Australasian Myrtle Rust Conference 2025 - Programme

Schedule and abstracts

Schedule

Monday 16 June

9:00-9:30	Welcome, pōwhiri, introductions	
	Community-led action	
9:30-9:50	Kaitiakitanga and Māori led solutions to Myrtle rust	Alby Marsh (Better Border Biosecurity) – pg3
9:50-10:10	Conservation of critically threatened swamp maire (*Syzygium maire*) in Auckland	Rob Beresford (Plant & Food Research) – pg4
10:10-10:30	Community conservation of swamp maire (*Syzygium maire*) in Kaipātiki	Lucy Kelly (Pest Free Kaipātiki) – pg4
10:30-11	**Morning tea**	
11-11:20	He ahi kā roa: Kaitiakitanga and resilience in the face of myrtle rust – a mātauranga Māori response	Tauranga Moana Biosecurity Capital – pg5
11:20-11:40	Ngāti Kuri-led conservation of rātā moehau (*Metrosideros bartlettii*) and kahikā rangitāhua (*Metrosideros kermadecensis*)	Te Haumihi (Ngāti Kuri) – pg5
11:40-12	Te whānau a Apanui, Ngāti Porou and Te Aitanga-a-Hauiti hapū response to myrtle rust	Te Whakapae Ururoa – pg6
12-12:20	A First Nations Australian response	Adrian Bauwens and Seth Henaway – pg6
12:30-1:30	**Lunch**	
	New technologies, solutions, and research insights Part 1: Tools and fungal genetics	
1:30-1:50	dsRNA solutions for myrtle rust: Field success on lemon myrtle	Anne Sawyer (University of Queensland) – pg7
1:50-2:10	New surveillance systems for the detection of airborne Austropuccinia psidii in Australia's Botanic Gardens	Ash Jones (Australian National University) – pg8
2:10-2:30	Decision-making tools for myrtle rust management in plant production	Jacinta Harrop (Plant Pass) – pg8
2:30-2:50	E heke e Heka! Bilingual apps	Taiāwhio Bryers (Scion) – pg9
3:00-3:30	**Afternoon tea**	
3:30-3:50	Genome evolution of the broad host range fungal pathogen, *Austropuccinia psidii*	Peri Tobias (University of Sydney) – pg9
3:50-4:10	The enigma of the wide-host range obligate pathogen *Austropuccinia psidii*	Grant Smith (Plant & Food Research) – pg10
4:10-4:30	Evidence for sexual reproduction in New Zealand populations of the myrtle rust pathogen *Austropuccinia psidii*	Michael Bartlett (Scion) – pg10

Tuesday 17 June		
9:00-9:10	Housekeeping and field trip info	
	Early career initiatives and research	
9:10-9:30	Characterisation of *Austropuccinia psidii* effector proteins expressed during infection of Myrtaceae	Jovarn Sullivan (University of Canterbury) – pg11
9:30-9:50	Cryopreservation for conserving *Gossia* species threatened by myrtle rust in Australia	Jingyin Bao (University of Queensland) – pg12
9:50-10:10	Establishing a cryopreservation protocol for critically endangered Australian native *Lenwebbia* sp. Main Range	Van Anh Nguyen (University of Queensland) – pg12
10:10-10:30	Investigation of fungal communities associated with myrtle rust infection and the use of mycoparasites as potential biocontrol agents against the disease	Dan Cu (Lincoln University) – pg13
10:30-11	**Morning tea**	
11-11:20	Could variation in susceptibility to myrtle rust infection of *Metrosideros excelsa* be linked to the endophytic microbiome?	Vladislav Kholostiakov (University of Auckland) – pg13
	New technologies, solutions, and research insights Part 2: Environmental and microbial insights	
11:20-11:40	He aha te whakaaweawe o te heka kahika ki ngā moroiti rau? What is the impact of myrtle rust on the leaf microbiome?	Hanareia Ehau-Taumaunu (Bioprotection Aotearoa, Plant & Food Research) – pg14
11:40-12	Sustainable myrtle rust management: Experimental approaches to bacterial suppression of rust disease	Fernanda Nieto-Jacobo (Plant & Food Research) – pg14
12-12:20	Correlations between historical land use and host density can help to prioritise management of a wet sclerophyll forest community in Eastern Australia	Kristy Stevenson (Queensland University of Technology) – pg15
12:30-1:30	**Lunch**	
1:30-1:50	The influence of forest edge effects on myrtle rust infection of *Lophomyrtus bullata*	James McCarthy (Manaaki Whenua – Landcare Research) – pg15
	Species conservation	
1:50-2:10	Identifying potentially suitable and accessible refugia to mitigate impacts of an emerging disease on a rare tree	Sarah Herbert (Te Herenga Waka—Victoria University of Wellington) – pg16
2:10-2:30	Myrtle rust in NSW: Strategies for species conservation	Craig Stehn (NSW DCCEEW) – pg16
2:30-2:50	Ex situ conservation of myrtle rust affected species at the Botanic Gardens of Sydney	Lyndle Hardstaff (Botanic Gardens of Sydney) – pg17
3:00-3:30	**Afternoon tea**	
3:30-3:50	Key learnings/recommendations from the 8th IUFRO workshop on resistance mechanisms and breeding in forest trees	Mia Townsend (Dieback Working Group) – pg17
3:50-4:10	Seed banking in Aotearoa – The kaupapa Māori approach	Marcus Shadbolt (Te Tira Whakamātaki) – pg18

Abstracts

Community-led action – Day 1

Kaitiakitanga and Māori led solutions to myrtle rust

Marsh AT[1]*, Wood AW*[2]*, Ropata H*[3]*, Campbell RE*[4]*, Fehlmann C*[5]*, Waiariki TL*[6]*, Sutherland R*[7]*, Bartlett M*[8]
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The Beyond Myrtle Rust research programme focused on four interlinking areas: Pathogen Dynamics (RA 1.1), Ecosystem Impacts (RA 1.2), Novel Mitigation Techniques (RA 1.3), and Kaitiakitanga & Māori-Led Solutions (RA 1.4). Collaborating with Māori partners, RA1.4 explored kaupapa Māori approaches to build capacity and develop strategies for understanding the implications of myrtle rust's establishment and spread. Key considerations included the values and impacts on Te Ao Māori, seeking Māori-driven solutions that integrate mātauranga to protect ecosystems and enhance kaitiakitanga in MR-affected areas.

A key piece of work was to collate key indicators and values—cultural, economic, environmental, and social—that will impact Māori, addressing both regional and national consequences of myrtle rust in Aotearoa. It was important that the team engaged Māori communities actively, to drive participation in operational responses, and explore Mātauranga Māori approaches to disease management. By assessing cultural and environmental priorities alongside disease impacts, BMR aimed to develop a Te Ao Māori values framework and protection plan template, and to foster connections with Pacific communities affected by invasive species.

This project aimed to engage Māori, drive participation in operational responses, and investigate Mātauranga Māori approaches to disease management. This included:

- Working with Māori partners to extend kaupapa Māori approaches
- Build capacity and develop strategies for Māori to understand the implications of myrtle rust establishment and/or spread
- Understand the values and impacts for Te Ao Māori
- Identify what mātauranga could be utilised for Māori-led solutions to protect ecosystems and plant health
- Enhance kaitiakitanga of MR-affected plants and ecosystems.

Conservation of critically threatened swamp maire (*Syzygium maire)* in Auckland

R Beresford[1]*, K McCormick*[2]*, M Valkova*[2]*, R Fuller*[3]*, W Bullôt*[1]*, B Lawrence*[1]*, H Geddes*[4]
[1] *Plant & Food Research,* [2]*Friends of Bushglen Reserve,* [3]*Auckland Council.*

Swamp maire (maire tawake) is a wetland forest species endemic to New Zealand that is highly susceptible to myrtle rust. Its distribution is restricted due to habitat destruction and since myrtle rust arrived in 2017, its conservation status has become 'Threatened - Nationally Critical'. In Auckland's favourable climate, myrtle rust started affecting swamp maire in Auckland Council (AC) reserves during summer 2020-2021. At Bushglen Reserve on the North Shore, observations of the upper leaf canopies of mature trees in February 2022 showed shoots, flowers and fruit all killed by myrtle rust and this pattern has been repeated at multiple sites, with slow decline leading to tree death in 3-5 years. A fungicide spray programme was started by the community group 'Friends of Bushglen Reserve' in April 2022 to protect juvenile trees and lower branches of selected mature trees. This has been very successful, allowing flowering, fruiting, seed collection and propagation of seedlings, now numbering in the hundreds. Regular monitoring at Bushglen has provided information to understand seasonal changes in tree health and myrtle rust intensity. The monitoring protocol uses a relative 0-10 scale for five key variables: 1) overall leaf canopy health, 2) presence of new growth, 3) active rust (juvenile trees), 4) shoot dieback and dead flower clusters (mature trees) and 5) flower and fruit development stages (mature trees). The success of the tree protection programme and subsequent seedling propagation has allowed the project to enter its next phase of screening the seedling progeny for naturally resistant types.

Community conservation of swamp maire (*Syzygium maire*) in Kaipātiki

L. Kelly[1]*, R. Beresford*[2]*, M. H. Murray*[1]*, K. McCormack*[3]*, R. Fuller*[4]*, J. Stenersen*[1]*, T. Todd*[1]*, N. Balfour*[1]
[1]*Pest Free Kaipātiki,* [2]*Plant & Food Research,* [3]*Friends of Bushglen Reserve,* [4]*Auckland Council.*

Swamp maire (*Syzygium maire*) is an endemic wetland tree that has been severely impacted by the arrival of myrtle rust in New Zealand, becoming functionally extinct in many areas. Pest Free Kaipātiki is a community restoration organisation based in Kaipātiki on Auckland's North Shore and since 2023 has been part of an ongoing collaborative project to assess the efficacy of fungicide treatment on swamp maire, with the goal of collecting fruit for propagation and seedling resistance screening. In Cecil Eady Reserve the approximately 54 trees have since been sprayed on a rotating schedule of three fungicides, with the help of volunteer labour. Over the summer of 24/25 over 300 ripe berries were collected for propagation, an increase from zero berries the previous year. These seedlings along with others from various sites across Auckland are currently being prepared to enter a trial to screen for natural myrtle rust resistance. The success of this project illustrates the importance of community-based conservation work and the benefits of collaboration with local volunteers.

He ahi kā roa: Kaitiakitanga and resilience in the face of myrtle rust – A mātauranga Māori response

Carlton Bidois[1], Matire Duncan[1], Riki Nelson[1], and Reon Tuanau[2]
[1]Tauranga Moana Biosecurity Capital (TMBC), [2]Manaaki Te Awanui

Myrtle rust poses a significant threat to indigenous ecosystems and to the cultural integrity of Aotearoa's ngahere. From a Māori worldview, taonga species such as ramarama, rōhutu, and pōhutukawa are not only ecological keystone species, but also deeply woven into the whakapapa, identity, and wellbeing of hapū and iwi. Their decline through disease is experienced not just as a biodiversity loss, but as a severing of ancestral relationships and mātauranga tuku iho (intergenerational knowledge).

This presentation shares a kaupapa Māori approach to understanding and responding to the impacts of myrtle rust. Drawing on localised narratives, hapū-led research, and mātauranga Māori frameworks, we explore how tikanga, whakapapa, and the role of kaitiaki can inform effective surveillance, restoration, and resilience strategies. We discuss how culturally grounded biosecurity practices offer a path toward healing – for the forest, the people, and our shared future.

We also reflect on the tensions and opportunities in weaving mātauranga Māori with Western science, and how co-governance models can better reflect the constitutional place of tangata whenua in protecting Aotearoa's unique biodiversity.

Field work observations in the Far Far North – Mahi Taiao mo te whenua 'Te Haumihi', the lands of Ngāti Kuri Iwi

Erik Kaihe-Wetting *(Te Haumihi, Ngāti Kuri)*

At the very tip of New Zealand's North Island lie the traditional lands of Ngāti Kuri Iwi, an area encompassing Te Rerenga Wairua (Cape Reinga), Manawatawhi (The Three Kings Islands, and even the remote Rangitahua/Raoul Island and the other Kermadecs. The mainland part of this area consists of several unique biomes and a high level of endemism resulting from their previous separation from the rest of NZ for many millions of years. One unique species here is the Rata Moehau tree (*Metrosideros bartlettii*), which was 'rediscovered' in 1975 and is now known from fewer than twenty wild trees, which as a *Metrosideros* is vulnerable to Myrtle Rust.

A small but dedicated team of Taiao Rangers work for Ngāti Kuri Iwi in the field, conducting pest control, propagation and replanting programmes, and protecting rare and endangered species such as the endemic 8cm land snail Pupu Whakarongotaua (*Placostylus ambagiosus*). Over the last three years, this team has also become also responsible for work in the prevention and monitoring of plant pathogens such as myrtle rust. Te Haumihi is a meteorologically distinct area with unique weather patterns and together with unusual distributions of vulnerable Myrtaceae species, Ngāti Kuri Taiao Rangers are realising that research into the patterns of myrtle rust infection (or lack thereof) has only just begun.

Te whānau a Apanui, Ngāti Porou and Te Aitanga-a-Hauiti hapū response to myrtle rust

Mere Tamanui and Graeme Atkins, Te Whakapae Ururoa

Te Whakapae Ururoa was formalised as a Jobs for Nature project/collaboration in 2021. Jobs for Nature was a $1.185 billion programme that benefitted the environment, people and the regions as part of the COVID-19 recovery package. Te Whakapae Ururoa has been tracking spread and infestation at critical sites across a 27,800ha stretch of the East Coast coastline ever since. This area has been identified as being critically vulnerable to myrtle rust infestation. Led by local communities, the work is grounded in local knowledge and biocultural monitoring approaches. Protocols for the collection and propagation of native seeds for the East Coast region were also developed. Te Whakapae Ururoa has now grown beyond the initial Jobs for Nature project, and they are excited to share their recent updates.

A First Nations Australian response to myrtle rust

Adrian Bauwens and Seth Henaway

Galang gumba daru! G'day all! I'm Adrian, a Wakka Wakka man based out at the Bunya Mountains - working as a forest health officer - with a strong focus on pathogens such as *Phytophthora* and now myrtle rust. I'll be discussing the impacts of such pathogens on culture and well-being, as well as the work that goes into monitoring and preparing to work with it.

New technologies, solutions, and research insights – Day 1
Part 1: Tools and fungal genetics

dsRNA Solutions for Myrtle Rust: Field Success on Lemon Myrtle

*Louise Shuey[1], Alistair McTaggart[2,3], Rebecca Degnan[4], Sebastian Orellana-Quinteros[4], Donald Gardiner[2], Bernie Carroll[4], Neena Mitter[2,5], **Anne Sawyer**[2,4]*

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RNA biopesticides have emerged as a game-changing plant protection platform that does not leave harmful residues in the environment or impact beneficial organisms. The approach involves spray application of pathogen-specific double-stranded RNA (dsRNA) on host plants to trigger RNA interference (RNAi) in the invading pathogen. This leads to the silencing of essential pathogen genes, inactivation of the pathogen and prevention of disease. We previously demonstrated that dsRNA targeting essential *Austropuccinia psidii* genes is effective as both a preventative and curative treatment against myrtle rust, inhibiting disease on *Syzigium jambos* cuttings when applied two days pre-infection and improving plant health and recovery from disease when applied up to two weeks post-infection under glasshouse conditions. The next step was to test the efficacy of the dsRNA in the field. We therefore conducted a small field trial on lemon myrtle (*Backhousia citriodora*) tress at Australian Native Products, The Channon, New South Wales. Trees were sprayed with water, *Green Fluorescent Protein (GFP)* dsRNA as a non-specific dsRNA control, *A. psidii translation elongation factor 1α (EF1α)* or *A. psidii beta-tubulin (BTUB)* dsRNA. Trees were scored for disease prior to spraying with dsRNA and again 12 weeks later. The preliminary results show that trees treated with *EF1α* dsRNA had signficantly fewer symptoms compared to the controls 12 weeks post spray. The dsRNA was stable on the trees for at least 9 weeks but had degraded by 6 months. These results indicate that dsRNA has great promise as a sustainable control for myrtle rust.

New surveillance systems for the detection of airborne *Austropuccinia psidii* in Australia's Botanic Gardens

Ashley Jones[1], *Rohan Kimber*[2], *Kelly Hill*[2], *Daniele Giblot-Ducray*[2], *Nicole Thompson*[2], *Benjamin Schwessinger*[1], *Mareike Moeller*[1], *Yapeng Lang*[1], *Zhenyan Luo*[1], *Andrew Baker*[3]
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A new surveillance system will be discussed for the early detection of airborne *Austropuccinia psidii*. This system will deploy new generation air samplers and environmental monitoring devices within strategically chosen Botanic Gardens across Australia. Samples will undergo downstream molecular analysis to both quantify myrtle rust detections in the air by quantitative PCR and sequence the DNA to enable identification at the strain level and detect novel strains. Detection of strains of concern will generate valuable data to national coordinated approaches that address the risks posed by myrtle rust, including community action and engagement to prevent spread and raise awareness. The systems will also provide completely new epidemiological insights that are important for long-term conservation strategies of many threatened species, currently housed in Botanic Gardens. Linkage to the Gardens also capitalises on on-ground expertise to link airborne detections to these unique sites for symptom scouting of disease outbreaks. The project team will report activities to a website to promote these novel strategies and to visualise the dynamics of airborne myrtle rust at each site using a data dashboard. This aims to enhance pathogen surveillance data available to custodians of Australia's living plant collections and inform plant conservation experts and special interest groups tasked with improving the long-term management strategies for myrtle rust in regions with new and/or established infections. This project, supported by the Saving Native Species Program within the Department of Climate Change, Energy, the Environment, and Water (DEECCW), is a collaboration between plant health surveillance systems and commercialised molecular diagnostic pipelines at SARDI, innovative automation technologies and data management systems at Data Effects, and cutting-edge molecular plant pathology techniques at ANU Research School of Biology.

Decision-making tools for myrtle rust management in plant production

Jacinta Harrop*, NZ Plant Producers Incorporated (NZPPI)*

With a growing body of research on myrtle rust, one of the key challenges for the plant production sector is turning this knowledge into practical tools that support day-to-day decision-making. NZ Plant Producers Incorporated (NZPPI) has been working alongside Robert Beresford from Plant & Food Research and HortPlus, with funding from Te Uru Rākau – New Zealand Forest Service, to address this challenge by developing an online disease management platform for nurseries. Central to this platform is the Myrtle Rust Climate Model, which uses real-time data from local weather stations to predict periods of heightened myrtle rust risk. The model provides plant producers with tailored, timely information to guide disease management practices and the protection of vulnerable species. In September 2024, the platform was further expanded to include other disease models and a weekly email reporting feature to improve accessibility and on-the-ground uptake. This initiative sits within wider developing plant biosecurity management resources. Including Plant Pass, Aotearoa New Zealand's nursery biosecurity scheme. The platform is becoming a critical decision-support tool for disease management in the plant production industry. With almost 240 active users across the country, This presentation will explore how the model works, how producers are using it, and the role of extension and engagement in improving adoption. It also highlights the importance of connecting science with practice to build resilient nurseries and strengthen biosecurity outcomes.

E heke e Heka!

***Taiāwhio Bryers**, Katerina Pihera-Ridge, Michael Barlett, Piata Raroa, Sierra De La Croix*

Kahika (native Myrtaceae species) are an essential component of our native forests. Preserving vitality in Te-Wao-nui-ā-Tāne, they heal the land in times of intensity/extremity and preserve the sanctity/integrity of the forest. The arrival of *Austropuccinia psidii* to our shores has significantly impacted our ngahere. This plant pathogen affects the Myrtaceae family, including our native Kahika species, causing the symptoms of what we see as 'myrtle rust'. Myrtle rust research in New Zealand has broadened our understanding of how each of our native Kahika are affected by the disease. From low impact in Mānuka and Kānuka, to high impact in Ramarama and Rōhutu (*Lophomyrtus* spp.), the high impact of disease for some species is concerning for future succession of Kahika in Aotearoa. We currently lack solutions that can efficiently control or prevent myrtle rust infection long term. With the persistence of ongoing seasonal impacts of Myrtle rust and limited collective knowledge, it becomes imperative to raise awareness beyond science communities. Supported with Unlocking Curious Minds funding, a Scion team led by a Te Ao Māori approach, have developed digital tools that presents science knowledge about Kahika and how they are affected by Myrtle rust. With rangatahi Māori in mind, two bilingual applications; “E heke e Heka!” and “Mātaihia te heka”, were created in the hope these tools will inspire the next generation of Kaimātai Taiao (Explorers of the environment). We will demonstrate their functionality and share key highlights of our journey to develop this virtual ngahere tool.

Genome evolution of the broad host range fungal pathogen, *Austropuccinia psidii*

Zhenyan Luo[*1], **Peri Tobias**[*#2], Lavi Singh[1], Chongmei Dong[3], Peng Zhang[3], Alyssa Martino[2], Maria Quecine[4], Nelson Massola[4], Lilian Amorim[4], Ziyan Zhang[1], Ashley Jones[1], Robert F Park[3], Benjamin Schwessinger[1#], Richard J. Edwards[5#], Thais Boufleur[4#] — [1]Research School of Biology, The Australian National University, Canberra, [2]School of Life and Environmental Sciences, University of Sydney, Camperdown, NSW, [3]School of Life and Environmental Sciences, Plant Breeding Institute, University of Sydney, Narellan NSW, [4] Luiz de Queiroz College of Agriculture, University of São Paulo, Brazil, [5]Evolution & Ecology Research Centre, School of Biotechnology and Biomolecular Sciences, UNSW Sydney, Kensington NSW 2052, Australia — *equal contributions; #co-corresponding*

Rust diseases on plants are caused by fungi in the order Pucciniales. Typically, rust fungi have narrow host specificity however the pandemic biotype of *Austropuccinia psidii* (myrtle rust) has an unusually broad host range. Here we assembled a fully phased chromosome-level genome for the pandemic *A. psidii* and identified key biological findings. We confirm a conserved rust fungal karyotype of 18 haploid chromosomes, in line with fungi for distantly related cereal rusts. Cytological studies supported the karyotype and indicated a bimodal size structure of twelve large and six small chromosomes, in accordance with the assembled sequence data. An interesting observation was chromosomal re-assortment between the two nuclei, with one nucleus carrying 19 and the other 17 chromosomes. The duplicated chromosome, determined with chromatin interaction data, is further supported by chromosome homology analysis. Synteny of universal single-copy orthologs is mostly maintained with the distantly related rust fungus *Puccinia graminis* f. sp. *tritici*, however nucleotide composition and methylation profiles are distinct compared to rust fungi with smaller genome sizes. Our analysis of full mating type loci supports a tetrapolar mating system for *A. psidii* with a novel finding of expanded numbers of peptide pheromone precursors. We show that infection dynamics of *A. psidii* are consistent on four different susceptible host species and transcriptional regulation reveals two distinct waves of gene expression in early and late infection, including allele-specific expression of candidate effectors. These findings provide resources and enhance the understanding of the genome biology and pathology of *A. psidii*.

The enigma of the wide-host range obligate pathogen *Austropuccinia psidii*

Rebekah Frampton[1], Louise Shuey[2], Rebecca Degnan[3], Anne Sawyer[3,4], Alistair McTaggart[4], Shea Addison[1], Beccy Ganley[5], David Chagné[6], Jovarn Sullivan[7], Nicky Hambrook[7], Michael Currie[7], Sophie Eccersall[7], Claudia-Nicole Meisrimler[7], Renwick Dobson[7], **Grant Smith**[1]*

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The obligate biotrophic basidiomycete *Austropuccinia psidii* has a host range of around 500 myrtaceous species including *Leptospermum scoparium* (mānuka). Analysis of RNA samples taken over time from pathogen challenged mānuka plants revealed the presence of a number of differentially expressed putative effector genes. Effectors are relativity small cysteine-rich proteins that facilitate pathogen entry into and manipulation of the host plant cell, including suppression of plant defences responses and altering plant cell physiology to benefit the pathogen. In the phased double-haploid *A. psidii* genome, 1,233 putative effector genes have been identified. Pathogen gene expression of three putative effectors, APSI_P014.1260.t1 (Effector Candidate 1(EFC1)), APSI_P001.5292.t1 (EFC2), and APSI_P005.10948.t1 (EFC3), were differential over the first 48 h after inoculation. The pathogen differential gene expression was relatively consistent irrespective of the pre-determined plant resistance phenotype (resistant immune, resistant hypersensitive, susceptible) at least for the first 48h after inoculation. Samples taken 20 min after inoculation contained multiple copies of some effector transcripts suggesting that these transcripts were pre-expressed by the pathogen and are packaged into the urediniospores during their genesis. Research to understand selected effectors as proteins, and identify their plant cell targets, revealed that the rough endoplasmic reticulum and nuclear envelope are potential plant cell targets for EFC1, whilst initial studies using detached *Syzygium jambos* leaf assays targeting EFC2 with dsRNA resulted in almost complete infection knockdown. A second study on the effect of dsRNA on spore germination found that both EF1 and EF2 significantly decreased *A. psidii* spore germination, suggesting additional potential roles for both EF1 and EF2 in spore biology.

Evidence for sexual reproduction in New Zealand populations of the myrtle rust pathogen *Austropuccinia psidii*

***Michael Bartlett**, Louise S. Shuey, Luciano Nunes Leite, Julia Soewarto, Roanne Sutherland, Gayathri Vaidyanathan, Kristin Gillard, Maria Zhulanov, Flávia Bonora, Rebecca M. Degnan, Mahajabeen Padamsee, Alistair R. McTaggart, Stuart Fraser*

Whether fungal pathogens reproduce clonally or sexually impacts their potential for change, such as to overcome host resistance or develop fungicide resistance. It is uncertain whether *A. psidii* is strictly clonal in invasive populations and the degree to which sexual reproduction may play a role. We hypothesized that in invasive populations of *A. psidii* with low founding diversity, clonal reproduction would predominate, with prevalence of a few highly successful genotypes. We used whole genome amplification to enable genotyping for 379 single pustules of *A. psidii* collected from ten geographic populations in New Zealand over three years, across three different host species, including samples from the original 2017 incursion, to test whether genotypic diversity changed over time, on hosts, and across long distances. We found high genotypic diversity, a high effective population size, no evidence of linkage among loci based on the index of association, and the production of sexual spores in most populations, all supporting the occurrence of frequent recombination, likely driven by sexual reproduction, in an invasive population of *A. psidii*. This finding has implications for management, including current resistance in endangered host populations and resistance breeding, the potential for fungicide resistance and potential outcrossing with different strains if new diversity arrives in New Zealand.

Early career initiatives and research – Day 2

Characterisation of *Austropuccinia psidii* Effector Proteins Expressed During Infection of Myrtaceae

Jovarn Sullivan[1]*, Michael Currie*[1]*, Sophie Eccersall*[1]*, Tara Curtis*[1]*, Nicky Hambrook*[1]*, Rebekah Frampton*[2]*, Ashish Sethi*[3]*, Vanessa Morris*[1]*, Grant Smith*[2]*, Claudia Meisrimler*[1]*, Renwick Dobson*[1]
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The study of effector proteins is essential for understanding the molecular mechanisms that enable plant pathogens to infect host species. *Austropuccinia psidii*, the causal agent of myrtle rust, utilises a repertoire of effector proteins to manipulate host plant cellular processes. Given that *A. psidii* has been observed to infect over 500 species within the Myrtaceae family, understanding its infection mechanism is critical for developing effective treatments. Characterising effector proteins often requires a multidisciplinary approach that combines cell biology, structural biology, and protein biochemistry techniques. These techniques depend on obtaining pure protein in milligram quantities, typically achieved through recombinant expression in *Escherichia coli*. We aim to elucidate the roles of four putative *A. psidii* effector proteins during infection through bioinformatic and biophysical analysis. However, as is the case with *A. psidii*, obtaining large quantities of proteins with high cysteine content has proven challenging, with previous efforts often resulting in poor yield and solubility. One of these effector proteins, AP1260, has been successfully expressed and purified, though *A. psidii*'s dikaryotic nature has led to the presence of two haplotypes of this protein. Biophysical studies have sought to determine the physical characteristics of both haplotypes in solution. These include analytical ultracentrifugation, circular dichroism, small-angle X-ray scattering, and nuclear magnetic resonance. Functional analysis of AP1260 uses agrobacterium-mediated transformation of *Nicotiana benthamiana* to determine its localisation and potential *in planta* interaction partners. The characterisation of AP1260 and other effector proteins unveils previously unknown knowledge of the mechanisms of *A. psidii* infection.

Cryopreservation for conserving *Gossia* species threatened by myrtle rust

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Many *Gossia* species, including *Gossia fragrantissima*, are severely threatened by myrtle rust and face a high risk of extinction. As affected species produce few seeds in the wild, and as the seeds are considered likely to be short-lived in storage, alternative *ex situ* conservation strategies are urgently needed. This study presents a high-efficiency cryopreservation protocol for *G. fragrantissima*. With only very limited wild populations and viable fruits often absent due to myrtle rust, shoot tips were used for cryopreservation to enable the capture and long-term storage of remaining germplasm. Initial trials using sucrose-pretreated explants cultured on standard Woody Plant Medium (WPM) achieved moderate regrowth (~70%) after liquid nitrogen treatment. However, explant health prior to cryopreservation was highly variable and influenced post-cryopreservation regrowth. To address this, we developed a new basal medium (PB) to improve nutrient uptake and shoot vigour before cryopreservation. Shoot tips grown on PB showed improved quality—less necrosis, better leaf colour, and more consistent callusing—and achieved nearly 100% regeneration after liquid nitrogen treatment, without the need for additional pretreatments. These results highlight that explant condition before cryopreservation is critical to success. Our protocol provides a reliable method for preserving *G. fragrantissima* and may be adapted for other Myrtaceae species affected by myrtle rust across Australasia. Incorporating tailored tissue culture systems into conservation programs offers a long-term strategy to safeguard these species when other options, such as seed banking, are not viable.

Establishing a cryopreservation protocol based on droplet vitrification to secure the germplasm of critically endangered native *Lenwebbia* sp. Main Range

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Lenwebbia sp. Main Range (P.R.Sharpe + 4877) - a member of the *Myrtaceae* family that is currently being threatened with myrtle rust disease - is now listed as "critically endangered" in the International Union for Conservation of Nature's Red List. Development of *ex situ* conservation techniques, including cryopreservation, will facilitate efficient germplasm capture of this, and other myrtle-rust-threatened species, and provide materials for possible future tolerance breeding and re-vegetation. In this study, we present the first attempt to establish a disease-free *in vitro* propagation and cryopreservation workflow for *Lenwebbia* sp. Main Range. A tissue culture system was developed and able to support multiplication, rooting and acclimatization of healthy *Lenwebbia* plantlets to *ex vitro* conditions. To date, 100% survival and regrowth of excised *Lenwebbia* apical shoot tips has been achieved after dissection. Dissected shoot tips exposed to Plant Vitrification Solution 2 (PVS2) for 10 and 20 minutes, followed by liquid nitrogen storage, have achieved survival rates of 20 and 30%, respectively. These findings have established the first crucial baseline for optimizing protocols and advancing efforts to cryobank endangered *Lenwebbia* and potentially other *Myrtaceae* species. Optimization of culture media to improve culture vigor and cryobanking recovery rates for this species is underway. The progress in creating "frozen collections" of *Myrtaceae* stands as an example of a timely response plan, made possible through the collaboration of research institutes, governmental bodies, and industry partners, to protect biodiversity under imminent threat of extinction.

Investigation of fungal communities associated with myrtle rust infection and the use of mycoparasites as potential biocontrol agents against the disease

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This study investigated the fungal communities associated with myrtle rust and identified potential mycoparasites for biocontrol. Leaf samples were collected from two native plant hosts, ramarama (*Lophomyrtus bullata*) and pōhutukawa (*Metrosideros excelsa*), in forests (Taranaki and Rotorua) and urban areas (Auckland and Christchurch). Metabarcoding revealed that Ascomycota (58.7%) and Basidiomycota (39.7%) dominated the fungal communities. At the genus level, an ASV assigned to rust pathogen *Austropuccinia* was relatively more abundant in *M. excelsa* than *L. bullata*, and higher relative abundance in urban than forest environments. From fungal isolation, 208 fungal isolates representing 64 genera were obtained. Among these, 23 putative mycoparasites from 11 genera were selected for antagonistic screening against *A. psidii*. Three *in vitro* assays including detached branchlet, spore germination, and pathogenicity tests were conducted. Two promising isolates (*Cladosporium* and *Trichoderma*) colonized 33–35% of rust pustules and inhibited 63–70% of urediniospore germination. Neither isolate caused disease symptoms on inoculated leaves. Greenhouse trials were carried out to evaluate their effectiveness under preventive (two days before rust inoculation) and curative (seven days after inoculation) applications. Preventive treatments significantly reduced the disease severity index to 19%, compared to 30% in the curative treatment and 33% in the untreated control. *Trichoderma* also promoted plant regeneration by increasing new shoot growth compared to *Cladosporium* and the control. These findings contribute to understanding the role of microbial communities in myrtle rust infection and inform the development of biocontrol strategies.

Could variation in susceptibility to myrtle rust infection of *Metrosideros excelsa* be linked to the endophytic microbiome?

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Metrosideros excelsa, pōhutukawa, is a New Zealand tree from the Myrtaceae family, often planted in the country. *Austropuccinia psidii* arrived in New Zealand in 2017, causing myrtle rust disease of native Myrtaceae. Observations suggested that *M. excelsa* display different levels of susceptibility to *A. psidii*; therefore, during summers 2022-23, 2023-24, and 2024-25, we surveyed 86 *M. excelsa* trees across nine sites in urban Auckland, recording infection levels and factors that might be linked to the infection. The highest mean infection was recorded in the 2022-23 summer, significantly higher than infection rates in the following 2023-24, and 2024-25. These data align with climate-based disease risk modelling predictions. Notably, the individual trees remained at the same level of relative susceptibility year-on-year, with some highly susceptible trees located close to individuals with mild symptoms of infection, suggesting susceptibility is an internal characteristic of individual trees. As we observed that *M. excelsa* seedlings also displayed various susceptibility to myrtle rust, we further investigated the vertical transmission of *M. excelsa* microbiome and the variation of microbial communities among 30 individual healthy trees. The results demonstrate that individual trees accumulate different microbial communities, and seedlings of each tree retain this difference after being grown in identical conditions. Some seed-borne bacteria suppressed seed-borne fungal pathogens in a dual culture assay. One *Bacillus* isolate significantly inhibited the germination of *A. psidii*. In the seed inoculation experiment, several microbial taxa enhanced seedling development. These results indicate that the seed microbiome may influence seedling growth and protection against pathogens.

New technologies, solutions, and research insights – Day 2
Part 2: Environmental and microbial insights

He aha te whakaaweawe o te heka kahika ki ngā moroiti rau? What is the impact of myrtle rust on the leaf microbiome?

Hanareia Ehau-Taumaunu *— Plant & Food Research, Auckland; Bioprotection Aotearoa, Lincoln*

Maire tawake (*Syzygium maire*) is the sole endemic representative of the *Syzygium* genus in Aotearoa and is uncommon owing to land clearing and swamp draining. Maire Tawake is now critically endangered because of its extreme susceptibility to myrtle rust. This research explores the maire tawake microbiome and the impact of myrtle rust on microbiome composition. Leaf samples were collected from the bottom canopy of asymptomatic and symptomatic maire tawake in Tāmaki Makaurau and Taranaki during the 2024/25 summer. The microorganisms (e.g. bacteria, fungi, viruses) were washed off the leaf surface and their DNA was extracted. Following whole genome sequencing, the resulting reads were processed, and taxonomic classification was performed using Kraken2 with the PlusPFP database. Results showed that asymptomatic leaves had a larger microbial diversity of assigned sequence reads than for sequences of leaves infected with myrtle rust. Although, fungi are hard to capture in the sequence data, the phylum of myrtle rust, Basidiomycota, was dominated by the genus *Puccinia*, whereas Ascomycota was dominated by multiple genera. This is work is the first step in understanding the microbiome's role for susceptible and resistant Myrtaceae plants to myrtle rust.

Sustainable myrtle rust management: Experimental approaches to bacterial suppression of rust disease

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Myrtle rust infection poses a serious threat to some native and exotic species in the Myrtaceae family. There is an urgent need to develop alternative control methods for the disease to reduce reliance on conventional synthetic fungicides. Three novel bacterial antagonists isolated from healthy myrtaceous plants, with potential biocontrol activity, were analysed for their effect on the infection of susceptible *Lophomyrtus* sp. 'Red Dragon' plants. All bacterial antagonists were tested alone and in different combinations against myrtle rust in vitro, using detached plant twiglets, and in vivo using young potted plants. In vitro and in vivo experiments showed that bacterial antagonists worked better as curative agents applied after rust infection. The results with potted plants showed that the antagonist *Bacillus* sp. together with the combination of *Pseudomonas* sp./ *Serratia* sp., when applied after infection by myrtle rust, significantly reduced rust infection relative to the positive control (rust only) by 54% and 49%, respectively, compared with 35% reduction by the commercial control Bacstar™. The positive effect of the bacteria was most evident in the new plant tissue produced during the experiment. The dynamics of the bacterial antagonists on the leaf surface was examined using metabarcoding. Metabarcoding analysis demonstrated that genera encompassing the bacterial antagonists had greater relative abundance on the leaf surface after they were inoculated, suggesting that these strains had survived and colonised the leaf surface in the presence of myrtle rust. Further research is needed to understand the commercial potential of the promising bacterial antagonist.

Correlations between historical land use and host density can help to prioritise management of a wet sclerophyll forest community in Eastern Australia.

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Plant pathogens such as myrtle rust pose a significant threat to native forests, and their impact can be influenced by environmental pressures like land clearing. The extent to which land clearing alters the density and distribution of susceptible species is crucial to understanding how myrtle rust affects forest landscapes. We hypothesized that patches of wet sclerophyll forest with greater human disturbance—particularly land clearing—would show higher densities of susceptible species in the understory layer. This is likely due to the ability of some highly susceptible species to act as early colonisers and their capacity to coppice, enabling rapid recovery after disturbance. To test this, we surveyed 21 patches of wet sclerophyll forest in eastern Australia, varying in land tenure and historical clearing. We found a positive interaction between past land clearing and myrtle rust impacts, largely driven by the abundance of rose myrtle (*Archirhodomyrtus beckleri*), a highly susceptible species. Sites with more of these trees also showed more severe branch dieback. Additionally, we observed greater species richness in the regeneration layer at sites with higher densities of susceptible trees. This may support the Janzen–Connell hypothesis, where high densities of susceptible hosts increase pathogen pressure, reducing dominance and promoting diversity. Our findings suggest that regrowth patches are more vulnerable to myrtle rust because of the nature of their understory composition and this result has management implications. Formerly heavily cleared sites may benefit from thinning and weeding, while less disturbed areas should receive targeted conservation to protect healthier endangered species.

The influence of forest edge effects on myrtle rust infection of *Lophomyrtus bullata*

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The small rain forest tree *Lophomyrtus bullata* is one of the most susceptible species in New Zealand to myrtle rust, and it is infected across most of its natural range which covers the northern half of New Zealand. Infection has caused the death of mature individuals in highly-affected areas, and there is concern that recruitment might be affected due to the infection of fruit and flowers, and the death of highly-susceptible seedlings. Shortly after the arrival of myrtle rust in New Zealand, it was observed that *L. bullata* was infected more heavily at forest edges. Infection was also higher with high humidity and temperature. To explore these observations, we established a set of transects running from forest edge to 60 m into the interior in a lowland rain forest in Taranaki where *L. bullata* was abundant. Along these transects we measured abundance and density of *L. bullata* and their co-occurring species, canopy cover, and temperature and humidity. We also did a detailed survey of myrtle rust infection at the time of peak infection in 2021, 2022, and 2023 with almost 100,000 leaves inspected across 145 plants. We show that infection was more severe further from the edge, where the forest canopy was more intact, forest structure more complex, and humidity higher, but only in the first year. In subsequent years, the influence of edge was no longer evident as severity became more even across the site.

Species conservation – Day 2

Identifying potentially suitable and accessible refugia to mitigate impacts of an emerging disease on a rare tree

***Sarah Herbert**, Te Herenga Waka | Victoria University Wellington*

Identifying refugia from emerging threats is vital for ensuring the persistence of rare and threatened species, but modeling habitats for these species is challenging. Moreover, current approaches to refugia modeling rarely consider people, who are essential for ensuring persistence of small populations. The introduction of myrtle rust to Aotearoa New Zealand represents a grave threat to the threatened and culturally important wetland tree maire tawake (*Syzygium maire*). We urgently need to identify refugia in accessible locations to enable the conservation of this species. Focusing on the capital city region, we demonstrate a novel combination of high-resolution hydrological modeling and integrated species distribution modeling. We map two myrtle rust infection risk scenarios throughout the region to identify areas of lower disease risk and use distance to road as a proxy for human accessibility. We identify 1,230 km^2 of waterlogged habitats for *S. maire* in the region. Of these, 1-52 km^2 are the most feasible for conservation management because they are predicted to potentially support high relative abundances of *S. maire*, are road accessible, and offer lower risk of myrtle rust infection under the mapped scenarios. Finally, we show that only protecting trees in low risk or accessible refugia is unlikely to be sufficient to maintain the regional population as the myrtle rust pandemic proceeds. We highlight the advantages of a highly local approach to refugia modeling for an endangered tree species and recommend leveraging human-nature interactions to create, expand, and protect habitat for rare species in a rapidly changing world.

Myrtle Rust in NSW: Strategies for Species Conservation

***Craig Stehn**, Senior Threatened Species Officer, NSW Department of Climate Change, Energy, the Environment and Water, Coffs Harbour, NSW 2450*

Myrtle rust has led to the rapid decline of several species in New South Wales and its effects are now modifying entire ecosystems. In 2019, two previously widespread and common species, *Rhodomyrtus psidioides* and *Rhodamnia rubescens*, were listed as critically endangered under the NSW Biodiversity Conservation Act due to impacts from the pathogen. Two additional species – *Lenwebbia* sp. Main Range and *Rhodamnia maideniana* – have since been listed as well. All four species have effectively ceased recruitment due the impact of myrtle rust infection on flowering, fruit set and seedling establishment. Since listing, staff from the NSW Saving our Species program, the Australian Botanic Gardens Mt Annan, the Australian Network for Plant Conservation, and the Research Centre for Ecosystem Resilience have been working together to understand these impacts and implement recovery actions. Due to the rapid declines, actions have focused on field surveys, germplasm collection, genetic studies, and the establishment of ex situ collections. Rust resistant lineages have been identified in *Rhodamnia rubescens* and these are now being tested through a series of field trails at Mt Annan and on the NSW north coast (Coffs Harbour Botanic Garden and the Minyumai Indigenous Protected Area). These field trails will provide important information on the durability of resistance under field conditions and will potentially produce open pollinated seed stock from known resistant lineages for future reintroduction into the wild populations.

Ex situ conservation of myrtle rust-affected species at the Botanic Gardens of Sydney

***Lyndle Hardstaff**, Curtin University and Botanic Gardens of Sydney*

Living collections at the Botanic Gardens of Sydney (BGoS) are an essential resource for the long-term conservation of species severely affected by myrtle rust in the wild. Myrtaceae species representing a substantial amount of wild diversity are maintained as specimens in the gardens, potted collections in the nursery, and in tissue culture and seedbank collections. Conservation strategies for each species are dependent on the storage potential of seeds, the availability of plant material for propagation, and the ease of propagation; however, each collection type has its own benefits and challenges. Tissue culture collections at BGoS have become increasingly valuable for conservation research as the number of species and accessions for each species increases, guided by genetic analysis to improve diversity in collections. These collections provide an important back-up for wild, potted and garden collections in an environment that is disease free and unaffected by environmental stresses such as drought and fire. Recent progress in optimisation of tissue culture media for *Syzygium paniculatum*, *Rhodamnia rubescens*, and *Rhodomyrtus psidioides* suggests that lower levels of nitrates, higher levels of micronutrients, and higher levels of iron support better recovery of shoot tips. These results will guide optimisation of cryopreservation protocols that may be used for long-term and less labour-intensive conservation.

Key Learnings and Recommendations from the 8th IUFRO Workshop on Resistance Mechanisms and Breeding in Forest Trees

***Mia Townsend**, Chief Executive Officer, Dieback Working Group Inc.*

The recent introduction of the invasive myrtle rust pathogen (*Austropuccinia psidii*) has had immensely destructive impacts on natural ecosystems throughout Australia and New Zealand. In an Australian context, *A. psidii* is listed as a key threat driving native plant species towards extinction in the wild and is highlighted as an issue of environmental significance in the National Threatened Species Action Plan 2022-2032 (Commonwealth of Australia, 2022).

To date, efforts to prevent these extinctions have extended to germplasm collection, screening for resistance, and research to understand the genetic diversity across remaining populations of species at risk. It is now critical to consider the next steps for these species, including how to best support their persistence outside of ex situ conservation collections. This presentation will outline key findings and recommendations after attendance of a representative from the National Myrtle Rust Working Group at the International Union of Forest Research Organisations' (IUFRO) 8th Workshop on Resistance Mechanisms and Breeding in Forest Trees.

Attendance at this workshop, to be held from 01/06 to 06/06 in British Columbia, Canada, along with the production of a post-conference report has been jointly funded by the Dieback Working Group and the Commonwealth of Australia's Department of Climate Change, Energy, Environment and Water (DCCEEW).

Seed Banking in Aotearoa – The Kaupapa Māori approach

Marcus-Rongowhitiao Shadbolt, *Te Tira Whakamātaki*

For a long time, Aotearoa, New Zealand has not had a formal, targeted approach to seed banking. However, since the initial incursion of Myrtle rust into Aotearoa in 2017, Te Tira Whakamātaki (TTW), hosts of the Māori biosecurity network, have been working across the country to inform, upskill, and resource our communities to better identify the rust, and to store seeds. This has involved work at all levels, from policy and legal rights, to training and resourcing communities, and even lab-based research projects looking into the storage behaviour of native species. International partnerships and relationships have also been a vital part of our response, and this talk will additionally discuss how we have incorporated and benefitted from connections in Australia, Hawai'i, and the UK. In this presentation, Marcus-Rongowhitiao Shadbolt will be discussing how TTW has engaged and trained Māori communities to tackle these challenges by looking at both the journey so far, and where we hope to go next.