Spatial Analysis of Risks Posed by Root Rot Pathogen, *Phytophthora cinnamomi*: Implications for Disease Management

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Phytophthora cinnamomi, a soil-borne pathogen that infects the roots of plants, is listed as a Key Threatening Process under Commonwealth and NSW state biodiversity legislation due to its deleterious effects on native flora. In warm temperate eastern Australia, the disease may cause insidious declines in plant species that have slow rates of population turnover, and thereby threaten their long term persistence. *Phytophthora cinnamomi* has been known to occur in Royal National Park since the 1970s and systematic surveys for the pathogen were carried out a decade ago. Development of effective management strategies to mitigate the impacts of the disease requires information on the spatial distribution of risks posed by the disease. In this study, we use limited disease survey data to identify areas that are most at risk. We propose and apply a simple risk model in which risks of disease impact are proportional to the product of habitat suitability for the pathogen and abundance of susceptible biota. We modelled habitat suitability of the pathogen from available survey data and found that soil landscapes and topographic variables were the strongest predictors. Susceptible flora were concentrated on sandstone plateaus. Disease risks were greatest on the sandstone plateaus and lowest in the shale gullies with intermediate levels of risk on shale ridges and the coastal sand plain. The outcomes of this spatially explicit risk assessment will help inform the development of management strategies and priorities for the disease in the Park. Our approach lends itself to broader application to conservation planning in other landscapes and to other threats to biodiversity.

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KEYWORDS: disease susceptibility, conservation planning, risk assessment, risk mapping, Royal National Park, species distribution model.

INTRODUCTION

Phytophthora cinnamomi Rands is a soil-borne plant pathogen with a very broad host range. It is damaging to crops and native vegetation in many countries. Genetic evidence suggests that it is a recent introduction to Australia (Dobrowolski et al. 2003) but has been present in most States since at least the early 20th Century (Cahill et al. 2008).

Since the association between infection by *P. cinnamomi* and death in native plants in Australia was established in the late 1960s (Podger 1968), severe damage in native vegetation has been documented in all Australian States (Cahill et al. 2008). Many plants in the families Ericaceae, Fabaceae, Proteaceae and Xanthorrhoeaceae are especially susceptible (McDougall 2006; Figure 1). The threat from *P. cinnamomi* is recognised in its listing as a key threatening process nationally under the *Environment Protection and Biodiversity Act 1999* and in NSW under the *Threatened Species Conservation Act 1995*.

Phytophthora cinnamomi spreads by motile spores in moist soil over short distances or by vegetative growth between roots. Spores also enable long distance dispersal in storm run off and creeks, or in soil attached to cars and boots. For this reason, it is often found beside roads, tracks and other places of soil-disturbance, and waterways. Infection occurs when motile spores germinate on or near plant roots

Figure 1. Sporadic mortality of susceptible plant species (e.g. *Banksia marginata*) in spring is characteristic of root rot disease caused by *Phytophthora cinnamomi* in Royal National Park.

or stem bases. These produce vegetative strands (mycelia) that grow in host tissue, destroying water conducting cells. Infected plants therefore typically display drought-like symptoms. Death may occur where a host is especially susceptible to infection or where other stresses are operating on the host (e.g. drought or insect attack). The mycelia may then produce sporangia (the structure that releases motile spores) or, under unfavourable conditions, a resting spore, which is resistant to drying (Cahill et al. 2008). Importantly, *P. cinnamomi* is not dispersed in the air.

Host plants vary in their susceptibility, ranging from tolerant (where there are no visible symptoms) to highly susceptible (where plants are rapidly killed). Hosts may be tolerant in some habitats but not others, or only under some climatic conditions (Shearer & Dillon 2006). The overall impact of *P. cinnamomi* on native vegetation is determined by local environmental conditions, host availability and time since infestation (Cahill et al. 2008). For instance, *P. cinnamomi* can be present and have no visual impact if hosts are tolerant, can have an impact in one area but not another, despite similar susceptible hosts, if environmental conditions are not conducive to spread and infection, or the impact can appear minimal long after infestation if susceptible hosts disappear. At sites dominated by highly susceptible species, the impact will commonly involve major structural change with flow-on effects to habitat-dependent plants and animals (McDougall et al. 2005). Importantly, once introduced to a site that favours its life cycle, *P. cinnamomi* is likely to persist because of the presence of tolerant hosts and the production of resting spores. Recolonisation of infested sites by susceptible hosts may occur and has been recorded (e.g. Weste et al. 1999; McDougall and Summerell 2003) but these colonists will be highly vulnerable to further infection and their likelihood of long-term survival is low. *P. cinnamomi* is putting many species at risk of extinction (Cahill et al. 2008).

The susceptibility to infection is known for very few native Australian species (McDougall 2006) but there are taxonomic patterns that can allow the susceptibility of other species to be inferred (Cahill et al. 2008). For instance, all species of *Andersonia* (family Ericaceae) in Western Australia, for which susceptibility is known, are highly susceptible (Wills and Keighery 1994), and species of *Xanthorrhoea* (family Xanthorrhoeaceae) tend to be moderately to highly susceptible (McDougall 2006). Curiously, all Western Australian species of *Banksia* are moderately to highly susceptible whereas few eastern Australian

Banksia species are highly susceptible (McCredie et al. 1985). However, almost all *Banksia* species are susceptible to infection to some extent (Figure 1). Extrapolation of susceptibility will not always be reliable within genera and families but offers a means of assessing likely vulnerability of communities or local floras to *P. cinnamomi*.

Site environmental conditions can greatly influence the impact of *P. cinnamomi* (Wilson et al. 2000; Cahill et al. 2008). It is able to complete its life cycle under a great range of temperature (mean annual temperature > 7°C) and rainfall (> 400 mm / annum) conditions. Some soil types, however, have been found to be less favourable to *P. cinnamomi* activity (e.g. those with antagonistic micro-organisms (Halsall 1982), high fertility (Shearer and Crane 2003), or high pH / high calcium content (Shearer and Hill 1989)). Putative relationships have also been reported between the incidence of *P. cinnamomi* and soil texture, as well as topographic features that influence soil moisture (Wilson et al. 2000; 2003).

There is no effective, long-term treatment for *P. cinnamomi* once it enters an ecosystem. A chemical (phosphonate) increases plant resistance but can be phytotoxic and needs frequent re-application. Prevention is therefore the most important form of management for sites suspected to be free of the pathogen. Preventive measures include routine surveillance of symptoms, restriction of access when soils are wet and the likelihood of spread is greatest, hygiene stations for cleaning shoes or vehicles, construction of well-drained tracks that will not support the pathogen, or chemical control (Cahill et al. 2008).

Phytophthora cinnamomi was first located in Royal National Park in 1974 (Gerrettson-Cornell 1986). No importance was attached to its presence until recently when deaths of *Xanthorrhoea resinosa* were linked to infection by *P. cinnamomi* (McDougall and Summerell 2003). Walsh et al. (2006) found that *P. cinnamomi* is widespread in Royal National Park, concluding that hygiene measures were likely to be ineffective at containing its spread. The pathogen was, however, found not to be ubiquitous or evenly distributed. It was, for instance, not located at any sites containing *Telopea speciosissima* (Waratah), which is typically highly susceptible to *P. cinnamomi*. This suggests that some parts of the Park are still free of *P. cinnamomi* and that preventive measures are worthwhile to protect iconic species such as this and localised or threatened species that may be susceptible. Spatial patterns in occurrence of the pathogen may be investigated using models of habitat suitability that link observed occurrence to environmental variables (Wilson et al. 2003). An understanding of the spatial pattern of risks posed to biodiversity by *P. cinnamomi* will help direct threat abatement actions to areas where they address the greatest risks.

In this paper we illustrate a method for mapping the spatial pattern of risks by combining a habitat suitability model for the pathogen with a map showing the abundance and diversity of susceptible flora. Our study area includes Royal and Heathcote National Parks, Garrawarra State Conservation Area and adjacent areas, approximately 30 km south of Sydney city (Figure 2). We first developed a habitat suitability model for the pathogen using data for *P. cinnamomi* presence obtained by Walsh et al. (2006) to relate the occurrence of infested soil samples to a set of spatially explicit environmental predictor variables. We then produced a distribution map of susceptible flora by combining vegetation survey data with susceptibility ranks for each species and weighting species association with mapped vegetation types using their frequencies of occurrence. Finally, we combined habitat suitability for the pathogen with susceptibility of flora to produce a *Phytophthora* risk map for the study area - we used this to identify areas where threat abatement efforts should be focussed.

METHODS

Phytophthora cinnamomi detection

Soil sampling of *P. cinnamomi* within Royal National Park was conducted in 2001 and 2002 for two distinct projects: a targeted survey of 14 sites, nine containing *Xanthorrhoea resinosa* and five containing *Telopea speciosissima* (Waratah); and a systematic survey of the plant communities. For the targeted survey, soil was sampled from the bases of 20 plants of the target species at each site. Sampling was repeated in the following year on two randomly selected plants at each site, giving a total of 308 samples over two years. Each sample consisted of three 100 g subsamples. For the plant community survey, walking tracks were selected such that they approximately represented the proportional distribution of the five broad vegetation types: heathland/open scrub, *Eucalyptus* forest, *Eucalyptus* woodland, wetland and rainforest. Along each track, a pair of samples was collected approximately every 150 m, one sample from directly adjacent to the track on the downslope side, and the other approximately 30 m from the track in an upslope direction. In total, 120 pairs of samples were collected. All samples were taken from the top 15 cm of the soil profile and included root fragments, as soils near the root zone yield higher populations of

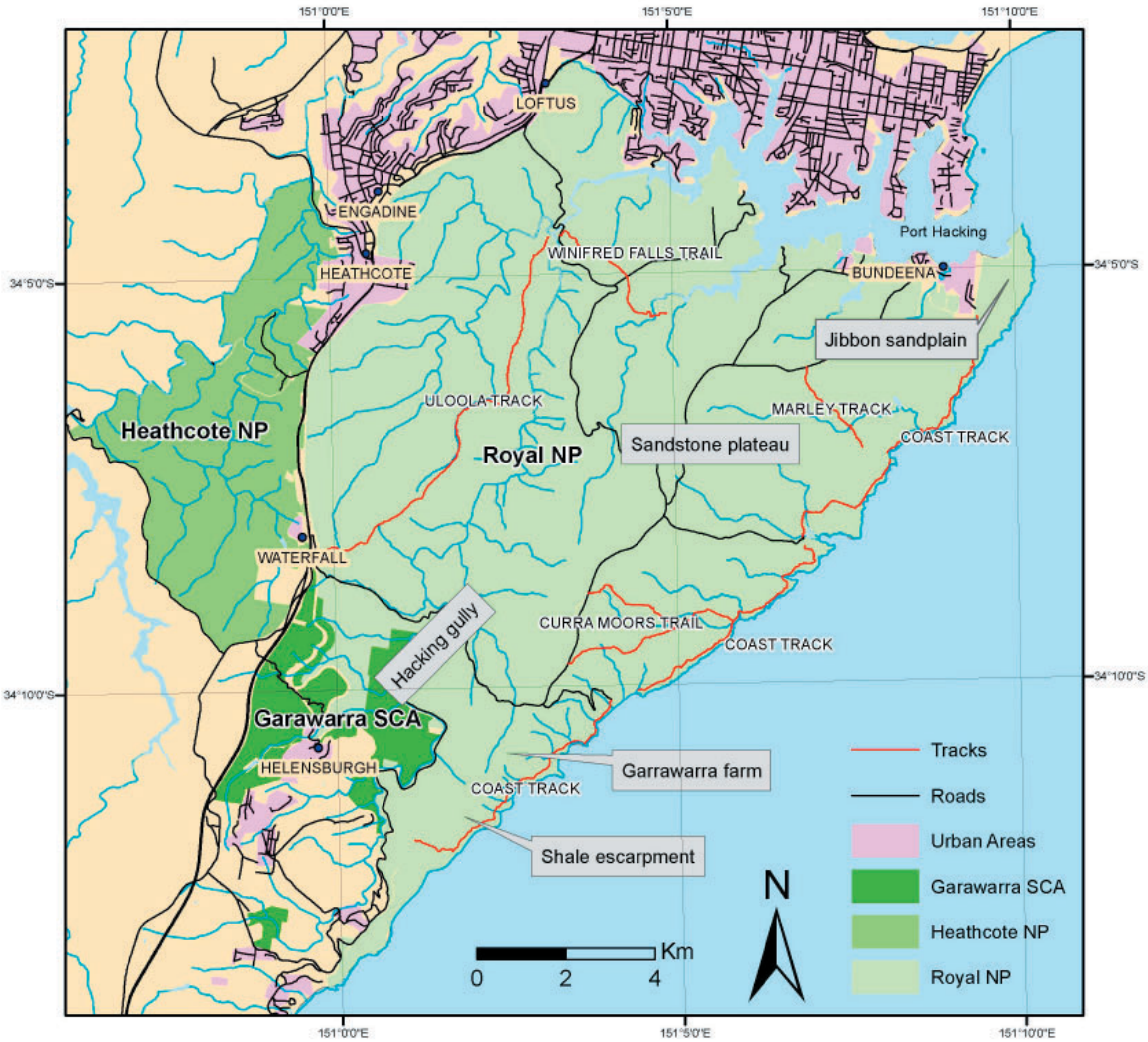

Figure 2. Study area.

P. cinnamomi (Tsao 1983). Equipment was sprayed with methylated spirits after each sample to ensure that inoculum was not transferred between samples. Samples were stored in sealed plastic bags and processed the following day. The baiting technique used to isolate *P. cinnamomi* is described in Walsh et al. (2006). The presence of *P. cinnamomi* was confirmed by examining selective media containing baits under a compound microscope. The location co-ordinates of all sample sites were recorded with a global positioning system and recorded as present or absent depending on the outcomes of baiting tests.

Model of habitat suitability

To model habitat suitability for *P. cinnamomi*, spatial data were assembled within a geographic information system (GIS) for seven environmental variables that we hypothesised may influence the distribution of *P. cinnamomi*. The seven predictor variables were: soil landscapes (Hazelton & Tille 1990); slope, aspect (sine-tranformed); wetness index (number of grid cells in the catchment above the focal cell); local topographic position (proportional distance between local ridge and local gully); topographic position (difference between elevation of focal cell and mean of neighbouring cells within a 250 m radius); topographic roughness (sum of absolute differences in elevation between the focal cell and neighbouring cells within a 250 m radius). These represent spatial proxies for local environmental variables such as soil fertility and pH, site moisture status and temperature that have previously been implicated as having an influence on the development and life cycle of the pathogen (Wilson et al. 2000; Cahill et al. 2008). All layers were projected onto a standard 25 m grid.

To ensure spatial independence of samples, we pooled samples within pairs from the plant community survey. The presence-absence records and environmental spatial data were used to construct a Maximum Entropy model (MaxEnt) of habitat suitability for *P. cinnamomi* (Phillips et al. 2006). This approach estimates a target probability distribution of occurrence by finding a distribution that is closest to uniform, subject to constraints represented by observations of presence and absence in relation to the predictor variables. The estimated distribution maximises agreement with the set of observations, without assuming anything that is not known about their underlying distribution (Jaynes 1990). MaxEnt performed well in comparative accuracy tests of numerous alternative methods of species distribution modelling (Elith et al. 2006).

All seven predictors were included in the initial model with a hinging value set to 0.5. Predictor variables were excluded from the model if they explained less than 5% of variation in the data, given inclusion of other predictors, or if they were correlated ($r>0.4$) with another predictor that explained more variation in the data. After checking the range of environmental data values across the study area in relation to the coverage of the training data set, model fit was evaluated by inspecting the area under the receiver operating curve (AUC). A map of habitat suitability for *P. cinnamomi* was produced by projecting the final model onto the study area using the spatial data layers.

Ranking species and mapping susceptibility of vegetation

The susceptibility of vascular plant taxa recorded in the study area to infection by *P. cinnamomi* was scored using lists of known susceptibility (Weste 2001; McDougall 2006) and personal observations (Table 1). Taxa were ranked as low, moderate or high susceptibility based on the severity of symptoms in the wild or glasshouse experiments. In some cases, susceptibility has been inferred from patterns of plant death observed in the field at sites that were known to be infested with *P. cinnamomi* (McDougall 2006). Those taxa that do not commonly develop symptoms regardless of whether colonisation by *P. cinnamomi* occurs were treated as field resistant. Taxa not directly known to be susceptible, but with known susceptible congeneric taxa were recorded as suspected susceptibility.

A set of 230 floristic quadrats collected in a stratified systematic survey was used to estimate the relative frequency of susceptible plant species in each vegetation type within the study area (NPWS, unpubl. data). A vegetation classification was generated from the data using a cluster analysis (see Tozer et al. 2010 for methods) and a map of the resulting units was drafted with the aid of aerial photographs and soil landscape maps. The mean frequency of each plant taxon in each vegetation type was calculated from their occurrences in quadrats assigned to respective types. An index of disease susceptibility was calculated for each vegetation type by summing the frequencies of all susceptible plant taxa and dividing by the sum frequencies of all recorded taxa. A second index was calculated from the summed frequencies of only the moderately and highly susceptible taxa. Both indices were mapped by joining vectors of the values for each vegetation type to the attribute table of the vegetation map in a GIS.

Risk mapping

Risks to biodiversity from *P. cinnamomi* at any given site were assumed to be a function of the likelihood of infection by the disease and the susceptibility of vegetation. We therefore produced

Table 1. Descriptions of susceptibility classes of vascular plant taxa to root rot disease caused by *Phytophthora cinnamomi.*

Susceptibility class
Field resistant
Of unknown susceptibility
Not known to be susceptible but other species in genus known to be of low to moderate susceptibility
Not known to be susceptible but other species in genus known to be highly susceptible
Known to be of low susceptibility or susceptible but degree of susceptibility not documented
Known to be of moderate susceptibility
Known to be of high susceptibility

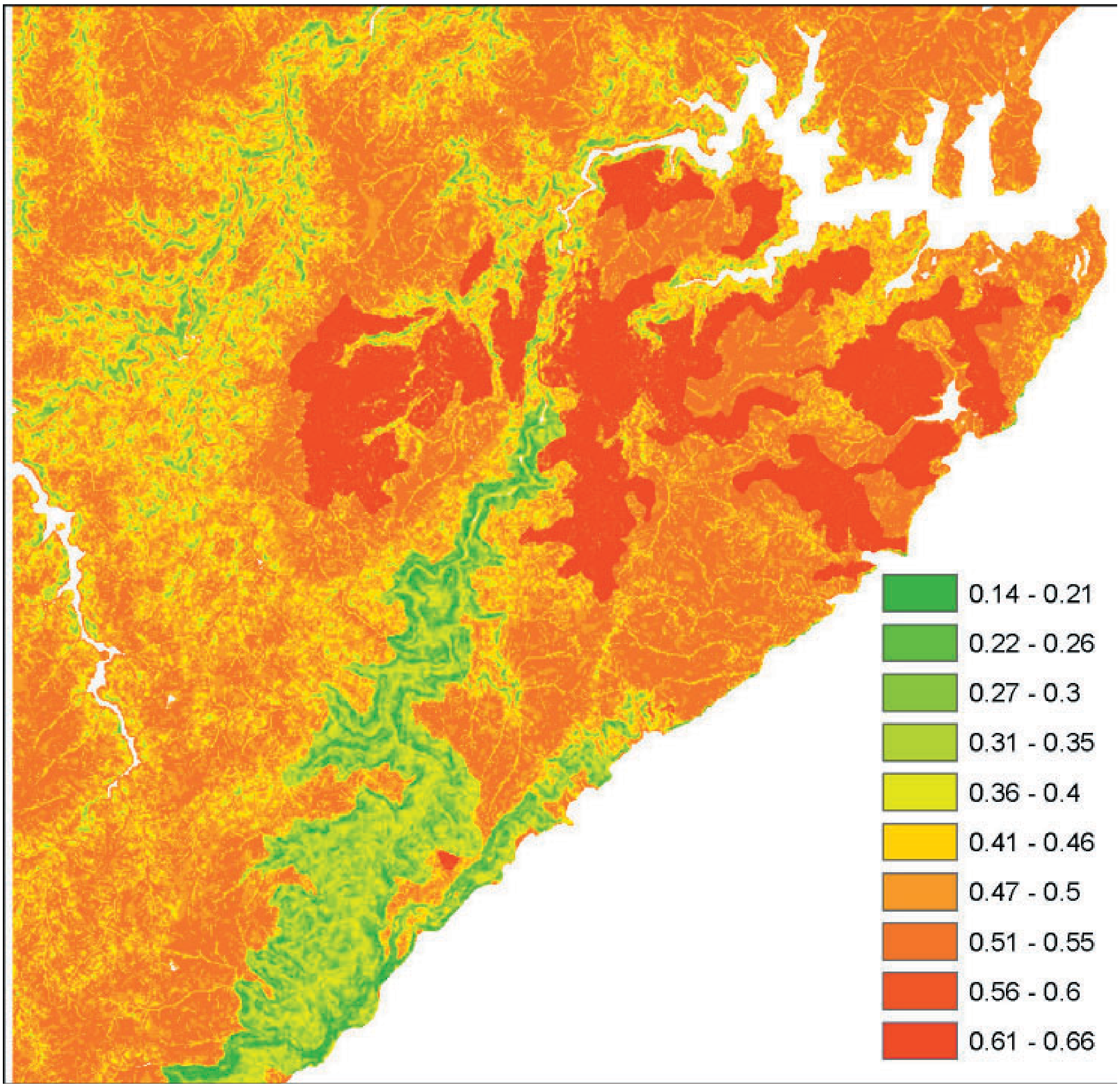

Figure 3. Predicted habitat suitability for *Phytophthora cinnamomi* in the study area.

a map of risk by multiplying spatial data layers for habitat suitability and the relative susceptibility indices.

RESULTS

Habitat suitability

The best distribution model of *P. cinnamomi* included three predictor variables. Soil landscape was the most important predictor, explaining 71% of variation, while slope explained a further 20% and topographic position explained 9%. Sites with clay loam soils derived from Narrabeen Group shales had lower probability of *P. cinnamomi* presence than other soil types. Presence was also less likely on steep slopes than flat slopes and less likely in deep gullies than shallow gullies, slopes and ridges.

More than 95% of the study area was modelled within the range of the training data. The remaining area was on steeper slopes than any of the sampled sites. The best model was a relatively poor fit to the data with an AUC of 0.69.

When projected on a map of the study area, the upper Hacking River valley and southern coastal escarpment showed a conspicuously low probability of *P. cinnamomi* presence compared to the surrounding sandstone plateau (Figure 3). Within the Hacking valley itself and also on the sandstone plateau, gullies and steep slopes had a subtly lower probability of presence than other landscape elements.

Susceptibility of vegetation

Two hundred and eighty-four vascular plant taxa recorded in a systematic vegetation survey of the study area were identified as known or suspected to be susceptible to disease caused by *P. cinnamomi*, representing approximately one-quarter of the total vascular flora of the reserves (Appendix 1). The most widespread dry sclerophyll forest communities had susceptibility scores of 40 or more, while the most widespread heathland community had a susceptibility score of 35 (Table 2). In contrast, rainforests and estuarine wetlands had the lowest susceptibility scores, generally less than 8, and wet sclerophyll forests and freshwater wetlands generally had susceptibility scores of less than 20 (Table 2). Of the 284 susceptible taxa, 128 were identified as moderately or highly susceptible. The susceptibility relationships between plant communities based on this subset of taxa were generally similar to those based on all susceptible taxa except that moderately or highly susceptible taxa were more abundantly represented in heathlands relative to dry sclerophyll forests (Table 2).

Susceptible plant taxa were most abundant across northern and central parts of the study area on the sandstone plateau, and least abundant in the southern part of the area in the upper Hacking valley and along the coastal escarpment (Figure 4). Localised saline wetlands along the shores of Port Hacking also had low abundances of susceptible taxa. Localised patches with intermediate abundance of susceptible taxa include the Jibbon sand plains in the far northeast of the study area and shale capped ridges at Loftus and Garrawarra farm, respectively, in the north and south of the study area. Spatial patterns in the relative abundance of all susceptible species were similar to those for highly and moderately susceptible species (Figure 4a cf. 4b). The main differences were on the sandstone plateau. All susceptible taxa were slightly more abundant on western parts of the plateau dominated by dry sclerophyll forests (Figure 4a). In contrast, moderately and highly susceptible taxa were more abundant on eastern parts of the plateau, reflecting the greater frequency of occurrence of these taxa in heathlands, which are more widespread in the east, and slightly lower frequencies of these taxa in dry sclerophyll forests of sandstone gullies, which are more widespread in the west (Figure 4b).

Spatial patterns of risk

Spatial patterns in risks to vegetation posed by *P. cinnamomi* are shown in Figure 5. Risks were greatest on the sandstone plateaus and lowest in the shale gullies with intermediate levels of risk on shale ridges and the coastal sand plain, reflecting patterns in habitat suitability for the pathogen and distribution of susceptible flora, described above. A focus on the most susceptible flora (Figure 5b) showed a slightly greater contrast in risks between different geological parent materials and higher risks in the eastern heathlands relative to the western sclerophyll forests.

DISCUSSION

Spatial patterns in disease risks

Phytophthora cinnamomi poses the greatest risk to native vegetation in heathlands and dry sclerophyll woodlands of the sandstone plateau, particularly on flat terrain of the plateau surface, ridges and upper slopes. Rainforests in deep gullies on shale-derived soils are at least risk, while wet sclerophyll forests and wetlands are at low levels of risk. These generalisations hold irrespective of whether the risk analysis includes all species known or suspected to be susceptible to the disease or only those that are highly or moderately susceptible. They are also consistent with previous reports that disease impacts appear to be greatest in seasonally dry oligotrophic landscapes (Cahill et al. 2008).

Comparatively low levels of risk were estimated for heathlands and sclerophyll woodlands on the Jibbon coastal sand plain relative to adjoining sandstone landscapes. This is a surprising result, given that sandplain habitats elsewhere have suffered major impacts from the disease, for example on the Swan coastal plain in southwestern Australia (Shearer & Hill 1989). Examination of the susceptibility data and soil survey data shows that modest levels of estimated risk are driven primarily by the fact that a relatively low number of vascular plant taxa recorded in plant communities of the Jibbon sand plain are currently known to be susceptible to the disease. Furthermore, soil sampling on the sand plain was extremely limited. Until more comprehensive soil testing and a more comprehensive appraisal of susceptible flora is carried out, our inferences about disease risks on the Jibbon sand plain should be treated with caution and similar management strategies and priorities should be applied to this area as applied to the high-risk heathlands of the sandstone plateau.

Limitations of risk assessment

Our risk assessment was limited primarily by the available data. Although the habitat suitability predictions for *P. cinnamomi* were largely within

Table 2. Susceptibility scores (summed frequencies of susceptible taxa) for each vegetation map unit (see DECCW 2010). Map unit codes: DSF- dry sclerophyll forests; FoW forested wetlands; FrW- freshwater wetlands; GL- grasslands; HL- heathlands; RF- rainforests; SW- saline wetlands; WSF- wet sclerophyll forests (after Keith 2004a).

Map unit code	Map unit name	Susceptibility score (all susceptible taxa)	Susceptibility score (moderately& highly susceptible taxa)
S_DSF03	Coastal Sand Apple-Bloodwood Forest	18	6
S_DSF04	Coastal Enriched Sandstone Sheltered Forest	20	6
S_DSF05	Coastal Sandstone Exposed Scribbly Gum Woodland	39	19
S_DSF06	Coastal Sandstone Foreshores Forest	16	5
S_DSF07	Coastal Sandstone Gully Moist Heath	44	20
S_DSF08	Coastal Sandstone Riparian Forest	21	8
S_DSF09	Coastal Sandstone Sheltered Peppermint-	39	17
S_DSF13	Southern Sydney Sheltered Forest	26	9
S_DSF14	Sydney Ironstone Bloodwood-Silvertop Ash Forest	37	14
S_DSF15	Woronora Sandstone Exposed Bloodwood Woodland	40	19
S_DSF16	Woronora Sandstone Mallee-Heath Woodland	45	22
S_DSF21	Coastal Sand Bangalay Forest	9	4
S_FoW01	Coastal Alluvial Bangalay Forest	8	2
S_FoW05	Hinterland Riverflat Paperbark Swamp Forest	3	1
S_FoW08	Estuarine Swamp Oak Forest	0	0
S_FrW01	Coastal Upland Damp Heath Swamp	25	9
S_FrW02	Coastal Upland Wet Heath Swamp	17	8
S_FrW04	Coastal Sand Swamp Paperbark Scrub	4	2
S_FrW05	Coastal Sand Swamp Sedgeland	5	0
S_GL02	Coastal Headland Grassland	5	3
S_HL02	Coastal Tea-tree-Banksia Scrub	8	3
S_HL04	Coastal Sandplain Heath	25	11
S_HL06	Coastal Headland Banksia Heath	20	9
S_HL08	Coastal Sandstone Heath-Mallee	35	18
S_HL09	Coastal Sandstone Plateau Rock Plate Heath	11	7
S_HL10	Hinterland Sandstone Dwarf Apple Heath-Woodland	23	10
S_RF01	Illawarra Escarpment Subtropical Rainforest	1	0
S_RF03	Coastal Warm Temperate Rainforest	3	1
S_RF07	Coastal Escarpment Littoral Rainforest	7	3
S_RF08	Coastal Headland Littoral Thicket	2	0
S_RF09	Coastal Sandstone Riparian Scrub	16	6
S_SW01	Estuarine Mangrove Forest	0	0
S_SW02	Estuarine Saltmarsh	0	0
S_WSF02	Coastal Enriched Sandstone Moist Forest	20	7
S_WSF03	Coastal Sand Littoral Forest	6	2
S_WSF04	Illawarra Escarpment Bangalay-Banksia Forest	11	5
S_WSF05	Illawarra Escarpment Blackbutt Forest	13	4
S_WSF06	Coastal Shale-Sandstone Forest	25	9
S_WSF07	O'Hares Creek Shale Forest	9	3
S_WSF09	Sydney Turpentine-Ironbark Forest	22	5

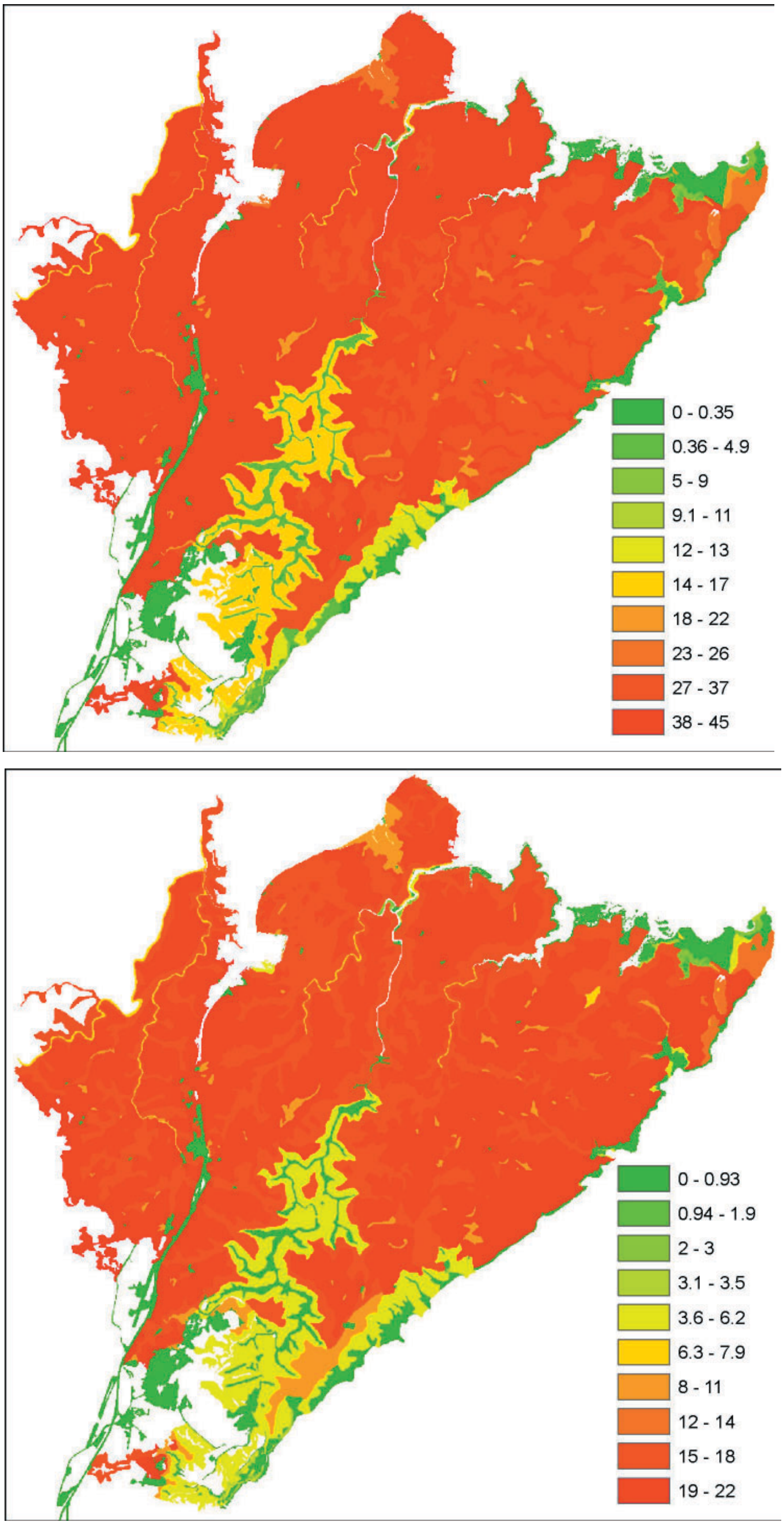

Figure 4. Spatial patterns in the relative abundance of a) all susceptible vascular plant taxa and b) highly and moderately susceptible vascular plant taxa.

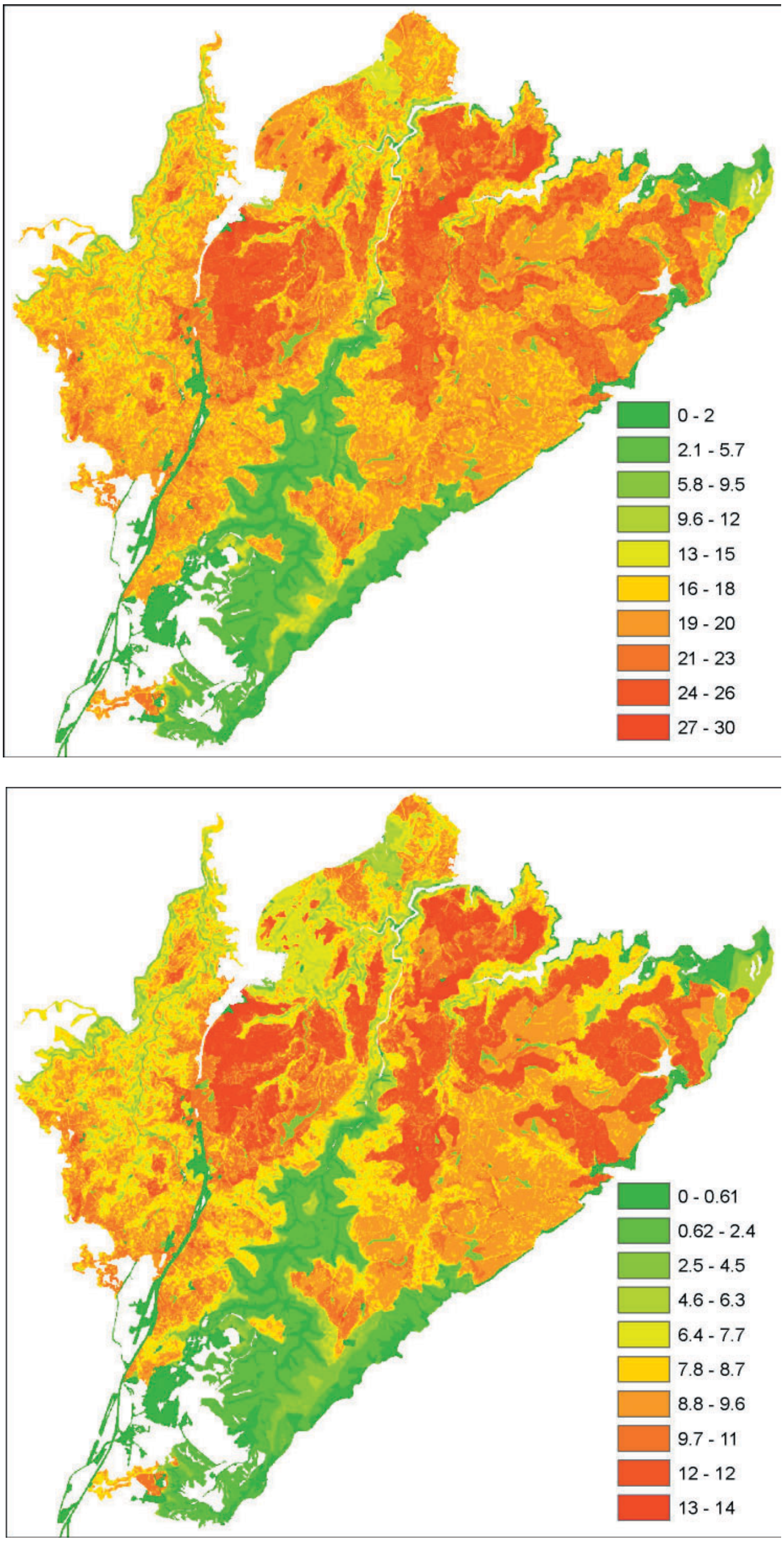

Figure 5. Spatial patterns in risks posed to native vegetation by *Phytophthora cinnamomi* based on (a) all susceptible taxa and (b) highly and moderately susceptible taxa.

the domain of the training data, some of the more restricted landscape types were not well sampled, notably the Jibbon sand plain. In addition, high levels of variability and some false negative test outcomes may be expected due to difficulties in detecting the disease, and may have been responsible for the mediocre performance of the habitat suitability model. Consequently, relatively large numbers of subsamples may be required to detect the disease (or confirm its absence) at any given site. Hierarchical Bayesian detectability models are well suited to deal with these uncertainties by modelling the probability that the disease is detected given that it is present at a site (McCarthy 2008).

An alternative approach to modelling habitat suitability for the pathogen based on occurrence in soil survey sites would be to model expression of disease symptoms in vegetation. This would be informative for risk assessment because the disease may not cause significant impacts on plant diversity in every habitat and location in which a habitat suitability model predicts it could occur. However, diagnosis of symptoms can be uncertain because there may be other causes of plant tissue death and because the symptoms can be relatively transient and hence difficult to detect in early stages of infection and several years after infection when dead remains have decayed. Thus both types of models have strengths and limitations.

Outcomes of the risk assessment may also be sensitive to incomplete data on the susceptibility of vascular flora to the disease. Precise assessments of susceptibility require experimental inoculation of test plants under a range of environmental conditions or thorough field investigations. This has not been done for a large majority of the local flora, although the susceptibility ranks for many species in Royal National Park were assigned by extrapolation from recovery of *P. cinnamomi* from symptomatic plants that were sampled elsewhere (McDougall 2006). This assumes that host susceptibility relationships are consistent within taxa across their geographic distributions. While some intraspecific genetic variation and environmentally regulated variation in susceptibility may be expected across the distribution of each host taxon, our approach was precautionary because it assumes that a species could be susceptible in the study area if symptoms have been recorded on individuals of the same or related species anywhere within their broader range. Although we believe that taxonomic patterns of host susceptibility are sufficiently strong (Cahill et al. 2008) to justify our approach, the models would benefit from improved susceptibility data to produce a more precise spatial representation of risks posed by the pathogen.

While we caution against interpretation of fine scale spatial patterns in disease risk, and interpretation of risk levels at precise locations, we believe that the major generalisations about the landscapes and areas that are most and least susceptible to the disease (outlined above) are likely to provide a robust basis for disease management, despite the limitations in the underlying data. This is because frequencies of the disease recorded in shale gullies were extremely low (7% positive test results recorded from 114 locations in shale gullies, cf. 23% from 109 locations on sandstone plateau and gullies), and few of the known susceptible species occur within plant communities of shale landscapes. Both of these results contrast markedly with findings for heathlands and sclerophyll woodlands on the sandstone plateau. Secondly, the spatial patterns in disease habitat suitability were reinforced by similar patterns in the distribution of susceptible biota that were derived from independent data. Furthermore, the results are corroborated by more general patterns of disease impacts reported from other parts of temperate Australia (Cahill et al. 2008). The distinction between sandstone ridges, upper slopes and gullies is more subtle and together with risk assessment for the Jibbon sand plain, warrants more precautionary treatment in the design of management strategies until uncertainties can be resolved.

Our model did not address the risks of pathogen introduction. As *P. cinnamomi* can be spread through earthworks and mud on footwear and vehicle tyres, an association may be expected between infestation and roadsides, fire trails, walking tracks and associated drains into bushland. Walsh et al. (2006) failed to detect diminished infestation over distances of 30 m from walking tracks, although a relationship may exist over larger distances extending to remote areas that are more buffered from movement of humans and other dispersal agents. Modelling of risks associated with these relationships would require improved survey data on the occurrence of *P. cinnamomi* that is more evenly stratified in relation to distance and drainage from locations of past and present anthropogenic disturbance. Ideally, it would also incorporate data on the frequency and pattern of track usage, especially when soil surfaces are saturated after rain, as well as fine-scale drainage patterns.

Disease management

Impacts of *P. cinnamomi* are less conspicuous in the Sydney region than in parts of south western

Australia, Victoria and Tasmania (Cahill et al. 2008). Nonetheless, the disease may cause insidious declines in key biota that have major implications for ecosystem diversity and function, especially on the sandstone plateau where we have shown that risks of disease impacts are greatest. For example, populations of *Xanthorrhoea resinosa,* a major structural component of heathlands on the plateau, are currently undergoing insidious declines related to synergistic effects of fire and disease (Regan et al. 2011). These declines are projected to continue, but the rate of decline will depend on how both disease and fire are managed. There are essentially two groups of management actions for the disease: those that seek to minimise spread; and direct treatment of the disease or its effects. The relative merits of these options depend on context. For example, Keith (2004b) found that quarantine measures to limit the spread of *P. cinnamomi* were likely to have little effect on the viability of highly susceptible *Epacris barbata* populations, whereas direct treatment could be more effective, but only if the treatment reduced plant mortality by at least 90%.

Although the disease is widespread across the study area, there still appear to be some areas that are at considerable risk of impact that are not yet infected. For example, *P. cinnamomi* was not recorded at any of the five sites supporting susceptible populations of *Telopea speciosissima*, despite comprehensive soil sampling. For these and similar sites, hygiene measures, such as restrictions on access during wet conditions and washdown or change of footwear protocols, may help to reduce the risk of infection by limiting dispersal of infected mud.

The habitats most at risk from *P. cinnamomi* are widely distributed and are traversed by some of the most popular walking tracks, including the Coast track, Marley track, Winifred Falls track, Curra Moors track and Uloola track, each of which is used by thousands of walkers each year. High-usage unkerbed roadways also traverse the study area; maintenance of their verges may increase the likelihood of pathogen spread, especially if undertaken during wet weather. As infections are already scattered along these routes, the major management task will be to limit further spread and protect the most valuable assets at risk. These routes, because of their high visitation rates, also provide opportunities to increase public awareness about the impacts of the disease and support for research and management initiatives to minimise its impact. Educational signage, strategically located wash-down stations, adherence to formed tracks, wash-down protocols for offroad vehicles, precautionary track closures, restrictions on wet weather use and regular dry-weather track maintenance to minimise development of muddy sinks are all appropriate measures to limit disease impacts in these circumstances.

CONCLUSIONS

By combining spatial data on habitat suitability for a disease and the distribution of susceptible biota, it is possible to carry out a spatial analysis of risks posed by disease to support the development of strategies and priorities for disease management. We were able to construct a disease risk map that is likely to be robust for this general purpose using relatively limited disease survey data, available vegetation survey data, existing data bases on plant susceptibility and simple modelling techniques. The axiom of our approach that risks should be proportional to the product of proneness to a threatening process and abundance of susceptible assets should be widely applicable to other management areas as well as other threats to biodiversity. Furthermore this risk model is readily transformed into spatial dimensions, providing a simple information resource for conservation planning.

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Appendix 1

Susceptibility to *Phytophthora cinnamomi* of plant taxa recorded in Royal National Park, Heathcote National Park and Garrawarra State Conservation Area. Nomenclature follows Pellow et al. (2009). 1 - known or suspected to be susceptible. 0 - not known or suspected to be susceptible (includes taxa with no data). Known susceptibility is based on isolation of the pathogen from plants exhibiting disease symptoms. Suspected susceptibility is based on evidence from a congeneric taxon.

Taxon	High, moderate or low susceptibility to Phytophthora (known or suspected)	High or moderate susceptibility to Phytophthora (known or suspected)
Abrophyllum ornans	0	0
Acacia binervata	1	0
Acacia binervia	1	0
Acacia brownii	1	0
Acacia elongata	1	0
Acacia floribunda	1	0
Acacia hispidula	1	0
Acacia implexa	1	0
Acacia irrorata subsp. irrorata	1	0
Acacia linearifolia	0	0
Acacia linifolia	1	0
Acacia longifolia subsp. *longifolia*	1	0
Acacia longifolia subsp. *sophorae*	1	0
Acacia longissima	1	0
Acacia maidenii	1	0
Acacia mearnsii	1	0
Acacia melanoxylon	0	0
Acacia myrtifolia	1	0
Acacia obtusifolia	1	0
Acacia stricta	1	0
Acacia suaveolens	1	0
Acacia terminalis	1	1
Acacia ulicifolia	1	0
Acmena smithii	0	0
Acronychia oblongifolia	0	0
Acrotriche divaricata	1	1
Actinotus helianthi	0	0
Actinotus minor	0	0
Adiantum aethiopicum	0	0
Adiantum formosum	0	0
Adiantum hispidulum	0	0
Adiantum silvaticum	0	0

Taxon	High, moderate or low susceptibility to Phytophthora (known or suspected)	High or moderate susceptibility to Phytophthora (known or suspected)
Aegiceras corniculatum	0	0
Alectryon subcinereus	0	0
Allocasuarina distyla	1	1
Allocasuarina littoralis	1	0
Allocasuarina nana	1	1
Allocasuarina paludosa	0	0
Allocasuarina torulosa	1	1
Allocasuarina verticillata	0	0
Almaleea paludosa	0	0
Alphitonia excelsa	1	0
Alternanthera denticulata	0	0
Amperea xiphoclada	1	0
Amphipogon strictus var. *strictus*	1	0
Angophora costata	1	0
Angophora floribunda	1	0
Angophora hispida	1	0
Anisopogon avenaceus	0	0
Aotus ericoides	1	1
Aphanopetalum resinosum	0	0
Apium prostratum	0	0
Aristida vagans	0	0
Aristida warburgii	0	0
Arthropodium milleflorum	0	0
Arthropteris tenella	0	0
Asplenium australasicum	0	0
Asplenium flabellifolium	0	0
Asplenium polyodon	0	0
Astroloma humifusum	1	1
Astroloma pinifolium	1	0
Austrodanthonia monticola	0	0
Austrodanthonia racemosa var. *racemosa*	0	0
Austromyrtus tenuifolia	0	0
Austrostipa puberula	0	0
Austrostipa pubescens	1	0
Avicennia marina subsp. *australasica*	0	0
Backhousia myrtifolia	0	0
Baeckea imbricata	1	1
Baeckea linifolia	1	1

Taxon	High, moderate or low susceptibility to Phytophthora (known or suspected)	High or moderate susceptibility to Phytophthora (known or suspected)
Baloskion gracile	0	0
Banksia ericifolia subsp. *ericifolia*	1	0
Banksia integrifolia subsp. *integrifolia*	1	1
Banksia marginata	1	0
Banksia oblongifolia	1	1
Banksia robur	1	1
Banksia serrata	1	0
Banksia spinulosa	1	0
Bauera microphylla	1	1
Bauera rubioides	1	0
Baumea acuta	0	0
Baumea articulata	0	0
Baumea juncea	0	0
Baumea rubiginosa	0	0
Baumea teretifolia	0	0
Bertya pomaderroides	0	0
Billardiera scandens	0	0
Blandfordia nobilis	1	1
Blechnum camfieldii	0	0
Blechnum cartilagineum	0	0
Blechnum indicum	0	0
Blechnum nudum	0	0
Blechnum patersonii	0	0
Blechnum wattsii	0	0
Boronia ledifolia	1	1
Boronia parviflora	0	0
Boronia serrulata	1	1
Bossiaea ensata	1	1
Bossiaea heterophylla	1	1
Bossiaea rhombifolia subsp. *rhombifolia*	1	1
Bossiaea scolopendria	1	1
Bossiaea stephensonii	1	1
Brachyloma daphnoides	1	0
Brachyscome angustifolia	1	0
Breynia oblongifolia	0	0
Brunoniella australis	0	0
Brunoniella pumilio	0	0
Burchardia umbellata	0	0

Taxon	High, moderate or low susceptibility to Phytophthora (known or suspected)	High or moderate susceptibility to Phytophthora (known or suspected)
Bursaria spinosa	0	0
Callicoma serratifolia	0	0
Callistemon citrinus	0	0
Callistemon linearis	0	0
Callistemon subulatus	0	0
Callitris muelleri	0	0
Callitris rhomboidea	0	0
Calochlaena dubia	0	0
Calystegia marginata	0	0
Calystegia sepium subsp. *roseata*	0	0
Calytrix tetragona	1	1
Carex appressa	0	0
Carex breviculmis	0	0
Carex brunnea	0	0
Carex gaudichaudiana	0	0
Carpobrotus glaucescens	0	0
Cassinia aculeata	0	0
Cassinia aureonitens	0	0
Cassinia denticulata	0	0
Cassinia trinerva	0	0
Cassytha glabella	0	0
Cassytha pubescens	0	0
Casuarina glauca	0	0
Caustis flexuosa	0	0
Caustis pentandra	0	0
Caustis recurvata	0	0
Cayratia clematidea	0	0
Cenchrus caliculatus	0	0
Centella asiatica	0	0
Centrolepis fascicularis	0	0
Centrolepis strigosa subsp. *strigosa*	0	0
Ceratopetalum apetalum	0	0
Ceratopetalum gummiferum	0	0
Cheilanthes sieberi subsp. *sieberi*	0	0
Chloanthes stoechadis	0	0
Chordifex dimorphus	0	0
Chordifex fastigiatus	0	0
Chorizandra cymbaria	0	0

Taxon	High, moderate or low susceptibility to Phytophthora (known or suspected)	High or moderate susceptibility to Phytophthora (known or suspected)
Chorizandra sphaerocephala	0	0
Christella dentata	0	0
Chrysocephalum apiculatum	0	0
Cissus antarctica	0	0
Cissus hypoglauca	0	0
Citronella moorei	0	0
Claoxylon australe	0	0
Clematis aristata	1	0
Clematis glycinoides var. *glycinoides*	1	0
Clerodendrum tomentosum	0	0
Comesperma defoliatum	0	0
Comesperma ericinum	1	0
Comesperma retusum	0	0
Comesperma sphaerocarpum	0	0
Comesperma volubile	0	0
Commelina cyanea	0	0
Conospermum ellipticum	1	0
Conospermum longifolium	1	0
Conospermum taxifolium	1	0
Conospermum tenuifolium	1	0
Convolvulus erubescens	0	0
Coprosma quadrifida	0	0
Coronidium elatum	0	0
Coronidium scorpioides	0	0
Correa alba var. *alba*	1	0
Correa reflexa	1	0
Corymbia gummifera	1	0
Crassula sieberiana	0	0
Crowea saligna	1	0
Cryptandra amara	1	0
Cryptandra ericoides	1	0
Cryptocarya glaucescens	0	0
Cryptocarya microneura	0	0
Cupaniopsis anacardioides	0	0
Cyathea australis	0	0
Cyathea leichhardtiana	0	0
Cyathochaeta diandra	0	0
Cyclophyllum longipetalum	0	0

Taxon	High, moderate or low susceptibility to Phytophthora (known or suspected)	High or moderate susceptibility to Phytophthora (known or suspected)
Cymbopogon refractus	0	0
Cyperus enervis	0	0
Cyperus gracilis	0	0
Cyperus imbecillis	0	0
Cyperus polystachyos	0	0
Cyperus sanguinolentus	0	0
Cyperus tetraphyllus	0	0
Dampiera purpurea	1	0
Dampiera stricta	1	0
Darwinia diminuta	1	1
Darwinia fascicularis	1	1
Darwinia leptantha	0	0
Davallia solida var. *pyxidata*	0	0
Daviesia acicularis	0	0
Daviesia alata	1	1
Daviesia corymbosa	1	1
Daviesia ulicifolia	1	0
Dennstaedtia davallioides	0	0
Desmodium brachypodum	0	0
Desmodium rhytidophyllum	0	0
Desmodium varians	0	0
Dianella caerulea	1	0
Dianella longifolia	1	0
Dianella prunina	1	0
Dianella revoluta var. *revoluta*	1	0
Dichelachne crinita	0	0
Dichelachne micrantha	0	0
Dichelachne rara	0	0
Dichondra repens	0	0
Dicksonia antarctica	0	0
Digitaria parviflora	0	0
Dillwynia elegans	1	1
Dillwynia floribunda	1	1
Dillwynia glaberrima	1	1
Dillwynia ramosissima	1	1
Dillwynia retorta	1	1
Dioscorea transversa	0	0
Diospyros australis	0	0

Taxon	High, moderate or low susceptibility to Phytophthora (known or suspected)	High or moderate susceptibility to Phytophthora (known or suspected)
Diploglottis cunninghamii	0	0
Dodonaea triquetra	0	0
Doodia aspera	0	0
Doodia caudata	0	0
Doryanthes excelsa	0	0
Doryphora sassafras	0	0
Drosera auriculata	1	0
Drosera binata	1	0
Drosera peltata	1	0
Drosera pygmaea	1	0
Drosera spatulata	1	0
Duboisia myoporoides	0	0
Echinopogon caespitosus var. *caespitosus*	0	0
Echinopogon ovatus	0	0
Einadia hastata	0	0
Einadia nutans	0	0
Elaeocarpus reticulatus	1	1
Elaeodendron australe	0	0
Eleocharis acuta	0	0
Eleocharis sphacelata	0	0
Empodisma minus	0	0
Endiandra sieberi	0	0
Entolasia marginata	0	0
Entolasia stricta	0	0
Epacris longiflora	1	1
Epacris microphylla	1	1
Epacris obtusifolia	1	0
Epacris pulchella	1	1
Epaltes australis	0	0
Eragrostis brownii	0	0
Eriostemon australasius	0	0
Eryngium vesiculosum	0	0
Eucalyptus agglomerata	1	0
Eucalyptus botryoides	1	0
Eucalyptus botryoides <--> *saligna*	1	0
Eucalyptus camfieldii	1	0
Eucalyptus capitellata	1	0
Eucalyptus consideniana	1	0

Taxon	High, moderate or low susceptibility to Phytophthora (known or suspected)	High or moderate susceptibility to Phytophthora (known or suspected)
Eucalyptus globoidea	1	0
Eucalyptus haemastoma	1	0
Eucalyptus luehmanniana	1	0
Eucalyptus multicaulis	1	0
Eucalyptus oblonga	1	0
Eucalyptus obstans	1	0
Eucalyptus paniculata subsp. *paniculata*	1	0
Eucalyptus pilularis	1	0
Eucalyptus piperita	1	0
Eucalyptus punctata	1	0
Eucalyptus racemosa	1	0
Eucalyptus resinifera	1	0
Eucalyptus saligna	1	0
Eucalyptus scias	1	0
Eucalyptus sieberi	1	0
Eucalyptus squamosa	1	0
Eucalyptus tereticornis	1	0
Euchiton gymnocephalus	0	0
Eupomatia laurina	0	0
Euroschinus falcatus var. *falcatus*	0	0
Eurychorda complanata	0	0
Euryomyrtus ramosissima subsp. *ramosissima*	1	0
Eustrephus latifolius	0	0
Exocarpos cupressiformis	0	0
Exocarpos strictus	0	0
Ficinia nodosa	0	0
Ficus coronata	0	0
Ficus obliqua var. *obliqua*	0	0
Ficus rubiginosa	0	0
Ficus superba var. *henneana*	0	0
Flagellaria indica	0	0
Gahnia aspera	0	0
Gahnia clarkei	0	0
Gahnia erythrocarpa	0	0
Gahnia melanocarpa	0	0
Gahnia microstachya	0	0
Gahnia radula	0	0
Gahnia sieberiana	0	0

Taxon	High, moderate or low susceptibility to Phytophthora (known or suspected)	High or moderate susceptibility to Phytophthora (known or suspected)
Galium propinquum	0	0
Geijera salicifolia	0	0
Geitonoplesium cymosum	0	0
Geranium homeanum	0	0
Geranium solanderi	0	0
Gleichenia dicarpa	1	0
Gleichenia microphylla	1	0
Gleichenia rupestris	1	0
Glochidion ferdinandi	0	0
Glycine clandestina	0	0
Glycine microphylla	0	0
Gompholobium glabratum	1	1
Gompholobium grandiflorum	1	1
Gompholobium latifolium	1	1
Gompholobium minus	0	0
Gonocarpus micranthus	1	0
Gonocarpus tetragynus	1	0
Gonocarpus teucrioides	1	0
Goodenia bellidifolia subsp. *bellidifolia*	1	0
Goodenia dimorpha	1	0
Goodenia hederacea subsp. *hederacea*	1	0
Goodenia heterophylla	1	0
Goodenia ovata	1	0
Goodenia paniculata	0	0
Goodenia stelligera	1	0
Grammitis billardierei	0	0
Grevillea buxifolia subsp. *buxifolia*	1	1
Grevillea diffusa	1	1
Grevillea longifolia	1	1
Grevillea mucronulata	1	1
Grevillea oleoides	1	0
Grevillea parviflora subsp. *parviflora*	1	1
Grevillea sericea subsp. *sericea*	1	1
Grevillea sphacelata	1	1
Guioa semiglauca	0	0
Gymnoschoenus sphaerocephalus	0	0
Gymnostachys anceps	0	0
Haemodorum corymbosum	0	0

Taxon	High, moderate or low susceptibility to Phytophthora (known or suspected)	High or moderate susceptibility to Phytophthora (known or suspected)
Haemodorum planifolium	0	0
Hakea dactyloides	1	0
Hakea gibbosa	1	1
Hakea propinqua	1	1
Hakea salicifolia	1	1
Hakea sericea	1	1
Hakea teretifolia	1	1
Hardenbergia violacea	0	0
Harmogia densifolia	0	0
Hedycarya angustifolia	0	0
Hemarthria uncinata var. *uncinata*	0	0
Hemigenia purpurea	0	0
Hibbertia acicularis	0	0
Hibbertia aspera subsp. *aspera*	1	1
Hibbertia bracteata	1	1
Hibbertia dentata	1	1
Hibbertia empetrifolia subsp. *empetrifolia*	1	1
Hibbertia fasciculata	1	1
Hibbertia linearis	1	1
Hibbertia monogyna	1	1
Hibbertia nitida	1	1
Hibbertia obtusifolia	0	0
Hibbertia riparia	1	1
Hibbertia scandens	1	1
Hibbertia serpyllifolia	1	1
Histiopteris incisa	0	0
Hovea linearis	1	1
Hovea longifolia	1	1
Hybanthus monopetalus	1	0
Hydrocotyle acutiloba	0	0
Hydrocotyle geraniifolia	0	0
Hydrocotyle laxiflora	0	0
Hydrocotyle sibthorpioides	0	0
Hydrocotyle tripartita	0	0
Hymenophyllum cupressiforme	0	0
Hypericum gramineum	0	0
Hypericum japonicum	0	0
Hypolaena fastigiata	0	0

Taxon	High, moderate or low susceptibility to Phytophthora (known or suspected)	High or moderate susceptibility to Phytophthora (known or suspected)
Hypolepis muelleri	0	0
Hypoxis hygrometrica	0	0
Imperata cylindrica	0	0
Indigofera australis	0	0
Ipomoea brasiliensis	0	0
Isachne globosa	0	0
Isolepis cernua	0	0
Isolepis inundata	0	0
Isopogon anemonifolius	1	0
Isopogon anethifolius	1	1
Isotoma fluviatilis	0	0
Joycea pallida	0	0
Juncus continuus	0	0
Juncus kraussii subsp. *australiensis*	0	0
Juncus planifolius	0	0
Juncus prismatocarpus	0	0
Juncus usitatus	0	0
Kennedia rubicunda	1	1
Korthalsella rubra	0	0
Kunzea ambigua	1	0
Kunzea capitata	1	0
Lachnagrostis filiformis	0	0
Lagenophora stipitata	0	0
Lambertia formosa	1	0
Lasiopetalum ferrugineum	1	0
Lasiopetalum parviflorum	0	0
Lasiopetalum rufum	1	0
Lastreopsis acuminata	0	0
Lastreopsis decomposita	0	0
Lastreopsis microsora subsp. *microsora*	0	0
Laxmannia gracilis	0	0
Legnephora moorei	0	0
Leionema dentatum	1	0
Lepidosperma concavum	0	0
Lepidosperma filiforme	0	0
Lepidosperma forsythii	0	0
Lepidosperma gunnii	0	0
Lepidosperma latens	0	0

Taxon	High, moderate or low susceptibility to Phytophthora (known or suspected)	High or moderate susceptibility to Phytophthora (known or suspected)
Lepidosperma laterale	0	0
Lepidosperma limicola	0	0
Lepidosperma longitudinale	0	0
Lepidosperma neesii	0	0
Lepidosperma urophorum	0	0
Lepidosperma viscidum	0	0
Leptinella longipes	0	0
Leptocarpus tenax	0	0
Leptomeria acida	1	0
Leptospermum arachnoides	1	0
Leptospermum continentale	1	0
Leptospermum grandifolium	1	0
Leptospermum juniperinum	1	0
Leptospermum laevigatum	1	0
Leptospermum morrisonii	1	0
Leptospermum parvifolium	1	0
Leptospermum polygalifolium subsp. *polygalifolium*	1	0
Leptospermum squarrosum	1	0
Leptospermum trinervium	1	0
Lepyrodia anarthria	0	0
Lepyrodia scariosa	0	0
Leucopogon amplexicaulis	1	1
Leucopogon ericoides	1	1
Leucopogon esquamatus	1	1
Leucopogon juniperinus	1	1
Leucopogon lanceolatus var. *lanceolatus*	0	0
Leucopogon microphyllus	1	1
Leucopogon parviflorus	1	0
Leucopogon setiger	1	1
Leucopogon virgatus	0	0
Lindsaea linearis	1	0
Lindsaea microphylla	1	0
Lissanthe strigosa	1	1
Livistona australis	0	0
Lobelia anceps	0	0
Lobelia andrewsii	0	0
Lobelia dentata	0	0

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Logania albiflora	1	0
Lomandra brevis	1	1
Lomandra confertifolia	0	0
Lomandra cylindrica	0	0
Lomandra filiformis	1	1
Lomandra fluviatilis	1	1
Lomandra glauca	1	1
Lomandra gracilis	1	1
Lomandra longifolia	0	0
Lomandra multiflora subsp. *multiflora*	1	1
Lomandra obliqua	0	0
Lomatia myricoides	1	0
Lomatia silaifolia	1	0
Lophostemon confertus	0	0
Ludwigia peploides subsp. *montevidensis*	0	0
Lycopodium deuterodensum	1	0
Macrozamia communis	0	0
Macrozamia spiralis	1	1
Marsdenia flavescens	0	0
Marsdenia rostrata	0	0
Marsdenia suaveolens	0	0
Melaleuca armillaris subsp. *armillaris*	1	1
Melaleuca deanei	1	1
Melaleuca ericifolia	1	1
Melaleuca hypericifolia	1	1
Melaleuca nodosa	1	1
Melaleuca styphelioides	1	1
Melaleuca thymifolia	1	1
Melodinus australis	0	0
Mentha satureioides	0	0
Micrantheum ericoides	0	0
Microlaena stipoides var. *stipoides*	0	0
Micromyrtus ciliata	0	0
Microsorum scandens	0	0
Mirbelia rubiifolia	0	0
Mirbelia speciosa	0	0
Mitrasacme paludosa	0	0
Mitrasacme polymorpha	0	0

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Monotaxis linifolia	1	0
Monotoca elliptica	1	0
Monotoca scoparia	1	1
Morinda jasminoides	0	0
Muellerina celastroides	0	0
Muellerina eucalyptoides	0	0
Myrsine howittiana	0	0
Myrsine variabilis	0	0
Nematolepis squamea subsp. *squamea*	0	0
Neolitsea dealbata	0	0
Notelaea longifolia	0	0
Notelaea ovata	0	0
Notelaea venosa	0	0
Notodanthonia longifolia	0	0
Olax stricta	1	0
Olearia microphylla	1	0
Olearia viscidula	1	0
Omalanthus nutans	0	0
Opercularia aspera	1	0
Opercularia diphylla	1	0
Opercularia hispida	1	0
Opercularia varia	1	0
Oplismenus aemulus	0	0
Oplismenus imbecillis	0	0
Oxalis chnoodes	0	0
Oxalis exilis	0	0
Oxalis perennans	0	0
Oxalis rubens	0	0
Ozothamnus diosmifolius	0	0
Palmeria scandens	0	0
Pandorea pandorana	0	0
Panicum simile	0	0
Parsonsia straminea	0	0
Paspalidium distans	0	0
Paspalum distichum	0	0
Passiflora herbertiana subsp. *herbertiana*	0	0
Patersonia fragilis	1	1
Patersonia glabrata	1	0

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Patersonia longifolia	1	1
Patersonia sericea	1	1
Pelargonium australe	0	0
Pelargonium inodorum	0	0
Pellaea falcata	0	0
Pellaea paradoxa	0	0
Peperomia blanda var. *floribunda*	0	0
Peperomia tetraphylla	0	0
Persicaria decipiens	0	0
Persicaria praetermissa	0	0
Persoonia lanceolata	1	1
Persoonia laurina	1	1
Persoonia levis	0	0
Persoonia linearis	0	0
Persoonia pinifolia	1	1
Petrophile pulchella	1	1
Petrophile sessilis	1	1
Phebalium squamulosum	1	1
Philotheca buxifolia	0	0
Philotheca salsolifolia	0	0
Philotheca scabra subsp. *scabra*	0	0
Philydrum lanuginosum	0	0
Phragmites australis	0	0
Phyllanthus gunnii	0	0
Phyllanthus hirtellus	0	0
Phyllota phylicoides	1	1
Pimelea linifolia	1	0
Pittosporum multiflorum	0	0
Pittosporum revolutum	0	0
Pittosporum undulatum	0	0
Planchonella australis	0	0
Plantago debilis	0	0
Platycerium bifurcatum	0	0
Platylobium formosum	1	1
Platysace ericoides	1	0
Platysace lanceolata	0	0
Platysace linearifolia	1	0
Platysace stephensonii	1	0

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Plectranthus parviflorus	0	0
Poa affinis	0	0
Poa labillardierei var. *labillardierei*	0	0
Poa poiformis var. *poiformis*	0	0
Podocarpus spinulosus	1	0
Polymeria calycina	0	0
Polyosma cunninghamii	0	0
Polyscias elegans	1	0
Polyscias murrayi	1	0
Polyscias sambucifolia	1	0
Polystichum australiense	0	0
Pomaderris andromedifolia	0	0
Pomaderris discolor	0	0
Pomaderris elliptica subsp. *elliptica*	0	0
Pomaderris ferruginea	0	0
Pomaderris intermedia	0	0
Pomaderris lanigera	0	0
Pomax umbellata	0	0
Poranthera corymbosa	0	0
Poranthera ericifolia	0	0
Poranthera microphylla	0	0
Potamogeton tricarinatus	0	0
Pratia purpurascens	0	0
Prostanthera densa	1	1
Prostanthera incisa	1	1
Prostanthera linearis	1	1
Pseudanthus pimeleoides	0	0
Pseuderanthemum variabile	0	0
Psilotum nudum	0	0
Psychotria loniceroides	0	0
Pteridium esculentum	1	0
Pteris tremula	0	0
Ptilothrix deusta	0	0
Pultenaea blakelyi	1	1
Pultenaea daphnoides	1	1
Pultenaea dentata	1	1
Pultenaea flexilis	1	1
Pultenaea hispidula	1	1

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Pultenaea linophylla	1	1
Pultenaea parviflora	0	0
Pultenaea retusa	1	1
Pultenaea scabra	1	0
Pultenaea stipularis	1	1
Pultenaea tuberculata	1	1
Pyrrosia rupestris	0	0
Ranunculus inundatus	0	0
Ranunculus lappaceus	0	0
Rhagodia candolleana subsp. *candolleana*	0	0
Rhodamnia rubescens	1	0
Rhytidosporum procumbens	0	0
Ricinocarpos pinifolius	0	0
Ripogonum album	0	0
Rorippa gigantea	0	0
Rubus moluccanus var. trilobus	0	0
Rubus parvifolius	0	0
Rubus rosifolius	0	0
Rulingia hermanniifolia	0	0
Rumex brownii	0	0
Samolus repens	0	0
Santalum obtusifolium	0	0
Sarcocornia quinqueflora subsp. *quinqueflora*	0	0
Sarcopetalum harveyanum	0	0
Scaevola ramosissima	1	0
Schelhammera undulata	0	0
Schizaea bifida	0	0
Schizaea fistulosa	0	0
Schizaea rupestris	0	0
Schizomeria ovata	0	0
Schoenus apogon	0	0
Schoenus brevifolius	0	0
Schoenus ericetorum	0	0
Schoenus imberbis	0	0
Schoenus lepidosperma subsp. *pachylepis*	0	0
Schoenus melanostachys	0	0
Schoenus moorei	0	0
Scolopia braunii	0	0

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Selaginella uliginosa	1	0
Senecio bipinnatisectus	0	0
Senecio hispidulus	0	0
Senecio lautus	0	0
Senecio linearifolius	0	0
Senecio minimus	0	0
Sigesbeckia orientalis subsp. *orientalis*	0	0
Sloanea australis	0	0
Smilax australis	0	0
Smilax glyciphylla	0	0
Solanum americanum	0	0
Solanum aviculare	0	0
Solanum prinophyllum	0	0
Solanum stelligerum	0	0
Sowerbaea juncea	0	0
Sphaerolobium vimineum	1	0
Spinifex sericeus	0	0
Sporadanthus gracilis	0	0
Sporobolus virginicus	0	0
Sprengelia incarnata	1	1
Stackhousia viminea	0	0
Stenocarpus salignus	0	0
Stephania japonica var. *discolor*	0	0
Stylidium graminifolium	1	1
Stylidium laricifolium	0	0
Stylidium lineare	1	1
Stylidium productum	1	1
Styphelia triflora	1	1
Styphelia tubiflora	1	1
Styphelia viridis subsp. *viridis*	1	1
Symphionema paludosum	0	0
Syncarpia glomulifera subsp. *glomulifera*	0	0
Synoum glandulosum subsp. *glandulosum*	0	0
Syzygium australe	0	0
Syzygium oleosum	1	0
Syzygium paniculatum	0	0
Tasmannia insipida	1	1
Telopea speciosissima	1	1

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Tetragonia tetragonioides	0	0
Tetraria capillaris	0	0
Tetrarrhena turfosa	0	0
Tetratheca ericifolia	1	1
Tetratheca neglecta	1	1
Tetratheca shiressii	1	1
Tetratheca thymifolia	1	1
Thelionema umbellatum	0	0
Themeda australis	1	0
Thysanotus juncifolius	1	0
Thysanotus tuberosus subsp. *tuberosus*	1	0
Todea barbara	0	0
Toona ciliata	0	0
Trachymene incisa subsp. *incisa*	0	0
Trema tomentosa var. *aspera*	0	0
Tricoryne elatior	0	0
Tricoryne simplex	0	0
Tricostularia pauciflora	0	0
Triglochin procera	0	0
Triglochin striata	0	0
Tristania neriifolia	0	0
Tristaniopsis collina	0	0
Tristaniopsis laurina	0	0
Trochocarpa laurina	1	0
Trophis scandens subsp. *scandens*	0	0
Tylophora barbata	0	0
Urtica incisa	0	0
Utricularia australis	0	0
Utricularia dichotoma	0	0
Utricularia lateriflora	0	0
Utricularia uliginosa	0	0
Vernonia cinerea var. *cinerea*	0	0
Veronica plebeia	0	0
Villarsia exaltata	0	0
Viminaria juncea	0	0
Viola betonicifolia subsp. *betonicifolia*	0	0
Viola hederacea	0	0
Viola sieberiana	0	0

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Wahlenbergia gracilis	0	0
Westringia fruticosa	0	0
Wilkiea huegeliana	0	0
Woollsia pungens	1	0
Xanthorrhoea arborea	1	1
Xanthorrhoea latifolia subsp. *latifolia*	1	1
Xanthorrhoea macronema	1	1
Xanthorrhoea media	1	1
Xanthorrhoea resinosa	1	1
Xanthosia pilosa	0	0
Xanthosia tridentata	0	0
Xerochrysum bracteatum	0	0
Xylomelum pyriforme	1	0
Xyris gracilis	0	0
Xyris operculata	0	0
Zieria compacta	0	0
Zieria laevigata	0	0
Zieria pilosa	0	0
Zieria smithii	0	0
Zornia dyctiocarpa var. *dyctiocarpa*	0	0