also known as the yellow-eyed penguin.

This year's case study *Metagenomics Uncovers the Hidden Diversity of Groundwater Ecosystems*, describes how this research is improving our understanding of the diversity and function of organisms found in water, our most precious resource, and one that faces many threats.

PROJECT LEAD:

Assoc Prof Kim Handley (University of Auckland)

Environmental Microbiomes

Microbial Dynamics of Aquatic Systems

Our aquatic environments are under increasing pressure from land use intensification, habitat modification and climate change. Metagenomics offers tools to help understand and predict the impacts of these pressures, as well as solutions to mitigate them. The *Environmental Microbiomes* project combines viral ecology, microbial population dynamics, and stress tolerance study, to increase our understanding of how microorganisms interact to affect ecosystem function.

Metagenomics is the study of genetic material directly recovered from environmental samples. Sets of genomes are assembled from complex DNA mixtures found in an environment.

The team published the first comprehensive 'omics-based study of an aquifer virome this year (see the case study *Metagenomics Uncovers the Hidden Diversity of Groundwater Ecosystems*). This work illustrates the diversity of viruses in groundwater, their contributions to host function, implications for groundwater biogeochemical cycles, and putative bacterial and archaeal hosts.

In addition, the project's work on the estuarine (freshwater-to-marine) virome (all viruses in the system) illustrates the implications of salinity on viral genomes. The project has also assessed a large global database from diverse aquatic ecosystems, and excitingly has identified genomic signatures of viral environmental adaptation.

Work on salinity tolerance in aquatic estuarine bacteria is in review, and work on estuarine organic carbon degradation is being prepared for publication.

Alongside four recent publications, the *Environmental Microbiomes* project has a major impact on Genomics Aotearoa's training offerings, and provides the only free, publicly available course on metagenomics in the country. This year the team trained 32 domestic and four international researchers.

The team are grateful to all the collaborators involved in iwi consultations, including Prof Kathleen Campbell (School of Environment, University of Auckland), Central North Island (CNI) Iwi Holdings Ltd and Ngāti Tahu – Ngāti Whaoa Runanga Trust for Orange Spring, Tauhara North No 2 Trust (Ngāti Tahu-Ngāti Whaoa) for Parariki Stream, Lake Rotokawa, Ngāti Tahu – Ngāti Whaoa Runanga Trust for Te Kopia and Waiotapu, Ngāti Kearoa/Ngāti Tuara for Kuirau Park, including Ngāti Whakaue for Te Kuirau/Turipuku, Ngāti Tahu – Ngāti Whaoa Runanga Trust for Ōrākei Korako and Te Kopia and Rotokawa (Tauhara North), and Ngāti Rangitahi/Tuhourangi for Waimangu. The team is working with Tracey Godfery to translate and communicate research outcomes back to iwi.

CASE STUDY:

Metagenomics Uncovers the Hidden Diversity of Groundwater Ecosystems

Viruses are found in all forms of life and all ecosystems. Although we associate them with disease, they are an essential component of natural ecosystems, and often have beneficial roles. Viruses in aquatic environments are historically understudied. And while we have some knowledge about viruses in oceans and waterways, few studies have explored the ecology of viral communities in groundwater ecosystems, or aquifers.

Aquifers are natural underground stores of water. Like all water systems, aquifers are home to complex communities of interacting micro-organisms, including prokaryotes (bacteria and archaea), microeukaryotes (tiny multicellular organisms), and little-studied viruses. Because they are completely dark environments, many aquifer organisms are unique to a specific system.

The *Environmental Microbiomes* team took 16 groundwater samples of two aquifers in Canterbury, from which they recovered more than 400 DNA viruses using novel metagenomic approaches. Most of these viruses were new to science, that is, they had never been found before.

The results provide valuable insights into the underexplored diversity in Aotearoa New Zealand's underground ecosystems. "This is a significant discovery – we now have a bank of new knowledge, and modern genomic technology has been a game changer in enabling this," says Genomics Aotearoa researcher Dr Michael Hoggard.

Currently Aotearoa New Zealand has limited capacity to use metagenomic technologies in environmental management. The Genomics Aotearoa *Environmental Microbiomes* project is changing that by developing national capabilities in metagenomics and by producing clear methods and guidelines.

Dr Hoggard explained that we need a baseline to improve environmental monitoring. "It's about understanding the little-known world of microbes in water – what is there, how they live and how they interact. We commonly think of viruses as negative agents affecting human, animal, or plant health. But environmental viruses also play essential and beneficial roles in ecosystems, including decomposing microorganisms and influencing environmental nutrient cycling processes."

Because viruses have a major impact on how bacteria live and interact in waterways, the more we understand about their biology, the better we can predict the consequences of ecosystem changes.

That understanding makes us better placed to analyse the impacts of climate change for instance, or what could happen when nutrients leach from farmland into groundwater. Better understanding of Aotearoa New Zealand's microbial ecosystems provides major benefits for environmental, primary production and health research.

PROJECT LEAD:

Prof Jemma Geoghegan (University of Otago)

The Genomics of Disease Risk in Hoiho
the Yellow-eyed Penguin

Hoiho (*Megadyptes antipodes*)

Unique to Aotearoa New Zealand, the hoiho (*Megadyptes antipodes*) is one of the world's rarest penguins and is nationally endangered. The hoiho population in Aotearoa New Zealand has declined by 65% in 20 years, due to lack of food, disease and predators. The Department of Conservation initiated a new recovery strategy and five-year action plan in 2020 with partners Te Rūnanga o Ngāi Tahu, Te Tautiaki Hoiho/the Yellow-eyed Penguin Trust, and Tini a Tangaroa/Fisheries New Zealand.

With small populations at risk from invasive predators, human disturbance, climate change and fisheries, the 2019 discovery of a viral disease that was killing a quarter of newborn chicks was devastating for the species and conservation efforts.

The Genomics Aotearoa hoiho project, which started this year, is supported by DOC and builds on the tools developed for kākāpō to understand genetic associations with disease risk. This is the first time hoiho genomes will be sequenced at depth to allow these associations to be discovered.

The project involves collaboration between DOC, University of Otago, University of Auckland, Te Rūnanga o Ngāi Tahu, Te Tautiaki Hoiho, and the Wildlife Hospital in Dunedin.

DOC will use the data generated to inform species management, such as translocations and breeding strategies, and Ngāi Tahu will have more information to make key decisions regarding species management.

Hoiho chicks (*Megadyptes antipodes*)

Image Credit (lower): **Janelle Wierenga**

PROJECT LEADS:

Dr Björn Oback and Dr Goetz Laible (AgResearch)

Dr Catherine Collins (University of Otago)

Assoc Prof Maren Wellenreuther (Plant & Food Research)

Assoc Prof Ocean Mercier and Dr Sara Belcher (Victoria University of Wellington)

Norwegian Rat (*Rattus norvegicus*)

Tactical Genetic Control of Rats

Aotearoa New Zealand's Predator Free 2050 goal is an ambitious initiative aimed at eradicating the country of its most harmful invasive species, namely stoats, ferrets, weasels, possums, and rats. Recent advances in genetic technologies offer new possibilities for pest control, potentially reducing reliance on environmental toxins and providing more cost-effective and eco-friendly solutions.

The *Tactical Genetic Control Tools of Rats* project is aiming to develop innovative methods for controlling rat populations, working towards a future where native ecosystems can thrive, free from invasive pests.

Since last year's annual report, the research teams from AgResearch, the University of Otago, and Victoria University of Wellington have made significant progress.

The two focal species of this project are the Norwegian rat (*Rattus Norvegicus*) and the ship rat (*Rattus Rattus*). Norwegian rats arrived in the late 1700s on settler and whaling ships. Strong swimmers, they have adapted well to both urban and rural environments. They threaten ground-dwelling native species, especially ground-nesting birds located near braided rivers and beaches. Ship rats, introduced after the 1860s, prefer forests and are skilled climbers and nest invaders, not only endangering native birds but also consuming native plants, wētā, spiders, and beetles.

Leading research aim one, AgResearch has employed two postdocs to help develop a transgenic rat suppression containment system. They have successfully created DNA constructs targeting germlines to produce transgenic male rats with impaired sperm motility. Additionally, they have developed and validated Cas9 with guide RNA constructs to produce sterile female rats by targeting the female ovary homeobox gene. This work is being carried out in secure containment with no release planned.

The University of Otago, in collaboration with Plant & Food Research, is working on research aim two, which involves analysing genomic data to understand the differences between Norway rats and Ship rats. By studying the spatial distribution of genomic clusters and factors such as gene flow, they are identifying the best strategy for introducing gene suppression technologies to both these species. Over the past year, they have sequenced around 200 genomes from both species from around New Zealand and are making significant progress in understanding their population dynamics, which will help inform the best strategy for introducing transgenic rats.

Victoria University of Wellington is leading the project's final research aim, which involves assessing tangata whenua attitudes toward single-sex offspring (SSOS) technologies for pest management. Through a series of interviews, researchers have found that while interviewees recognised the impact of pests on taonga and were open to innovative solutions like SSOS, they also emphasised the need for culturally appropriate approaches. Addressing these concerns will enable the project to account for tikanga and mātauranga Māori in future decision-making, helping to mitigate potential issues and ensuring all future work adopts an inclusive approach.

Cross-cultural environmental modelling has been completed to project the outcomes of using genetically modified rats as a control measure and the influence of gaining te ao Māori engagement and acceptance with the use of this technology. This modelling suggests that continuing with current management regimes will result in continued degradation of our environment and biodiversity. However, when SSOS technology is actively engaged with by te ao Māori, the outcomes for the environment are much improved. If we are to fully protect our ecosystems and biodiversity, we need to utilise SSOS technology, but we need to do it in a way that is tika, protects whakapapa and ensures rangatiratanga.

PROJECT LEAD:

Prof Peter Dearden **(University of Otago)**

Department of Conservation
Te Papa Atawhai

Understanding Darwin's Ant

Darwin's Ant (*Doleromyrma darwiniana*)

Darwin’s ant (*Doleromyrma darwiniana*), an invasive species native to Australia, has been spreading rapidly across the country, from the northern regions of Aotearoa New Zealand, all the way down to Christchurch in the south. This expansion is alarming conservationists, as recent evidence indicates that Darwin's ants may form super colonies. Such colonies could pose a serious threat to native ecosystems, potentially disrupting biodiversity in affected areas.

Since mid-2024, Genomics Aotearoa has been working with the Department of Conservation to investigate genetic diversity within New Zealand's Darwin’s ant populations. This research, led by Professor Peter Dearden from the University of Otago, aims to determine whether genetic techniques can be used to trace the origin of newly discovered ant populations, particularly on off-shore islands where eradication efforts are currently underway.

The project involves sequencing the genomes of 96 ants collected from a dozen sites across Aotearoa New Zealand. By studying ants from geographically isolated populations, the team aims to assess genetic variability at three different levels: within individual nests; between nests in infested areas; and across different geographical locations.

By identifying genetic differences within and between these ant populations, the researchers hope to trace the origin of new colonies. This data will be crucial for understanding how Darwin's ants are spreading and whether genetic markers can be used to identify the source of new populations.

In addition to providing valuable population data, this research also serves as an early case study exploring the potential of using genetic methods to identify how invasive ant species, such as Darwin’s ants, spread to off-shore islands. If successful, these methods could be applied to other invasive species in the future, providing a powerful tool for conservation efforts aimed at protecting New Zealand’s ecosystems.

Darwin's Ant (*Doleromyrma darwiniana*) eggs

Images Credit: **Grahame (CC-BY-NC-ND) - iNaturalist**

PROJECT LEADS:

Prof Peter Dearden **(University of Otago)**

Prof Thomas Buckley **(Manaaki Whenua – Landcare Research)**

Department of Conservation
Te Papa Atawhai

Mount Augustus snail (*Powelliphanta augusta*)

The Mount Augustus Snail

The Mount Augustus snail (*Powelliphanta augusta*) is a large, carnivorous land snail which is critically endangered, whose last known habitat was a tiny area on the Mount Augustus ridge-line on the West Coast of the South Island.

Open-cast mining has largely destroyed its natural habitat, and remnant populations, now in captivity, are divided into three distinct breeding groups. These are labelled based on their original locations along the mountain’s ridge-line: northern, central, and southern.

Researchers are now investigating gene flow within the Mount Augustus snail population, which could provide valuable insights into the breeding dynamics of this species. One major question is how gene flow occurred between these three breeding groups before their habitat was destroyed. With the population now experiencing a genetic bottleneck, the critical issue is, how can we best preserve genetic diversity to ensure this species' long-term survival?

Genomics Aotearoa, Manaaki Whenua Landcare Research, and the Department of Conservation are working together to address this issue. However, gathering genomic data from molluscs poses unique challenges. The snails’ tissues are covered in mucus, which complicates the DNA extraction process.

Manaaki Whenua Landcare Research was tasked with obtaining high-quality DNA sequences from over 90 snails. By the end of June this year, the necessary DNA sequences were successfully collected, and the research team at Genomics Aotearoa is now analysing the genomes of the snails using SNP (single nucleotide polymorphism) data. This analysis compares the genetic makeup of the northern, central, and southern breeding groups, allowing the team to uncover important information such as genetic differentiation, genome structure, and estimates of genetic diversity and population size within the three groups.

The project is ongoing and set to be completed by the end of 2024. The results will help determine whether the current approach of maintaining three separate breeding groups (northern, central, and southern) is the best way to preserve the species’ genetic health and ensure its continued survival.

Stockton Opencast Mine in 2007. Mt Augustus was part of the Stockton Mine site and was removed to recover the underlying coal

PROJECT LEADS:

Prof Thomas Buckley (Manaaki Whenua – Landcare Research)
Dr Shannon Clarke (AgResearch)
Dr David Chagné (Plant & Food Research)
Assoc Prof Anna Santure (University of Auckland)

High Quality Genomes and Population Genomics

Rewarewa (*Knightia excelsa*) flowers

High-quality genomes are increasingly being used as tools to help threatened species recovery. Potential adaptive resilience to environmental instability, such as climate change, requires knowledge of the genomes of entire populations of a species (the pangenome), and their variation (the variome). Increasingly, population genomics tools are within reach of conservation managers. Honouring Te Tiriti o Waitangi is critical to the success of research on taonga species, and conservation outcomes.

SUB-PROJECT LEAD:

Assoc Prof Anna Santure (University of Auckland)

Understanding Hihi Genomics to Maximise Conservation Management

Hihi/Stitchbird (*Notiomystis cincta*)

Hihi are a threatened forest bird, with low genetic diversity and small populations. These populations are actively managed by DOC on advice from the Hihi Recovery Group. The group includes DOC staff, research scientists, conservation practitioners and Ngāti Manuhiri, who are a kaitiaki for hihi. The hihi genomics sub-project investigates the potential of these small populations to adapt to environmental change.

Last year the team developed a genetic health check to inform conservation management of hihi and found that high levels of inbreeding in the important Tiritiri Matangi population were associated with higher juvenile mortality. Inbreeding-induced homozygosity at a specific part of the genome is also predictive of low lifetime reproductive success.

These genomics insights suggest that active management interventions that increase genetic diversity, such as translocating individuals between populations, will benefit species survival. This is known as genetic rescue.

This year, the research team leveraged the existing genome assembly, and whole genome re-sequencing data, to detect and genotype structural variants (SVs) and single nucleotide polymorphisms (SNPs). Combined with the exceptional life history information from the Tiritiri Matangi population of hihi, the team were able to assess the impact of variation on the fitness of individual birds.

The project also achieved technical milestones, including testing and optimising pipelines for structural variant discovery and analysis.

Research fellow Dr Katarina Stuart developed and led a workshop on Selection Scan Outlier analysis, with five workshops delivered to date in Aotearoa New Zealand and Australia including one for the Genomics Aotearoa training programme. Workshops in Australia were supported by BioPlatforms Australia and strengthened links to the Australian genetics research community.

In the past year, Anna Santure was voted Vice President of the AustralAsia Genetics Society and has just become Acting President.

In accordance with the wishes of Ngāti Manuhiri, all genomic data for hihi have been generated in Aotearoa New Zealand and are safeguarded within the *AGDR*. The project team acknowledges Ngāti Manuhiri as kaitiaki for Te Hauturu-o-Toi and for its taonga species hihi.

SUB-PROJECT LEAD:

Assoc Prof Libby Liggins (University of Auckland)

Australian long-spined urchin (*Centrostephanus rodgersii*)

Genomics to Inform Management of Urchins and Cultivation of Kelp

The goal of this sub-project is to generate high-quality genome assemblies for two marine species that are ecologically significant in our coastal rocky reef ecosystems and have economic potential. The Australian long-spined urchin (*Centrostephanus rodgersii*) and kelp (*Ecklonia radiata*) have a close ecological relationship, influencing each other's population dynamics. As the range, extent and numbers of the urchin increase on our northeastern coastlines, our reefs are losing kelp cover.

The Australian Long Spined urchin genome is complete and undergoing annotation. The genome is being used as a reference for population genomic investigations across Australasia, revealing the colonisation and range extension pathways of the species. The urchin is being actively moved/culled by DOC from some regions where it is a pest. Concurrently, commercial fishers are starting to harvest the species for a burgeoning local market. Developing a means to molecularly monitor the populations, and its re-colonisation dynamics post-culling/fishing is important for informing the long-term management of the populations for both fisheries and conservation.

Te Whānau ā Apanui's aspirations in algal aquaculture are motivating the generation of a high-quality genome for kelp. The kelp genome will guide selective breeding for favourable traits and aid in population genomic assessments of wild kelp in the rohe of Te Whānau ā Apanui. This will provide a baseline understanding of genotypic diversity, inform the selection of individuals for cultures, and monitor the region for genetic pollution.

Despite the isolation of high-quality DNA, difficulty in sequencing has initiated collaboration with other algal geneticists and the submission of a manuscript describing the chemical properties of the DNA causing the problem.

Te Whānau ā Apanui will attach Biocultural Labels to the completed genomes and sampled biological material. These labels will ensure that future use of these resources requires consent by Te Whānau ā Apanui as kaitiaki and that they benefit from sharing these resources.

SUB-PROJECT LEADS:

Prof Neil Gemmell and Dr Alana Alexander (University of Otago)

Genomics of Taonga Species

Deriving Genomic Information from Imperfect Samples

Hector's Dolphins (*Cephalorhynchus hectori*)

This sub-project's goal is to create and analyse high-quality genome assemblies for several taonga species to enhance species recovery and management plans in partnership with iwi, DOC, and other stakeholders. The team has completed assemblies of genomes of Hector's and Māui dolphins, kanakana (New Zealand lamprey), takahē and pekapeka (short-tail bat), and analysis continues.

The continued focus in the last year was on the generation of genomes from samples of mixed quality (old, low quality, poorly stored) using a variety of approaches to improve analysis outcomes.

Highlights this year include completion of the pekapeka genome to the Vertebrate Genomics Project high-quality standard. The genome is currently being analysed as a part of the Bat1k initiative. A kanakana population genomics paper has been drafted and is with iwi partners for review.

The team's work on dolphin genome assembly has received positive feedback from iwi/hapū/rūnanga partners: "I would like to mihi to you for all your mahi on this", "What a massive amount of work you and your team have put in, congratulations on nearing the completion of this project." To look after the taonga that are these genomes, they will be placed on the *AGDR*, and they are forming the basis for Alana Alexander's (Te Hikutū: Ngāpuhi, Pākehā) Rutherford Discovery Fellowship, investigating past and present threats to the dolphins utilising genomics.

A manuscript has been drafted that describes the dolphin genome assembly pipeline, which has broad application to other species where optimal tissue for genome assemblies is limited. The pipeline is freely available on GitHub.

The team have been working with the DOC Bat Recovery Group, and Marine Mammal Team, MPI Biosecurity (on kanakana diseases), the NIWA Freshwater Biodiversity Group, Vertebrate Genome Project, Bat1K project, Cetacean Genome Project and other researchers working with species where only 'non-optimal' tissue is available.

For each study species, the team have built strong working relationships and partnerships with hapori Māori. Jane Kitson (Ngāi Tahu, Ngāti Mamoe me Waitaha) for kanakana work. Takahē iwi relationships are managed via the DOC Takahē Recovery Group through Tāne Davis (Ngāi Tahu). Ngati Rangi are the team's iwi contacts for peka peka.

The work on Hector's and Māui dolphins involves many iwi/hapū/rūnanga around the country: Awarua Rūnanga, Kāti Huirapa Rūnaka ki Puketeraki, Ngāi Tai ki Tāmaki, Ngāti Apa ki te Rā Tō, Ngāti Kōata, Ngāti Kuia, Ngāti Maru (Hauraki), Ngāti Rārua, Ngāti Tama ki Te Tau Ihu, Ngāti Tamaoho, Ngāti Tamaterā, Ngāti te Ata, Ngāti Toa Rangatira, Ngāti Whātua, Ōnuku Rūnanga, Ōraka-Aparima Rūnaka, Rangitāne o Wairau, Te Ākitai Waiohua, Te Atiawa o Te Waka-a-Māui, Te Iwi o Te Roroa, Te Kāhui o Taranaki Trust, Te Kawerau a Maki, Te Ngāi Tūāhuriri Rūnanga, Te Rūnanga o Arowhenua, Te Rūnanga o Hokonui, Te Rūnanga o Kaikōura, Te Rūnanga o Koukourārata, Te Rūnanga o Makaawhio, Te Rūnanga o Moeraki, Te Rūnanga o Ngāi Tahu, Te Rūnanga o Ngāti Waewae, Te Rūnanga o Ōtākou, Te Rūnanga o Waihao, Te Taumutu Rūnanga, Te Uri o Hau, Waihōpai Rūnaka, Waikato-Tainui, Wairewa Rūnanga.

SUB-PROJECT LEADS:

Prof Thomas Buckley (Manaaki Whenua – Landcare Research)

Prof Tammy Steeves (University of Canterbury)

Genomic Solutions for Threatened Species and those with Large and Complex Genomes

Black Stilt/Kakī (*Himantopus novaezelandiae*)

This sub-project supports the conservation management of threatened species and enhances our understanding of biodiversity unique to Aotearoa New Zealand. Iterative engagement with relevant iwi and hapū and DOC is key to the success of the project. Our focal species include kuaka Whenua Hou (Whenua Hou diving petrel), wētāpunga (giant wētā), huhu (huhu beetle), rātā Moehau (endangered rātā tree), rewarewa (*Knightia excelsa* tree), kihikihi (cicada), rō (stick insect), pepeketua (*Leiopelma* frogs), tara iti (fairy tern), and kakī (black stilt).

This year the rātā moehau genome assembly was completed and is being annotated. Variant calling of 30 re-sequenced samples of wild and cultivated rātā moehau is underway. Relationship building, knowledge sharing and engagement with iwi partners Ngāti Kuri has been a recent highlight. Thanks to co-funding from Ngā Rakau Taketake, Jessie Prebble joined Ngāti Kuri and the Auckland Museum for a bioblitz at Te Paki in April 2024; and in May 2024 Ngāti Kuri organised two days of rātā Moehau hui, at Otāri Wilton's bush in Wellington, and the Auckland Botanic Gardens.

The team are using stick insects as a model to explore genomic tools to study the evolution of polyploid genomes. Using these tools, the team have revealed that species of the genus *Acanthoxyla* arose from multiple hybridisation events. Following hybridisation, the lineages lost the ability to reproduce sexually and now have female only lineages.

The team presented new and improved long-read genome assemblies for two of Aotearoa New Zealand's rarest birds, tara iti (New Zealand fairy tern), and kakī (black stilt). We then used these foundational resources to incorporate SNPs and SVs into a more holistic assessment of genomic diversity for the nationally critical tara iti. To contextualise these data, we used resequence data for two close relatives, the more populous and widespread Australian fairy tern and the nationally critical kakī. This work was made possible due to our long-standing relationships with the DOC's Tara Iti Recovery Group (RG) and Kakī RG, and the newly established Tara Iti Research Advisory Group (RAG). RAGs are formed to provide strategic and technical advice to species recovery programmes to ensure that the most urgent and impactful research is funded. Working with the Tara Iti RAG, and alongside the Tara Iti RG, our combined data are being used to develop a position statement regarding the efficacy of genetic rescue for tara iti.

The team has also published on rewarewa and cicada, with a further three publications in review. The suite of tools the team has produced for genome assemblies and population genomic analyses are available on GitHub. Outputs from the project have included three new bioinformatics pipelines, 11 presentations at events and one co-funded DOC technical report.

SUB-PROJECT LEADS:

Prof Peter Dearden and Dr Joseph Guhlin (University of Otago)

New Tools for Kākāpō Genomics

Kākāpō (*Strigops habroptilus*) - "Ako"

Kākāpō, Aotearoa New Zealand's charismatic critically endangered night parrot has had new genomic tools developed this year. The work on kākāpō genomics reached several important milestones, was published in *Nature Ecology and Evolution*, and received wide reporting in more than 35 scientific and mainstream media outlets globally including Cosmos, Nature, and New Scientist.

The team have now sequenced the genomes of all living kākāpō, as well as some deceased individuals, including early embryo failure. These data have been variant called and are being analysed for DOC. This new data will provide insights into how the new generations are changing at the genetic level, improve and test our trait models, and provide deeper insights into genetic causes of early embryo failure. The team has worked closely with DOC to transform these research activities into pipelines and processes that the department can use without the need for input from genomics researchers. The tools developed with DOC include dashboards translating genomic data, relatedness, and pedigree into clear information supporting management decisions. This dashboard assists with translocation and artificial insemination decisions and has been well received by the conservation team. Additionally, individuals have been tested for genetic susceptibility to cloacitis ("crusty bum"), a recurrent disease and severe problem for the species. These results have been shared with DOC, and as more cases arise, the model is updated, and results are shared.

In addition to the six manuscripts published this year, two manuscripts are in draft: one describing the pipelines and dashboard as exemplars for conservation management of any species with genomic data, and a second on the analysis of chicks from the previous generation, which tests and sharpens predictions.

Many of the tools developed are already publicly available on GitHub, with more to be added soon. These tools are already changing how worldwide conservation genomics is done. International researchers are exploring the Kākāpō trained AI model for variant calling for Song Sparrows and King Penguin studies, and it will be adapted for use in the hoiho project later this year.

Kākāpō (*Strigops habroptilus*) - "Mother "Alice" and chick "Rupi"

Images Credit: **Jake Osbourne**

Health

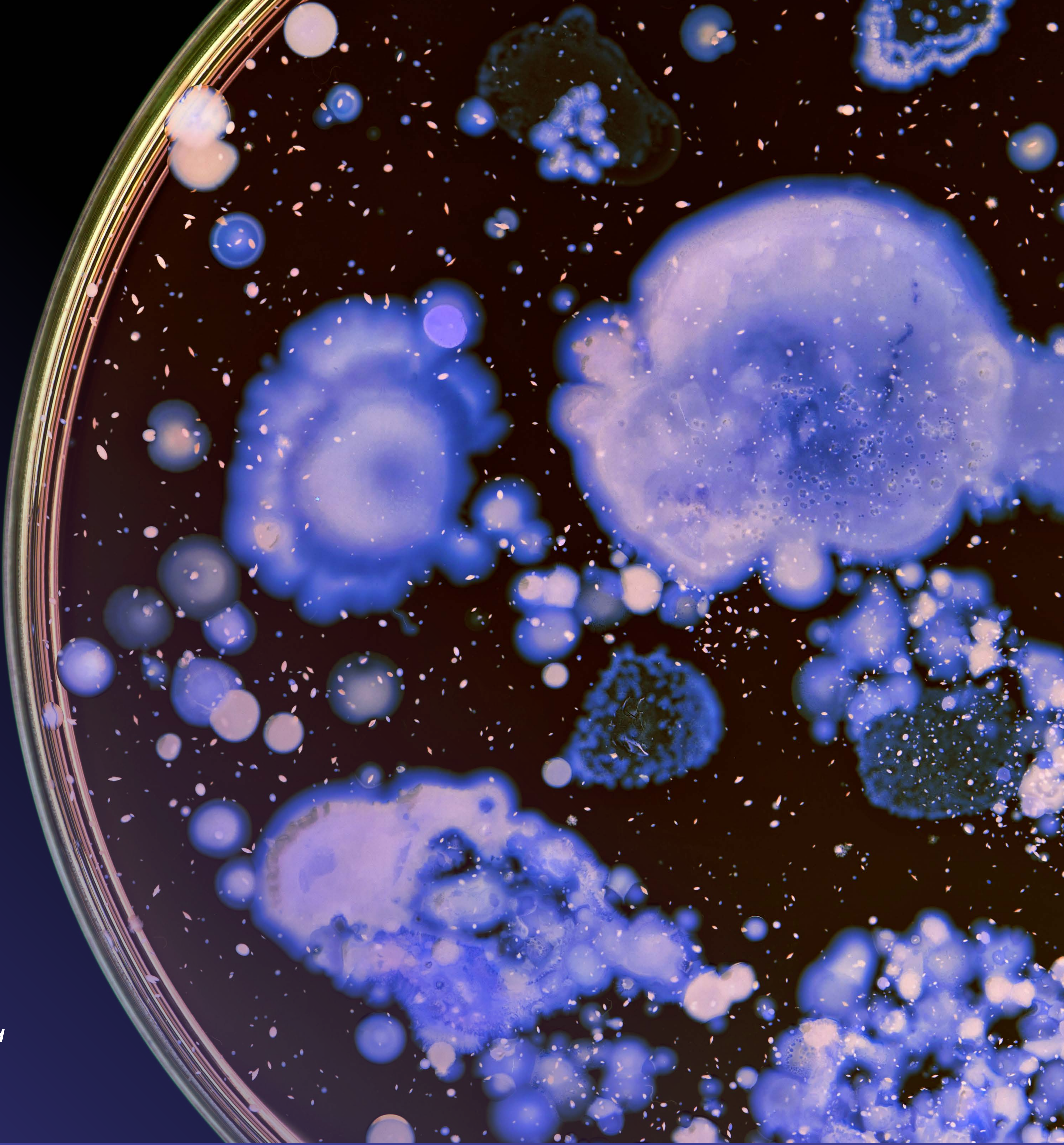
This year we report on five projects in the health theme. Last year the ground-breaking *Rakeiora* project was completed, along with the *Aotearoa New Zealand Variome* project. The latter research was granted additional funding and is reported this year as *He Kākano: the Aotearoa Māori Variome*.

As well as the five ongoing projects, the completed Health projects are:

- *Aotearoa New Zealand Variome,*
- *Cell Free Genomics,*
- *Genomic Translational Oncology,*
- *Culture-Independent Genomic Typing of Bacterial Pathogens,*
- *Epigenome Wide Association Study Technology,*
- *Clinical Genomics,* and
- *Rakeiora.*

One new health project has been initiated, *Marine Fungi as a Source of Antimicrobial Agents*, which is notable as our first project led by a Pasifika researcher, Dr Helen Woolner. Helen is combining Cook Islands Māori Indigenous knowledge and genomics for drug discovery.

There are two health case studies this year; one on how the outcomes of the *Variome* projects provide a genetic dictionary for tāngata of Māori descent; and the second on how *Distributed Sequencing* has been used at Wellington Hospital for early detection of disease outbreaks.



PROJECT LEADS:

Prof Stephen Robertson and Assoc Prof Phil Wilcox (University of Otago)

He Kākano

The Aotearoa Māori Variome

Variomes define the unique genetic signatures of populations. Without a comprehensive variome for Aotearoa New Zealand, shaped as it is by our unique human history, genomic tools based on overseas non-Māori populations have limited use in genomic medicine for people with Māori ancestry.

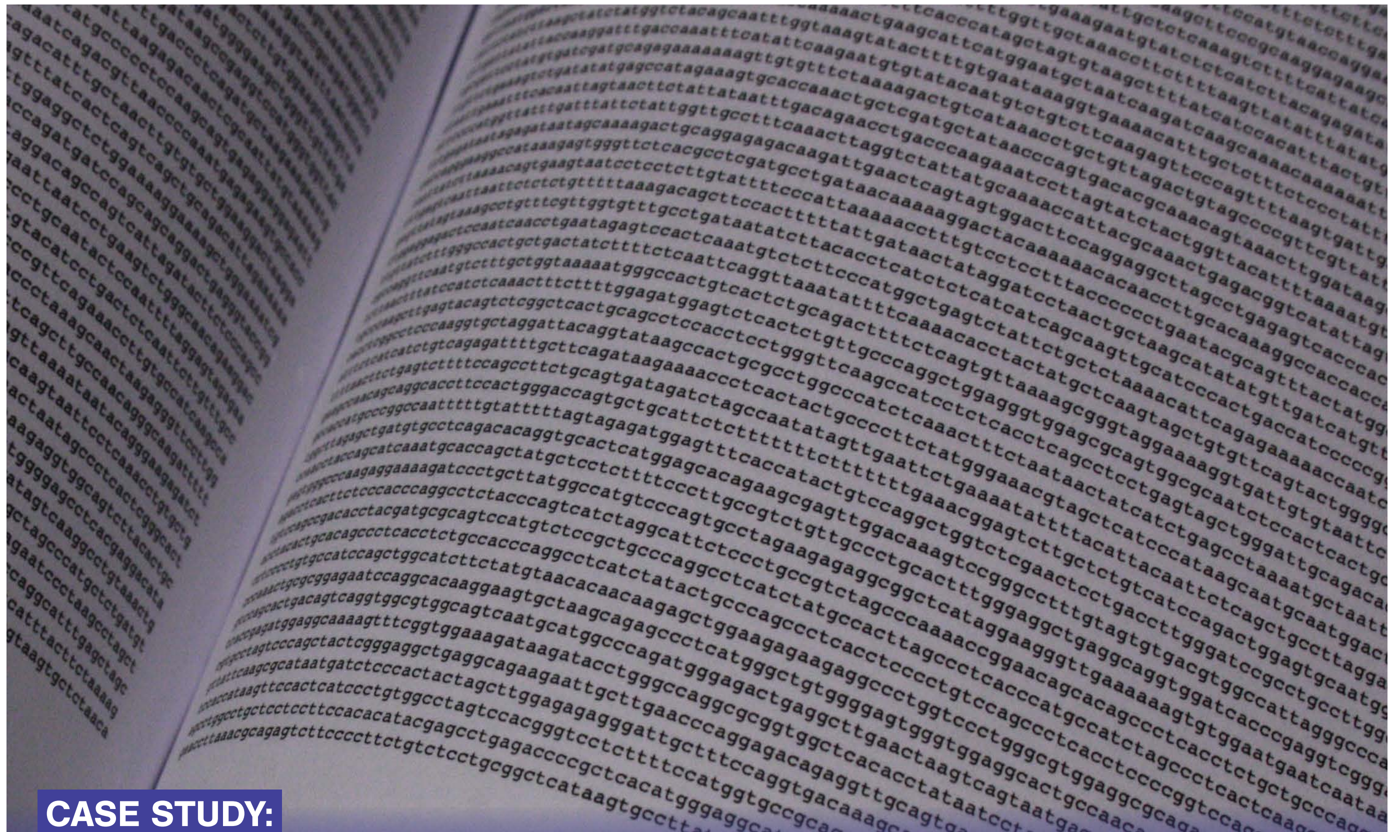
Following on from the successful *Aotearoa New Zealand Variome* project, this project extends the recruitment of participants and sequencing to provide an even fuller catalogue of variation. To date, the genomes of over 1000 people have been sequenced. A pilot implementation with clinical scientists has been completed as well, and collaboration continues with the University of California at Santa Cruz (UCSC) who are co-leading the Human Pangenome Reference Consortium (HPRC).

Construction of a portal tool is nearly complete. This tool will enable controlled access by approved clinicians for querying genotype frequencies of specific genetic variants. This information will help with clinical decision-making for individuals with Māori ancestry.

The continuing refinement of the Aotearoa New Zealand variome in a culturally appropriate way places the country's health genomics research community in a good position to support precision medicine.

HE KĀKANO RESEARCHERS WITH SOME OF THE MEMBERS OF THE LEADERSHIP RŌPŪ (FROM LEFT):
PHIL WILCOX, STEPHEN ROBERTSON, HELEN WIHONGI, HUTI WATSON, ANA ROLLESTON, MAUI HUDSON,
TE URUROA FLAVELL (FORMER CHAIR), ANDREW SPORLE, IRENE KEREAMA-ROYAL, JENNY HARRE-HINDMARSH

Carving Credit: **John Collins and Sunnah Thompson (Te Kawerau ā Maki)**



CASE STUDY:

He Kākano, a Genetic Dictionary for Aotearoa New Zealand

The *Aotearoa New Zealand Variome* project had primarily been using short-read sequencing approaches to resolve genomic variation. The ongoing collaboration between Genomics Aotearoa funded researchers and scientists at the UCSC introduced the power of long-read sequencing to enhance genome resolution.

Currently, long-read sequences are being prepared for the genomes of six Māori participants. Associate Professor Phil Wilcox explains "This collaboration is very much a knowledge exchange, where UCSC share their methods for constructing long read genome assemblies, and in return we share our knowledge and experiences of introducing Māori/Indigenous content into university-level education in bioethics, as well as aspects of culturally informed co-design of genomics research."

The technology being used is the most up to date in the world. Long-read sequences are assembled using the recently developed Telomere-to-Telomere (T2T) techniques pioneered by the group at UCSC. These techniques produce the most detailed genome assemblies currently possible. Professor Stephen Robertson says that the use of several genomic sequencing and assembly techniques will give a much more comprehensive understanding of Māori genomes.

The aim of sequencing and accurately understanding genomic variation in Māori populations is to ensure that the expansion of genomics into healthcare and medicine is accurate and fit-for-purpose. "It's simple - if we don't do this, no one will do it for us, and Māori will miss out because we don't have the necessary genetic information to accurately diagnose and prescribe precision treatments," he said.

"Put another way, we can't check the spelling in a person's genome if we don't have a genetic dictionary informed by their ancestry. *He Kākano, The Aotearoa New Zealand Māori Variome* is that genetic dictionary."

Diagnostic scientists at Health New Zealand have already used some of these data in a trial for clinical diagnosis of Māori patients with inherited disease. This trial produced useful information, showing genetic variations that helped clinical diagnosis for some individuals.

Producing genomes from Indigenous populations is a major step forward in broadening the western-biased global databases currently available, as Associate Professor Phil Wilcox emphasises, "Māori ways of designing and conducting a research project deliver benefits both diagnostically and scientifically and these are world leading. Our relationship with UCSC shows that we can link to world leaders who are respectful of tikanga, to help deepen our understanding of our own local realities, effectively placing Aotearoa New Zealand at the leading edge of human health genomics."

Just as importantly, this project has paved the way for local real-world clinical solutions, meeting Te Tiriti responsibilities to deliver equity in healthcare, while implementing protocols that respect Māori data sovereignty.

Image Credit: **Stephen C Dickson (CC BY-SA 4.0) - Wikimedia Commons**

PROJECT LEADS:

Dr David Winter, Dr Donia Macartney-Coxson, and Dr Joep de Ligt (ESR)
Prof Patrick Biggs and Dr Kristene Gedye (Massey University)

Distributed Sequencing for the Health of People and Animals

DR RHYS WHITE - ESR

Small, portable sequencing devices are now able to capture genomic data in real time without the need for specialised facilities. This distributed sequencing has promising benefits for a range of applications. This project develops and implements pipelines to enable real-time analysis and reporting for decision making at the point-of-need: in the hands of human and animal healthcare professionals.

Animal Health

Aotearoa New Zealand has a shortage of parasitologists, which is a major challenge in a country so reliant on primary industries. The *Distributed Sequencing* project intends to enable the accurate diagnosis of parasites in the absence of expert parasitologist analysis.

The animal health component of the project has undergone a substantial restructure due to a late-start in recruitment, changes in leadership and the passing of Dr Kristene Gedye earlier in 2024. The knowledge, expertise and relationships Kristene brought to the project are irreplaceable.

The team have trialled many DNA extraction methods to identify those suitable for working with the very small amounts of nematode material found within the samples (e.g., faecal) handled by veterinary labs. The team have been optimising sample preparation to maximise high-quality nematode DNA prior to Oxford Nanopore sequencing.

Human Health

The ongoing collaboration with Dr Max Bloomfield has had a direct impact on infection prevention and control. Oxford Nanopore genomic surveillance allowed for the detection of a ward-based outbreak of *Clostridioides difficile* at Wellington Regional Hospital.

This work was published in *Infection Control and Hospital Epidemiology*, and is an example of the value of point-of-need sequencing that can be followed by others. The approach has contributed directly to the management of infections within the hospital, and the detection of outbreaks in wards with vulnerable patients.

A prototype laboratory process and bioinformatic pipeline for culture-free antimicrobial resistance detection has been developed. This proof-of-concept will be optimised for use in a real-world situation later in 2024. Ethical and safety agreements are in place to work with residual samples from other testing, allowing the metagenomic aspects of this project to proceed.

Image Credit: **ESR**

CASE STUDY:

Distributed Sequencing Speeds Diagnosis and Response

When Dr Miles Benton (who then worked at ESR) was awaiting the results of a meningitis test for his premature baby boy, he realised the 48-hour wait could, and should, be a lot shorter. Dr Benton knew that in his bioinformatics work he could make a difference to thousands of New Zealanders every year, speeding up diagnosis and improving outcomes for patients.

This concern was the genesis of the *Distributed Sequencing for the Health of People and Animals* project to implement and prototype rapid, real-time genomic sequencing in hospitals and veterinary clinics.

The human health component of the research saw Dr Rhys White work on-site at Awanui labs in Wellington Regional Hospital with Dr Max Bloomfield, the pathology lab lead. This partnership has had a huge impact on infection control and prevention at the hospital and its successes have led to wider interest in on-site sequencing amongst the Aotearoa New Zealand microbiology lab community.

One success was the prospective genomic surveillance of *Clostridioides difficile* that detected an outbreak of potentially lethal sequence type (ST)2 infection on the haemato-oncology ward. For these vulnerable patients, early detection of the outbreak was potentially lifesaving.

The collaboration also supported genomic surveillance and early detection of methicillin-resistant *Staphylococcus aureus* (MRSA) in the Neonatal Intensive Care Unit, another group of highly vulnerable patients. This early detection facilitated prompt screening of infants on the ward, again, very probably saving lives.

The on-site early interventions protected patients and avoided ward-closures; saving lives, saving money, and allowing the hospital to continue providing care. These outcomes indicate the potential impact of the project and are an impetus to roll the technology out more widely.

“The key to success has been the partnership,” said Dr David Winter. “It wouldn’t have worked without that. Dr Bloomfield has been a leader in adopting sequencing in the diagnostic laboratory. We supported him from the outset, but the Genomics Aotearoa project provided the opportunity for Dr White to work closely with Dr Bloomfield in the hospital setting. Working together and sharing skills really made a difference in generating the results that we have."

The project used Oxford Nanopore MinION technology, a stapler-sized DNA sequencer, which has a minimal footprint and a low up-front cost, making it ideal as an accessible, economic genomic sequencing option.

“The big challenge now is scaling up the benefits of this project to hospitals around the country,” said Dr Donia Macartney-Coxson.

PROJECT LEAD:

Prof Stephen Robertson (University of Otago)

Extending Whole Genome Analysis into Healthcare

Sequencing and analysing a person's entire genome – whole genome analysis (WGA) – is the most comprehensive method of genetic diagnosis. In Aotearoa New Zealand the benefits of WGA in healthcare have yet to be fully realised, and WGA services here are almost entirely dependent on overseas providers.

Now complete, this project trialled the generation, analysis, interpretation, and clinical delivery of genomic diagnostics by teams based in hospitals across Aotearoa New Zealand.

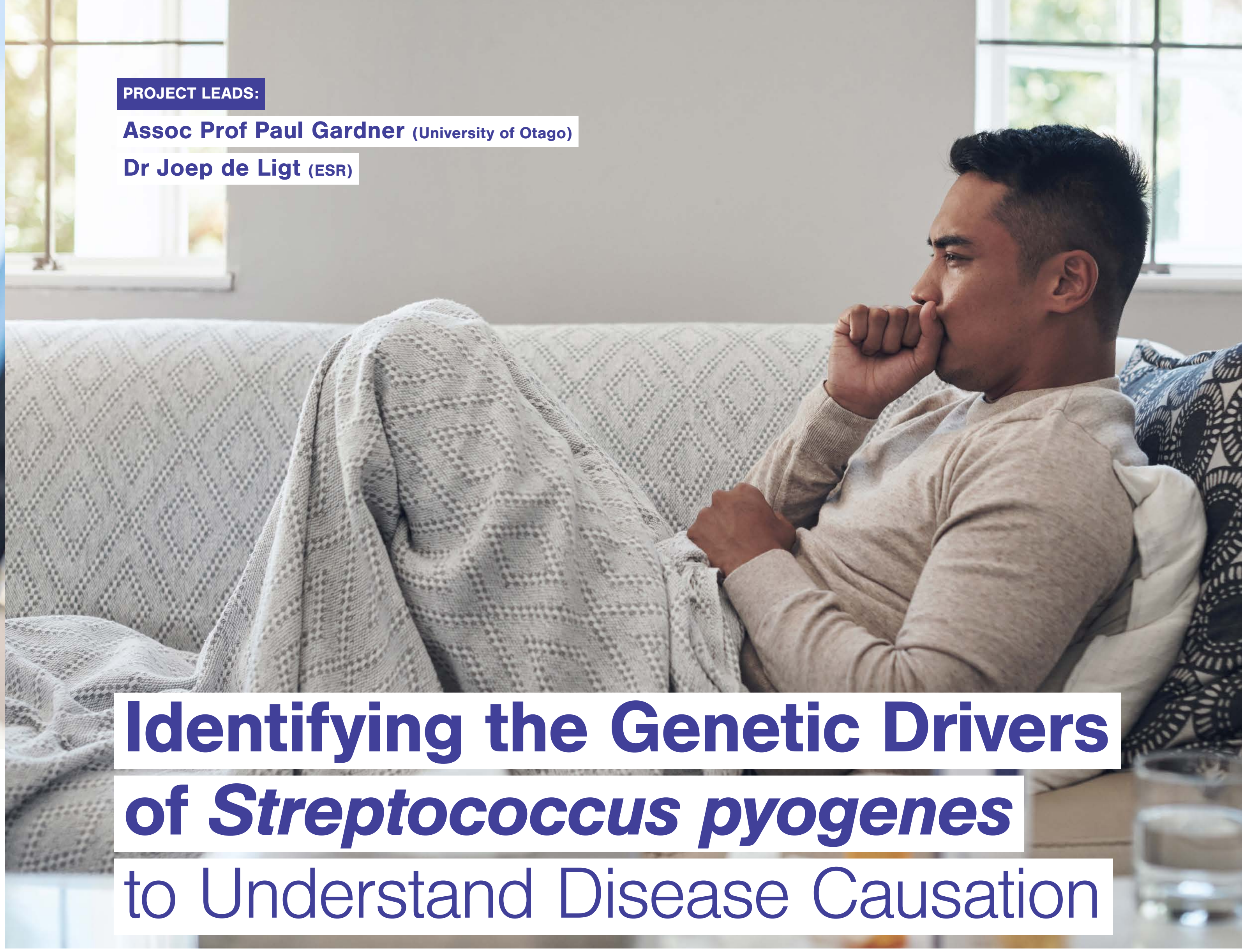
A cohort of 103 people (45 whānau) were enrolled in the project over a term of 18 months. 42% of participants were Māori. Almost all diagnostic evaluations were through Canterbury Health Laboratories, with a diagnostic rate of 38%. All diagnoses by the clinical lab were corroborated by the host research laboratory (the Laboratory for Genomic Medicine, Dunedin School of Medicine).

The associated genomics wānanga raised awareness and appreciation of genomic analysis by Māori medical students and attendees at SING Aotearoa.

The outcomes of the project included:

- Creating comfort, familiarity and increased competence with clinical genomics diagnostic processes.
- Developing a mode of practice in clinical genomics diagnostic evaluation aligned with tikanga Māori.
- Establishing a diagnosis for almost 40 people and their whānau.
- Contributing to the establishment of Aotearoa New Zealand's first clinically accredited Exome sequencing diagnostic service, Canterbury Health Laboratories, in 2023.

The team look forward to seeing increased local capacity for genetic diagnosis.



PROJECT LEADS:

Assoc Prof Paul Gardner (University of Otago)

Dr Joep de Ligt (ESR)

Identifying the Genetic Drivers of *Streptococcus pyogenes* to Understand Disease Causation

More than 600 million Group A Streptococcus (GAS; *Streptococcus pyogenes*) infections occur globally each year, with a variety of clinical outcomes, from minor sore throats to rheumatic fever and heart disease. Children are particularly susceptible.

Now complete, the project aimed to better understand the causes of the range of GAS outcomes by:

- gaining insights into the genetic diversity and population structure of invasive and non-invasive GAS amongst children in Aotearoa, and
- identifying genetic drivers responsible for invasive phenotypes.

Community engagement was a major component of the project and was led by the National Hauora Coalition. This engagement led to community insights from Māori, Tongan, Samoan and Cook Island Māori, including youth, and identified three fundamental requirements: informed consent, culturally informed guidelines, and ensuring Indigenous sovereignty of isolates.

The project led to a deeper understanding of the genetics of *Streptococcus pyogenes* that causes rheumatic fever. Following on from this project, the data generated are being used in the national Ministry of Health-funded *Streptococcus* vaccination research led by the University of Auckland.

PROJECT LEAD:

Dr Helen Woolner (Victoria University of Wellington)

Marine Fungi as a Source of Antimicrobial Agents

Genomics Aotearoa is pleased to welcome researcher Dr Helen Woolner to the team. Helen is a talented early career researcher of Cook Islands Māori descent and is a lecturer at Victoria University of Wellington. Her specialisation is in identifying new biological compounds for healthcare applications, and she is particularly enthusiastic about promoting Pasifika interests and participation in the benefits of this research and its translation into outcomes.

Antimicrobial agents – and antibiotics in particular – are a cornerstone of modern healthcare. However, according to the World Health Organization the research and development pipeline for new antimicrobial tools is not keeping pace with the growing need, due to antimicrobial resistance.

Pacific peoples have a long history of using naturally sourced medicines. We now recognise that natural chemicals known as secondary metabolites are the sources of the therapeutic effects of these traditional medicines.

Exploring Pacific marine microbial natural products requires combining Pacific-led scientific innovation and Pacific Indigenous wisdom. By prioritising collaborative research practices with Indigenous knowledge holders, Helen will ensure the research is conducted in a culturally appropriate manner, that customary practices are adhered to throughout the research, and that benefits accrue to the appropriate knowledge holders.

Helen's project combines Cook Islands Māori Indigenous knowledge together with a genomics approach for an in-depth exploration of Cook Islands marine microbes, which will lead to a greater likelihood of discovering antimicrobials.

Primary Production

Two Primary production projects are reported on this year (*Invasomics for Better Biosecurity and Invasive Species Management* and *High Quality Genomes and Population Genomics II*).

Completed Primary production projects are:
- ***High Quality Genomes,***
- ***Better Breeding Values,* and**
- ***High Quality Genomes and Population Genomics.***

Five sub-projects are currently being executed under the *HQG+PG II* project within this theme. These sub-projects encompass diverse research targets including mānuka, karaka and blueberry, pasture genomics and finfish for aquaculture and fisheries.

The case study, *Fisheries Genomics for a Changing Climate, Changing Seas*, describes the fine-scale local adaptation of snapper, and the potential for overfishing without prudent management.

PROJECT LEADS:

Prof Thomas Buckley (Manaaki Whenua – Landcare Research)
Dr Shannon Clarke (AgResearch)
Dr David Chagné (Plant & Food Research)
Assoc Prof Anna Santure (University of Auckland)

High Quality Genomes and Population Genomics

Primary production end-users can use high-quality genomes and population genomics tools to better predict biological traits such as the reproduction, appearance, behaviour, or disease susceptibility of a variant, and understand how these traits differ among populations. Understanding this variation will improve economic yields and increase resilience to environmental change.

SUB-PROJECT LEAD:

Prof Maren Wellenreuther (Plant & Food Research)

Finfish Genomics: Improved Hoki and Chinook Salmon Genomes

Chinook Salmon (*Oncorhynchus tshawytscha*)

The genomics field is constantly changing, and tools and resources that were state-of-the-art only a few years ago are already outdated. This sub-project and the next are investigating different tools for genome sequencing and assembly of economically and culturally important fish species, to improve fisheries management.

This sub-project has developed improved genomes for hoki and Chinook salmon for the fisheries and aquaculture industries, respectively. Further investigation this year discovered that last years' draft assemblies using PacBio hi-fidelity technology were not of satisfactory quality.

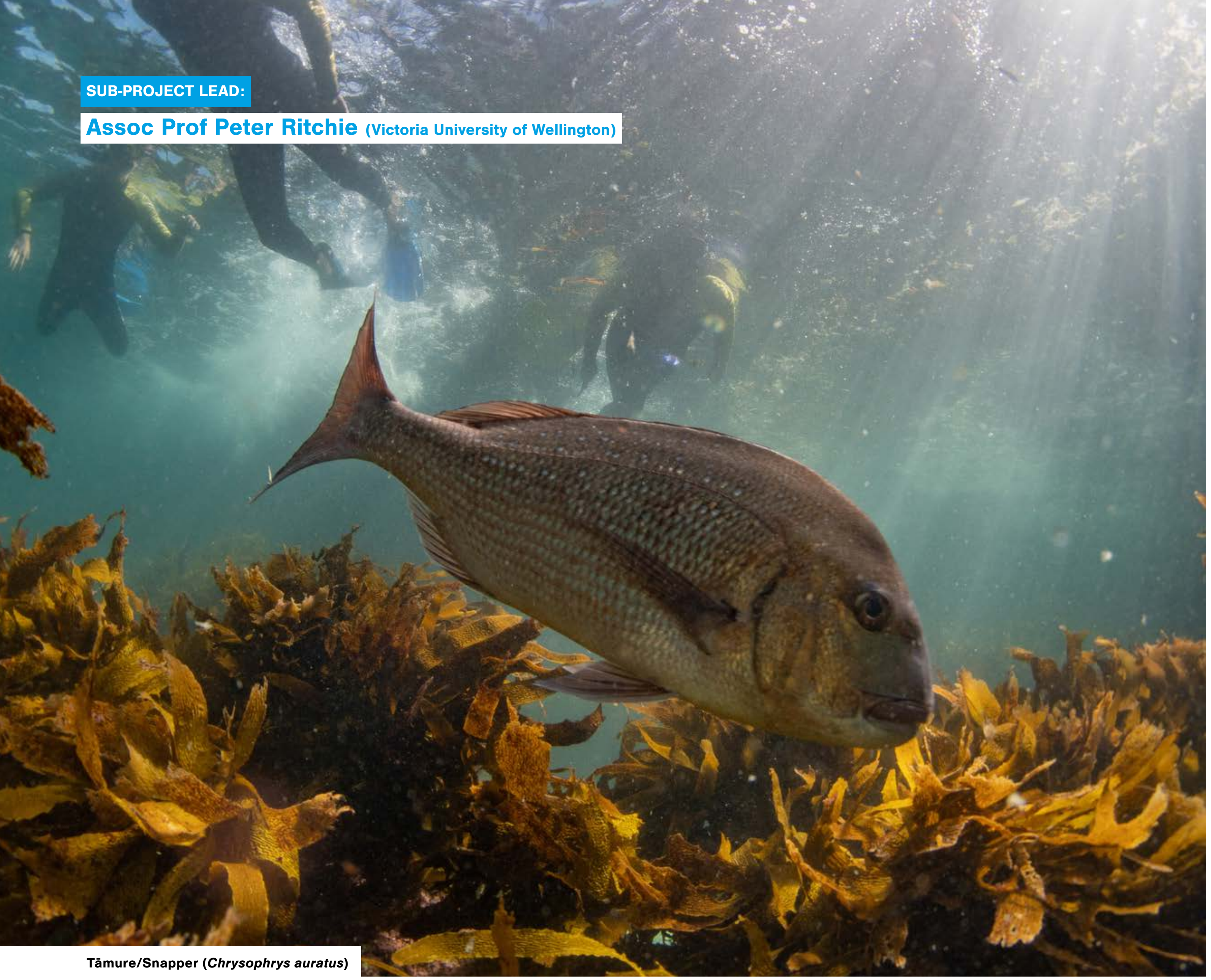
Consequently, the team used the original good quality assembly for hoki to analyse new population genomic data from previously unsampled regions, including the sub-Antarctic islands, where adult hoki annually migrate. Preliminary analyses suggest that these regions may contain fish populations that are genetically divergent from hoki around Aotearoa New Zealand.

For Chinook salmon, the team extended its collaborations with AgResearch and the Cawthron Institute. Recent MBIE Endeavour funding (Climate Adapted Finfish, Fast-Tracking Finfish Climate Change Adaptation Research Programme - Cawthron Institute) will enable the team to continue a New Zealand-specific assembly for this species. This ongoing work aims to obtain Hi-C data, additional PacBio data and possibly linkage mapping data.

Chinook Salmon (*Oncorhynchus tshawytscha*)

SUB-PROJECT LEAD:

Assoc Prof Peter Ritchie (Victoria University of Wellington)



Tāmure/Snapper (*Chrysophrys auratus*)

New Tools for Fisheries Genomics

Like the Chinook salmon and hoki sub-project, this sub-project is using genomics to develop new tools for fisheries. Oxford Nanopore sequencing technology is being used by the researchers, who initially sequenced the tāmure (snapper; *Chrysophrys auratus*) genome.

Genome assemblies have now been generated for four more fish species – kahawai, blue moki, john dory, and hāpuka. These four genomes are now ready for use in future fisheries studies.

The insights that the team has produced have drawn attention from fisheries managers, policy teams, and Māori fisheries businesses, who need to understand how fisheries adapt to climate change. Some species demonstrate evolutionary adaption to changing sea temperatures and others are simply expanding their distribution. These insights support a priority-based approach to managing climate-change-induced fisheries, helping determine which species may require minimal intervention and which need additional management tools to ensure stock resilience.

The outcomes of this sub-project demonstrate the enormous value population genomics can bring to planning and mitigation of critical challenges to future food production. A range of end-users will soon be able to incorporate these findings into their planning, and provide feedback on the priorities for the next genomics analyses of fisheries species.

The methods developed for this sub-project are focussed on an easy-to-adapt protocol for researchers with limited experience in bioinformatics. The team created a public GitHub repository, presented in a way that people with limited bioinformatics experience can follow, making these tools accessible to a wider audience.

Image Credit: **Samara Nicholas (CC-BY-NC) - iNaturalist**

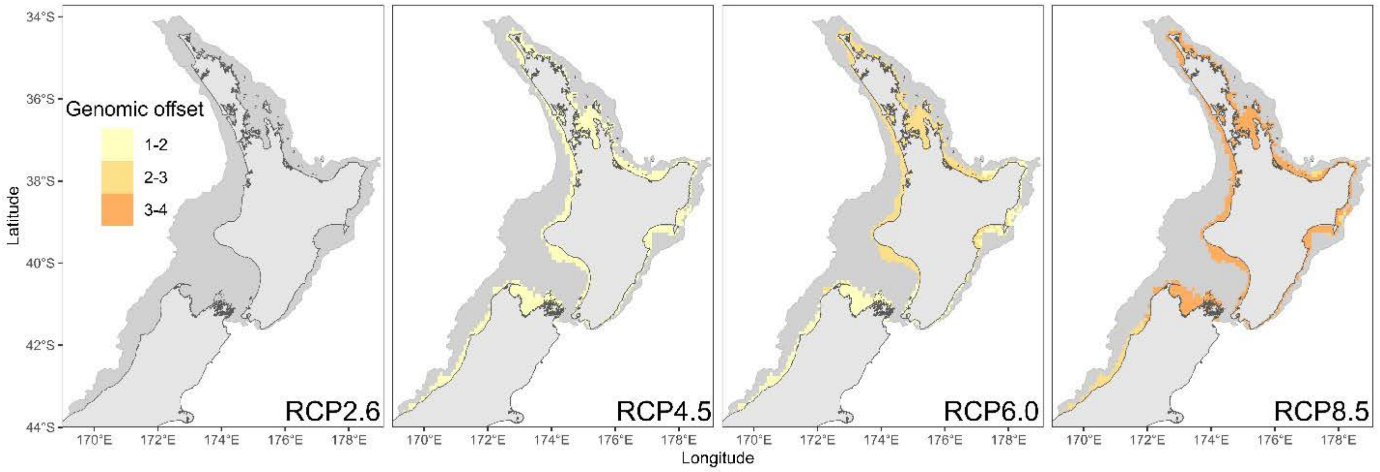


Figure: The grey shaded area is the 200m bathymetry line (tāmure maximum depth). Plots show increasing genomic offset across different climate scenarios (severity increases from left to right). Genomic offset measures adaptations (traits) that were beneficial in a previous environment and are no longer beneficial, that is, the traits are now maladaptive.

CASE STUDY:

Fisheries Genomics for a Changing Climate, Changing Seas

We often perceive climate change as impacting our land, but life in our oceans is also changing. Genomics can help us better manage this change and protect the realm of Tangaroa, along with the people and economy that rely on it.

Tāmure (snapper) have historically been limited to the coastal areas of the North Island, Marlborough Sounds, and Tasman Bay, but are increasingly appearing in catches further south along the East and West Coast of the South Island. This change in distribution is seen as evidence of a species response to warming oceans, a phenomenon which will increase as sea temperatures continue to rise. This project sought to answer two questions:

1. how are warming oceans affecting the tāmure and
2. how can we protect our fishing industry and ensure the species survives into the future?

Dr Tom Oosting, of Victoria University of Wellington, performed genotype-by-environment analyses on tāmure. Tom compared genomic variation with key environmental indicators, such as temperature, salinity, and dissolved oxygen concentrations. Hundreds of tāmure genomes have been sequenced, resulting in one of the largest datasets for a fisheries species in Aotearoa New Zealand.

This project has shown that sea temperature is exerting selective pressure on the species. The work has also identified the areas in the genome where these adaptations occur. Detecting natural selection is an exciting finding that indicates that different genotypes can be linked to physical characteristics, such as growth rates.

The research also raises critical questions about the future of tāmure. Intergovernmental Panel on Climate Change (IPCC) climate projections were used to estimate the mismatch between the environment and tāmure genotypes (see figure).

The change in distribution of tāmure populations requires careful management. If we can use proactive fisheries management to secure the locally adapted populations of species, fisheries will be sustainable in the long-term.

“As tāmure move into new environments, we need to prevent a gold rush approach to these new fishing stocks. Early management will ensure that long-term fisheries prospects are secure for the species,” said Associate Professor Peter Ritchie of Victoria University of Wellington.

Mark Fenwick (Taranaki Whānui) of NIWA and Te Ātiawa ki te Ūpoko o te Ika ā Māui Pōtiki (Fisheries) Trust, adds, “If fisheries in the south are founded by fish that are better adapted to the novel environment and they are immediately overfished, there is a risk the adaptive response to climate change will collapse. Genomic research has a critically important role in supporting Māori fisheries interests and maintaining the value of our people's fisheries assets."

“We desperately need to expand this research to fisheries species that we know have range limits just south of Whanganui-a-Tara,” says Associate Professor Ritchie. “Species such as tāmure, kingfish, hāpuka and kahawai are showing similar patterns. Adaptive fronts might not be a feature of all expanding fisheries species. But we need to find those that are experiencing climate-induced adaptation and develop more responsive fisheries management to protect them during that adjustment phase”.

SUB-PROJECT LEADS:

Prof Maren Wellenreuther and Dr David Chagné (Plant & Food Research)

Mānuka (*Leptospermum scoparium*) flowers

The Mānuka Microbiome

Mānuka is a taonga species and a high value production resource. Before this sub-project, nothing was known of the role of the plant's microbiome. Using metagenomics, this sub-project, in partnership with Associate Professor Kim Handley (University of Auckland) investigates the microbiomes from mānuka populations throughout Aotearoa New Zealand.

The team is working with Māori landowners including representatives from Ngati Porou, Te Arawa, Te Rarawa, Ngāi Tahu and Rangitāne o Manawatū who have mānuka growing on their land. This research will contribute to understanding which types of microbes live in association with mānuka and what role these organisms play, especially around adaptation to environmental conditions.

Sampling of mānuka populations from the East Cape has been completed and sequence data has been produced for six tissue types, using three replicates from five locations. Data analysis is in progress. A complete assembly of the mānuka metagenome will determine what microbial species live in association with mānuka and what is their abundance and function between tree parts and regions.

SUB-PROJECT LEADS:

Dr David Chagné and Dr Chen Wu (Plant & Food Research)

Developing a High Quality Genome for Karaka

Karaka (*Corynocarpus laevigatus*) berries

Karaka is an iconic taonga tree that was planted at traditional fishing sites as a seasonal food source for early Māori settlers.

Mana whenua Rangitāne o Manawatū would like to explore the commercial potential of this taonga in their rohe.

This sub-project is associated with an MBIE Vision Mātauranga Capability Fund project that is led by Rangitāne o Manawatū with PFR and Massey University, and which seeks to understand the phenotypic composition of the toxin in the karaka fruit.

The high-quality, highly complete genome and transcriptome assembly for karaka that was produced last year has helped researchers uncover some unique centromeric repeats which need further analysis to resolve their exact structure. The data are also being used to inform the associated project on the variability of the karaka toxin between trees growing in the Manawatū.

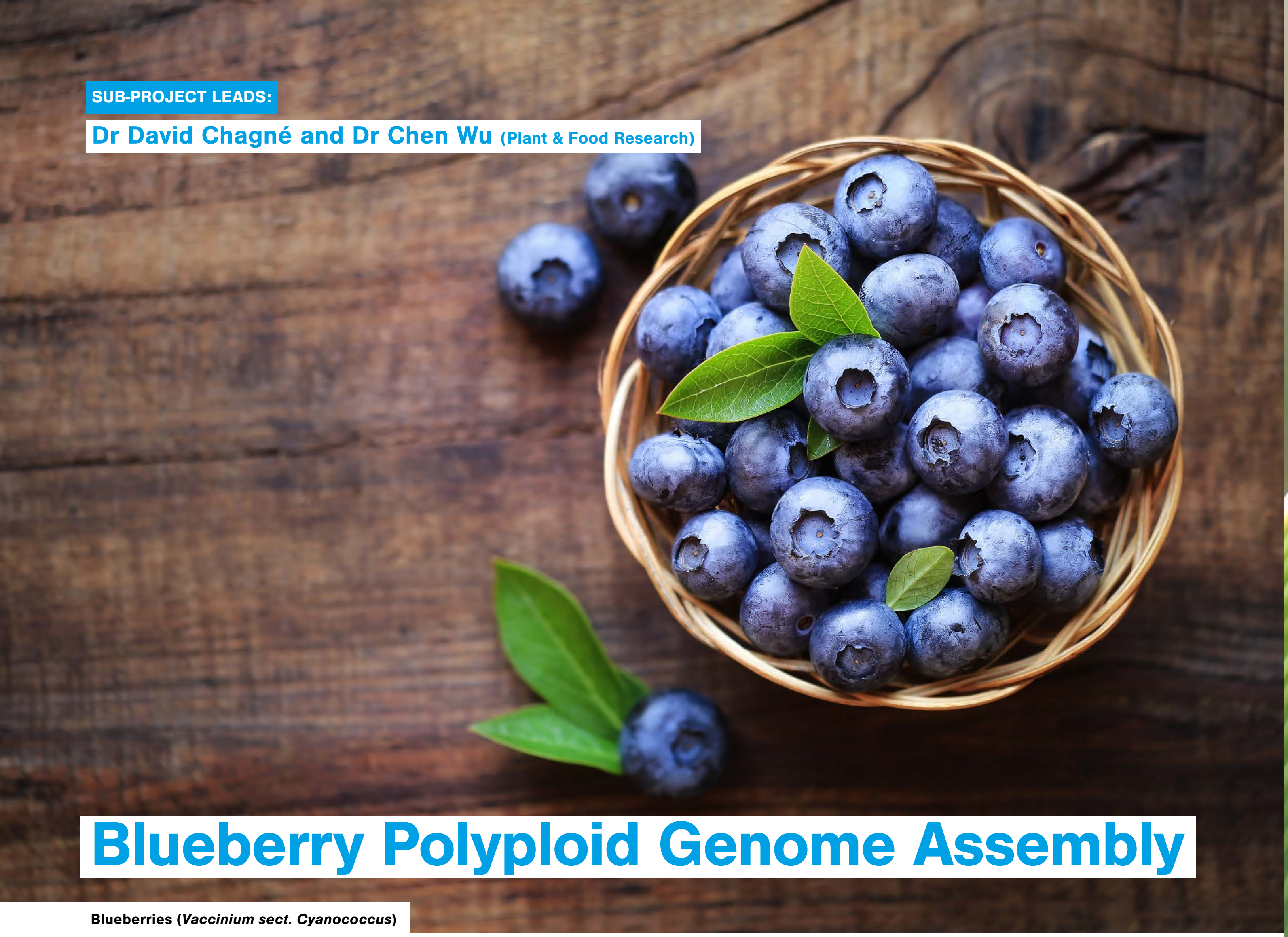
Karaka (*Corynocarpus laevigatus*) leaves

Lower Image Credit: **Ben Ackerley (CC-BY-NC) - iNaturalist**

SUB-PROJECT LEADS:

Dr David Chagné and Dr Chen Wu (Plant & Food Research)

Blueberry Polyploid Genome Assembly



Blueberries (*Vaccinium sect. Cyanococcus*)

Blueberry is a commercially valuable crop species whose fruit also has important antioxidant health-promoting properties.

The Plant & Food Research team works with Turners & Growers (who represent blueberry growers) to ensure this research is fit for real-world impact on their business, blueberry breeders who need genomics solutions to effectively develop new cultivars, and international researchers from the Vaccinium CAP USDA project.

Blueberry plants are autopolyploid and tetraploid. Autopolyploids have more than two sets of chromosomes from the same species and tetraploids have four sets of chromosomes. This year the *Blueberry Polyploid Genome Assembly* sub-project built haplotyped complete autopolyploid genome assemblies using long read sequencing technologies and the trio-binning method, which leverages a parents-offspring relationship.

The high-quality genome of tetraploid blueberry obtained last year was used to resolve the four sets of autotetraploid chromosomes. This enabled the team to identify and characterise an allele of an anthocyanin acyltransferase (*AAT*) gene that is likely the source of the high antioxidant properties of blueberry.

Blueberries (*Vaccinium sect. Cyanococcus*)

PROJECT LEADS:

Dr Manpreet Dhami (Manaaki Whenua – Landcare Research)

Dr Ang McGaughran (University of Waikato)

Invasomics for Better Biosecurity and Invasive Species Management

Queensland Fruit Fly (*Bactrocera tryoni*)

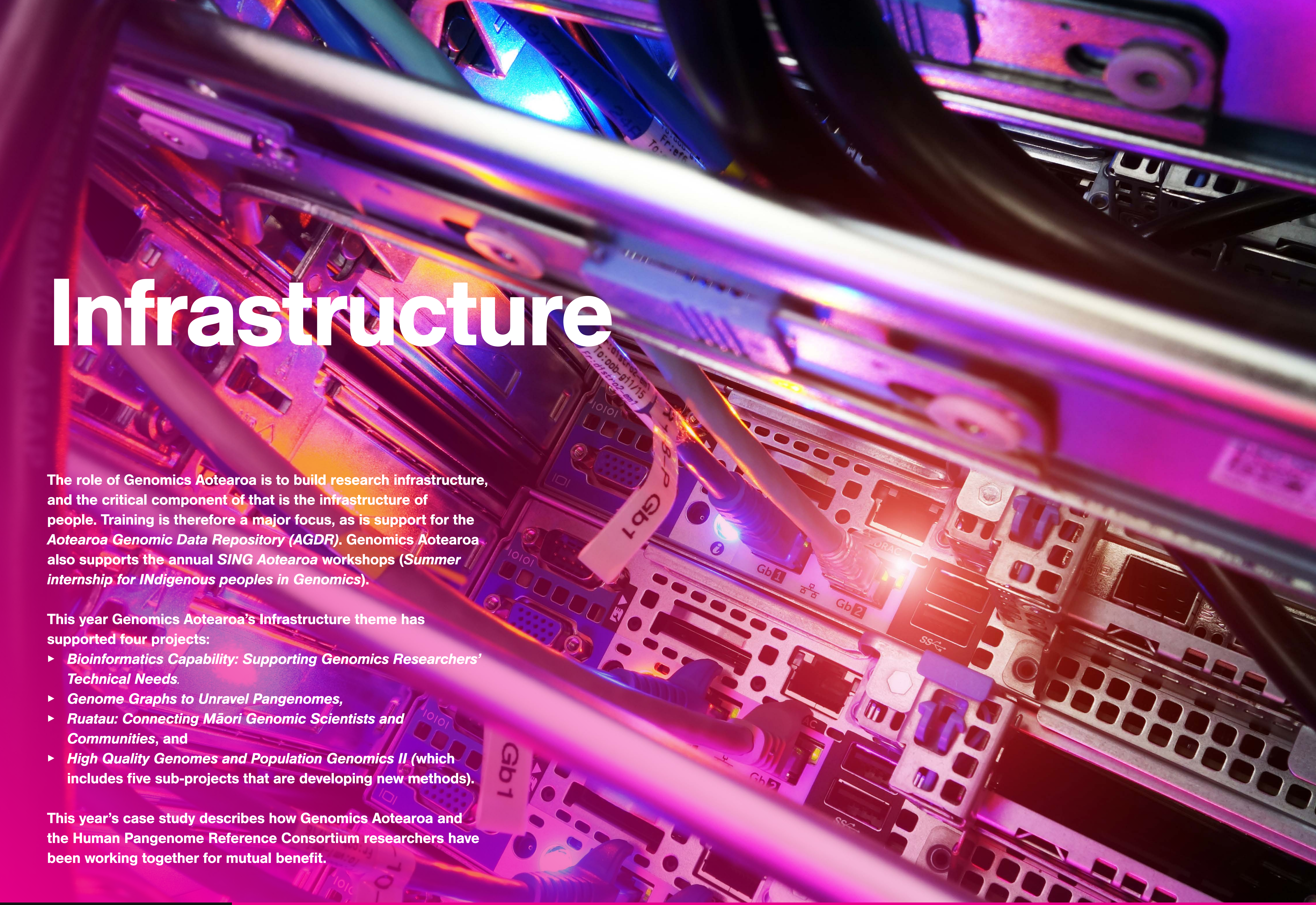
Ever-increasing international trade, mobility, and the uncertainties of climate change all influence the threats that invasive species pose to biodiversity, primary industries, and health in Aotearoa New Zealand.

The recently completed *Invasomics* project aimed to develop models to identify genomic features that underlie successful biological invasions and predict the invasion potential of species that pose a high risk to the country. What was proposed was a validated, generalisable tool that would aid prioritisation of potential new invasive species, whereby stakeholders and end-users could accentuate their risk categorisation pipelines.

Upon completion of the research, the team had identified several barriers to developing the tool and laid the groundwork for future work in this area. Perhaps most importantly, they identified adaptive genomic signals associated with high priority pest species, such as the Queensland fruit fly and the brown marmorated stink bug - resources that could help predict the impacts of these species in changing and new environments.

As well as enhancing relationships with key stakeholders, such as the Ministry for Primary Industries, the project has resulted in six publications in high-ranking journals to date. The researchers plan to continue their unique invasomics work.

Image Credit: **Cinclosoma (CC BY-NC) - iNaturalist**



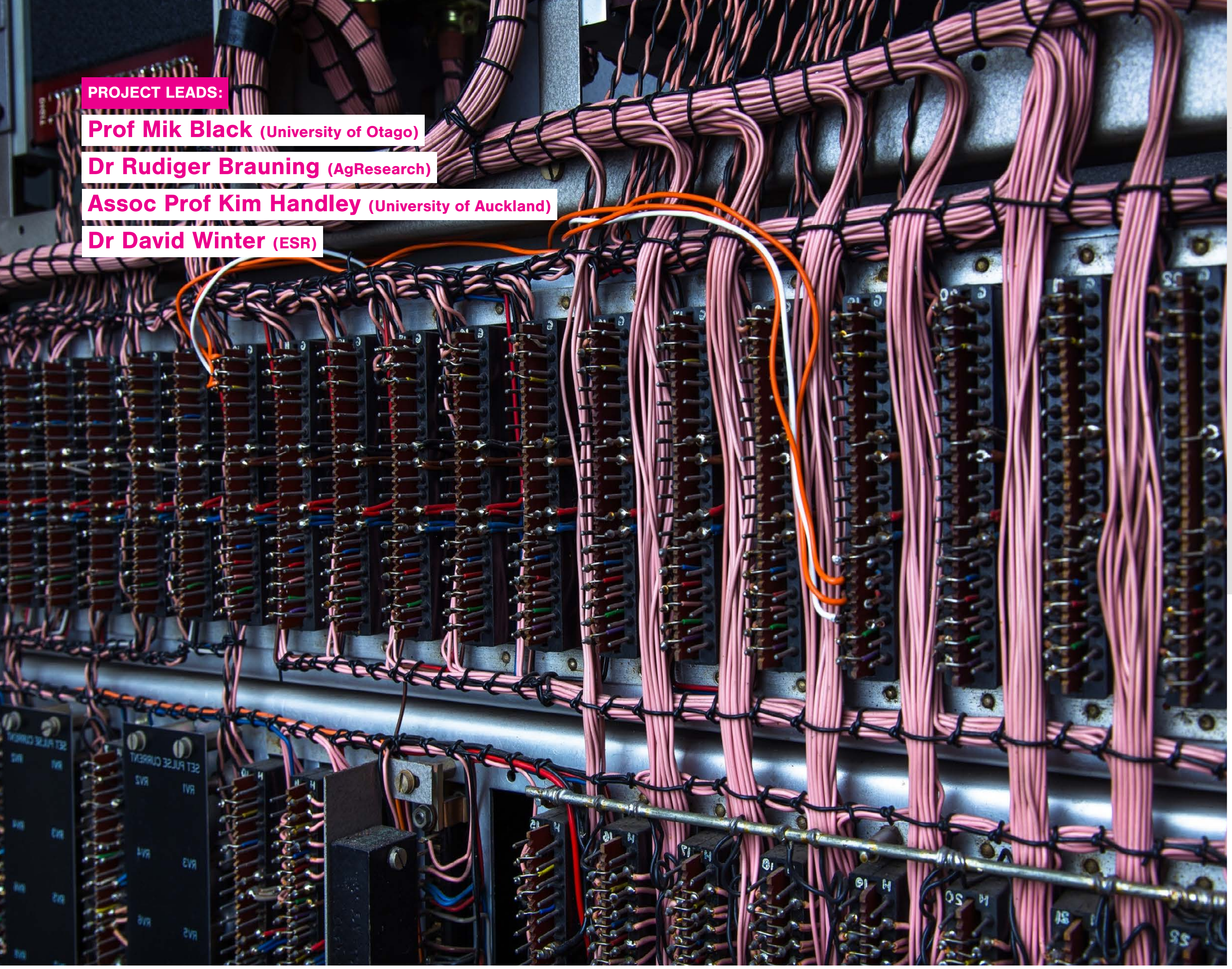
Infrastructure

The role of Genomics Aotearoa is to build research infrastructure, and the critical component of that is the infrastructure of people. Training is therefore a major focus, as is support for the *Aotearoa Genomic Data Repository (AGDR)*. Genomics Aotearoa also supports the annual *SING Aotearoa* workshops (*Summer internship for INdigenous peoples in Genomics*).

This year Genomics Aotearoa's Infrastructure theme has supported four projects:

- *Bioinformatics Capability: Supporting Genomics Researchers' Technical Needs*.
- *Genome Graphs to Unravel Pangenomes*,
- *Ruatau: Connecting Māori Genomic Scientists and Communities*, and
- *High Quality Genomes and Population Genomics II* (which includes five sub-projects that are developing new methods).

This year's case study describes how Genomics Aotearoa and the Human Pangenome Reference Consortium researchers have been working together for mutual benefit.



PROJECT LEADS:

Prof Mik Black (University of Otago)

Dr Rudiger Brauning (AgResearch)

Assoc Prof Kim Handley (University of Auckland)

Dr David Winter (ESR)

Bioinformatics Capability

Supporting Genomics Researchers' Technical Needs

Bioinformatics underpins much of Genomics Aotearoa's work, providing the tools, software and workflows that enable genomic data analysis. It is highly interdisciplinary, combining elements of biology, computer science, mathematics, statistics and data science to extract biological meaning from large and complex data sets.

The research community's bioinformatics needs also require substantial infrastructure: computing resources, data management and training. The *Bioinformatics capability 2* project supports and develops on-going capacity and capability in Aotearoa New Zealand. The project also fulfils the technical requirements to support the cultural infrastructure of Genomics Aotearoa, such as the *AGDR*.

The computing resources provided by NeSI saw researchers across 17 different projects using more than 1.7 million hours of CPU and GPU time in the past 12 months. This is an increase of 800,000 computing hours since last year, indicating the increasing need for these resources.

SUB-PROJECT LEAD:

Prof Mik Black (University of Otago)

Little Bush Moa (*Anomalopteryx didiformis*) bones

Aotearoa Genomic Data Repository

The *AGDR* provides a secure data facility for genomic and genetic data from taonga species in a way that supports the principles of Māori data sovereignty. The *AGDR* has been implemented in conjunction with NeSI and aligns with the *Te Mata Ira* and *Te Nohonga Kaitiaki Guidelines.*

The *AGDR* helps organisations and individuals exercise their kaitiakitanga over taonga species, while facilitating controlled data management and sharing.

Seven access requests were received this year:

- three for mānuka. Two were approved and one lapsed due to non-response from requester.
- one for *Venenivibrio*, an endemic bacterial genus found in the Taupō Volcanic Zone, which was approved.
- one for kanakana, which is at the stage of consultation with kaitiaki.
- one for little bush moa, also at the consultation stage.
- one for virome genomic data from geckos and skinks, which is awaiting more information from the requester.

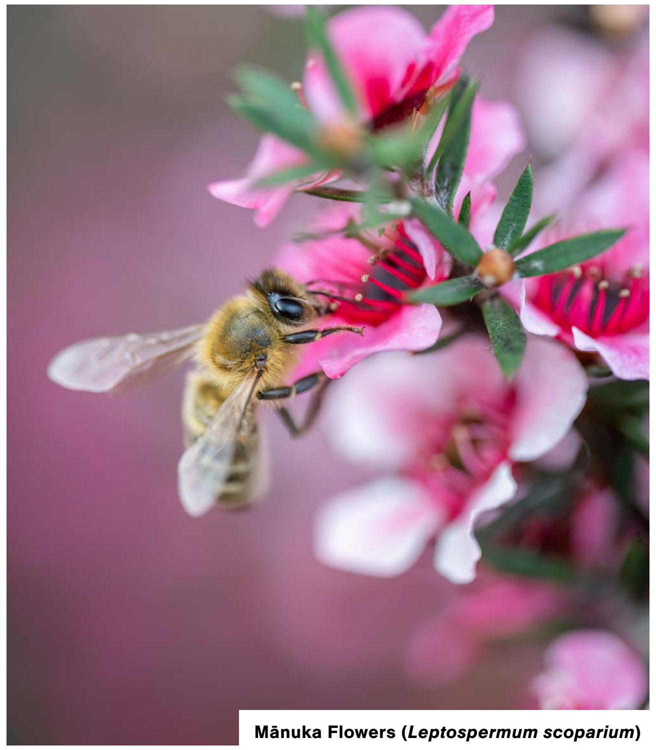
Thirteen datasets were added to the repository over the past year: little bush moa, kuku (two datasets), eDNA samples including lake water, soil (two datasets), seawater, virome samples from skinks and geckos, rewarewa, snapper, kiwi infectome, Hector's and Maui dolphin, and haku.

We acknowledge the complex issues surrounding Māori and Indigenous sovereignty over genetic data, and work to overcome these challenges in partnership and with commitment to Te Tiriti.

Our Advisory Board, who oversee the *AGDR*, continues to provide expert guidance and advice and had a productive first in-person meeting with members of the Genomics Aotearoa and NeSI teams in April 2024.

The *AGDR* Advisory Board is comprised of:

- **Nick Roskruge** (Te Ātiawa whānui, Ngāti Tama-āriki, Ngāti Porou) (Chair)
- **Wayne Blissett** (Ngāpuhi)
- **Jan Hania** (Ngāti Tuwharetoa, Ngāti Raukawa-te-au-ki-te-Tonga, Ngāti Huia, Te Ātiawa, Ngāti Tama)
- **Taoho Patuawa** (Te Roroa, Ngāti Whatua, Ngāpuhi)
- **Hema Wihongi** (Ngāpuhi, Te Rarawa)



Mānuka Flowers (*Leptospermum scoparium*)

Upper Image Credit: **Auckland War Memorial Museum** (CC by 4.0)

SUB-PROJECT LEADS:

Dr Tyler McInnes (University of Otago)

Dr Jian Sheng Boey (University of Auckland/NeSI)

Bioinformatics Training

Over the past year Dr Tyler McInnes and Dr Jian Sheng Boey have continued to manage the Genomics Aotearoa component of the joint Genomics Aotearoa/NeSI training programme.

The training programme is a portfolio of workshops which range in duration from one day to one week and run either online or in person. Workshops are taught by subject matter experts and assisted by volunteers from the research community (with volunteers themselves gaining valuable teaching and community service). Workshops are written by and with the help of bioinformatics and genomics researchers from the ten institutions that make up Genomics Aotearoa together with our international collaborators.

Early September 2024 will mark the 100th workshop hosted since the training programme launched six years ago. In that time over 2,000 participants from across Aotearoa New Zealand have attended workshops that cater to everyone from absolute beginner to specialist. Interest in training workshops continues to grow with an increasing demand for bioinformatics skills across the biological sciences and beyond. This year 582 participants have attended 28 workshops offered by the training programme.

Genomics Aotearoa also holds internal training to promote the growth and development of our early career researchers. The Genomics Aotearoa Annual Meeting hosted training for specialised workflow-management software for 11 researchers, and in May, 15 early career researchers assembled in Wellington for two days of workshops which included mental health training, strategic career planning, and bioinformatics tool kits.

CASE STUDY:

Sharing learnings with Human Pangenome Reference Consortium researchers

In July 2023 Genomics Aotearoa and NeSI hosted world leaders in genomics to share their experiences developing the human pangenome reference, released in May 2023.

Julian Lucas, Senior Bioinformatics Systems Analyst at UCSC Genomics Institute, held a masterclass on human genome assembly using long-read sequencing. Julian was supported by Brandon Pickett (NIH/NHGRI Bethesda MD) and Linelle Abueg (The Rockefeller University).

Dr Karen Miga, Director of the Reference Production Center for the HPRC at UCSC, presented a Genomics Aotearoa Friday seminar on Expanding Studies of Global Genomic Diversity with Complete, Telomere-to-Telomere (T2T) Assemblies.

Dr Miga, one of Time's 100 Most Influential People for 2022, co-founded the Telomere-to-Telomere (T2T) Consortium in 2012. The consortium is an open, community-based effort to generate the first complete human genome assembly. This work laid the foundation for use of the T2T assembly methods in the generation of the first human pangenome reference.

As well as sharing techniques, Dr Miga discussed appropriate engagement with Indigenous communities with the He Kākano: the Aotearoa Māori Variome team and is now using this knowledge to help develop her own Indigenous-informed practice.

“Karen Miga and her team came here to discuss working alongside Indigenous communities. It was a wonderful demonstration of how engaging with Māori communities gives us all opportunities to strive for better research,” said Dr Ludovic Dutoit, Lecturer in the Department of Zoology at the University of Otago.

Ludovic learnt tools and approaches that several students in his team are now using. “It can be hard to keep up with all the new techniques, understand which ones are worthwhile, and which are achievable. This workshop was an amazing opportunity to learn from the best and to incorporate new tools into our research. We are now using Hi-C data to help assemble the sex chromosomes of a mokomoko (gecko) and to assemble a high-quality reference genome to support gecko conservation programmes.”

Genomics Aotearoa training manager Dr Tyler McInnes said it was exciting for local researchers to be learning from scientists leading the world in pangenome research “The T2T reference genome is a leap forward in the field of human genomics, and equally important is the development of the methodology used to build this new resource.”

The techniques have been taught again in the Otago Bioinformatics Spring School 2023 and as a stand-alone Genomics Aotearoa workshop.

Researchers are now adapting and refining methods to develop resources in evolutionary genomics, conservation genomics, aquaculture, and microbiological genomics.

Image Credit: **UC Santa Cruz - Karen Miga**

PROJECT LEADS:

Prof Mik Black (University of Otago)

Dr Joep de Ligt (ESR)

Genome Graphs to Unravel Pangenomes

Pangenome approaches are used to catalogue the entire genomic variation in a population, or an entire species. Graph-based analyses can improve the detection of genomic variation and are increasingly being used internationally, as in several Genomics Aotearoa projects.

This project continues to explore the use of genome graphs for pangenome construction, and for genomewide variant analysis using graph-based methodology. There are two strands to the research, encompassing microbial and human genomics.

The microbial research component was completed by Zoe Yang and Joep de Ligt at ESR, with a paper describing the analysis using data generated by Oxford Nanopore sequencing. A workshop on genome graph construction for microbial genomes was delivered, and the content is freely available on GitHub. The content for a second, more advanced workshop session on simulating sequencing data for alignment to genome graphs is also available on GitHub.

Work is continuing at the University of Otago on the human genomics component of the project, with a human pangenome workshop scheduled for later this year.. Material for an advanced human pangenomics workshop is in development. Professor Mik Black has incorporated genome graph learning into the "GENE360 – Extension Topics and Research Skills" course in third year Genetics at the University of Otago.

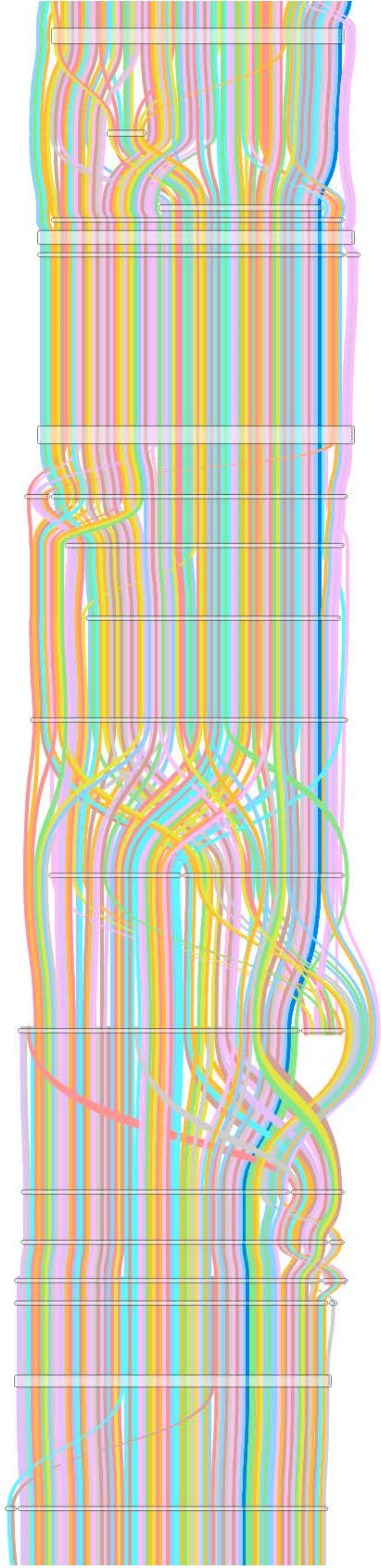


Figure: A "sequence tube map" visualisation of the draft human pangenome, from a small region of Chromosome 5. Each coloured line represents one copy of an individual chromosome, with the path taken through the nodes of the graph (the horizontal bars) defining the exact genomic sequence for that haplotype.

PROJECT LEADS:

Dr Alana Alexander and Dr Catherine Collins (University of Otago)

Dr Simon Hills (Massey University)

Ruatau

Connecting Māori Genomic Scientists and Communities

Empowering Māori communities to make informed decisions about genomics for hauora of people and kaitiakitanga of taonga species is vital. Kaipūtaiao Māori (Māori scientists) are uniquely placed to understand community perspectives, priorities, and concerns, however, Māori are under-represented in genomics research. Māori genomics researchers who grew up in Te Ao Pākehā may feel that they need more grounding in Te Ao Māori prior to establishing relationships with hapori Māori who are interested in genomics research. *Ruatau* bridges these gaps.

Ruatau is developing processes and resources to increase the capability of Māori communities and Māori scientists to mutually contribute to genomic mātauranga aspirations. The project supports unique whānau-led research, culturally informed genomics research, and Māori participation in research, culminating in a network of Māori with interests in genomics.

All project leads and advisors are Māori. *Ruatau* supports the capability and capacity of these researchers, together with the development of community leaders in genomics.

Following on from an initial wānanga held with Kāti Huirapa ki Puketeraki last year, a wānanga this year focused on the outcomes of genomic science and data management.

The wānanga led to the development of a "genomics tono template", which includes guided questions to facilitate conversations among researchers and hapori. Puketeraki Marae in Karitane, Otago, will pilot the template during interactions with scientists, with plans to share with other communities and scale up as a "scientific tono template".

The most exciting outcome of the past year was the enthusiasm and gratitude of Puketeraki for the tono template, which would not have been developed without the support of MBIE and the *Ruatau* project.

PROJECT LEAD:
Assoc Prof Maui Hudson (University of Waikato)

SING Aotearoa
Mentoring Emerging Māori Genomics Researchers

Genomics research promises a range of benefits for Māori. The Summer Internship for INdigenous Genomics (SING) Aotearoa brings together pakeke and tauira Māori to discover genomics and bioinformatics and explore the ethical and cultural issues around genomics research.

Genomics Aotearoa is proud to have financed and enabled SING Aotearoa over the past six years.

This year, for the first time, the annual event took place within a community setting, rather than a tertiary institution. *SING 2024 Te Tai Tokerau* was held in Whangārei with daily excursions throughout rohe o Ngāti Hine.

Several past and current Genomics Aotearoa researchers participated in the event including Stephen Robertson and Phillip Wilcox from Ōtākou Whakaihu Waka and Maui Hudson from Te Whare Wānanga o Waikato, along with many other kaipūtaiao Māori (Māori scientists) and esteemed speakers. It was a privilege for the group to have Cheyenne Reuben-Thomas of SING Canada as an international manuhiri and guest speaker.

SING 2024 Te Tai Tokerau could not have taken place without the kaimahi support from Te Kotahi Research Institute, Waipapa Taumata Rau (University of Auckland), Ōtākou Whakaihu Waka (University of Otago), and Te Whare Wānanga o Awanuiarangi.

Fourteen new tauira from rohe across Aotearoa New Zealand attended the two-day wānanga. The event delivered a comprehensive introduction to genetics and genomics from an Indigenous perspective, offering engaging wānanga sessions and diverse interactions on various topics.

Learning was supported by hands-on experiences of genetic sequencing, mātauranga Māori, and whakawhānaungatanga (connecting). Feedback from tauira was overwhelmingly positive.

The SING Aotearoa programme nurtures hononga (connections) and camaraderie (whānaungatanga), providing a haven of whakaruruhau (protection) for Māori who may feel marginalised in a field that can alienate Indigenous perspectives.

SING Aotearoa has established a platform for Māori to engage with genomics in a culturally respectful and secure environment. Its success underscores the need to promote diversity and inclusivity in scientific endeavours and serves as a model for future initiatives.

PROJECT LEADS:

Prof Thomas Buckley (Manaaki Whenua – Landcare Research)
Dr Shannon Clarke (AgResearch)
Dr David Chagné (Plant & Food Research)
Assoc Prof Anna Santure (University of Auckland)

High Quality Genomes and Population Genomics

Common Myna (*Acridotheres tristis*)

This year, the *High Quality Genomes and Population Genomics* project supported five infrastructure sub-projects:

- *New Chromatin Conformation Capture Methods for Scaffolding Genomes*
- *Characterising Epistasis with High Density Single Nucleotide Polymorphism Chip Data*
- *Methods and Tools to Improve Reference Genomes for Ryegrass and Greenshell Mussel*
- *BEAKERtaxa: Natural Language Processing Methods to Identify Species from DNA Kmers*
- *Combining Structural Variation and SNP Variants for Genomic Prediction*

These projects are all developing, customising and streamlining methods to resolve some of the more challenging genomes found in our natural and production systems.

SUB-PROJECT LEADS:

Dr David Chagné and Dr Elena Hilario (Plant & Food Research)

New Chromatin Conformation Capture Methods for Scaffolding Genomes

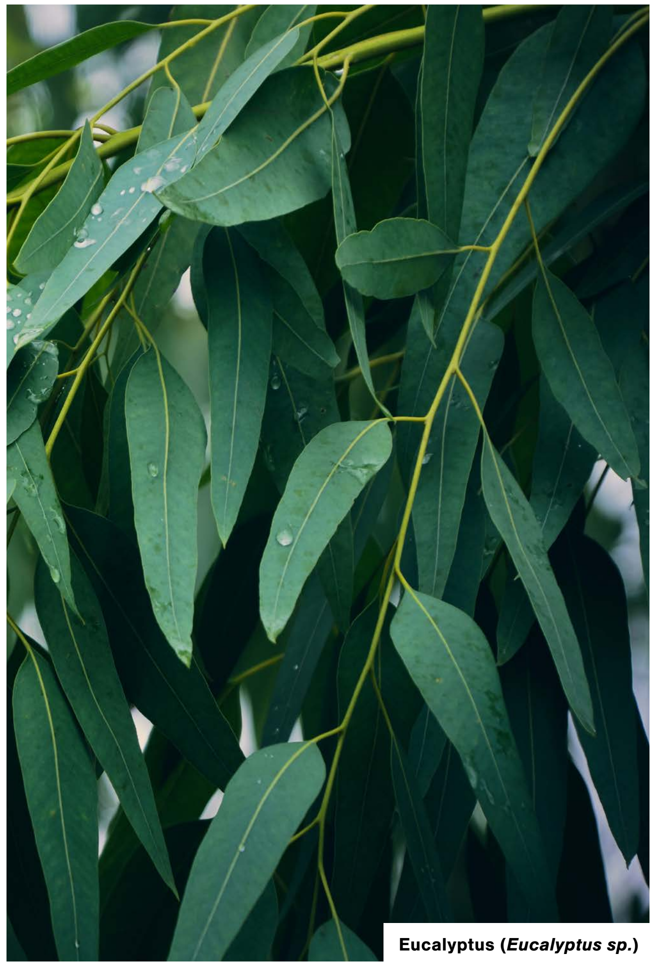
Chromosome conformation capture (CCC) techniques are a set of methods used to analyse the spatial organisation of chromatin (the mixture of DNA and proteins that make up chromosomes) in a cell.

Hi-C sequencing is a high-throughput CCC technique that helps researchers construct genome assemblies. Although commercial solutions are available for Hi-C techniques, for species with complex genomic architecture these often do not work or need extensive optimisation.

Based on the optimised protocols developed by the team last year, this year Hi-C libraries were produced for myna bird, peka peka, several different polyploid strains of kiwifruit, karaka, Eucalyptus, grape and Wahlenbergia. Protocols are currently being optimised for gecko, skink, salmon, relatives of karaka and for the mānuka microbiome.

Protocols are available for Hi-C library preparation using DNAse fragmentation, plant nuclear genomic DNA preparation and nuclei enrichment for tricky Hi-C samples. Resources for checking protocols are freely available on GitHub.

The team is grateful for the continuing collaboration of Ashley Jones from the Australian National University, Canberra.



Eucalyptus (*Eucalyptus sp.*)

SUB-PROJECT LEAD:

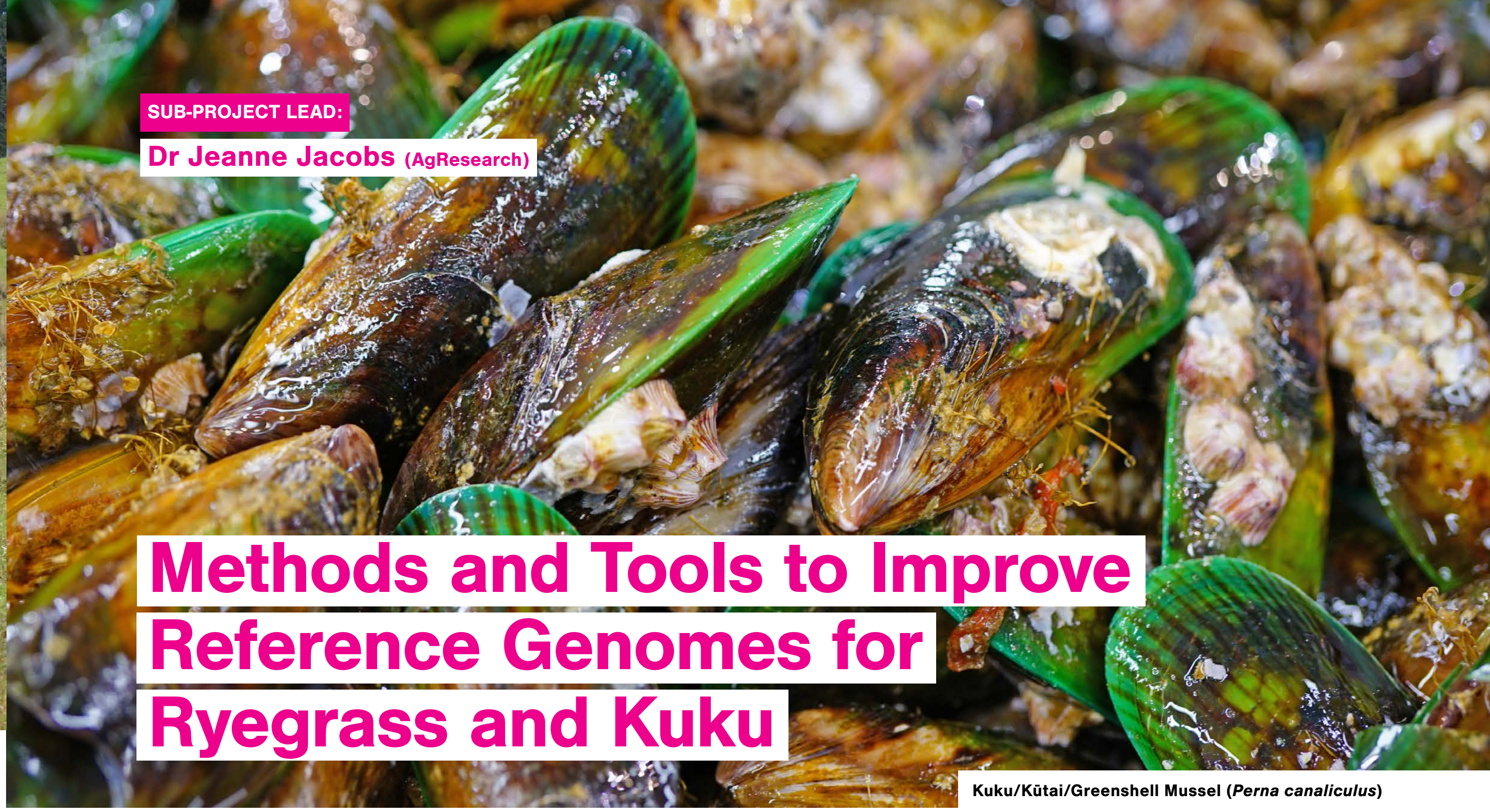
Dr Michael Lee (University of Otago)

Characterising Epistasis with High Density Single Nucleotide Polymorphism Chip Data

Primary producers require a better understanding of genomic data to better predict genetic merit and increase the rate of genetic improvement. Beef + Lamb NZ Genetics is a key collaborator on this sub-project, which uses sheep as an exemplar.

Epistasis is likely to account for some of the phenotypic variation seen within a population but is poorly understood. We used block partitioning of matrices to calculate the pairwise linkage disequilibrium (LD) of markers on a high density ovine (sheep) genotyping chip. About 200 billion pairwise comparisons, based on data from about 28,000 animals, allowed us to identify markers displaying interchromosomal LD implying that genes may be interacting across chromosomes (epistasis). A manuscript in preparation shows that the integration of SNPs imputed up to WGS in GWAS better captures genetic differences for several traits important for the sheep industry.

Completed this year, the study's results dovetail into the sub-project on genomic variation in the sheep genome described on page 77. The epistatic variants that were discovered were added to the updated ovine genotyping array (chip). Understanding this variation will help to validate the genetic interactions in a wider population alongside identifying the biological constraints that give rise to the variations.



SUB-PROJECT LEAD:

Dr Jeanne Jacobs (AgResearch)

Methods and Tools to Improve Reference Genomes for Ryegrass and Kuku

Kuku/Kūtai/Greenshell Mussel (*Perna canaliculus*)

Ryegrass is an important livestock fodder in Aotearoa New Zealand, particularly for dairy cows and grazing cattle. Ensuring quality fodder is essential for maximising productivity.

Kuku or kūtai (greenshell mussel) are an important aquaculture species, and a taonga. Both kuku and perennial ryegrass have highly heterozygous genomes, which is yet another challenge that complicates genome assembly. This sub-project is developing methods and tools for improving reference genomes for these species.

For ryegrass, this year RNA sequencing (Illumina) was undertaken for three tissue-types (leaf, root, flowerheads) and eight lines of ryegrass (two parents and six F1 progeny). The same RNA samples are also being sequenced at Bragato Research Institute using Oxford Nanopore sequencing, with the support of a PromethION development grant. This technology yields full length sequences of RNA, improving the annotation of the draft genome. Data analyses are planned next.

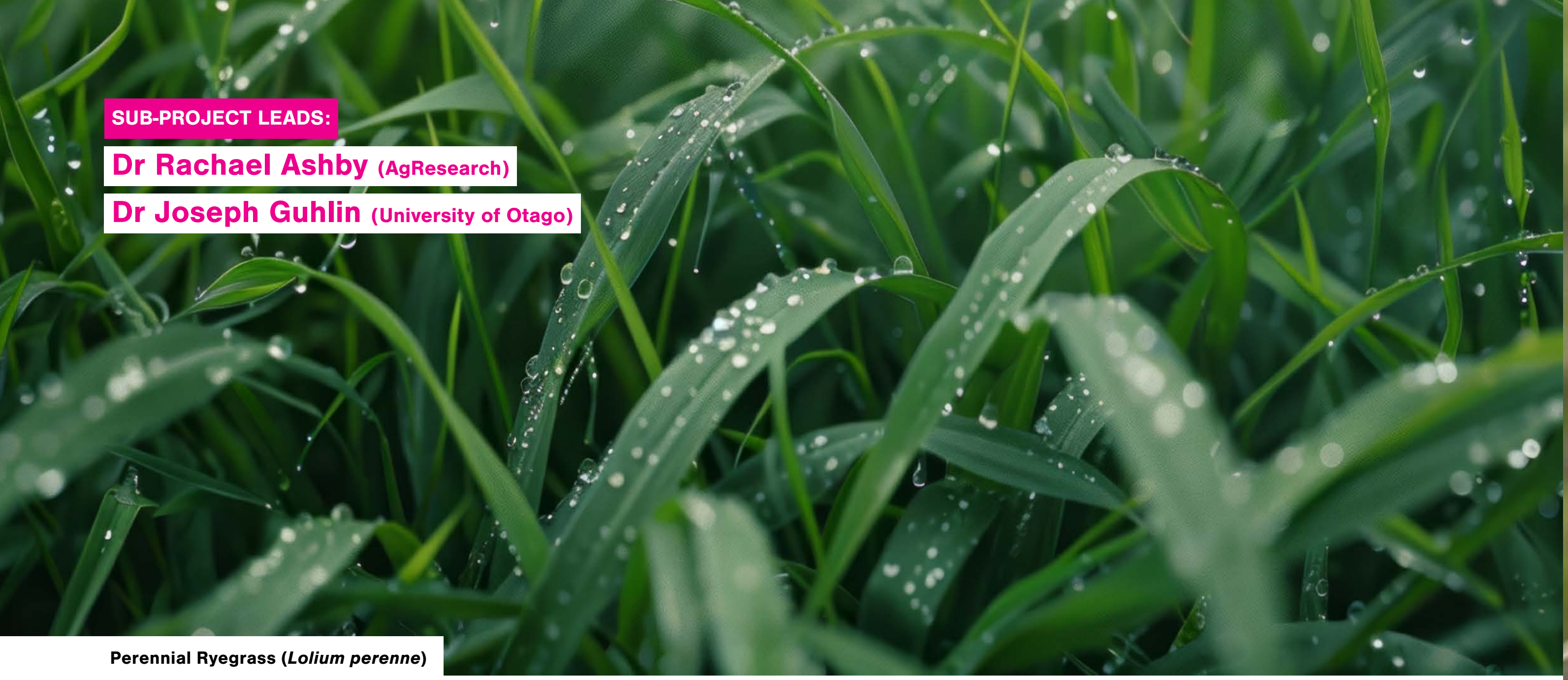
An improved genome assembly has been produced for kuku utilising technology within Aotearoa New Zealand, through this sub-project our researchers and partners are working through the challenges of annotating this genome.

Perennial Ryegrass (*Lolium perenne*)

SUB-PROJECT LEADS:

Dr Rachael Ashby (AgResearch)

Dr Joseph Guhlin (University of Otago)



Perennial Ryegrass (*Lolium perenne*)

BEAKERtaxa

Natural Language Processing Methods to Identify Species from DNA Kmers

The BEAKERtaxa sub-project investigates if natural language processing methods would assist bioinformaticians and researchers to identify species from short DNA sequences that are used for genome analysis (DNA kmers). The focal species was ryegrass, together with its symbiotic *Epichloë festucae* endophytes.

Epichloë festucae on Perennial Ryegrass (*Lolium perenne*)

Image Credit: **Walter Wimmer (CC-BY-NC) - iNaturalist**

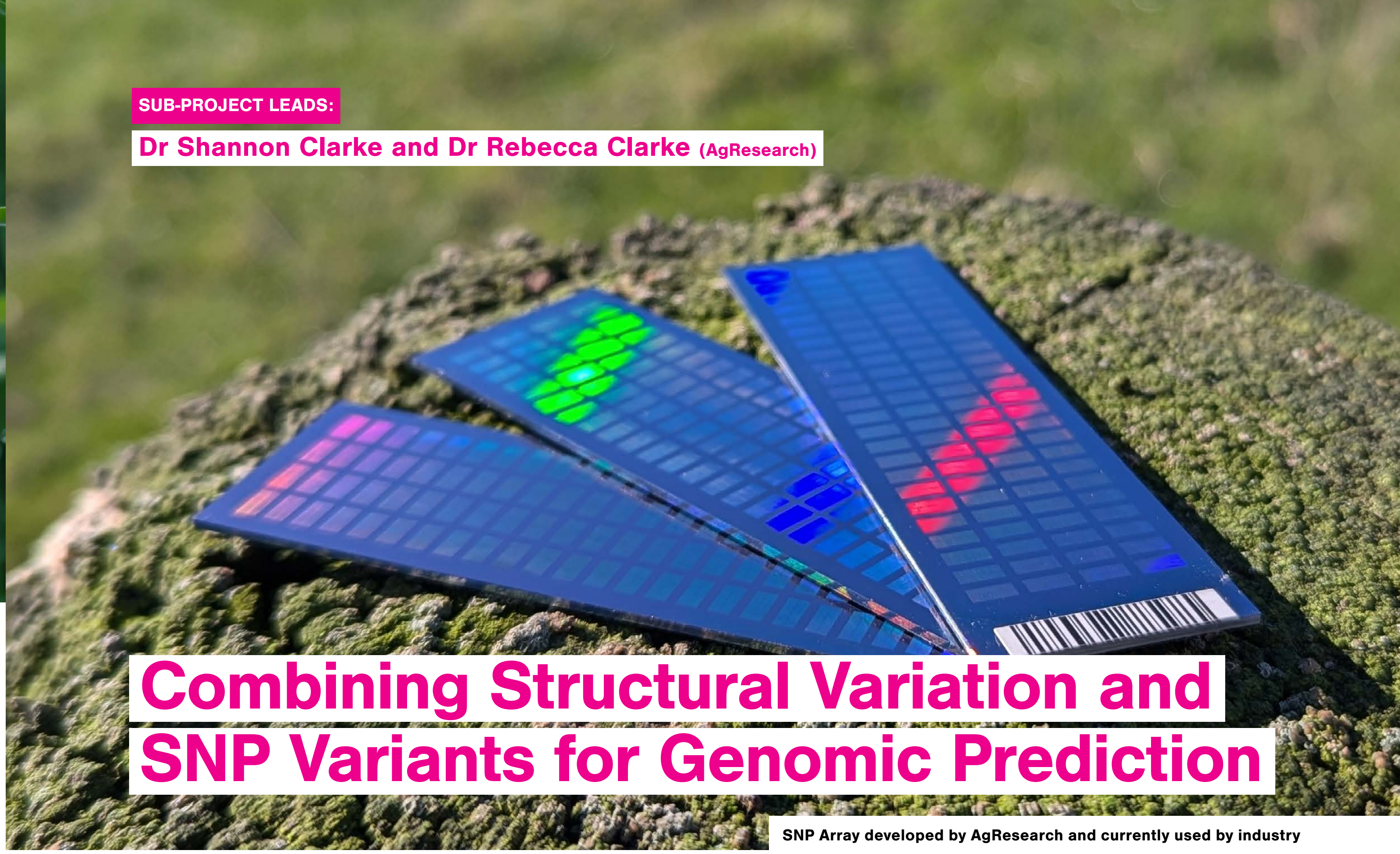
The BEAKERtaxa sub-project applies large-language models (LLM) and natural language processing to species identification of short DNA sequences used for genome analysis. Using a model similar to that which powers ChatGPT, we can treat DNA as short sequences of "words" or "kmers" and allow the model to identify species from sequence similarity, as is the current practice, and patterns viewed within the data. This approach is accomplished using a transformer model with multiple layers and attention models but using a novel input mechanism that considers the relatedness of DNA sequences, an innovation not currently used in other models.

We are working with artificial microbial communities, generating our own, and testing with novel data; we are utilising ryegrass and its symbiotic *Epichloë festucae* endophytes. Selecting, growing, and sequencing five perennial ryegrass cultivars with three *Epichloë festucae* symbiotic endophytes was completed last year, with the refinement of benchmarking with this exemplar dataset almost complete.

This year, a comprehensive review of current taxonomic binning methods was successfully completed, marking a significant step forward. The creation of datasets for testing and benchmarking is currently underway, with the transition from simulations to real-world datasets being a major milestone. Additionally, tools designed to facilitate data intake by the LLM have been completed, with a manuscript in preparation. The model has also been tested and trained on various tasks and performs well. The following steps will be to bring all of the components together and train the model. The final steps will be to bring all of the components together and train the model. This is currently underway and due for completion in November 2024.

SUB-PROJECT LEADS:

Dr Shannon Clarke and Dr Rebecca Clarke (AgResearch)



Combining Structural Variation and SNP Variants for Genomic Prediction

SNP Array developed by AgResearch and currently used by industry

The national and international sheep research and breeding communities need new genotyping tools to improve genomic prediction of desired traits.

This sub-project uses existing resources to investigate methods for the detection of structural variation and genomic prediction. Genomic resources from pangenome assembly, copy number variation inclusion on SNP array platforms, and long read adaptive sequencing were investigated last year.

This year the team continued the use of Oxford Nanopore long read sequences for adaptive sequencing. The team have shown that multiplexing of samples can be done in conjunction with adaptive sequencing, but while this tool is useful for discovery and validation, it is not ready for industry to use. Increasing the number of samples in one multiplexing run would be a more cost-effective option for the industry.

The team also investigated enrichment of both host and parasite DNA from faecal samples and found that this technique is effective for different sample types. Adaptive sampling targeting the ITS2 region may also provide better sequencing enrichment of parasite DNA from faecal samples.

Finally, several software packages to identify copy number variations (CNVs) from SNP Chip data have been evaluated. Manuscripts are in preparation to describe the inclusion of SNPs that span the CNVs on the next Ovine SNP array.

Various Species of New Zealand Sheep at AgResearch

Engagement

Genomics Aotearoa’s engagement and outreach activities have continued to grow this year. Our genomics exhibition *Genome: Science of Life* originally staged at Tūhura Otago Museum, has been touring various parts of the country with the museum’s Outreach team.

In addition, four videos explaining genomics solutions have been produced in a series entitled “*What If...*”.

Our annual meeting provided opportunities for networking among the research community and we were delighted to welcome our International Advisory Panel to the event.

We offered several strategic grants this year, and our early career researcher scholarships are another new initiative. We also continued our interactions with the media, our fortnightly *Friday Seminar Series* with over 980 attendees across the year, our monthly newsletters, and public engagement via our YouTube channel.

Genomics Aotearoa Annual Meeting 2023

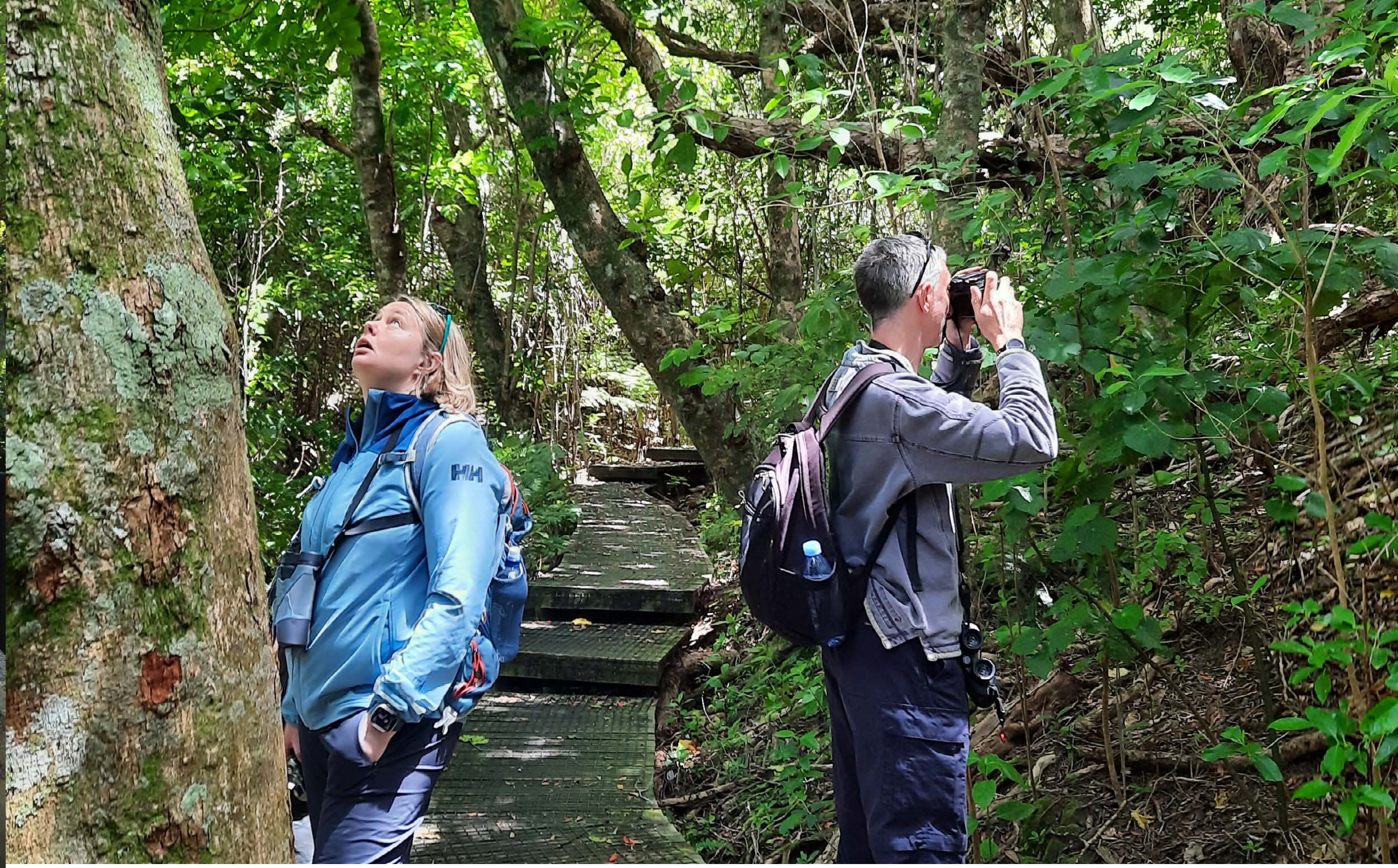
The 2023 Genomics Aotearoa Annual Meeting took place in Dunedin from 21-22 November, with 26 speakers and more than 100 people attending. The opening remarks from Board chair William Rolleston were followed by two days of lively debate and networking, capped off by a shared session with the MapNet Conference on the second afternoon.

Mik Black and Tracey Godfery highlighted the work done in the previous year across Genomics Aotearoa's research programmes, including an update on projects funded through the Indigenous Genomics Platform, while Jayashree Panjabi gave an overview of educational outreach activities. A major topic of discussion was the future direction of genomics in Aotearoa New Zealand, highlighted in presentations by Joep de Ligt (formerly ESR), Mike Bunce (Chief Science Advisor, DOC) and Peter Dearden.

Joep talked about the cost-benefit of genomic precision medicine and why this tool is not yet broadly used in Aotearoa New Zealand. Joep felt that while the country now has good technical capability, we need to better train clinical geneticists, raise awareness of the legal issues surrounding genetic testing, and increase research and engagement with Indigenous communities.

Mike suggested that genomics researchers needed to work together as "team genetics" and that embedding genomics in government decision making was critical. Like Joep, Mike highlighted the need for legislation around genetic testing and emphasised the importance of communicating research effectively.

Peter reflected that the past six years of genomics projects, training and outreach have been significant, but genomics research has barely begun responding to the key challenges facing our nation. He cited climate change, and the urgent need to develop genomic solutions that will make a difference to the country. Peter concluded that Genomics Aotearoa's mission was far from over, and that future work needed a fresh emphasis on building pathways to implementation and impact.

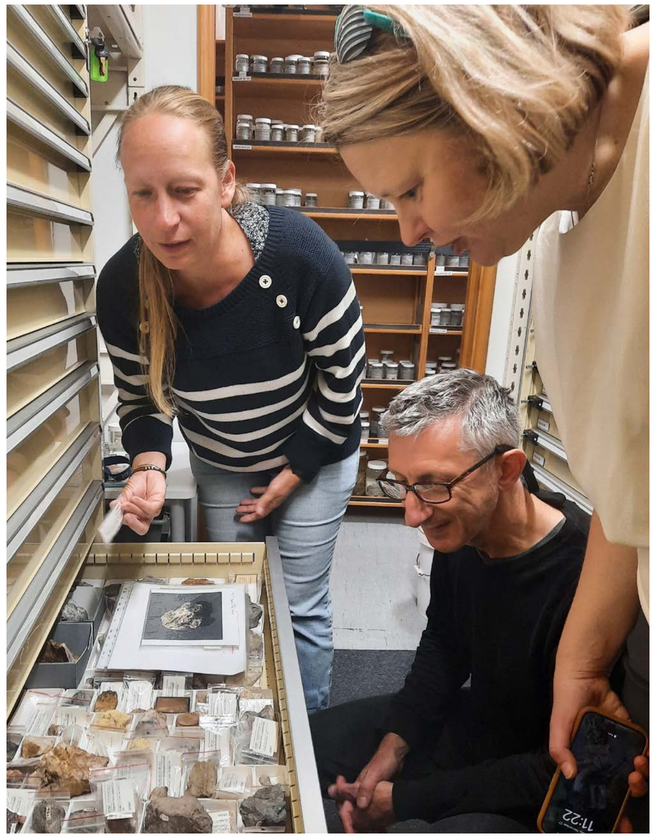


International Advisory Panel Tour of New Zealand

One highlight of the Annual Meeting was the attendance of all three members of Genomics Aotearoa's International Advisory Panel: Nick Goldman (EMBL, UK), Andrew Gilbert (BioPlatforms, Australia) and Elinor Karlsson (the Broad Institute, Cambridge, Massachusetts). The group all shared insights into their own genomics work.

After the meeting Nick and Elinor enjoyed a short tour across Aotearoa New Zealand accompanied by Operations Manager Jayashree Panjabi. They visited researchers and managers at Plant & Food Research, the Cawthron Institute and Wakatū Incorporation in Nelson, and Plant & Food Research in Auckland. They also enjoyed a trip to Tiritiri Matangi Island (arguably the largest and most impressive natural laboratory in the country) and a back-of-house tour of Auckland Museum.

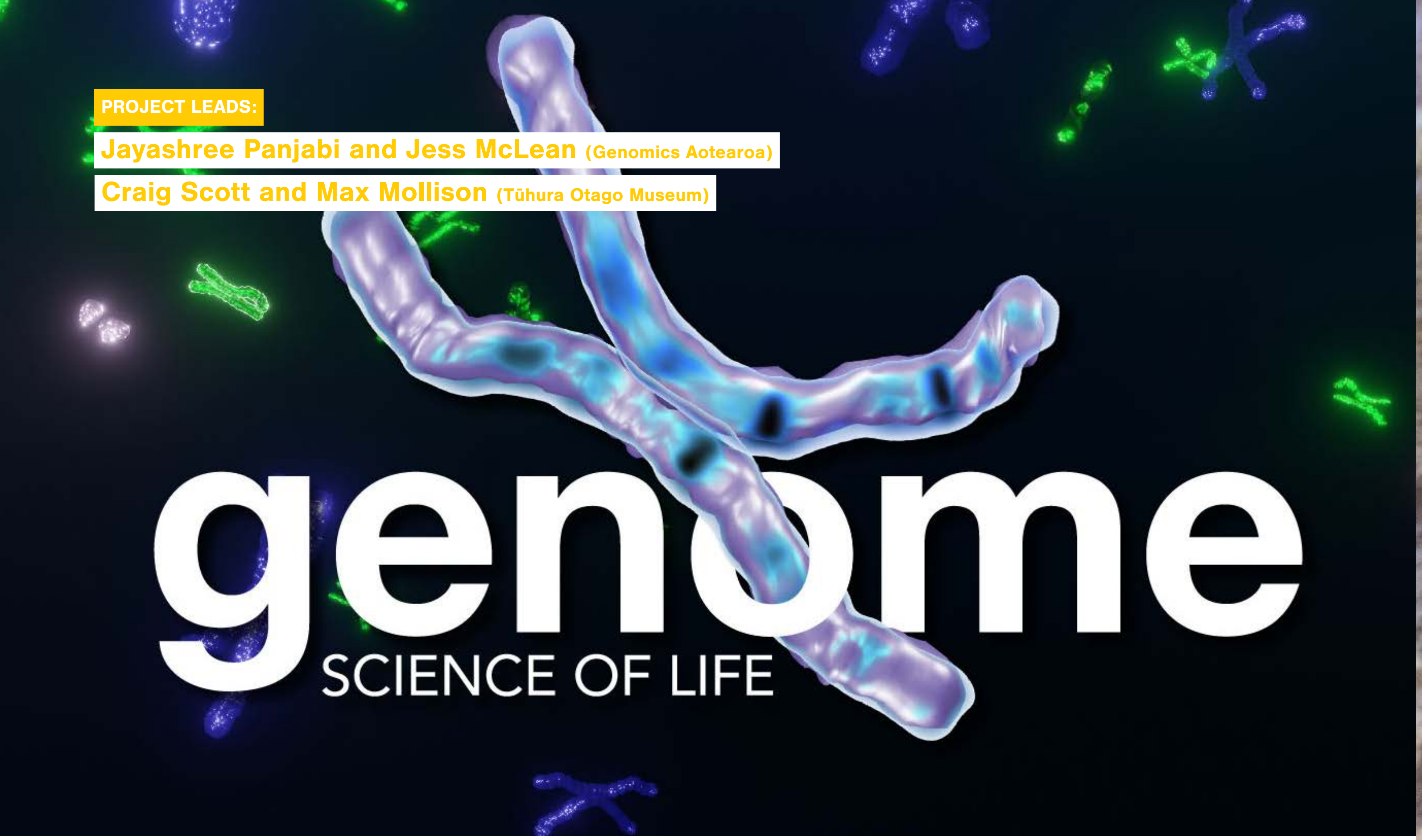
We are extremely grateful to Nick, Andrew and Elinor for their service to Genomics Aotearoa over the past six years, and hope for a continued association.



PROJECT LEADS:

Jayashree Panjabi and Jess McLean (Genomics Aotearoa)

Craig Scott and Max Mollison (Tūhura Otago Museum)



Genome: Science of Life

Update on Touring

Genomics Aotearoa's *Genome: Science of Life* digital showcase started its community engagement journey at the New Zealand International Science Festival's busy central Dunedin hub in June 2023. Hundreds of visitors were able to view the showcase.

The showcase then went to the University of Otago's Chiasma event in July 2023. Chiasma aims to connect students with the business community to highlight potential career paths. The showcase illustrated the varied applications of genomics.

Then it was off to Aotearoa's largest science conference, the Queenstown Research Week in August 2023. The showcase was displayed in a breakout area, which enabled visitors to relax and absorb the content. The conference organisers were positive about the showcase's vibrant contribution to the conference.

In September 2023, the opportunity arose to share the showcase with youth at the Edgar Centre in Dunedin, as part of Otago Polyfest. Thousands of tamariki and rangatahi viewed the showcase.

Genome: Science of Life was also displayed at the Genomics Aotearoa annual meeting in November.

The exhibition then headed to the Motueka District Museum. In parallel, a digital clone was displayed in Lab-in-a-Box at ASB Polyfest in March 2024, and then at MOTAT during their busy April school holidays. There it contributed to a programme on *Using science to see the unseen*.

Genome: Science of Life went to Parliament's Banquet Hall in late May 2024 as one of several exhibitions at *Science showcases – taking science to the country*, hosted by Green Party MP Scott Willis. More than 100 guests discussed the importance of public information and engagement for the future application of genomics technologies.

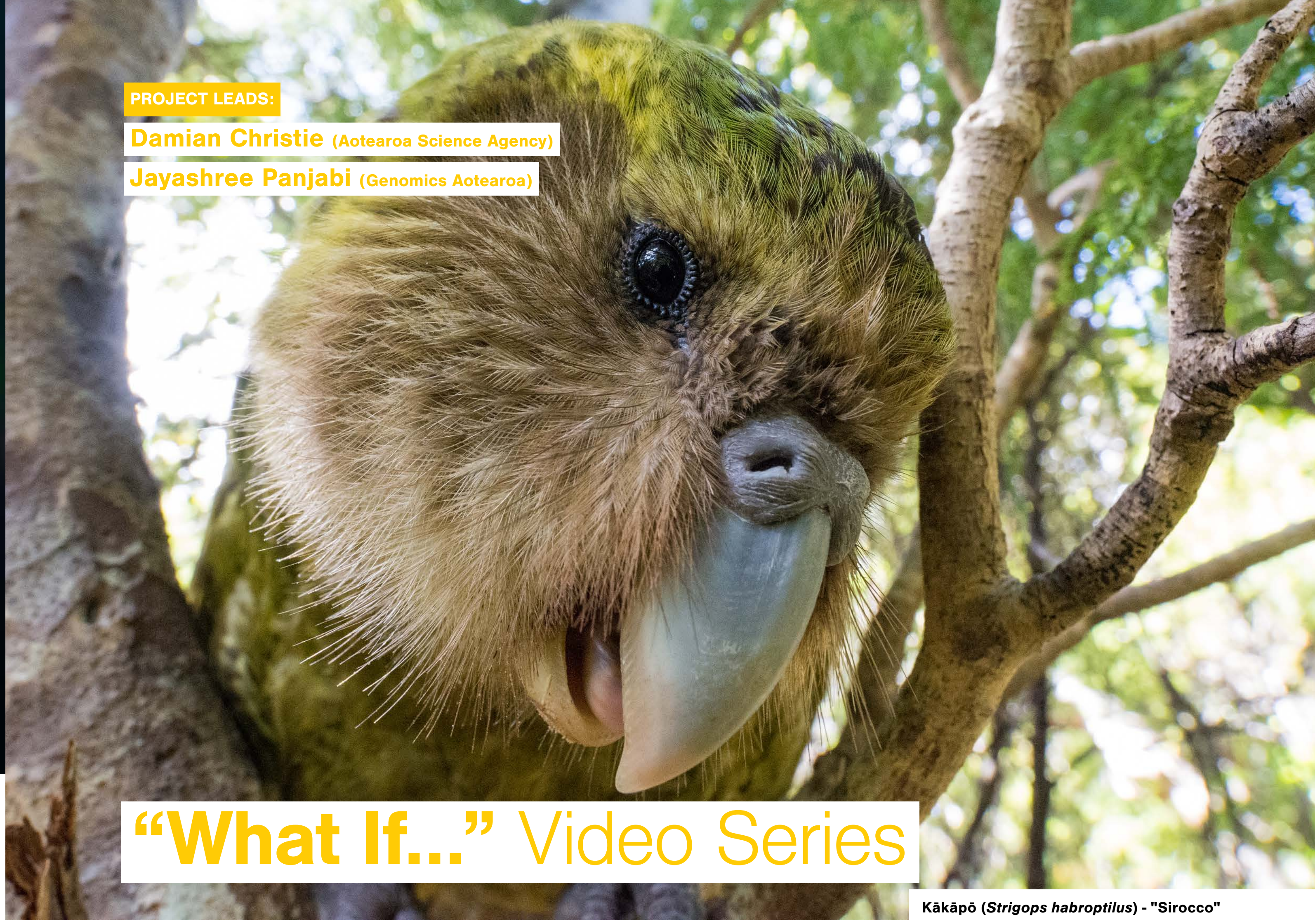
The exhibition was digitally shared with Niue High School, where it was hugely appreciated by science teachers who otherwise have limited access to such information. This interaction spurred national interest in the need for science support for students in Niue. To emphasise this need, Nathan Kenny from Genomics Aotearoa was interviewed for Breakfast TV.

After a very busy year, *Genome: Science of Life* is now on long-term display in Tūhura Otago Museum's Science Centre. The Science Centre attracts over 65,000 visitors a year, providing huge exposure for this well-travelled and well-received showcase.

PROJECT LEADS:

Damian Christie (Aotearoa Science Agency)

Jayashree Panjabi (Genomics Aotearoa)



"What If..." Video Series

Kākāpō (*Strigops habroptilus*) - "Sirocco"

Five videos have been produced by Damian Christie from the Aotearoa Science Agency, in order to promote the impact of genomics in our everyday lives.

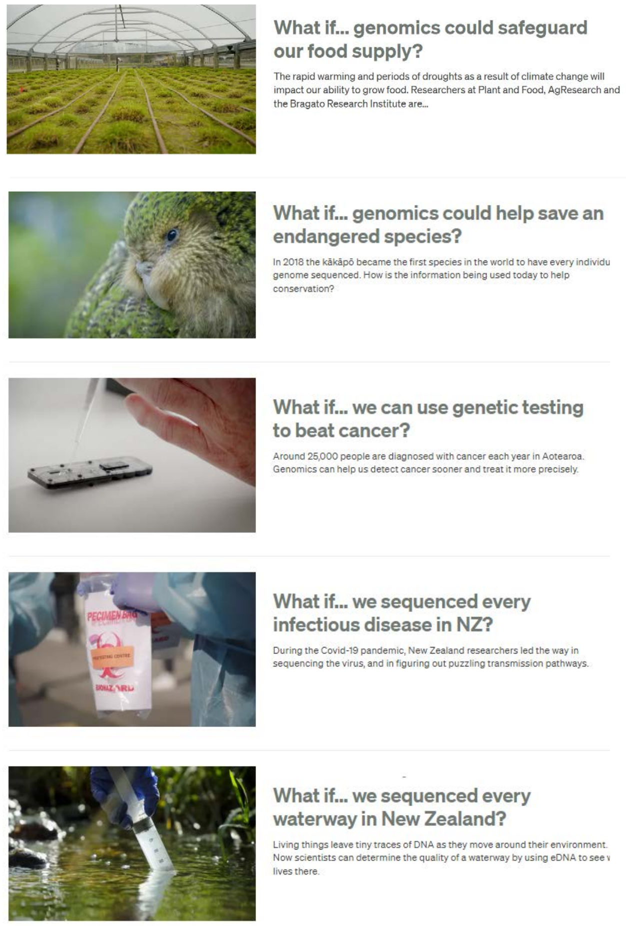
Topics covered are:

- Food security
- Conservation of the Kākāpō
- Genomics and cancer treatment
- Covid-19 in Aotearoa New Zealand
- eDNA work in our rivers

The videos are accessible via the Radio New Zealand website, accompanied by an entire episode of "Our Changing World" on the videos and the future of genomics in Aotearoa.

Two more videos are in development and will be released in 2025.

Find them all at www.rnz.co.nz/genomics/



What if... genomics could safeguard our food supply?

The rapid warming and periods of droughts as a result of climate change will impact our ability to grow food. Researchers at Plant and Food, AgResearch and the Bragato Research Institute are...

What if... genomics could help save an endangered species?

In 2018 the kākāpō became the first species in the world to have every individu genome sequenced. How is the information being used today to help conservation?

What if... we can use genetic testing to beat cancer?

Around 25,000 people are diagnosed with cancer each year in Aotearoa. Genomics can help us detect cancer sooner and treat it more precisely.

What if... we sequenced every infectious disease in NZ?

During the Covid-19 pandemic, New Zealand researchers led the way in sequencing the virus, and in figuring out puzzling transmission pathways.

What if... we sequenced every waterway in New Zealand?

Living things leave tiny traces of DNA as they move around their environment. Now scientists can determine the quality of a waterway by using eDNA to see v lives there.

Image Credit: **Jake Osbourne**

Early Career Researcher Scholarships

One of the main purposes of Genomics Aotearoa is to build an infrastructure for genomics, not of buildings and equipment, but of people. The intention is to ensure that there are pathways for early career researchers to connect with world-class researchers and nurture their careers for the benefit of science in Aotearoa New Zealand.

Since the inception of Genomics Aotearoa, we have supported 45 early career researchers or postdoctoral fellows at many universities and Crown Research Institutes. Most early career researchers have been employed for two years or more. Alongside salaries, our development programme delivers bioinformatics workshops and annual networking events. The success of this programme has led to a new initiative this year – early career travel scholarships. This initiative will help build a cohort of specialists who will be the foundation for future genomic science in Aotearoa.

“We reviewed scholarship programmes from around the world, and took the best ideas from all of them,” says Jayashree Panjabi, Genomics Aotearoa Operations Manager. “We were not prescriptive. Applicants could decide to go anywhere. They just needed to tell us where they wanted to go and why, what they would do, what they would gain from the experience, and, most importantly, what they would bring back to their team.”

Five researchers secured early career travel scholarships and will learn from the best international genomics experts in a variety of disciplines. Congratulations to the five recipients, Brooke Whitelaw, Astra Heywood, Katarina Stuart, Julie Blommaert, and SiMing Li.

Brooke Whitelaw: University of Adelaide, Australia

Dr Brooke Whitelaw is a postdoctoral fellow at the University of Otago, where she is part of a team working on the rapidly advancing science of genetic-based control for rat population suppression.

Brooke will use this scholarship to visit collaborative research groups specialising in gene drives in mice at the University of Adelaide, primarily with Dr Thomas Prowse. Dr Prowse studies the population biology of native and invasive species in Australia, and investigates components of wild population regulation, such as survival, reproduction, genetics, disease, and environmental change. Brooke will also be visiting Professor Paul Thomas who is developing CRISPR/CAS9 genome editing technology. Professor Thomas is generating and analysing mouse models to create synthetic gene drives for suppression of mammalian pest populations.

Brooke looks forward to bringing further knowledge of these new technologies to her work back in Aotearoa New Zealand. She says, “As an early career researcher still trying to establish myself, this scholarship provides a valuable opportunity to form lasting collaborations and further my work on an international level.”

Astra Heywood: North Carolina State University, United States of America

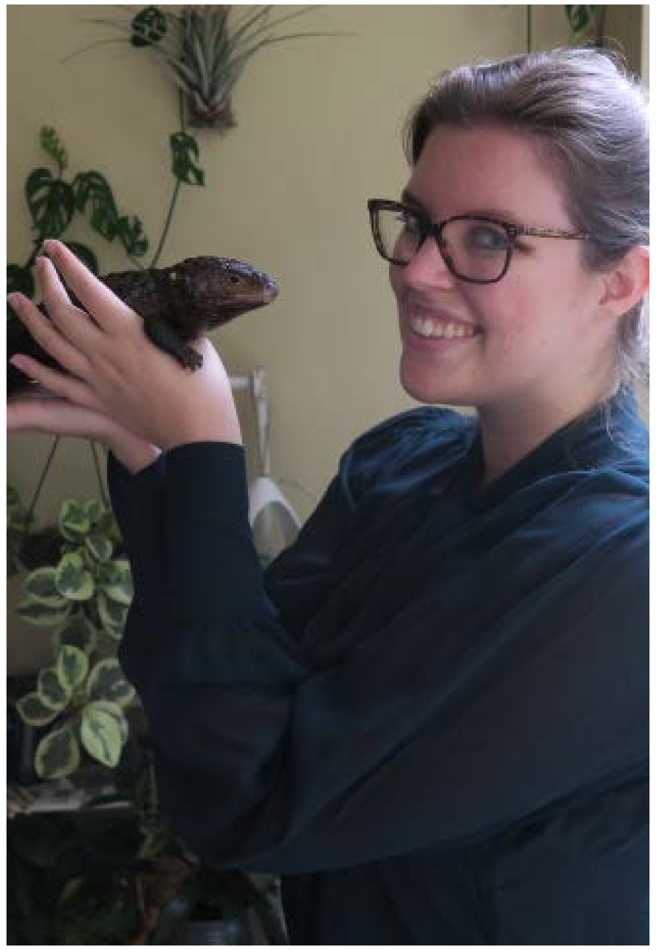
Dr Astra Heywood is a bioinformatics scientist at Plant & Food Research and will visit North Carolina State University to develop strategies and computational tools for determining inheritance patterns in mixed ploidy species.

Polyploidy is a significant feature that contributes to species diversification. Hybridisation and polyploidy are common features of many plants that are important to Aotearoa New Zealand. However, most statistical methods for determining inheritance patterns are developed for diploid or haploid species and rely on assumptions that might not be applicable in ploidy crosses and hybridisation.

Astra will be working with Dr Marcelo Mollinari, a Senior Research Scholar, and Dr Massimo Iorizzo, an Associate Professor. Dr Mollinari works with complex polyploid species. He created the MAPpoly R package, and co-created OneMap, an R package for linkage mapping in outcrossing species. Dr Iorizzo studies comparative structural genomics and the genetics of traits associated with desirable plant characteristics, including health properties.

“Working with these specialist researchers will help me develop computational and statistical methods for determining ploidy, inheritance and heterozygosity. I am so excited to work with leaders in this field, learn from them, and bring this knowledge back to inform science here,” said Astra.

Katarina Stuart: Institute of Zoology, Zoological Society of London, England



Dr Katarina Stuart seeks to understand the genetic mechanisms underlying rapid adaptation, mostly in invasive species. She also intends to grow her research scope to explore the overlap between invasive and native threatened species. Katarina will focus on anthropogenic selection, and the practical application of high-throughput genomics research to species conservation.

Winning this scholarship will allow Katarina to work towards this goal, learning from Dr John Ewen and Dr Patricia Brekke at the Institute of Zoology, Zoological Society of London.

Dr Ewen and Dr Brekke have been closely affiliated with research in Aotearoa New Zealand through their work on the hihi. They are leading experts in both theoretical and applied conservation genomics in small populations. They have worked on both invasive and threatened species and have translated genomic outputs to practical conservation outcomes, which aligns perfectly with Katarina’s goals.

"As a researcher who completed their PhD during the pandemic, I have had few opportunities to meet researchers from outside Australasia. This scholarship gives me the first opportunity to meet academics whose work I have been following my whole career. It has given me the chance to make strategic decisions around networking and my future career direction. And it means I can talk to project collaborators in depth about specific results and broader conservation implications, which is a major focus of my current fellowship," says Katarina.

Julie Blommaert: Minderoo OceanOmics Centre at University of Western Australia

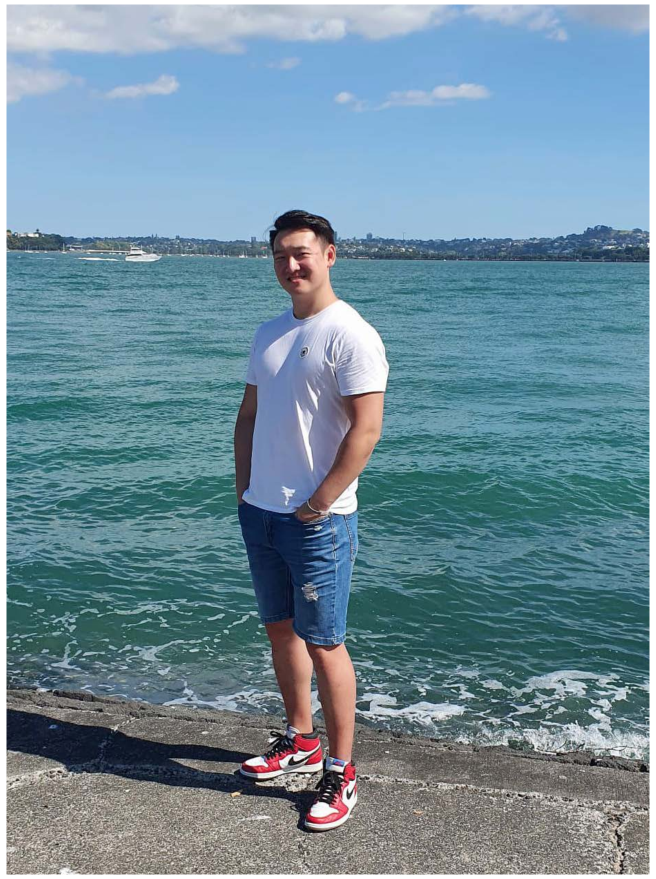
Dr Julie Blommaert's visit to the OceanOmics Centre will be the first collaboration in marine genomics research between Plant & Food Research and the Minderoo Foundation. OceanOmics Centre researchers study marine genomics and eDNA for conservation and ocean health. The team has expertise and infrastructure to enable high throughput sequencing and advanced data analysis.

Julie applies machine learning and artificial intelligence (ML/AI) to genomic selection and trait prediction for aquaculture breeding programmes as part of the Data Science for Aquaculture MBIE platform. She also develops high-quality genetic resources for marine species and conducts microbiome metagenomics research.

"The Genomics Aotearoa scholarship provides the opportunity to connect with research groups using machine-learning approaches that I am developing. I work on aquaculture systems, and the Minderoo OceanOmics Centre uses data science for ocean health. There are similar problems in both systems. I am so excited to see the work they do in person," said Julie.

This collaboration will accelerate the use of ML/AI genomic prediction tools in Julie's work and broaden perspectives on ocean health for both aquaculture and preservation of marine ecosystems. This work has promising potential to inform management decisions, identify environmental stressors, and develop targeted strategies to promote the resilience and sustainability of aquaculture and aquatic ecosystems.

SiMing Li: Guangzhou Institute of Biomedicine and Health, China

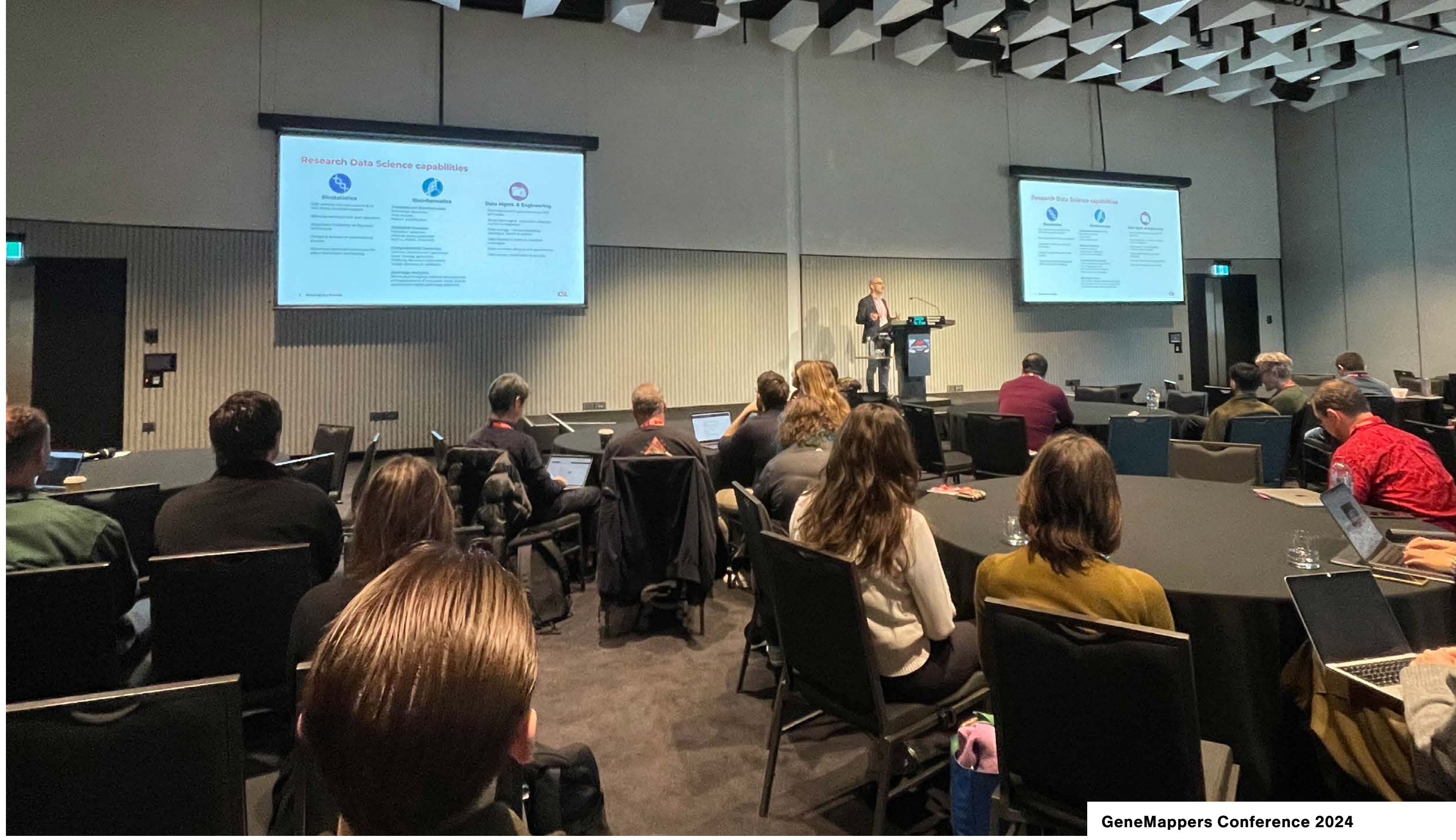


Soon, Dr SiMing Li will be joining Professor Lai at the Guangzhou Institute of Biomedicine and Health (GIBH), one of the largest transgenic facilities in the world. The GIBH team regularly publishes in top-rated journals such as *Cell*, *Nature*, and *Science*, and SiMing is eager to understand the team's approach.

SiMing will learn micromanipulation and pronuclear injection techniques at the GIBH. Understanding the technical nuances of these technologies and methodologies are skills SiMing will bring back to share and use in his work on the transgenic rat project. This project is funded by Predator Free 2050 and is developing genomic tools to aid the control of this invasive pest.

"Winning this travel scholarship is a significant milestone in my career. The scholarship has provided me with the invaluable opportunity to collaborate with leading experts in my field. This will further my research in gene editing and tactical population control as part of this project. I am deeply grateful for the opportunity provided by Genomics Aotearoa," Dr Li said.

Although considered to have tremendous promise for pest control to protect taonga species, genetic modification of animals is under-developed and under-resourced in Aotearoa New Zealand. SiMing's learnings, from top international researchers, will be invaluable in growing our country's capability in this field.



GeneMappers Conference 2024

Strategic Grants

Over the past seven years, Genomics Aotearoa has provided individual grants of up to $10,000, in order for researchers to attend international conferences, for satellite meetings to occur around Queenstown Research Week, travel assistance to enable early career researchers to attend conferences and workshops, and grants-in-aid for certain research projects.

This year, Genomics Aotearoa provided funding and support for IndigiData, a 5-day residential wānanga, designed to develop understanding of Indigenous data science and sovereignty. This was held in August 2023 and will be held again in late 2024. The Bioinformatics team ran training as part of the event, offering Coding - Intro to Shell. Sponsorship has also been given to support IndigiData 2024.

Conferences supported this year were as follows: GeneMappers 2024 (to fund an international speaker and postdoc travel scholarships), New Zealand Microbial Ecology Consortium 7.0 2024 (to fund a workshop on opportunities for interweaving of mātauranga Māori and environmental microbiology/microbial ecology), the annual Otago Bioinformatics Spring School, and two satellite meetings (Genomics and He Taonga Tuku Iho with BioProtection Aotearoa) as part of Queenstown Research Week 2023. We are also sponsoring a Pathogen Genomics satellite for Queenstown Research Week 2024. Alison Van Eenennaam, the MapNet keynote speaker at the joint session of the Genomics Aotearoa Annual Meeting was sponsored by Genomics Aotearoa.

The GeneMappers conference at Te Pae (the new Christchurch Convention Centre) drew in 127 delegates from 31 organisations from Australia, New Zealand, and further afield. They recieved 113 abstracts (more than 70% were from Early Career Researchers) from which they selected 35 speakers, on top of four invited overseas speakers, several speakers from Australia and New Zealand.

A strategic grant was also provided to support research led by Travis Horton and Sara Flanagan at the University of Canterbury, focusing on the use of field-based genomics to trace the ancestry of Paikea/Polynesian humpback whales in the Cook Islands. This research contributes to understanding the connections between these whales and their Polynesian heritage.

Additionally, a strategic grant was awarded to Genetics Otago to fund the purchase of four Genomics in Schools Suitcase Kits that will be used to support genomics education.


TE AO MĀORI NEWS

Honey battle back on: Aotearoa Mānuka proved to have different DNA from Aussie Manuka

Smithsonian MAGAZINE

Inside New Zealand's Quest to Save Its Rotund, Flightless Parrots

FARMERS WEEKLY

Nine million years between NZ and Australian mānuka

nature

Most rare kākāpō parrots have had their genome sequenced

Newshub.

Honey war heats up after research finds major genetic differences between NZ and Australia mānuka

SCI AM

Kākāpō Parrots Are Flightless, Adorable and Making a Comeback

The New Zealand Herald

World experts: Where NZ's genomic science is having global impact

POPULAR SCIENCE

New Zealand's quest to save its rotund, flightless parrots

LISTENER

Life savers: How genetic data will revolutionise your diagnosis and treatment

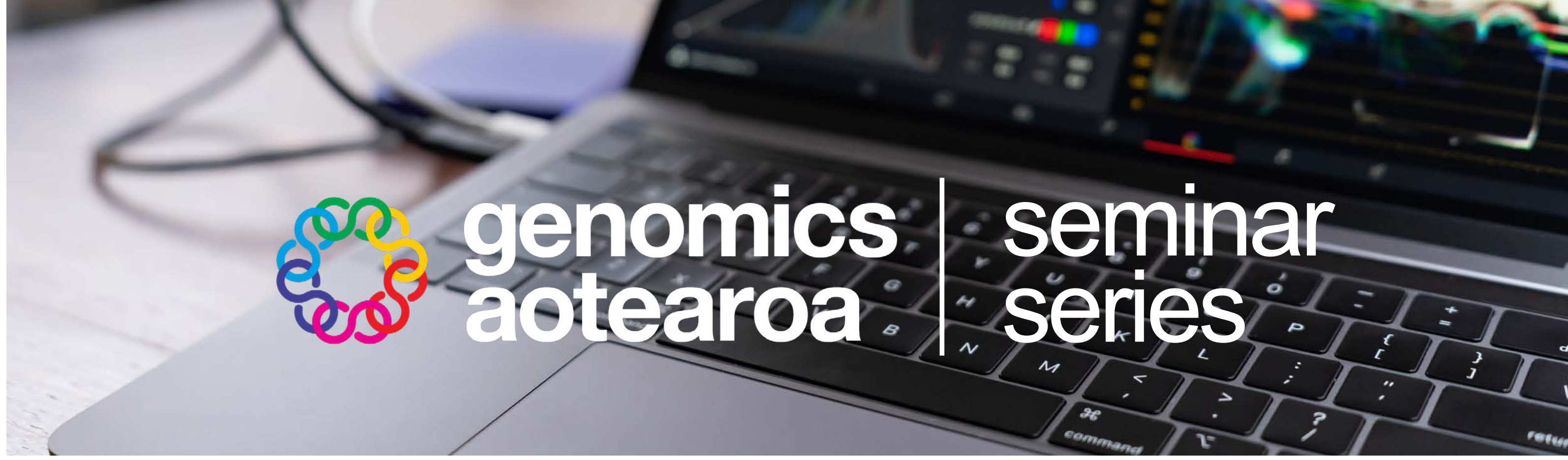
Media Engagement

This year, Genomics Aotearoa's research received considerable media coverage, both in New Zealand and internationally, drawing attention to key issues in conservation, the protection of Indigenous knowledge, and the application of genomics to global challenges.

The Kākāpō Genomics work, which involved sequencing nearly the entire kākāpō population, was a major focus. Coverage in Nature Genetics, Scientific American, Popular Science, and Smithsonian Magazine emphasised the importance of this work, while stories published in multiple languages further extended its international reach.

The trans-Tasman battle over mānuka honey also captured media attention, with research revealing significant genetic differences between New Zealand and Australian mānuka trees. This finding contributed to New Zealand's trademark discussions and drew interest due to its commercial implications and the cultural significance of mānuka to Māori.

During their visit for our annual meeting, members of our International Advisory Panel were interviewed by the NZ Herald. The article highlighted how our work, from combating COVID-19 to advancing conservation genomics, is positioning New Zealand as a leader in the global genomics landscape.



Seminar Series and YouTube

This year, Genomics Aotearoa has continued to connect and grow the genomics community through our Seminar Series and YouTube channel.

We hosted 14 fortnightly seminars via Zoom, featuring a mix of local and international speakers. Five of these were presented by international experts, including a second presentation from Karen Miga of the Human Pangenome Reference Consortium, which was a highlight as our first hybrid live and online seminar.

Our seminars saw strong attendance, maintaining high viewer engagement with topics ranging from the genomics of kākāpō to privacy issues in direct-to-consumer genetic testing.

In addition to the Friday seminars, we also hosted the Asia-Pacific Genetics Seminar Series, a quarterly collaboration with international genetics societies. This series has drawn a global audience, encouraged international exchange, and strengthened connections within the genetics community across the Asia-Pacific region.

The seminar recordings are available on our YouTube channel, which continues to grow as a platform for sharing valuable content and supporting the ongoing development of the genomics community.

Stephen Robertson and Phil Wilcox	University of Otago	He Kākano – The Aotearoa Māori Variome Resource
Dafni Anastasiadi	Plant & Food Research	Epigenetic Clocks for Age Prediction
Catherine Collins	University of Otago	Ruatau: Connecting Māori Genomic Scientists and Communities
Carla Finn	Victoria University of Wellington	Developing Genomic Resources of the Haku/Warehenga (Yellowtail Kingfish, S. Lalandi) to Support Māori-Led Aquaculture
Paul Gardner	University of Otago	Should I Trust My Bioinformatic Tools?
Ronald Jenner	Natural History Museum, London	Seeing Evolution Through a Cladistic Blindfold
Andelka Phillips and Jan Charbonneau	University of Oxford University of Tasmania	Privacy and the World of DTC - Data Breaches Are Already Happening
Manpreet Dhami and Ang McGaughran	Manaaki Whenua-Landcare Research University of Waikato	Invasomics for Biosecurity
Gabriel Gasque	Protocols.io, Berkeley, CA	The Power of Sharing Detailed Methods
Richard Newcomb	Plant & Food Research	Where an Interest in Genomes Can Take You
Andelka Phillips	University of Queensland	Think Before You Spit - Privacy Perceptions in Direct-to-Consumer Genetic Testing
Laura Duntsch	University of Auckland	Conservation Genomics and the Hihi
Joseph Guhlin	University of Otago	Species-Wide Genomics of Kākāpō
Karen Miga	University of California, Santa Cruz	Expanding Studies of Global Genomic Diversity With Complete, Telomere-to-Telomere Assemblies

Contributing Researchers

Katerina Achilleos	University of Otago
J. David Aguirre	University of Auckland
Alana Alexander	University of Otago
Sebastian Alvarez Costes	University of Otago
Simon Apang Semese	Massey University
Te Mauri Apiata	Tahuri Whenua
Vanessa Arranz	Massey University
Rachael Ashby	AgResearch
Carmen Astudillo-Garcia	University of Auckland
Sarah Bailey	Plant & Food Research
Marc Bailie	University of Otago
Colan Balkwill	Victoria University of Wellington
Paul Battersby	University of Auckland
Chris Battershill	University of Waikato
Sara Belcher	Victoria University of Wellington
Julie Bennett	University of Otago
Miles Benton	ESR
Max Berry	Wellington Hospital
Basharat Bhat	University of Otago
Louise Bicknell	University of Otago
Patrick Biggs	Massey University
Mik Black	University of Otago
Amanda Black	Lincoln University
Wayne Blissett	Rangitāne o Manawatū
Renata Blissett	Rangitāne o Manawatū
Jian Shen Boey	University of Auckland
Rudiger Brauning	AgResearch
Talia Brav-Cubitt	Manaaki Whenua Landcare Research
Manon Broadribb	Victoria University of Wellington
Robert Brookes	University of Waikato
Jamie-Lee Brown	Te Rarawa
Thomas Buckley	Manaaki Whenua Landcare Research
Matthew Calder	Department of Conservation
Iggy Carvajal	Plant & Food Research
Craig Cary	University of Waikato
M. Leticia Castro	ESR
David Chagné	Plant & Food Research
Aleisha Chalmers	University of Otago
Henry Chan	WDHB
Cheng-Yee Chan	CDHB
Aniruddha Chatterjee	University of Otago
Aakash Chhibber	University of Auckland
Seung-Sub (Shane) Choi	University of Auckland
Jane Clapham	ESR
Anna Clark	University of Otago
Amanda Clarke	University of Waikato
Rebecca Clarke	AgResearch
Shannon Clarke	AgResearch
Catherine Collins	University of Otago
Christine Couldrey	LIC
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Glossary of Genomics Terms

TERM	DEFINITION
Allele	Alternative versions of a single gene. Used to characterise variation in the genome and compare among individuals.
Assembly	DNA sequencing technology cannot read whole genomes in one go; instead, it reads short pieces of bases from a genomic sequence. Sequence assembly aligns and merges fragments to form a longer DNA sequence to reconstruct the original *genome*.
Allopolyploidy	*Allopolyploidy* is a form of polyploidy that occurs when organisms have multiple sets of genetically distinct *chromosomes.*
Autopolyploidy	Autopolyploidy is a form of polyploidy that occurs when organisms have multiple sets of chromosomes from the same species.
Bioinformatics	The science of analysing genomic data.
Candidate genes	Genes of interest related to phenotypes or disease states.
Chromatin	Chromatin is a mixture of DNA and proteins that form chromosomes in cells. Histone proteins package the massive amount of DNA in a genome into a highly compact form that can fit in the cell nucleus.
Chromosome conformation capture (CCC or 3C)	Chromosome conformation capture techniques are a set of molecular biology methods used to analyse the spatial organization of chromatin in a cell.
Clinical geneticist	This is a medical doctor with special training in genetics who meets with patients to evaluate, diagnose, and manage genetic disorders. Clinical geneticists also assist in the management of genetic diseases by identifying preventable complications through early and accurate diagnosis and surveillance.
CRISPR-Cas9	CRISPR-Cas9 (Clustered Regularly Interspaced Short Palindromic Repeats) is a method of genetic manipulation consisting of two key molecules that introduce a change into the DNA. The molecules are: An enzyme called Cas9 which can cut strands of DNA at a specific location in the genome so that short sections of DNA can then be added or removed. A piece of RNA sequence called guide RNA (gRNA), located within a longer RNA which guides Cas9 to the correct part of the genome to cut.
DNA methylation	DNA methylation is one type of epigenetic mechanism that modifies the expression of genes and therefore their effects. DNA bases are modified by addition of a methyl group. Methylation can change the activity of a DNA segment without changing the genome sequence.
eDNA	Environmental DNA, or eDNA refers to many tiny traces of genetic material that remain in the environment as living things pass through water or soil. It can be used to survey the environment to detect traces of diseases or invasive species or rare species. Environmental DNA can be assessed using metabarcoding.
Epigenetics/ Epistasis	Epigenetic mechanisms are those that regulate inherited (genomic) gene expression, that is how, and when those genes are switched on (or off). These epigenetic switches may be due to environmental exposure or lifestyle factors. Non-genetic factors include the environment like diet, gut microbiota, toxin, and drug exposure, psychological and physical stressors, and levels of activity throughout life. Measuring the epigenetic changes that occur in diseases, including cancer and heart disease, can provide understanding of the underlying mechanisms.
Epigenome	The set of all epigenetic modifications to an individual's genome.
Eukaryote	An organism whose cells contain a nucleus surrounded by a membrane and whose DNA is bound together by proteins (histones) into chromosomes. Animals, plants, and fungi are eukaryotes.
Exemplar research	A research model that provides leadership and examples for further research in similar fields.
Exposome	Exposome describes all environmental factors, both exogenous and endogenous, which we are exposed to in a lifetime. It is an important tool in the study of autoimmunity, complementing classical immunological research tools and genome-wide association studies (GWAS).
Finishing the sequence	Finishing an assembly involves refining the genomic sequence to eliminate sequencing errors and to close gaps.
Genetic admixture	The presence of DNA in an individual from a distantly related population or species, because of interbreeding between populations or species who have been reproductively isolated and genetically differentiated. Admixture results in the introduction of new genetic lineages into a population.
Genetic counsellors	These are healthcare professionals with training in human genetics and counselling who guide patients and their whānau with a genetic disorder through the process of understanding and making informed healthcare decisions.
Genetic gain	The rate of genetic improvement within a breeding population over time. An important concept in conventional quantitative genetics and breeding, genetic gain can be defined as the increase in performance achieved annually through artificial selection.
Genetic-linkage mapping	Used to determine the order of genes on a chromosome and the relative distances between those genes.
Genome annotation	The process of attaching biological information to genetic sequences.
Genome duplication	A widespread phenomenon in plant genome evolution, where an organism can sometimes inherit two copies of the genome of its parents, instead of only one copy. The doubling of DNA then persists over generations and the duplicated copies can result in the evolution of new functions.
Genome map	Helps scientists to define which parts of the genome are physically linked to each other. The landmarks on a genome map that aid navigation might include short DNA sequences, regulatory sites that turn genes on and off, and genes themselves.
Genomic offset	Genomic offset statistics predict the degree of maladaptation of populations to rapid habitat alteration based on associations of genotypes with environmental variation. *In a changing environment, adaptations* (traits) that were beneficial in a previous environment may no longer be beneficial, that is, the traits are now maladaptive.
Genomic signature	Genomic regions of DNA sequences that provide information about the activity of a specific group of genes in a cell or tissue.
Genome variation types	Genome variations include mutations and polymorphisms. Mutation is often used to refer to a variation that is associated with a specific human disease, while the word polymorphism implies a variation that may or may not affect a physical characteristic. Genetic variations also include gene deletions, gene additions and structural variations (see structural variants).
Genome-wide association studies	A search for parts of the genome associated with characteristics of interest, one example being human diseases.
Genotype (noun)	An organism's set of genetic variations.
Genotype (verb)	To determine genetic variation in a genome.
Germline	The cells which develop into eggs and sperm.
Haplotype	Combinations of alleles from several locations on the same chromosome that are inherited together. Used to infer the relationships among genes (and species) and the characterize the evolutionary processes that shape their ancestry.

TERM	DEFINITION
Hi-C	Hi-C sequencing is a high-throughput chromosome conformation capture technique to analyse spatial genome organization and map higher-order chromosome folding and topological associated domains.
Imputation	The mathematical process of replacing missing data with estimated values.
Infectome	The infectome is the part of the exposome (see definition earlier) referring to the collection of an individual's exposures to infectious agents.
Introns	Regions of non-coding DNA sequence within genes.
Long read sequencing (also known as third generation sequencing)	Involves new forms of sequencers that can read long distances down one strand of DNA. There are currently two effective technologies: Pacific Biosciences (PacBio) - an imaging approach that allows the detection of the incorporation of single labelled base pairs one after another into a strand of DNA being replicated. Oxford Nanopore (Nanopore) - uses tiny, charged pores that a strand of DNA is drawn into, and as each base passes through the hole it changes the charge in a way that can be measured. These changes in charge are then assigned to each base and the sequence is built up from there.
Linked read technology	Uses a unique barcode system to label short DNA sequences from individual molecules that are close to each other on the genome, so they can be linked to create longer sequence reads.
Metabarcoding	Metabarcoding is a type of sequencing that enables the simultaneous identification of many organisms within one sample. The aim is to assess species composition within a sample.
Metabolomics	This process detects chemicals or metabolites and provides a read-out of what chemicals are in a tissue at any one time.
Microbiome	The community of microorganisms (such as fungi, bacteria, and viruses) that exists in a particular environment. The environment could be anything from the body of an animal or plant or soils and waterways.
Mutations	The changing of the structure or function of a gene, caused by the alteration of single base units in DNA, or the deletion, insertion, or rearrangement of larger sections of genes or chromosomes. The resulting variant form may be transmitted to subsequent generations.
Non-coding DNA	Genes (coding DNA) account for a small percentage of the DNA in the genome - knowing the entire genome sequence will help scientists study the parts of the genome outside the genes. Non-coding DNA includes the regulatory regions that control how genes are turned on an off, as well as long stretches of DNA of unknown function.
Nonsense mutation	A DNA mutation that results in a non-functional protein.
Nucleotides and bases	A single *base* of DNA is made up of Adenine (A), Cytosine (C), Guanine (G) or Thymine (T). Base pairs are the two opposing nucleotides (a base, a sugar molecule, and a phosphate group) on a double-stranded DNA molecule. Adenine pairs with Thymine, and Cytosine pairs with Guanine.
Omics or 'omics	Omics is the collective name for the disciplines that characterise and quantify pools of biological molecules that translate into the structure, function, and dynamics of organisms. Examples include genomics, proteomics, metabolomics, metagenomics, phenomics and transcriptomics.
Pangenome	A pangenome (also pan-genome or supragenome) is a combined collection of genomes from all strains or varieties within a group of organisms.
Phenotype	Observable characteristics influenced both by an organism's genotype and by the environment.
Pathway	In genetics, a pathway is a set of genes that work together in a biological process.
Pharmacogenomics	This is the study of how genomic variation within the individual or their disease (including gene expression, epigenetics, germline, and somatic mutations) influences one person's response to drugs. The aim is to optimise drug therapy by maximising therapeutic effect and minimising adverse effects.
Pipeline	A process for the preparation, development, production, and analysis of genomic data.
Polishing (of the draft genome assembly)	Assembly polishing improves a draft genome assembly by removing artifacts of the assembly process. This results in improved local accuracy (specific parts of the genome) and consensus accuracy (genome quality).
Polyploidy	Polyploidy is the presence of more than one set of chromosomes in the genome. The two types of polyploidy are autopolyploidy and allopolyploidy. Autopolyploidy occurs when the multiple chromosome sets are from the same species, while allopolyploidy occurs when the multiple chromosome sets are genetically distinct.
Population genomics	The large-scale application of genomic information to study populations, including entire genomes of an entire species (e.g., kākāpō).
Prokaryote	Unicellular microbial organism that lacks a nucleus. All bacteria are prokaryotes. A related group are Archaea – these are also unicellular but are different to bacteria.
Proteomics	RNA (made from turned-on genes) is translated into protein. Proteomics is a technique to look at the broad range of proteins in a cell or tissue (using mass spectrometry). We can usually identify which proteins are present in a cell and what they are doing.
Re-sequencing	Once a reference genome has been assembled for a species, re-sequencing involves aligning sequences from other individuals to the reference to detect variants of interest.
RNA	RNA (ribonucleic acid) is the molecule that takes information from DNA to make protein and has many other activities. RNA is only made from genes in the DNA that have been activated.
Selection Scan Outlier analysis	Looks for outlier (unexpected or unusual) genomic variation (loci) that might be indicators of regions under divergent selection.
Short read sequencing (also known as next generation or second-generation sequencing)	A DNA sequencing method that produces relatively short fragments of DNA sequences, typically ranging from a few dozen to a few hundred base pairs in length. This sequencing approach is characterized by its ability to generate a large volume of sequencing data quickly and cost-effectively.
SNPs	About 90 percent of human genome variation can be accounted for by single nucleotide polymorphisms, or SNPs (pronounced *snips*). These are variations that involve just one nucleotide, or base. These markers are used to genotype individuals to better understand population genetic variation and can be used to detect genes that are under selection.
Somatic	Refers to the cells of the body in contrast to the cells that make sperm or eggs (germline cells).
Structural variation or Structural Variants (SVs)	Structural variation describes individual or group differences in genome structure which are generally larger than one nucleotide, such as gene deletions, insertions, duplications, inversions, and translocations. These variant regions are scattered throughout genomes and are often associated with gene expression changes and observable differences among individuals (phenotypic differences).
Topologically associating domain (TAD)	A topologically associating domain is a self-interacting genomic region. That is, DNA sequences within a TAD physically interact with each other more frequently than with sequences outside the TAD.
Transcriptomics	Sequencing RNA from a tissue or cell to measure the set of active (expressed) genes.
Variome	The complete set of genetic variations found in populations of species.
Whole genome sequencing (WGS)	The process of determining the complete DNA sequence of an organism's genome.

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The pikorua symbol was developed in a collaboration between Josh Byford-Pothan (student of Science Communication, of Māori whakapapa), Jess McLean, and Denise Narciso (Graphic Designer).

The natural shape of the three-twist pikorua depicts the growth of two pikopiko fern fronds and is a traditional Māori symbol that represents the strength of bonds between groups and cultures. The shape is also reminiscent of the DNA helix that connects us all.

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