

A PRELIMINARY BIOCLIMATIC APPROACH TO PREDICTING POTENTIAL DISTRIBUTION OF *Phellinus noxius* AND GEOGRAPHICAL AREAS AT RISK FROM INVASION

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INTRODUCTION

Phellinus noxius, the cause of brown root-rot disease, is an invasive pathogen that was first described by Corner in Singapore (Corner 1932). It has a wide host range of primarily woody plants representing over 200 species from diverse families (Ann *et al.* 2002). This pathogen is also widespread, and has been reported to occur in many tropical/subtropical areas of Asia, Australia, Central America, Africa, and Oceania, where it can be quite destructive. *Phellinus noxius* appears to attack hosts regardless of health condition, and it can survive in organic matter long after host death. Early symptoms of brown root-rot disease are similar to other root diseases, including leaf chlorosis, wilt, and branch dieback; however,

mortality can occur relatively quickly after infection (Sashashi *et al.* 2012). A prominent sign of brown root-rot disease is a dark brown or blackish mycelial crust covering the stem base and root collar (Figure 1A). The associated wood decay typically displays honeycomb-shaped zone lines of reddish-brown to black (Figure 1B). The pathogen is often spread via root-to-root contact, but dispersal via basidiospores is also possible.

The general objective of this study is to predict suitable climate space for *P. noxius*, based on documented occurrences of DNA-sequence verified samples. By comparing bioclimatic variables associated with the precise locations of verified *P. noxius*, bioclimatic variables that influence pathogen occurrence can be identified and geographic locations that have suitable climate space for the pathogen can be predicted. Such information can predict potential distribution of *P. noxius*, and predict areas at risk from this invasive pathogen.

MATERIALS AND METHODS

A Maxent (Maximum Entropy) Species Distribution Model (version 3.3.3k) was used, because of its applications designed for presence-only data (Phillips *et al.* 2005). For this model, 19 bioclimatic variables (e.g., annual mean temperature, annual precipitation, mean temperature of coldest quarter, precipitation in warmest quarter, etc.) were used from WorldClim (worldclim.org). Sequencing of the ITS rDNA and translation elongation factor 1 α gene confirmed the identity of ca. 100 isolates (Figure 2) used for

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pathogen locations (latitude and longitude) to create SWD (Samples With Data) files that served as a basis for the Maxent bioclimatic model (Auto Features) using WorldClim climate surfaces. The regularization multiplier was kept at default, response curves and jackknifes were added to measure variable importance, and default settings were used for all experimental options. The final output, which is an average of all replicates under set parameters, displays current areas with suitable climate space for *P. noxius*. Minimal evidence of outliers was found, and cross-validation was used to verify data results. A total of 10 replicates were run with data split into training and test groups to assure accuracy and provide a statistical analysis. Quantum GIS (QGIS) was used to create the final outputs of the maps (Figure 3).

RESULTS AND DISCUSSION

The preliminary prediction maps show potential distribution (areas with suitable climate space) of *P. noxius* and areas that are at risk from this invasive pathogen, based on known locations of ca. 100 confirmed isolates from southeastern Asia, Australia, and Pacific islands (Figure 3). Please note that *P. noxius* isolates from Central America, Caribbean, South America, and Africa were not included in this study. Continued DNA-based characterization will help determine if isolates

belong to different species or genetic groups. Until more is known, caution is warranted for geographic areas that have suitable climate space for *P. noxius*, especially where this invasive pathogen does not currently occur (e.g., movement of plant material, infected wood, and infested soil should be restricted from areas where *P. noxius* occurs).

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Figure 1. *Phellinus noxius* infection on a dying flame tree (*Delonix regia*) during the dry season (A) and associated wood decay (B).

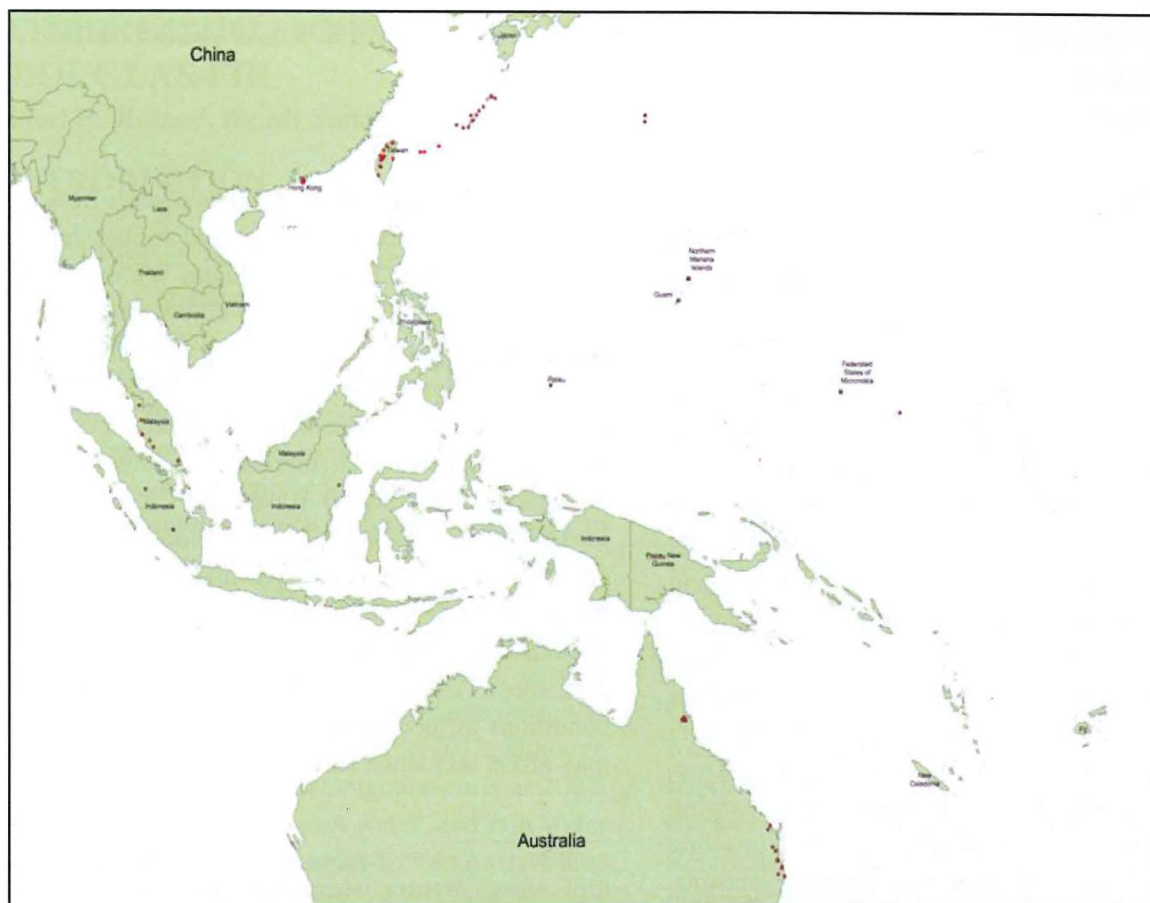


Figure 2. DNA-confirmed occurrences of *Phellinus noxius* that were used for bioclimatic modelling.

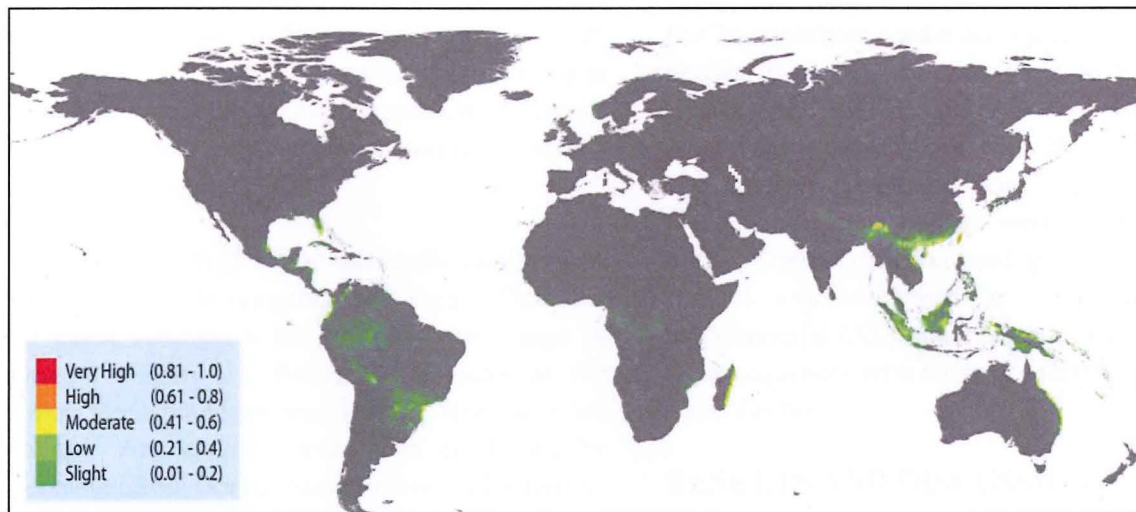


Figure 3. Preliminary predicted suitable climate space for *Phellinus noxius*. The colors indicate increasing climatic suitability from dark green (marginally suitable) to red (highly suitable). These predictions are based on 19 bioclimatic variables and the default settings in MaxEnt.