Natural area visitor network

Suitability of existing pathogen data and opportunities for new data collection to parameterise a natural area visitor network model

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REPORT INFORMATION SHEET

REPORT TITLE	SUITABILITY OF EXISTING PATHOGEN DATA AND OPPORTUNITIES FOR NEW DATA COLLECTION TO PARAMETERISE A NATURAL AREA VISITOR NETWORK MODEL
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SIDNEY OUTPUT NUMBER	57827
DATE	JUNE 2016
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EXECUTIVE SUMMARY

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This project

The increased access of visitors into natural areas provides new routes for the entry of pathogens into places of high biodiversity value, and could facilitate the spread of an unwanted, high risk pathogen when introduced. Currently the network connections between natural areas frequented by visitors is unknown and the aim of the Biological Heritage National Science Challenge Biosecurity Network Interventions project is to develop a network model linked with the potential for pathogen spread through these natural areas.

The objective of this report is to review the suitability of existing pathogen data in natural areas, highlight the gaps that exist with the current data and identify opportunities or methods to generate new data to parametrise or validate models.

Recommendations and conclusions

- There are several databases or datasets that contain records of pathogens identified in natural areas, however the applicability of these data for this project are low because the records are presence or absence information of an organism in a particular area and there is no information on mode of spread. Since this project focuses on visitor mediated spread of pathogens between natural areas in New Zealand, data for this project need to reflect this form of transmission.

- Picking a model pathogen system is not recommended for assessing biosecurity networks in natural areas. Instead, published data on propagule densities and viability of microorganisms in soil or on clothing or equipment should be used to model the likelihood of pathogen movement, combined with climatic mapping to evaluate the potential that these pathogens could establish.

- There is considerable data on propagule density, diversity and viability of microorganisms in soil or in association with visitors. Some of this research has been done in New Zealand from a border biosecurity perspective.

- Model validation for this project needs to target high risk networks identified between natural areas. An eDNA, or if available, an eRNA method is recommended to validate movement of microorganisms between areas.

- Specific stakeholder engagement with the Ministry for Primary Industries and the Department of Conservation (DOC) is required.

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June 2016

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Introduction

New Zealand's forests are relatively resilient to pathogens. Although there are a variety of diseases or declines that affect different plant species, very few of these are considered serious. The exception to this would be *Phytophthora agathadicida* that causes kauri dieback in *Agathis australis* (kauri) (Weir et al. 2015), and the sudden decline in *Cordyline australis* (cabbage trees), thought to be caused by a phytoplasma (Andersen et al. 2001).

Phytophthora agathadicida is an introduced pathogen that was first identified on Great Barrier Island in the 1970s (Gadgil 1974) and, more recently, causing dieback across kauri in the northern regions of the North Island (Beever et al. 2009; Waipara et al. 2013). Spread of the pathogen is thought to have occurred through movement of infected kauri stock, ground water, and potentially streams. Movement via humans and animals is also thought to have also contributed to the spread (Krull et al. 2013). *Phytophthora agathadicida* has infected and killed kauri of all ages across its natural range and highlights the vulnerability of New Zealand's native flora and risk unwanted overseas pathogens could pose.

Internationally there are three key diseases that are considered high risk to New Zealand's native forests. These are *Phytophthora ramorum*, *Phytophthora austrocedrae*, and *Puccinia psidii*. *Phytophthora ramorum* is an aerially dispersed pathogen that has a broad host range of over 100 plants, and has devastated native ecosystems in numerous overseas countries where it has been introduced and established. Notably *Phytophthora ramorum*'s host range includes herbaceous plants through to mature trees such as oak (sudden oak death) and larch (sudden larch death) (Brasier and Webber 2010; Rizzo et al. 2002). If introduced to New Zealand, this pathogen has the potential to impact our forest ecocsystems and could decimate any susceptible plant species, as it has done overseas.

Phytophthora austrocedrae causes dieback and mortality in *Austrocedrus chilensis*, and more recently a few other tree species within the Cuppressaceae have also been found to be highly susceptible (Green et al. 2015; Greslebin et al. 2007). The disease was first reported in Argentina and there is concern that if it were introduced to New Zealand closely related *Libocedrus* species could also be highly susceptible.

Puccinia psidii is a rust pathogen that affects members of the Myrtaceae (Pegg et al. 2014). There is variation in susceptibility to this pathogen (Tobias et al. 2016) and in Australia, some highly susceptible species are facing local extinction in some areas where pathogen is present (Carnegie et al. 2016). This rust is spread aerially and it is expected it will be introduced to New Zealand via human or commodity movement, or it could also blow over the Tasman Sea as has been documented for other rust pathogens introduced to New Zealand from Australia (McKenzie 1998). New Zealand has several native species of Myrtaceae that could be susceptible to this disease including taonga and iconic species such as pohutukawa and rātā (*Metrosideros* spp.) and mānuka (*Leptospermum scoparium*).

The increased access of visitors into natural areas provides new routes for the entry of pathogens into places of high biodiversity value, and could facilitate the spread of unwanted, high risk pathogen if introduced. Currently the network connections between natural visitor areas is unknown and the aim of the Biological Heritage National Science Challenge Biosecurity Network Interventions project is to develop a network model linked with the potential for pathogen spread through these natural areas. Ultimately the models will allow stakeholders to identify opportunities for interventions to either contain or slow the rate of spread of unwanted pathogens, thereby providing methods to safeguard New Zealand's native flora and ecosystems.

The objective of this report is to review the suitability of existing pathogen data in natural areas, highlight the gaps that exist with the current data and identify opportunities or methods to generate new data to parametrise or validate models.

Data collections

There are several databases or datasets that contain records of pathogens identified in natural areas. This includes Scion's Forest Health Database (FHDB), Landcare Research's NZFungi2 database, and several MPI databases such the Plant Pest Information Network (PPIN), Laboratory Information Management System (LIMS) databases, and more recently, survey results for *Phytophthora agathadicida* detection across the northern North Island by the Kauri Dieback Programme. The applicability of these data for this project are low as the records are presence or absence of an organism in a particular area and there is no information on mode of spread. These pathogens could have been spread independent of human intervention by infected plant material, livestock or waterways. As this project focuses on visitor mediated spread of pathogens between natural areas in New Zealand, data for this project should reflect this form of transmission, which could include transport on clothing, shoes, equipment, luggage, or vehicles by visitors. Some of the survey results from the Kauri Dieback Programme could be directly applicable to this project, if *Phytophthora* spp. were chosen as a model organism. In particular, information on pathogen movement along walking tracks, where this is thought to have occurred via visitors spreading infected soil.

Model pathogen systems

New Zealand's biosecurity measures are very effective at keeping unwanted pathogens out. However, there always remains the risk that pathogens like *Phytophthora ramorum*, *Phytophthora austrocedrae*, or *Puccinia psidii* could inadvertently be introduced and their spread throughout New Zealand could have devastating impacts on our native forests.

The introduction of *Puccinia psidii* via aerial dissemination across the Tasman Sea (McKenzie 1998) cannot be prevented. In view of this, using *Puccinia psidii* as an example of a pathogen system to model is desirable, because the findings from this project could be instrumental in preventing or slowing spread across the country through high frequency visitor areas. The aerial nature of dispersal by *Puccinia psidii* means that this pathogen could spread throughout New Zealand independent of human movement. However, despite this, human transmission is very important as has been described in Australia with the "yellow brick road" phenomenon, where pathways of yellow, infected plants between an infected forest and a research or response organisation have been observed. This has not been due to negligence by officials working on the disease but reflects how easily this pathogen can be dispersed on clothing or vehicles.

The ease by which spores can be carried by visitors between natural areas could increase the rate of spread and could also hamper government or local authority efforts to manage the pathogen and disease if it were to establish. Furthermore, results from this type of modelling would be applicable to movement of other pathogens, including *Phytophthora ramorum* and *Phytophthora austrocedrae*, especially so if the modelling considered variations in inoculum density.

Phytophthora agathadicida is not considered an appropriate model system for this project for multiple reasons, such as the limited range of its host (Steward et al. 2014) which means it is not suitable for modelling dispersal of an unwanted pathogen across New

Zealand, and issues with not being able to distinguish natural versus human mediated movement in areas where it is present. There has been considerable work done by Auckland Council and Landcare Research researchers, in conjunction with the Kauri Dieback Programme, looking the impacts and interaction of human transmission of *Phytophthora agathadicida* that could be used to contribute to and inform the models generated in this Biosecurity Networks project.

Other than *Phytophthora agathadicida* there are no other pathogens already established in New Zealand that are considered suitable for use as a model system. However, there is considerable data available in publications on propagule density and viability that is directly applicable to this project. Furthermore, a considerable amount of that research has been conducted in New Zealand. This work will be discussed further in Model Parametrisation.

The recommendation for assessing biosecurity networks in natural areas is not to pick a model system but to use published data on propagule densities and viability to model the likelihood of pathogen movement, and combine this with climatic mapping to evaluate the potential that these pathogens could establish.

Model parametrisation

Considerable work has been done in the border biosecurity space looking at propagule density, diversity and viability of microorganisms in soil or in association with visitors. This includes information on the density and diversity of fungi present on clothing, shoes and baggage of international travellers entering New Zealand and sizeable data on density, diversity and viability of microorganisms in soil (Gadgil et al. 2000; Gadgil et al. 2002; Gadgil and Flint 1983; Godfrey and Marshall 2002; McNeill et al. 2011; Sheridan 1989).

This New Zealand derived data in combination with overseas research into visitor aided pathogen spread or density, diversity and viability of microorganisms in soil (Curry et al. 2002; Cushman and Meentemeyer 2008; Davidson et al. 2005; Fichtner et al. 2012; Hughes et al. 2010; Hunt et al. 2006) should provide more than enough data to model the likelihood of pathogen spread under different inoculum level scenarios. In general, the pathogen data on visitor dispersed microorganisms has tended to focus on bacteria and fungi, however there is suitable data on *Phytophthora* spp. in soil that can be used (Davidson et al. 2005; Fichtner et al. 2007; Peterson et al. 2014).

It is recommended that the modelling aspect of this project focuses more on inoculum density loads because this can be used to inform likely spread of pathogens at an early stage of establishment (low levels of inoculum) through to a fully established and replicating pathogen (high levels of inoculum). This information would be key for eradication or slow the spread management of new pathogens. Different levels of inoculum could also be used to mimic different pathogens, for example a high inoculum level could mimic *Puccinia psidii*, whereas a low to medium inoculum loading would be more applicable to *Phytophthora ramorum* and *Phytophthora austrocedrae.* This would enable the model to be applicable to any pathogen incursion that could impact New Zealand's native ecosystems.

Another factor to be considered for model parametrisation is the establishment potential of a pathogen in a new area. In general, temperature and moisture conditions within nurseries are optimal for most pathogens regardless of their location across the country. For establishment outside of nursery settings there is more variation in disease establishment and severity. Soil borne pathogens tend to have fewer restrictions on disease establishment because microorganisms associated with soil often have structures

to withstand adverse conditions. Conversely, these resting structures aid dispersal and establishment of soil borne pathogens. Aerially dispersed pathogens tend to be more dependent on climate conditions and pathogen and disease establishment can vary across the country. A variety of climate maps for different aerial pathogens of *Pinus radiata* (grown across New Zealand) have been produced (Ganley et al. 2011; Ganley et al. 2009; Watt et al. 2011a, b; Watt et al. 2012; Watt et al. 2011c) and these could be used to predict likely establishment potential of other aerial pathogens across the country. In general the majority of the North Island and the top half of the South Island have higher risks of disease establishment and severity than other parts of New Zealand.

Dispersal by natural means (i.e. airborne, soil borne or animal unrelated to human movement), is outside of the scope of this project. Although aspects of dissemination are in common to both, human mediated transmission is different and the ramifications of dissemination via this pathway has different outcomes from natural dispersal through the environment.

Model validation

Model validation for this project needs to target high risk networks identified. There is scope for a variety of different methods to be used such as testing soil transferred on shoes, vehicles or equipment shared between visitor regions, vacuuming (Holliday et al. 2013) clothing or luggage, or comparing composition of microorganisms between high risk networks. As a model organism has not been recommended for this project, an environmental sampling method is recommended, specifically an eDNA, or if available, an eRNA method.

An eDNA technique amplifies DNA from all microorganisms specific to the primers used, including those present in very low levels. It has high-through put but is more time consuming because of the bioinformatics component. This technique does not tell you if an organism is viable, which is where an eRNA technique would be beneficial. From a new to New Zealand biosecurity point of view, any microorganisms identified as potentially new to New Zealand using eDNA techniques would need to be reported to MPI immediately. As identification of an organism to species level cannot be done using only one gene region, there is scope to work with MPI to develop a process that recognises these difficulties but focuses effort on detection of potential unwanted, high risk pathogens.

Currently there are no eRNA-based diagnostic methods that have been tested for use for diagnostic environmental sampling, such as required for this project. An eRNA method has the advantage over eDNA methods in that RNA is targeted and successful amplification shows the microorganism is viable. Both techniques have the same issues with of new to New Zealand identification and reporting. If an eRNA method were tested before the validation phase this technique would be recommended in combined with, or lieu of, an eDNA approach.

Culturing and other DNA techniques are not recommended for this project because, in general, there is not a lot of information of the diversity of microorganisms in natural areas, and these techniques are more suited to the identification of known pathogens or microorganisms.

Project risks

New to New Zealand organisms are known species (or in some cases genera) that have not previously been identified in New Zealand. Organisms that cannot be identified to species would not be reported as new to New Zealand if the genus was already present. For this project, new to New Zealand organisms roughly fall into two categories, those that are considered low risk and those considered high risk. Low risk pathogens are typically those that have been present in New Zealand for a considerable time (either native or introduced) but have not previously been identified as present, or pathogens that are newer introductions but are unlikely to adversely affect New Zealand plant-based economies or native flora. High risk pathogens are more recently established organisms that pose a serious threat to either specific plant-based industries or to our native estate.

To ensure the process of reporting and identifying any new to New Zealand organisms it is recommended that there is specific stakeholder engagement with MPI's Incursion Response team and Plant Health and Environment Laboratory, and staff from the Department of Conservation (DOC). Individuals from both organisations need to be fully aware of the project. It is recommended that this involvement is formalised at the MPI stakeholder engagement meeting on 2 August 2016. This formalised engagement with these groups would also be used to work through any issues with publication of microorganism datasets, if required. Separate engagement with DOC is also required and could be done through the wider Natural Area Visitor Network project.

Any natural visitor areas used for the model validation phase will need appropriate permits from DOC for sampling and/or local iwi permission depending on their location. Appropriate consultation with these groups during the design phase of the experimental workplan is needed. Appropriate care to ensure equipment and clothing are cleaned between visitor areas.

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