Biological Conservation 218 (2018) 154–162

Contents lists available at ScienceDirect

Biological Conservation

journal homepage: www.elsevier.com/locate/biocon

Assessment and prioritisation of plant species at risk from myrtle rust (*Austropuccinia psidii*) under current and future climates in Australia

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ARTICLE INFO

Keywords:
Invasive species
Maxent
Myrtaceae
Pathogen
Plant disease
Species distribution models

ABSTRACT

Myrtle rust (*Austropuccinia psidii*) is an invasive rust fungus that attacks species of the Myrtaceae family, one of the most dominant plant families in Australia. The potential extent of myrtle rust affected areas and the high number of potential host species make a species prioritisation scheme essential to direct conservation and management efforts. This study builds on previous work by: compiling an up-to-date list of myrtle rust occurrences and host species; mapping current and future climate suitability for myrtle rust; and identifying host species at risk based on range overlaps and susceptibility data.

Suitable habitat for myrtle rust is restricted to eastern and southern coastal areas of Australia, with minor areas in the Northern Territory and Western Australia. This coastal distribution remains present under future climates, with some extension in inland New South Wales and Tasmania, and a reduction of suitable habitat in northern Queensland and Western Australia. Contrary to previous studies, our results indicate that south-west Western Australia has low climatic suitability for myrtle rust. Under current climate, 1285 Myrtaceae species are at risk of exposure to myrtle rust. This number decreases to 1224 species under future climate.

We divide species exposed to myrtle rust into three priority categories, giving highest priority to species with at least 70% of their range overlapping regions climatically suitable for myrtle rust under current or future climates. We find 23 species are of high priority for conservation action. Finally, we provide a series of recommendations for management of species within each priority category.

1. Introduction

Austropuccinia psidii (formerly, *Puccinia* (Beenken, 2017), herein referred to as myrtle rust) is a pathogenic rust fungus native to Central and South America (Coutinho et al., 1998; Glen et al., 2007), that attacks a wide range of species of the Myrtaceae family (Carnegie and Lidbetter, 2012; Morin et al., 2012; Sandhu and Park, 2013; Giblin and Carnegie, 2014). Myrtle rust affects young growing tissues of plants, resulting in shoot dieback, reduced recruitment, and adult plant mortality in some species (Pegg et al., 2014; Carnegie et al., 2016). The fungus is a significant invasive pathogen globally, and in recent years has spread to the U.S.A (Uchida et al., 2006), South Africa (Roux et al., 2013), parts of Asia (Kawanishi et al., 2009; McTaggart et al., 2016) and the Pacific (Carnegie et al., 2010; Giblin, 2013), where it affects a range of horticultural, agricultural and native species (Glen et al., 2007).

Australian vegetation is likely to be particularly vulnerable to myrtle rust due to the widespread dominance of Myrtaceous species. Myrtle rust was first detected in Australia in 2010 (Carnegie et al., 2010), and has since spread rapidly along the coast of New South Wales (NSW) and Queensland (Pegg et al., 2014; Carnegie et al., 2016), to Victoria (Agriculture Victoria, 2017), Tasmania (Biosecurity Tasmania, 2017) and, more recently, the Northern Territory (NT) (Westaway, 2016), and Lord Howe Island (Bob Makinson *pers. comm.* 2016). There are 2250 Myrtaceae species within Australia with many forming the dominant component of vegetation communities, such as the eucalypts (*Eucalyptus*, *Angophora* and *Corymbia*), paperbarks and bottlebrushes (*Melaleuca* and, formerly, *Callistemon*), and tea-trees (*Leptospermum*) (Makinson and Conn, 2014). Inoculation and field studies have confirmed that there are at least 347 Australian hosts of myrtle rust, including species, subspecies and hybrids (Giblin and Carnegie, 2014). However, the majority of Myrtaceae species remain untested for myrtle rust susceptibility.

Currently, detailed understanding of the impact of myrtle rust on native plant populations in Australia is confined to two highly susceptible rainforest species: *Rhodomyrtus psidioides* and *Rhodamnia rubescens*. Both of these species have suffered severe population declines due to myrtle rust infection (Carnegie et al., 2016), and as a

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https://doi.org/10.1016/j.biocon.2017.11.035
Received 21 May 2017; Received in revised form 16 November 2017; Accepted 28 November 2017

consequence have been proposed as Critically Endangered in NSW (NSW Scientific Committee, 2017). More recent studies have reported severe impacts to a broader range of species in native ecosystems in south-east Queensland (Pegg et al., 2017). For many other susceptible species, the impact on wild populations is unknown.

A successful assessment of the vulnerability of plant species to myrtle rust requires knowledge of the ranges of the pathogen and host, as well as host susceptibility. Our knowledge of the current extent of myrtle rust in Australia is incomplete, as occurrence records are scattered, systematic surveillance programs in native forests are lacking, and there is no central reporting authority. Pioneer studies have mapped the potential extent of the fungus in Australia using the known distribution of the disease in its native range in South and Central America (Booth et al., 2000; Booth and Jovanovic, 2012; Elith et al., 2013). Subsequent physiological studies of the pathogen provided more detailed information about the climatic conditions that favoured spore germination, and these became the basis of later mechanistic climate suitability models (Kriticos et al., 2013).

Several potential issues may arise with respect to existing climate suitability maps for myrtle rust in Australia. Firstly, the exclusion of Australian occurrence records from model calibration (e.g. Elith et al., 2013) may lead to a miscalculation of the climatic niche of the rust (Gallagher et al., 2010). Secondly, only one strain of myrtle rust occurs in Australia (Machado et al., 2015) and this differs to the Brazilian strain (Stewart et al., 2017). Elith et al. (2013) and Stewart et al. (2017) demonstrated how variation in projections of climate suitability may arise as a result of different strains being used to calibrate models. Thus, it is possible that the inclusion of multiple strains in previous studies (Booth et al., 2000; Booth and Jovanovic, 2012; Kriticos et al., 2013) may lead to an overestimation of climatic suitability for myrtle rust in Australia.

Furthermore, numerous records of myrtle rust are based on sightings in nurseries and residential gardens — areas that may have different microclimates due to active management such as provision of water and shade. To the best of the authors' knowledge, there has not been an attempt to separate out nursery or garden locations from natural records in previous Maxent models (Elith et al., 2013; Stewart et al., 2017). The use of these occurrence data may overestimate the climate niche of this species. Finally, modelling studies have yet to address climate change, which will alter interactions between hosts and pathogens (Booth et al., 2015), and likely impact the distribution of myrtle rust.

The objective of this study was to collate data on the geographic extent of myrtle rust in Australia along with host plant distribution and susceptibility, and to develop a prioritisation scheme for managing hosts and reducing the impact of the pathogen. Specifically, we (i) compiled myrtle rust occurrence data and an updated list of host plant species, ii) mapped areas of climate suitability for the pandemic strain of myrtle rust (sensu Stewart et al., 2017) under current and future climate scenarios, iii) developed a decision-support tree to prioritise species most at risk of exposure to myrtle rust, and iv) provide recommendations for future conservation actions for each category of species at risk.

2. Methods

2.1. Myrtle rust and host plant occurrence data

We obtained Australian occurrence records for myrtle rust from NSW, Queensland, Victoria, Tasmania and NT government databases, recent literature (Machado et al., 2015; Potts et al., 2016), validated sightings from the Australian Myrtle Rust Environmental Impacts Working Group, and colleagues (see acknowledgements). These records date from the appearance of the fungus in Australia in 2010 until June 2016. Global occurrence data were gathered for locations known to have the same strain (pandemic) as Australian isolates (Costa Rica, Indonesia, Jamaica, Mexico, Puerto Rico and the U.S.A) (Machado et al., 2015; Stewart et al., 2017). Occurrence records were separated into three categories according to the primary land use and likely infection source: nurseries (N) – which likely contain imported infected material; gardens (G) – private residences and public gardens, which possibly contain imported infected material as well as natural infection; and natural environments (NE), which are likely naturally infected. Records were cleaned by removing occurrences with missing or incorrect co-ordinates (e.g. fell within ocean areas), or where location type could not be identified.

Occurrence records for Australian Myrtaceae species were obtained from the Australian Virtual Herbarium (AVH; http://avh.chah.org.au/) and cleaned similarly to the rust records and excluding cultivated records. To harmonise differences in taxonomy between the host species list (below) and AVH data, scientific names were checked using the statistical package 'Taxonstand' (Cayuela and Oksanen, 2016) in R version 3.1.2 (R Core Team, 2016). This package uses the accepted names in 'The Plant List' website (www.theplantlist.org),

Extent of occurrence (EOO) was calculated for each plant species with sufficient occurrence records (n = 2087, each with at least five occurrence records), using the minimum convex polygon method within the 'adehabitatHR' package (Calenge, 2006). Provisional EOO polygons were generated for a further 39 species with less than five records through duplication of records. Polygons were then clipped to the extent of the Australian coastline. EOO was chosen rather than area of occupancy due to likely inequalities in completeness of survey data between Myrtaceae species, and the possibility of underestimating risk for species with few and highly dispersed records.

2.2. Plant susceptibility data

An updated host susceptibility list was compiled from: i) existing host listings provided by the Australian Myrtle Rust Environmental Impacts Working Group; ii) a literature search for new records; and iii) attribute information from the myrtle rust occurrence records. For each host, susceptibility information was collated based on the metric of the original source. Susceptibility to myrtle rust was categorised into four classes: resistant, low, medium, and high (Table 1).

Resistant plants are those that show no signs of infection when exposed to the rust. Low susceptibility plants become infected, but show resistance through necrotic pathways (Tobias et al., 2016) and prevent the completion of the rust life cycle (i.e. no sporulation present). Some plants may show both signs of infection and resistance, and may be considered moderately susceptible (medium susceptibility). Highly susceptible plants show no signs of resistance and have high

Table 1

Susceptibility scales based on the reaction of the host species to myrtle rust exposure. A unified scale was created to describe the range of susceptibility reactions of hosts to myrtle rust based on previous studies. HR, highly resistant; R, resistant; MR, moderately resistant; RT, relatively tolerant; MS, moderately susceptible; S, susceptible; V, very susceptible; HS, highly susceptible; ES, extremely susceptible.

Score	Rating	Description	Equivalence for other scales			
			Morin[a]	Winzer[b]	Pegg[c]	S & P[d]
0	Resistant	No infection	1	0		HR
1	Low	Infection but no sporulation	2	1		R
2	Medium	Infection and minimal sporulation	3–4	2–3	RT-MS	MR-MS
3	High	Infection and abundant sporulation on leaves, twigs and/or fruits.	5	4–5	HS-ES	S-VS

[a] (Morin et al., 2012).

[b] (Winzer et al., 2017).

[c] (Pegg et al., 2014).

[d] (Sandhu and Park, 2013).