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NGĀ TAONGA

MPI 18607 Project Report

Scoping a resistance breeding programme: Strategy pathways for implementation

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Executive summary

The problem

The objective of this project was to develop a breeding framework to facilitate long-term maintenance of healthy populations of Myrtaceous species in New Zealand.

Myrtle rust has the potential to cause significant impacts upon native and introduced Myrtaceae species in New Zealand, including native species extinctions and broader environmental impacts. Breeding approaches, including germplasm conservation, genetic improvement for enhanced resistance, and reforestation with genetically improved material in severely impacted taxa, have clear potential to reduce the impacts of the disease (Sniezko and Koch 2017). However, myrtle rust will have variable impact across the c. 200 native and exotic Myrtaceae species in New Zealand, and different species will be a higher priority than others for action, so it will be important to formulate appropriate breeding responses on a case-by-case basis.

Key results

The major outcomes of the study were:

- Possible breeding responses were identified, including: genetic collections and the establishment of seed stands; cryopreservation and seed storage; building breeding programmes; and the use of molecular genetics/genomics.
- A decision framework was developed to prioritise and identify appropriate breeding responses for each species on the MPI list of important New Zealand Myrtaceae species (see MPI 18607 Project 3.5 report, September 2018, summarised in Appendix B).
- Simulations were performed to identify: i) sampling strategies to ensure genetic variation in the host species is captured; ii) the probability of host survival; and iii) how this probability is affected by the introduction of resistant host genotypes, for species with different distributions and levels of population structure.
- Strategy pathways were identified for MPI to implement breeding as part of the long-term response to myrtle rust.
- Discussion with Research team for Theme" Te Ao Māori" has identified four key themes which must be considered for application of these recommendations in Phase 2 of the MPI response to the myrtle rust incursion ─ ongoing consultation will be critically important.

Recommendations and conclusions

- A triage breeding system is recommended to identify appropriate breeding responses for different host species. Key targets for action include: threatened (nationally critical and nationally endangered) species, taonga species/trees and/or highly susceptible species.
- Geo-located seed collections for all native species. Structured collections will be beneficial for all at-risk species, providing the basis for future conservation, breeding and research programmes.
- Ex situ conservation plantings for high-risk species (priority 1; Appendix B, C).
- The genetic diversity of the pathogen needs to be monitored long-term to detect any changes.
- Te Ao Māori considerations must be adopted and used to co-develop culturally appropriate breeding programmes for selected species.
- Coordination and sharing information across projects and organisations within New Zealand and elsewhere will be crucial to maximise the efficiency and success of long-term management strategies (in line with the New Zealand Myrtle Rust Strategy 2019-2023).

Highest priority recommendations

We recommend the continuation of this scoping work through the formation of a cross-sector action group to co-develop, with the appropriate kaitiaki of indigenous flora, an implementation plan for the breeding programme triage system, coordination of further seed collections and their appropriate protections.

We recommend that the high-risk species (Priority 1; Appendix B, C) should have action plans developed and implemented as soon as possible.

Contents

1 Project background

To better understand myrtle rust and limit its impact in New Zealand, the Ministry for Primary Industries commissioned a comprehensive research programme in 2017 with more than 20 projects valued at over $3.7 million. Projects in this programme were completed by June 2019.

The projects covered research in the following themes:

- Theme 1 - Understanding the pathogen, hosts, and environmental influence.
- Theme 2 – Building engagement and social licence: Improved understanding of public perceptions and behaviours to allow better decisions about investment, improved design of pathway control strategies and maintain social license for use of management tools.
- Theme 3 – Te Ao Māori: Greater understanding of Te Ao Māori implications of myrtle rust in order to support more effective investments, and improved use of Mātauranga, specific Māori knowledge, and kaupapa Māori approaches in management regimes.
- Theme 4 – Improving management tools and approaches: Improved diagnostic and surveillance speed, accuracy and cost-effectiveness, supporting eradication efforts and enabling scaling up of surveillance efforts for a given resource. More effective treatment toolkits to avoid emergences of MR resistance to treatments and to enable disease control over increasingly large scales that will lead to reduced or avoided impacts.
- Theme 5 - Evaluating impacts and responses: Improved understanding of environmental, economic, social and cultural, impacts to inform risk assessment and management and to communicate implications to decision/makers and stakeholders.

This report is part of the MPI commissioned research under contract MPI18607 which addressed research questions within Theme 2, 4 and 5.

Text in the report may refer to other research programmes carried out under the respective theme titles.

2 Introduction

Myrtle rust (Austropuccinia psidii [G. Winter] Beenken) is a globally significant rust fungus that is native to South and Central America, but in recent years has spread to new areas with increasing speed. It has an unusually broad host range within the myrtle family (Myrtaceae), which includes taxa of cultural and economic importance in New Zealand, such as Leptospermum scoparium (mānuka) and Metrosideros spp. (pōhutukawa, rātā). Genetic diversity in A. psidii is highest in its native range, including different strains which have variable impacts on different hosts. In contrast, a single ‘pandemic’ genotype is found in most recently invaded countries in the Asia pacific region, including New Zealand and Australia.

Since the first detection on mainland New Zealand in May 2017, myrtle rust has spread to most areas that are climatically suitable for the disease, including sites across the North Island and northern parts of the South Island. Taranaki, Auckland and Bay of Plenty are the worst affected areas and most reports have been from Lophomyrtus spp. and Metrosideros spp. The potential long term impacts of myrtle rust on New Zealand’s native and exotic Myrtaceous flora are difficult to predict. However, findings from elsewhere suggest severe impacts, including species extinctions and broader ecological consequences, can be expected where highly susceptible taxa occur in areas which are climatically suitable for myrtle rust.

There are few cases globally of genetic improvement programmes to combat disease in native trees species and the re-introduction of more resistant individuals into wild populations. However, examples of successful selection/breeding programmes and reforestation using trees with enhanced resistance for pine blister rust in the white pines (Pinus spp.) and Phytophthora lateralis in Port-Orford-Cedar (Chamaecyparis lawsoniana) in the U.S.A. clearly demonstrate that such programmes can help alleviate the impacts of exotic diseases (Sniezko and Koch 2017). In combination with other initiatives in place to help monitor, predict and manage the impacts of myrtle rust in New Zealand, resistance characterisation of germplasm in susceptible hosts and (where appropriate) breeding for resistance can facilitate the long-term maintenance of healthy Myrtaceous populations, both in the wild and in plant-based industries.

The aims of this project were to:

1. Identify possible breeding responses.
2. Formulate a ‘decision framework’ to prioritise and allocate New Zealand’s Myrtaceous flora to appropriate breeding responses.
3. Perform simulation studies to identify sampling strategies, the probability of survival after the introduction of a new pathogen, and how this is affected by the introduction of resistant genotypes, for species with different population characteristics.

Together, this research is used to identify strategy pathways for MPI to implement breeding as part of the long term response to myrtle rust.

3 Methods and Insights

3.1 Possible high-level breeding responses and recommendations

Possible breeding responses were identified (Table 1), including:

- genetic collections and the establishment of seed stands;
- cryopreservation and seed storage;
- building breeding programmes; and the
- use of molecular genetics/genomics.

We suggest that species that are known to be highly susceptible or are threatened (nationally critical and nationally endangered; (de Lange et al. 2018), have all approaches developed (Priority

1 and 1/2; Appendix C). We also suggest that as a minimum, genetic collections of seed are undertaken for all native species (New Zealand Myrtle Rust Strategy 2019-2023). Targeted range-wide collections are recommended for all native species of moderate to high risk. The greatest value from these collections will be achieved where the collection point is known and geo-referenced to enable possible future returns to the site if any resistance is found. We recommend that cryopreservation techniques are developed at least for the most at-risk material. We also recommend additional collections of vegetative material for freezing to facilitate any possible future DNA-based genetic analyses. Where important species occur in areas of high myrtle rust risk (e.g. Beresford et al. 2018), as a minimum action to the incursion, seed collection and planting in areas of low risk should be done.

3.2 Decision framework to prioritise and identify appropriate breeding responses for New Zealand *Myrtaceae* species

We adapted the ‘risk assessment decision tree’ developed for Australia (Berthon et al. 2018) to consider the unique New Zealand flora and the unique role of Māori as kaitiakitanga (guardians), including whakapapa linkages, as well as the outstanding Wai262 Treaty Claim. Considerations for prioritisation for exotic versus indigenous Myrtaceae species are related but adapted for the New Zealand context (Appendix B).

3.3 Simulation studies

We simulated the effects of population sizes and distributions to answer three key questions.

- To inform seed collections in New Zealand’s native Myrtaceous species, we simulated the effectiveness of different sampling efforts in capturing the genetic variation in populations with different gene flow characteristics (i.e. migration rate and distance). Results showed that systematically sampling one in every 5, 10, 15 or 20 individuals/population across a species distribution had the same impact on the retention of genetic diversity (rare alleles) regardless of the intensity and distance of gene flow (Appendix A).
- To help predict the response of natural populations to myrtle rust, we simulated the evolutionary response of populations to environmental change (such as, the introduction of myrtle rust), and the probability of extinction if the evolutionary response is insufficient. Sub-population number (N; Wiser et al. 2017) and maximum population size (carrying capacity; K) were based on knowledge of *Metrosideros excelsa* and *Leptospermum scoparium*. The results showed that species with high population sizes, such as *L. scoparium*, have a high probability of survival, although this probability decreases as genetic diversity and migration rates between sub-populations decrease. In contrast, for species such as *M. excelsa*, small population sizes increased the probability of extinction. However, genetic diversity and gene-flow between sub-populations reduced the probability of extinction. Hence, monitoring genetic diversity and gene flow in populations across the native range of *M. excelsa* will be important to help predict its evolutionary response to myrtle rust. Facilitating gene flow, for example in recently isolated populations, either *in situ* or in *ex situ* conservation populations could be highly beneficial in cases where gene flow is limited.
- We examined how the probability of survival is influenced by the introduction of resistant genotypes into wild populations, from a breeding population which has undergone selection for myrtle rust resistance. The simulation results suggested that adding even a small number of resistant genotypes, increased the probability of population survival, which increased further with the introduction of a larger number of resistant genotypes. This suggests that breeding for resistance and the repatriation of genetically improved individuals into the wild would very likely improve the chance of survival of high-risk plant populations and species. However, in our simulations, small populations (K = 500) remained highly vulnerable to extinction regardless of the introduction of resistant genotypes.

4 Recommendations and Actions: Strategy pathways for MPI to implement breeding as part of the long-term response to myrtle rust

We recommend the development of a co-ordinated national-scale myrtle rust conservation/genetic improvement strategy supported by extensive consultation with stakeholders. Priorities and recommendations should be revised periodically as a better understanding of the impacts of myrtle rust in New Zealand are gained, and in order to incorporate the latest research findings. Many of the recommendations are currently being undertaken in various projects, e.g. Catalyst, but this could be improved through better co-ordination of activities.

Refine and implement a triage system to prioritise species to different breeding responses

A triage breeding system is recommended to prioritise and allocate appropriate responses to different host species and individuals (Appendix B). Key targets for action include: threatened (nationally critical and nationally endangered) species; taonga species/trees; highly susceptible species; and other species of economic, environmental and social importance.

ACTIONS

1) We recommend the formation of a cross-sector action group to co-develop, with the appropriate kaitiaki of indigenous flora:
   a. An implementation plan of the breeding programme triage, and
   b. Coordination of further seed collections and their appropriate protections.
2) Since the level of susceptibility of each species will depend on the genetic variation in resistance present and overlap with climatic suitability for myrtle rust, it will be important to integrate the findings from ongoing research. We recommend developing genetic management action plans for high risk species, including consideration of:
   a. Screening within New Zealand species for variation in myrtle rust susceptibility by artificial inoculation (MPI 18608/Catalyst programme), together with;
   b. The species distribution maps generated under MPI18607 project 3.2 and;
   c. Climatic modelling of disease risk in New Zealand (Beresford et al. 2018).

   Integrating the findings of this ongoing research will help predict the level of risk among species, and populations within species. The predicted climatic risk and genetic susceptibility of host species at different locations should be compared with the results from ongoing surveillance of disease outbreaks, to verify and enhance future predictions. In the longer term, actual observations of species decline due to myrtle rust will help to prioritise species for action (e.g. Makinson et al. 2018).
3) Consultation with iwi/hapū should be performed to identify taonga species, and individual populations or trees within taonga species to help prioritise actions.
4) Consultation with the wider New Zealand public and other relevant stakeholders, such as NZ Plant Producers Incorporated and Forest Growers Ltd, will be important to help prioritise species/populations and gauge the acceptance of management options. This will tie-in with the work within in MPI18607 on building engagement and social licence.

Ensure there is adequate seed capture and storage for at-risk species

It is crucial to preserve genetic diversity, to minimise the impact of myrtle rust and maintain adaptive potential to other risk factors (New Zealand Myrtle Rust Strategy 2019-2023).

ACTIONS

1. Range-wide individual-tree geo-located seed collections are recommended as essential for all at-risk species and important for other native species.
2. Determine the contributions of existing seed collections (Catalyst, etc.) and capture accessible metadata. Critical points include adequate numbers and representation of species distributions, availability of seed for different applications and accurate documentation and geo-locations are taken for each individual-tree collection.
3. Collect sufficient seed to allow for present and future research needs (including genetic screening and research into mechanisms underlying variation in resistance), ex situ conservation, and long-term seed banking.
4. Use the simulation sampling guidelines for sampling density in order to capture genetic diversity in populations with different levels of gene flow.
5. Adopt and/or further develop techniques for seed storage and cryopreservation as an alternative to seed storage, including those developed under the MPI 18608 Catalyst programme.
6. Identify or establish stands in areas of low climate risk, especially for seed production, is a possible approach for some species (Table 1). For example, ex situ conservation populations were successfully established to preserve the genetic diversity in lemon myrtle in Australia due to its economic importance, high susceptibility to myrtle rust, and small fragmented natural populations.
7. Consultation with iwi/hapū is recommended to identify representatives and establish seed collection protocols across New Zealand.

Compile structured collections for at-risk species

Structured collections would be beneficial for all at-risk species of high priority (Table 1), providing the basis for future conservation, breeding and research programmes.

ACTIONS

1) For high priority species, the genetic material used for screening New Zealand species for variation in myrtle rust susceptibility by artificial inoculation (MPI 18608/Catalyst programme), should be compared with the natural distribution and/or structured collections of host species to ensure each species is adequately represented. Structured collections could be initiated and used to supplement existing screenings, where necessary.
2) Population genetic/genomic studies are recommended for high priority species to determine their population status. Our simulation work highlights the importance of host population attributes (i.e. population size, genetic diversity and gene-flow between sub-populations), on the capacity of natural populations to respond to environmental change (such as, the arrival of myrtle rust), including the probability of survival after the introduction of resistant genotypes. Detailed information on population attributes is lacking for most New Zealand Myrtaceae but is required for informed management.
3) Initiate work with the iconic M. excelsa, which is highly susceptible to myrtle rust and represented by small, declining, fragmented populations, and the highly susceptible Lophomyrtus bullata. Engage with iwi/hapū to collect seed samples, which can then later be used to test for resistance.

Monitor for genetic change in the pathogen population

Since new strains/biotypes of myrtle rust can impact host species differently, it will be important to monitor the genetic diversity of A. psidii in New Zealand and the Asia-Pacific region for genetic differentiation, which may occur through mutation, recombination or the arrival of new strains.

ACTIONS

1) Monitor the genetic diversity of A. psidii in New Zealand. This is currently undertaken through (MBIE) research into the possible role of sexual recombination in the New Zealand population of A. psidii. Monitoring should be ongoing, including periodically genotyping A. psidii throughout New Zealand.
2) The establishment of an Asia-Pacific myrtle rust network would help in early warning of new strains entering the region (Makinson et al. 2018).
3) If new strains are detected, they should be included in screening host susceptibility by artificial inoculation.

Work with Te Ao Māori to co-develop conservation and breeding programmes

Kaitiakitanga and whakapapa considerations for native Myrtaceae, and the interconnectedmess between the land, the biota, and the mana whenua must be considered for the co-development and implementation of myrtle rust conservation/genetic improvement strategies. This mahi will align with existing Māori biosecurity solutions for taonga species, which were in place before the disease incursion. It will build on existing relationships, and help fulfil the objectives of the New Zealand Myrtle Rust Strategy (2019-2023).

Our simulation work, and programmes elsewhere, suggest that repatriation/assisted migration of germplasm with enhanced resistance would be a viable option for high-risk host species. However, this form of intervention would require broad consultation and consideration of diverse issues including ecological impacts and Te Ao Māori considerations.

ACTIONS

Through discussions with the research team from Theme "Te Ao Māori", we have identified four key themes which must be considered for application of these recommendations in Phase 2 of the MPI response to the myrtle rust incursion.

1) Taonga

   i) The principles of whakapapa can help to prioritise particular taonga species that are of greater significance, than others. Iwi/hapū should be consulted to identify localised distributions of taonga species and specific populations of high cultural importance.

   ii) Individual hapū have taonga trees that are culturally significant and must be recognised and conserved. For example, the ancient pohutukawa growing on the northern tip of New Zealand at Cape Reinga.

2) Seed collection protocols and identifying stakeholders/representatives

   i. Identification of the kaitiaki of Myrtaceae across New Zealand as contacts for seed collection.

   ii. Determining seed collection protocols, in partnership with Te Ao Māori researchers and the identified kaitiaki.

   iii. Seed tracking and barcoding to ensure integrity of rohe origin is maintained.

   iv. Seed collection agreements and protection plans to safeguard the ownership of the material.

3) Understanding the tools

   Attend regional hui with Te Ao Māori to raise awareness about different management options to help minimise the impact of myrtle rust, including: conservation genetics; sampling strategies to capture genetic diversity; breeding methodology; and raising awareness of the 'g' words (e.g. genetics, genomics, genetic modification).

4) Management plans

   i) Support iwi/hapū to develop their own management plans.

   ii) Inclusive of cultural and kaitiaki priorities.

Table 1: Possible breeding approaches and their application for resistance breeding.

Types of breeding approaches	Description	Possible application	New Zealand Myrtaceae Species in category
Genetic collections	Targeted and range-wide Individual-tree collections of seed. Individual-trees/plants are photographed and GPS location recorded. Consider collecting seed/leaves/vegetative material for freezing and future DNA analysis.	Approach to conserve the base genetic variation. Essential for high-risk species. Optional for others. Individual-tree collections essential for structured breeding programmes.	All species where myrtle rust is a medium-to-high risk (North Island species). e.g. Lophomyrtus spp., Metrosideros spp., Kunzea spp.
Seed stands	Identification or planting of stands specifically for seed production.	Possible approach for species in low risk climate areas for provision of seed for repatriation. Could be used for establishment of seed production areas outside areas where myrtle rust is a risk (e.g. South Island). May require moving outside original rohe.	All species where myrtle rust is a medium-to-high risk (North Island species) and where contiguous healthy stands exist. e.g. Lophomyrtus spp., Metrosideros spp.
Cryopreservation and seed storage	Banking of genetic material frozen as seeds or as tissue culture cell lines would provide a longer-term solution to preserving genetic diversity.	Adopt and/or further develop techniques for seed storage and cryopreservation from MPI 18608 Catalyst program.	Threatened spp., (e.g. Metrosideros bartletti, M. kermadecensis and those at high risk of decline e.g. Lophomyrtus bullata, Metrosideros excelsa and their hybrids.
Quantitative breeding	Development of structured species collections, tests and populations that will allow screening for quantitative resistance using various techniques and future planting for conservation, possible repatriation.	Applied and immediate approach for all at-risk species of high priority. Likely to require movement of plants outside rohe that are in common gardens. Breeding programmes within regions/rohes may be possible. Screening in nursery/glasshouse environments using quantitative approaches within New Zealand would be ideal.	Native species of high priority for conservation, (Metrosideros bartletti, M. kermadecensis) and highly susceptible species (Lophomyrtus bullata, Metrosideros excelsa and their hybrids). Exotic species of very high economic importance, where disease risk may potentially cause a significant impact such as mānuka, industrially important Eucalyptus spp., horticulturally important species, that are highly susceptible, such as Agonis flexuosa and Szygium spp should be considered, pending further discussions with NZ Plant Producers Incorporated and Te Ao Māori researchers.

Types of breeding approaches	Description	Possible application	New Zealand Myrtaceae Species in category
Quantitative breeding with genomics	DNA markers are developed and/or applied in quantitative and structured breeding programmes. The combination of markers and breeding approaches will speed up the selection and deployment of more resistance genotypes, where present.	Applied and immediate approach for all at-risk species of high and very high priority. Likely to require movement of plants outside rohe that are in common gardens. Breeding programmes within regions/rohes may be possible.	Native species of the highest priority for conservation and highly susceptible species (detailed above). Exotic species of very high economic importance, where disease risk may potentially cause a significant impact, should also be considered.
Molecular genetics	DNA markers are used to understand the population structure and/or the existence of resistance genes and their distribution. Detailed analysis of populations will inform management decisions across the species' range tested. Individual-tree/plant collections will be necessary.	Population genetics will allow the development of informed genetic management plans and informed decisions about the real differences within and among rohe. Using DNA science for resistance will be longer-term and in-depth analysis will be required.	Native species which are of the highest priority for conservation, and highly susceptible species (detailed above). Species where discussions about eco-sourcing are based on no evidence or understanding of genetic structure and gene flow in existing native populations.
Combination of all approaches	Using all approaches to maximise the chance of success where species under extreme risk have been identified.	Apply to Threatened species, taonga species, and highly susceptible species.	Native species which are of the highest priority for conservation, and highly susceptible species (detailed above).

5 Acknowledgements

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7 Appendix A

Simulation analyses

We performed simulations to identify how factors such as host population size, genetic diversity and gene flow affect three distinct areas of investigation:

1) efficiency of different sampling strategies;
2) probability of extinction after introduction of myrtle rust, and
3) how this probability is affected by the introduction of resistant genotypes.

i) Sampling strategies

Simulations were performed to address the key question: How do sampling strategies affect the probability of capturing rare alleles in species with differing levels of gene flow among populations?

Simulations were performed with software (IBDsim v2.0; Leblois et al. 2009) for the simulation of genotype data under isolation by distance, which can consider many different dispersal distributions and a large number of genotypes. Simulations were performed on a spatial grid of 70 x 70 points, each representing one individual with 10,000 SNP markers. The mutation rate was set to 0.001 and minor allele frequency to 0.01. Dispersal distribution was simulated through a stepping stone approach as follows:

$$f_k = \frac{M}{2|k|^n}$$

Where M is migration rate and k is number of steps following (-maximum distance < k < +maximum distance). Four scenarios were simulated regarding the intensity and distance of gene flow in the population:

1) Migration rate of 0.15 and maximum dispersal distance 30 points
2) Migration rate of 0.05 and maximum dispersal distance 30 points
3) Migration rate of 0.15 and maximum dispersal distance 10 points
4) Migration rate of 0.05 and maximum dispersal distance 10 points

Each scenario was simulated 100 times. The outcome of sampling (Figure 1) was simulated with one in every 5, 10, 15 and 20 points in the spatial grid.

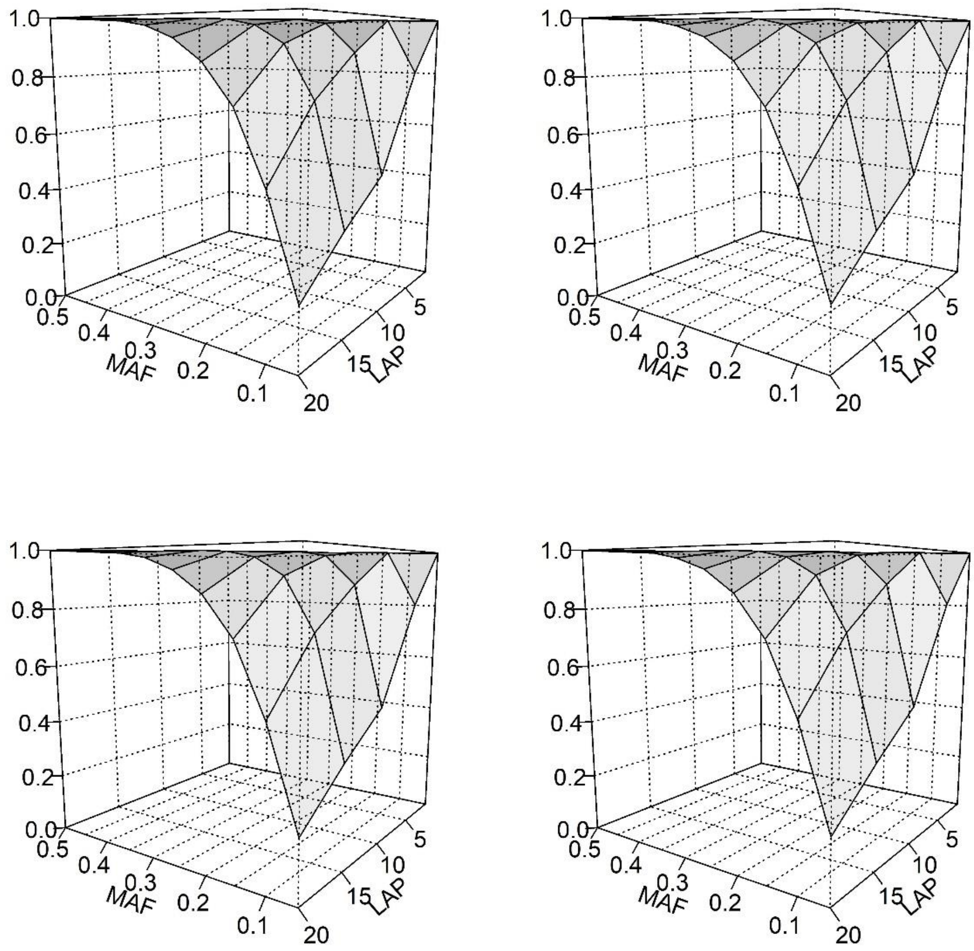

Figure1: Retention of alleles in the sample regarding allelic frequency and sampling effort: scenario 1 (upper left plot), scenario 2 (upper right plot), scenario 3 (bottom left plot) and scenario 4 (bottom right plot). MAF = minor allele frequency. LAP = number of points in the spatial grid between selected individuals; for example, LAP 5 means that selection was performed on one in every 5 points on the spatial grid.

Interpretation

The rarest alleles (minor allele frequency [MAF] of 0.05) were retained at ~20% probability at the lowest density sampling strategy simulated. Among the scenarios which were simulated, a spatially systematic sampling will have the same probability of retention of rare alleles regardless of sampling density and gene flow characteristics in the host population. Hence, relatively sparse sampling is sufficient to capture the genetic diversity within populations under the simulated conditions.

Recommendations

Higher sample numbers are always likely to be beneficial to capture the genetic variation within taxa, especially where life history traits such as the degree of selfing are unknown. However, providing sampling of seed is performed in a systematic manner across a species distribution (rather than transect or 'easy access' sampling, for example), and in the absence of a high rate of selfing, relatively low sampling density is likely to be adequate to capture rare genetic variants even in species with low dispersal.

ii) The probability of survival after the introduction of myrtle rust

The key questions we addressed were:

i) How do gene flow and migration rates influence the probability of survival of a population after the introduction of a new pathogen?

ii) How does the size of the distribution influence the probability of survival of a population after the introduction of a new pathogen?

iii) How does genetic diversity influence the probability of survival of a population after the introduction of a new pathogen?

We used the simulation package SLiM (Haller and Messer 2019) to simulate evolutionary responses to environmental change using their models for Evolutionary Rescue and Meta-population extinction and migration. We used the Evolutionary Rescue after Environmental Change model to examine the evolutionary response of a population to environmental change (in this case, change in optimum phenotype for resistance), and the probability of extinction if that response is insufficient. The probability of extinction was based on the number of extinction events from 100 runs of each evolutionary model (Figure 2).

Evolutionary rescue can be based upon standing genetic variation, new mutations that provide new adaptive potential, or genetic variation brought in by migrants. We focused on a QTL-based model where evolutionary rescue may (or may not) occur as a result of both standing genetic variation and new mutations.

Key parameters of the model that were likely to influence the evolutionary rescue after environmental change included the population carrying capacity, the distance from the old optimum to the new one, the mutational distribution and rate, the lowest fitness effect of the QTL, and the maximum fitness benefit from low population density. This was also a hermaphroditic model, where hermaphroditic selfing is not prevented, however inbreeding depression was not explicitly included in the model.

We defined a QTL mutation type, m1. Each QTL is drawn from a normal distribution centred on 0.0 with a standard deviation of 1.0 (which are important parameters for this model, since the exact nature of the standing genetic variation and mutational variance will be important). We defined constants for population carrying capacity (K), for the phenotypic optimum before and after environmental change (opt1 and opt2), and for the time when the environmental change will occur (Tdelta).

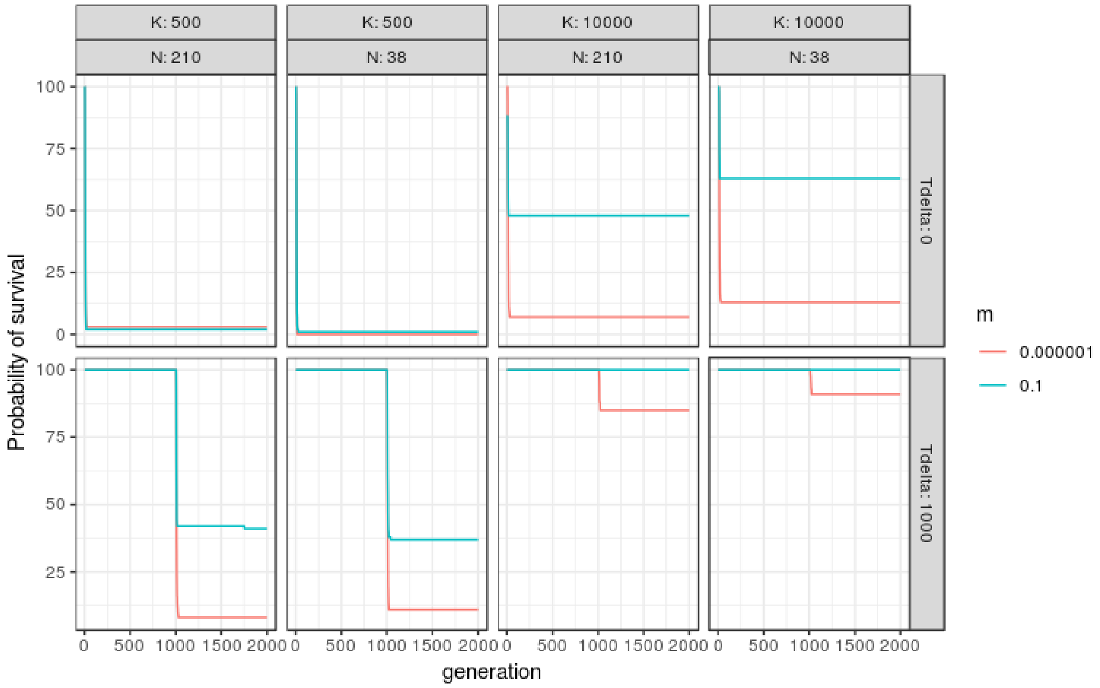

Figure 2. The effect of sub-population number (N), population carrying capacity (K), migration rate between subpopulations (m) and standing genetic diversity (Tdelta) on the probability of survival of the populations in the simulation. Values of N and K were chosen which may be representative of *Metrosideros excelsa* and *Leptospermum scoparium*. For standing genetic diversity, populations were allowed either 1000 generations to accumulate diversity before the introduction of the pathogen or the population was introduced at generation 0 at which point there was no diversity in the population.

Interpretation

We have interpreted our simulation results in the case of two indigenous species with different distribution types (mānuka and pohutukawa; see below). These results are based on assumptions and the theoretical simulation will require validation, but gives some relevance to how the simulation can be applied to a real-world event.

i) Mānuka is a species which is likely to have a high population size (e.g., K > 10,000) and a large number of populations. Low genetic variation in populations (e.g., Tdelta = 0) increased the probability of population extinction. This was exacerbated when migration rates between sub-populations were low (m=0.000001). Increasing migration rates and population sizes reduced the probability of extinction as the likelihood of spread of alleles that confer resistance was increased.

ii) Pohutukawa is a species which has suffered recent decline both in population number and population size, and may suffer from reduced genetic variation as a result of bottlenecks. Low existing genetic variation in populations (Tdelta = 0) almost always resulted in extinction. With increasing genetic variation, there was still a high probability of extinction (>30%) if population sizes were low. The probability of extinction was again reduced, if gene flow between populations occurred (m=0.1 vs m=0.000001), as it allowed the spread of resistant genotypes.

Recommendations

Sub-populations that have not undergone substantial bottlenecks are likely to have sufficient genetic diversity to increase the likelihood of resistance. If there is gene-flow between sub-populations, this would further reduce the likelihood of extinction of these populations.

iii) Does introducing resistant genotypes reduce the probability of extinction after introduction of a new pathogen?

We simulated two populations (**Figure 3**) which were selected for myrtle rust resistance - one with a carrying capacity of 500 individuals (as could be found in pohutukawa) and one with a carrying capacity of 10000 individuals (as could be found in mānuka). After 25 generations (to allow resistance to build up in our breeding population), we introduced myrtle rust into our wild population (by changing the evolutionary optimum). We simultaneously allowed the migration of 100 resistant genotypes from the breeding population into a single population in the wild (m=0.95). This was compared to the wild population where no resistant genotypes were introduced (m=0.000001). Only one introduction occurred in the same generation as the invasion of myrtle rust. The probability of extinction was defined as the number of simulation runs out of 100 where the wild population went extinct. To test the direct effect of introduction of resistant phenotypes, we increased the deleterious effect of myrtle rust so that extinction was more likely in the absence of resistance in the wild population.

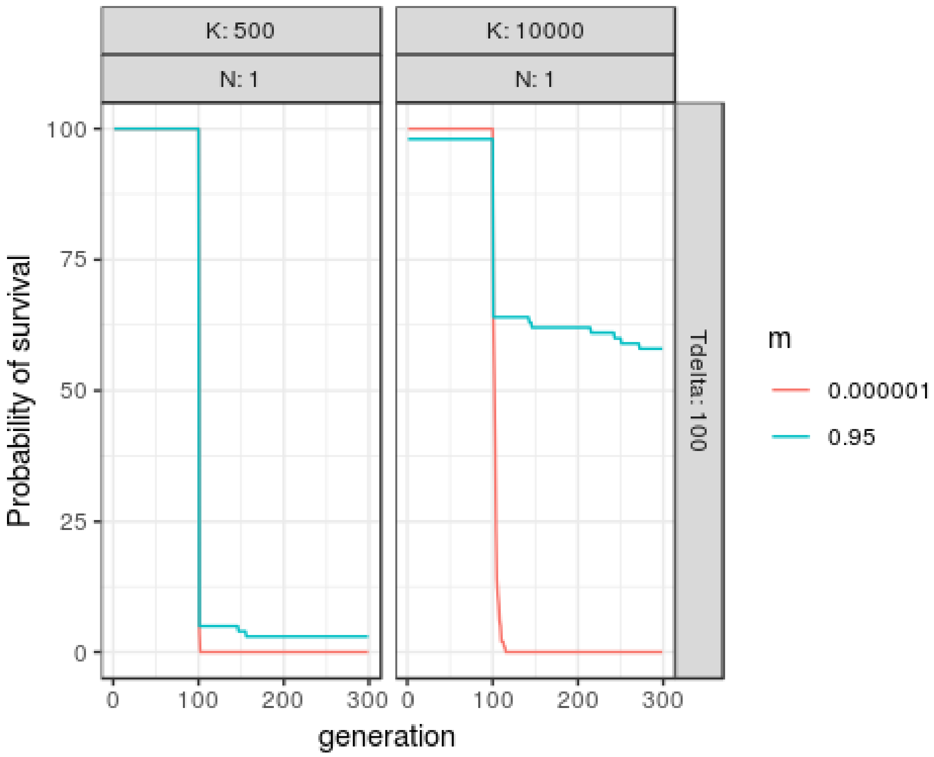

Figure 3: The effect of introducing resistant genotypes (m=0.95) into a single wild population at the same time as invasion by myrtle rust (generation 100). This was compared to the outcome when no resistant individuals were introduced into the wild population (m=0.000001). Two populations were considered: one with a carrying capacity of 500 individuals (K=500; as could be found in Pohutukawa) and one with a carrying capacity of 10000 individuals, as could be found in manuka (K=10000). The number of wild populations was kept at one for simplicity of interpretation (N=1).

Interpretation

Adding resistant genotypes increased the probability of survival of a population, although populations with low numbers of individuals (K=500) remained extremely vulnerable to extinction, even with the addition of resistant genotypes.

The addition of a very low number of resistant individuals (m=0.000001) can reduce the probability of extinction of a population. However, the more individuals introduced, the higher the chance of survival of a population.

Recommendations
Introducing resistant genotypes into wild populations will increase the probability of survival. This scenario should be investigated further using data on known levels of resistance in natural populations.

References

Haller, B. C., & Messer, P.W. (2019). SLiM 3: Forward genetic simulations beyond the Wright-Fisher model. *Molecular Biology and Evolution 36(3)*, 632-637. https://doi.org/10.1093/molbev/msy228

Leblois, R., Estoup, A., Rousset, F. (2009). IBDSim: a computer program to simulate genotypic data under isolation by distance. *Molecular Ecology Resources, 9(1),* 107-109. doi.org/10.1111/j.1755-0998.2008.02417.x

8 Appendix B

Proposed triage breeding system to prioritise and allocate appropriate responses to different host species and individuals

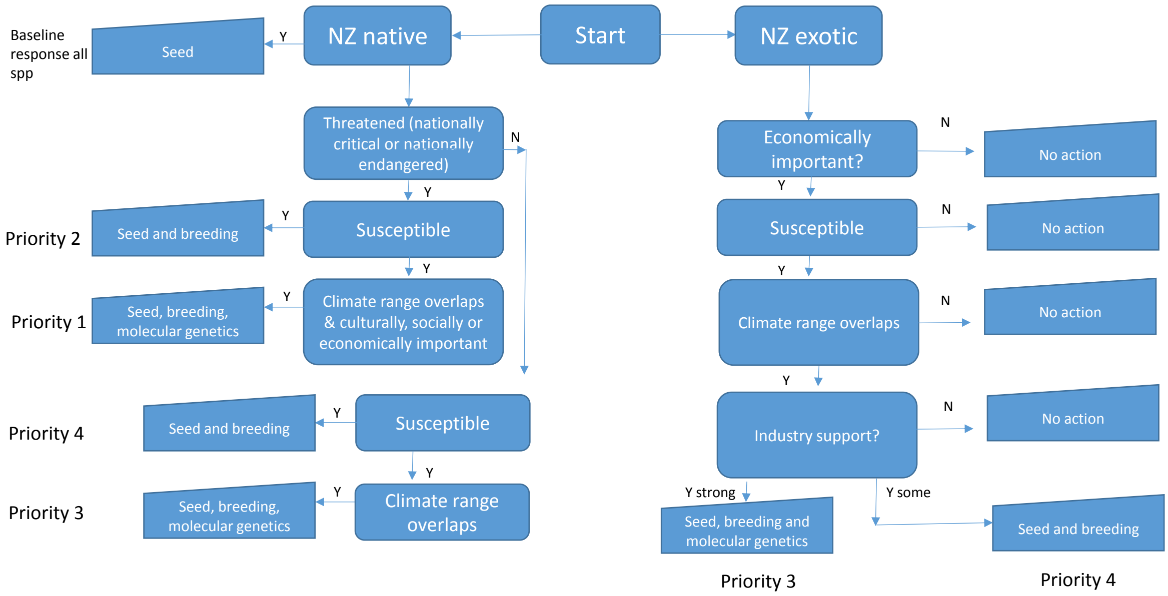

Figure 1: Decision framework adapted from Berthon et al. (2018), as a draft for consideration with New Zealand Myrtaceae species. For NZ native species, 'climate range overlaps' was determined based on whether c. >25% of the species distribution overlapped areas of high to very high maximum predicted infection risk for A. psidii (Figure 7; Beresford et al. 2018).-

Interpretation

Based on these criteria, all native species were allocated to priorities (Appendix C).

References

Beresford, R. M., Turner, R., Tait, A., Paul, V., Macara, G., Yu, Z. D., Lima, L., Martin, R. (2018). Predicting the climatic risk of myrtle rust during its first year in New Zealand. *New Zealand Plant Protection, 71,* 332-347.

Berthon, K., Esperon-Rodriguez, M., Beaumont, L. J., Carnegie, A. J., & Leishman, M. R. (2018). Assessment and prioritisation of plant species at risk from myrtle rust (*Austropuccinia psidii*) under current and future climates in Australia. *Biological Conservation, 218*, 154-162. doi:10.1016/j.biocon.2017.11.035

9 Appendix C

Provisional prioritisation list of important New Zealand Myrtaceae species for consideration in a post-incursion myrtle rust response.

High priority species are given in bold.

Species List	Importance	Tree or Shrub	Status*	Degree of Susceptibility**	Common name	Synonyms	Draft priority for consultation (Based on framework in Fig 4).
Acca sellowiana (O.Berg) Burret	Fruit (Feijoa)	Shrub	Exotic	Low	Feijoa	*Feijoa sellowiana* (O. Berg) O. Berg	Priority 3/4
Agonis flexuosa (Willd.) Sweet	Horticultural	Tree	Exotic	Extremely	Agonis, peppermint tree, peppermint myrtle, river myrtle		No specific action
Amomyrtus luma (Molina) D.Legrande & Kausel		Tree	Exotic		Luma		No specific action
Angophora costata (Gaertn.) Britten	Horticultural	Tree	Exotic	Susceptible	Sydney red gum		No specific action
Angophora floribunda (Sm.) Sweet		Tree	Exotic	Susceptible[1]	Rough-barked apple		No specific action
Astartea fascicularis (Labill.) DC.		Shrub	Exotic	Susceptible			No specific action
Backhousia citriodora F.Muell.		Tree	Exotic	Moderately-Highly[1]	Lemon myrtle		No specific action
Baeckea linifolia Rudge		Shrub	Exotic	Moderately[1]			No specific action
Beaufortia sparsa R.Br.		Shrub	Exotic	Susceptible[1]	Swamp bottlebrush		No specific action
Blepharocalyx salicifolius (Kunth) O.Berg		Tree	Exotic				No specific action
Callistemon citrinus (Curtis) Skeels	Horticultural	Shrub	Exotic	Susceptible	Bottlebrush		No specific action
Callistemon pallidus (Bonpl.) DC.		Shrub	Exotic	Susceptible[1]	Lemon bottlebrush		No specific action

Species List	**Importance**	**Tree or Shrub**	**Status***	**Degree of Susceptibility****	**Common name**	**Synonyms**	**Draft priority for consultation (Based on framework in Fig 4).**
Callistemon salignus (Sm.) Sweet	Horticultural	Tree	Exotic	Low[1]	Willow bottlebrush, white bottlebrush		No specific action
Callistemon viminalis (Gaertn.) Loudon	Horticultural	Shrub	Exotic	Moderately-Highly[1]	Weeping bottlebrush		No specific action
Calothamnus quadrifidus R.Br.		Shrub	Exotic	Susceptible[1]	One-sided bottlebrush		No specific action
Calytrix tetragona Labill.		Shrub	Exotic	Susceptible[1]	Common fringe-myrtle		No specific action
Chamaelaucium uncinatum		Shrub	Exotic	Extremely	Geraldton wax plant		No specific action
Corymbia calophylla (Lindl.) K.D.Hill & L.A.S.Johnson	Horticultural	Tree	Exotic				No specific action
Corymbia citriodora (Hook.) K.D.Hill & L.A.S.Johnson		Tree	Exotic	Susceptible[1]	Lemon-scented gum		No specific action
Corymbia ficifolia (F.Muell.) K.D.Hill & L.A.S.Johnson	Horticultural	Tree	Exotic	Susceptible[1]			No specific action
Corymbia gummifera (Gaertn.) K.D.Hill & L.A.S.Johnson		Tree	Exotic	Susceptible[1]	Red bloodwood		No specific action
Darwinia vestita (Endl.) Benth.		Shrub	Exotic				No specific action
Eucalyptus bosistoana F.Muell.	Timber	Tree	Exotic		Coast grey box		Priority 3/4
Eucalyptus botryoides Sm.	Timber	Tree	Exotic	Susceptible	Bangalay		Priority 3/4
Eucalyptus delegatensis R.T.Baker subsp. *delegatensis*	Timber	Tree	Exotic	Susceptible[1]	Alpine ash		No specific action
Eucalyptus elata Dehnh.		Tree	Exotic	Susceptible			No specific action
Eucalyptus eugenioides Spreng.	Timber	Tree	Exotic		Thin-leaved stringybark		No specific action
Eucalyptus fastigata H.Deane & Maiden	Timber	Tree	Exotic	Susceptible	Brown barrel		Priority 3/4

Species List	**Importance**	**Tree or Shrub**	**Status***	**Degree of Susceptibility****	**Common name**	**Synonyms**	**Draft priority for consultation (Based on framework in Fig 4).**
Eucalyptus fraxinoides (Dumort.) H.Deane & Maiden	Timber	Tree	Exotic		White ash		No specific action
Eucalyptus globoidea Blakely	Timber	Tree	Exotic	Susceptible[1]	White strinybark		Priority 3/4
Eucalyptus globulus	Timber	Tree	Exotic	Susceptible[1]	Blue gum		No specific action
Eucalyptus gunnii Hook.f.		Tree	Exotic	Susceptible[1]	Cider gum		No specific action
Eucalyptus leucoxylon F.Muell. subsp. *Leucoxylon*	Horticultural	Tree	Exotic				Priority 3/4
Eucalyptus macarthurii (Cheeseman) H.Deane & Maiden		Tree	Exotic				No specific action
Eucalyptus muelleriana (Vill.) A.W.Howitt	Timber	Tree	Exotic				Priority 3/4
Eucalyptus nicholii Maiden & Blakely		Tree	Exotic				No specific action
Eucalyptus nitens (H.Deane & Maiden) Maiden	Timber	Tree	Exotic	Susceptible	Shining gum		Priority 3/4
Eucalyptus obliqua (G.Forst.) L'Hér.	Timber	Tree	Exotic	Susceptible[1]	Messmate		No specific action
Eucalyptus ovata Labill.		Tree	Exotic	Susceptible[1]			No specific action
Eucalyptus pauciflora Spreng.		Tree	Exotic	Susceptible[1]	Blackbutt		No specific action
Eucalyptus pilularis (J.R.Forst. & G.Forst.) Sm.	Timber	Tree	Exotic	Susceptible	Blackbutt		Priority 3/4
Eucalyptus pulchella Desf.		Tree	Exotic	Susceptible[1]	White peppermint		No specific action
Eucalyptus radiata (Schwägr.) DC.		Tree	Exotic	Susceptible[1]	Narrow leaved peppermint		No specific action
Eucalyptus regnans F.Muell.	Timber	Tree	Exotic	Susceptible[1]	Giant gum		Priority 3/4

Species List	Importance	Tree or Shrub	Status*	Degree of Susceptibility**	Common name	Synonyms	Draft priority for consultation (Based on framework in Fig 4).
Eucalyptus saligna (A.Cunn.) Sm.	Timber	Tree	Exotic	Susceptible	Sydney blue gum		Priority 3/4
Eucalyptus viminalis Labill.	Horticulture	Tree	Exotic	Susceptible[1]	Manna gum		Priority 3/4
Eugenia uniflora L.		Tree	Exotic	Moderately[1]	Suriname cherry, Brazilian cherry, Cayenne cherry		No specific action
Heteropyxis natalensis Harv.		Tree	Exotic		Lavender tree		No specific action
Hypocalymma angustifolium (Endl.) Schauer		Shrub	Exotic	Low	White Myrtle		No specific action
Kunzea baxteri (Klotzsch) Schauer		Shrub	Exotic	Susceptible[1]	Scarlet Kunzea		No specific action
Kunzea ericifolia (Sm.) Heynh.		Shrub	Exotic		Spearwood, native tree, yellow kunzea		No specific action
Kunzea ericoides (A.Rich.) Joy Thomps.	Horticultural/ agricultural	Tree	Threatened - Nationally Vulnerable	Susceptible	Manuoea, Titira, Atitira, Kanuka	*Leptospermum ericoides* A.Rich.	Priority 3
***Kunzea sinclairii* (Kirk) W.Harris**		**Tree**	**Threatened – Naturally critical**		**Great Barrier Island kanuka**	***Leptospermum sinclairii* Kirk; *Leptospermum ericoides* var. *pubescens* Kirk**	**Priority 1**
Leptospermum grandifolium Sm.		Shrub	Exotic	Susceptible[1]	Mountain tea-tree		No specific action
Leptospermum laevigatum (Gaertn.) F.Muell.		Shrub	Exotic	Susceptible	Victorian tea tree		No specific action
Leptospermum lanigerum (Aiton) Sm.		Shrub	Exotic	Susceptible[1]	Wooly tea-tree		No specific action
Leptospermum petersonii F.M.Bailey		Shrub	Exotic	Low	Lemon scented tea tree		No specific action

Species List	**Importance**	**Tree or Shrub**	**Status***	**Degree of Susceptibility****	**Common name**	**Synonyms**	**Draft priority for consultation (Based on framework in Fig 4).**
Leptospermum scoparium J.R.Forst. & G.Forst.	cultural/ agricultural/ horticultural	Shrub	At Risk - Declining	Susceptible	Manuka, tea tree, kahikatoa	None - a myriad of varieties have been proposed none of which has been strictly synonymised within *L. scoparium*. Allan (1961) describes some of these, several may warrant further study.	Priority 3
***Lophomyrtus bullata* Burret**	**cultural/ horticultural**	**Shrub**	**Threatened - Nationally Critical**	**Susceptible**	**Ramarama, bubble leaf**	***Myrtus bullata* Sol. ex A.Cunn. non Salis. nom. illegit., *Myrtus aotearoana* (E.C.Nelson) E.C.Nelson nom. illegit., *Lophomyrtus aotearoana* E.C.Nelson nom. illegit.**	**Priority 1**
***Lophomyrtus obcordata* (Raoul) Burret**	**cultural/ horticultural**	**Shrub**	**Threatened - Nationally Critical**	**Susceptible[1]**	**Rohutu, New Zealand myrtle**	***Eugenia obcordata* Raoul, *Myrtus obcordata* (Raoul) Hook.f.**	**Priority 1**
Lophostemon confertus (R.Br.) Peter G.Wilson & J.T.Waterh.	horticultural	Tree	Exotic				No specific action
Luma apiculata (DC.) Burret		Tree	Exotic				Priority 3/4?
Melaleuca alterniflora (Maiden & Betche) Cheel		Shrub	Exotic	Susceptible[1]			No specific action
Melaleuca armillaris (Gaertn.) Sm.		Shrub	Exotic	Susceptible[1]			No specific action
Melaleuca bracteata F.Muell.	horticultural	Shrub	Exotic		Black tea tree, River tea tree		No specific action

Species List	**Importance**	**Tree or Shrub**	**Status***	**Degree of Susceptibility****	**Common name**	**Synonyms**	**Draft priority for consultation (Based on framework in Fig 4).**
Melaleuca diosmifolia Andr.		Shrub	Exotic		Green honey-myrtle		No specific action
Melaleuca glomerata F.Muell.		Shrub	Exotic		Desert honey-myrtle		No specific action
***Metrosideros albiflora* Gaertn.**	**cultural**	**Vine**	**Threatened - Nationally Vulnerable**		**White rata, Akatea**		**Priority 1/2**
***Metrosideros bartlettii* J.W.Dawson**	**cultural**	**Tree**	**Threatened - Nationally Critical**	**Susceptible[2]**	**Rata moehau, Bartlett's rata**	**None**	**Priority 1**
***Metrosideros carminea* W.R.B.Oliv.**	**cultural**	**Vine**	**Threatened - Nationally Vulnerable**	**Susceptible**	**Crimson rata, Carmine rata**	***Metrosideros diffusa* Hook.f.**	**Priority 1/2**
Metrosideros colensoi	**cultural**	**Vine**	**Threatened - Nationally Vulnerable**		**Rata**	***Metrosideros pendens* Colenso, *Metrosideros colensoi* Hook.f. var. *colensoi*, *Metrosideros colensoi* var. *pendens* (Colenso) Kirk**	**Priority 1/2**
Metrosideros collina (J.R.Forst. & G.Forst.) A.Gray	cultural	Shrub	Exotic	Low	Metrosideros Tahiti		Priority 3/4?
***Metrosideros diffusa* (G.Forst.) W.R.B.Oliv.**	**cultural**	**Vine**	**Threatened - Nationally Vulnerable**	**Susceptible[2]**	**White rata**	***Melaleuca diffusa* G.Forst., *Metrosideros hypericifolia* A.Cunn.**	**Priority 1/2**
***Metrosideros excelsa* Sol. ex Gaertn.**	**cultural/ horticultural**	**Tree**	**Threatened - Nationally Vulnerable**	**Susceptible**	**Pohutukawa, New Zealand Christmas tree**	***Metrosideros tomentosa* Richard**	**Priority 1**

Species List	Importance	Tree or Shrub	Status*	Degree of Susceptibility**	Common name	Synonyms	Draft priority for consultation (Based on framework in Fig 4).
Metrosideros fulgens Gaertn.	cultural	Vine	Threatened - Nationally Vulnerable	Susceptible[2]	Rata, Akatawhiwhi	*Leptospermum scandens* J.R.Forst. et G.Forst., *Metrosideros scandens* (J.R.Forst. et G.Forst.) Druce, *Metrosideros florida* Sm.	Priority 3
***Metrosideros kermadecensis* W.R.B.Oliv.**	**cultural**	**Tree**	**Threatened - Nationally Critical**	**Low[1]-Moderately**	**Kermadec pohutukawa**	***Metrosideros polymorpha* Hook.f. and *Metrosideros villosa* Kirk are heterotypic synonyms of *M. polymorpha* Gaudich., *Metrosideros villosa* Sm.**	**Priority 1**
Metrosideros parkinsonii Buchanan	cultural	Shrub/small tree	Threatened - Nationally Vulnerable		Parkinson's rata		Priority 3
Metrosideros perforata (J.R.Forst. & G.Forst.) A.Rich.	cultural	Vine	Threatened - Nationally Vulnerable	Susceptible[2]	White rata, akatorotoro, Akatea	*Leptospermum perforatum* J.R.Forst. et G.Forst., *Metrosideros scandens* Sol. ex Gaertn.	Priority 3
Metrosideros robusta A.Cunn.	cultural/ horticultural	Tree	Threatened - Nationally Vulnerable	Susceptible[2]	Northern rata	*Metrosideros florida* Hook.f.	Priority 3
Metrosideros umbellata Cav.		Tree	Threatened - Nationally Vulnerable		Southern rata	*Melaleuca lucida* G.Forst., *Metrosideros lucida* (G.Forst.) A.Rich.	Priority 3

Species List	Importance	Tree or Shrub	Status*	Degree of Susceptibility**	Common name	Synonyms	Draft priority for consultation (Based on framework in Fig 4).
Micromyrtus ciliata (Sm.) Druce		Shrub	Exotic		Fringed heath-myrtle	Baeckea gracilis A.Cunn.	No specific action
Myrteola nummularia (Poir.) O.Berg		Shrub	Exotic		Cranberry myrtle		No specific action
Myrtus communis L.	horticultural	Shrub	Exotic	Moderately-Highly[1]	Common myrtle		No specific action
***Neomyrtus pedunculata* (Hook.f.) Allan**	**cultural**	**Shrub**	**Threatened - Nationally Critical**		**Rohutu, myrtle**	***Myrtus pedunculata* Hook.f., *Eugenia vitis-idaea* Raoul, *Myrtus vitis-idaea* (Raoul) Druce, *Neomyrtus vitis-idaea* (Raoul) Burret**	**Priority 1**
Pimenta dioica (L.) Merr.		Tree	Exotic	Susceptible[1]	Allspice, Pimenta, Jamaica pepper		No specific action
Plinia cauliflora (Mart.) Kausel		Tree	Exotic		Jabuticaba, Brazilian grapetree		Priority 3/4
Psidium cattleianum Sabine	agricultural (Fruit (Guava))	Shrub/Small Tree	Exotic	Susceptible	Purple guava		Priority 3/4
Psidium guajava L.	agricultural (Fruit (Guava))	Shrub	Exotic	Susceptible	Yellow guava		Priority 3/4
Sannantha virgata (J.R.Forst. & G.Forst.) Peter G.Wilson		Shrub	Exotic				No specific action
Syncarpia glomulifera (Sm.) Nied.		Tree	Exotic	Moderately		Turpentine	No specific action
Syzygium australe (Link) B.Hyland	horticultural	Tree	Exotic	Low	Brush cherry	*Eugenia australis* Wendl. ex Link	No specific action
Syzygium floribundum F.Muell.	horticultural	Tree	Exotic	Low		*Waterhousea floribunda*	No specific action

Species List	Importance	Tree or Shrub	Status*	Degree of Susceptibility**	Common name	Synonyms	Draft priority for consultation (Based on framework in Fig 4).
***Syzygium maire* (A.Cunn.) Garn.-Jones**	**cultural**	**Tree**	**Threatened - Nationally Critical**	**Susceptible[2]**	**Swamp maire, Maire tawake, Waiwaka**	***Eugenia maire* A.Cunn.**	**Priority 1**
Syzygium paniculatum Gaertn.	horticultural	Tree	Exotic	Low		Eugenia *paniculata* Gaertn. J.Britt. nom. illeg.	No specific action
Syzygium smithii (Poir.) Nied.	horticultural	Tree	Exotic	Low-Moderately[1]	Lilly pilly, Monkey apple	*Acmena smithii, Eugenia smithii*	No specific action
Taxandria juniperina (Schauer) J.R.Wheeler & N.G.Marchant	horticultural	Tree	Exotic		Australian cedar, juniper myrtle	*Agonis juniperina*	No specific action
Taxandria marginata (Labill.) J.R.Wheeler & N.G.Marchant		Tree	Exotic	Low	Kanooka, Water gum		No specific action
Taxandria parviceps (Schauer) N.G.Marchant		Shrub	Exotic	Susceptible	Chilean guava		Priority 3/4
Thaleropia queenslandica (L.S.Sm.) Peter G.Wilson		Tree	Exotic	Susceptible[1]	Queensland golden myrtle		No specific action
Thryptomene calycina (Lindl.) Stapf	horticultural	Shrub	Exotic	Susceptible[1]	Grampians heath myrtle		No specific action
Tristaniopsis laurina (Sm.) R.Br.	horticultural	Tree	Exotic	Low	Kanooka, Water gum		No specific action
Ugni molinae Turcz.	agricultural (Fruit (Chilaean Guava))	Shrub	Exotic	Susceptible	Chilean guava		Priority 3/4
Xanthostemon chrysanthus (F.Muell.) Benth.		Tree	Exotic	Low-Moderately[1]	Golden penda		No specific action

*The conservation status of New Zealand native plants is taken from de Lange et al. (2018) NZ Department of Conservation report: Conservation status of New Zealand indigenous vascular plants, 2017. New Zealand Threat Classification Series 22

**Modified from Hood (2016; Scion internal report (57365) Myrtle Rust and the New Zealand Forest Industry) and updated to include additional hosts and range of susceptibility, where known, from more recently compiled host lists:

[1]Makinson (2018b) Australian Host List

[2]Host species *A. psidii* had been found on in New Zealand, as of April 2018. (MPI 18607 Project Report, project 3.2 Selection of indicator species for surveillance)

See source references for more information.