

POPULATION GENOMIC ANALYSES OF THE BROWN ROOT-ROT PATHOGEN (*Phellinus noxius*): EXAMINING POTENTIAL INVASIVE SPREAD AMONG PACIFIC ISLANDS

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INTRODUCTION

Phellinus noxius (Corner) G. H. Cunn is a vastly destructive, fast-growing fungal pathogen that affects a wide range of woody hosts in pan-tropical areas, including Asia, Australia, Africa, and Oceania (Ann *et al.* 2002; Figure 1). This pathogen causes brown root-rot disease on cacao, coffee, and rubber, as well as diverse fruit, nut, ornamental, and other native/exotic trees, with little indication of host specificity (Sahashi *et al.* 2010). Pathogenic symptoms of *P. noxius* infection can include reduced tree growth, defoliation, and branch dieback; however, *P. noxius* can survive as a saprophyte by colonizing heartwood and/or other organic matter. Brown root-rot disease can develop over several years, or in some cases, *P. noxius* infection can cause tree mortality within a year. Understanding the genetic diversity and evolutionary history of *P. noxius* populations worldwide well help assess the evolutionary origins, worldwide movement, and potential ecological differences within *P. noxius*.

The objectives of this study are to:

- 1) estimate the worldwide genetic diversity and evolutionary history of *P. noxius* movement;

- 2) determine if populations of *P. noxius* from Pacific islands show genetic signatures of introduced populations; and

- 3) characterize *P. noxius* for climatic modeling efforts to determine geographic areas at risk from *P. noxius* introductions.

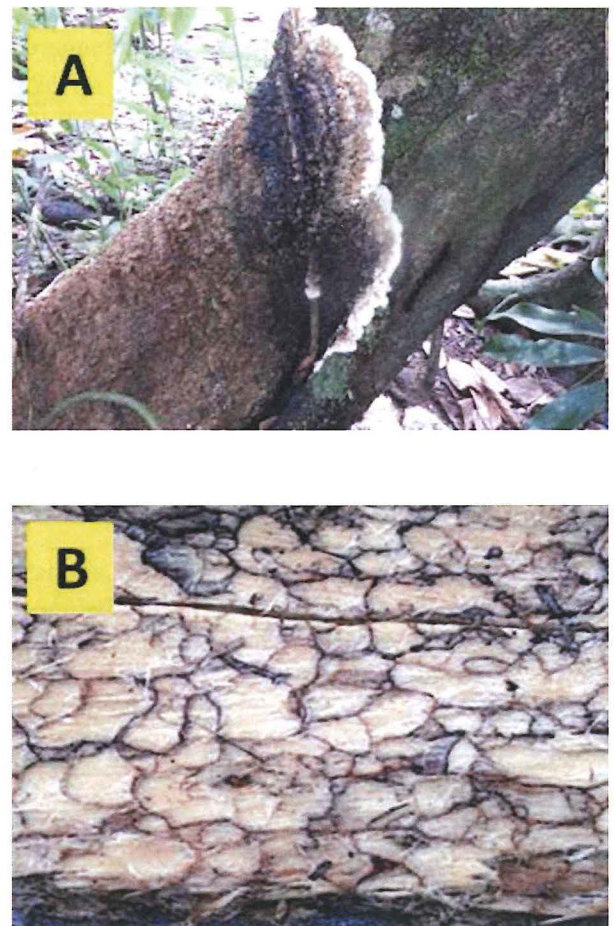


Figure 1. Characteristic symptoms/signs of brown root rot caused by *Phellinus noxius*: mycelial crust (A) and mycelial mats and reddish-brown hyphal zone lines between the infected bark and sapwood (B).

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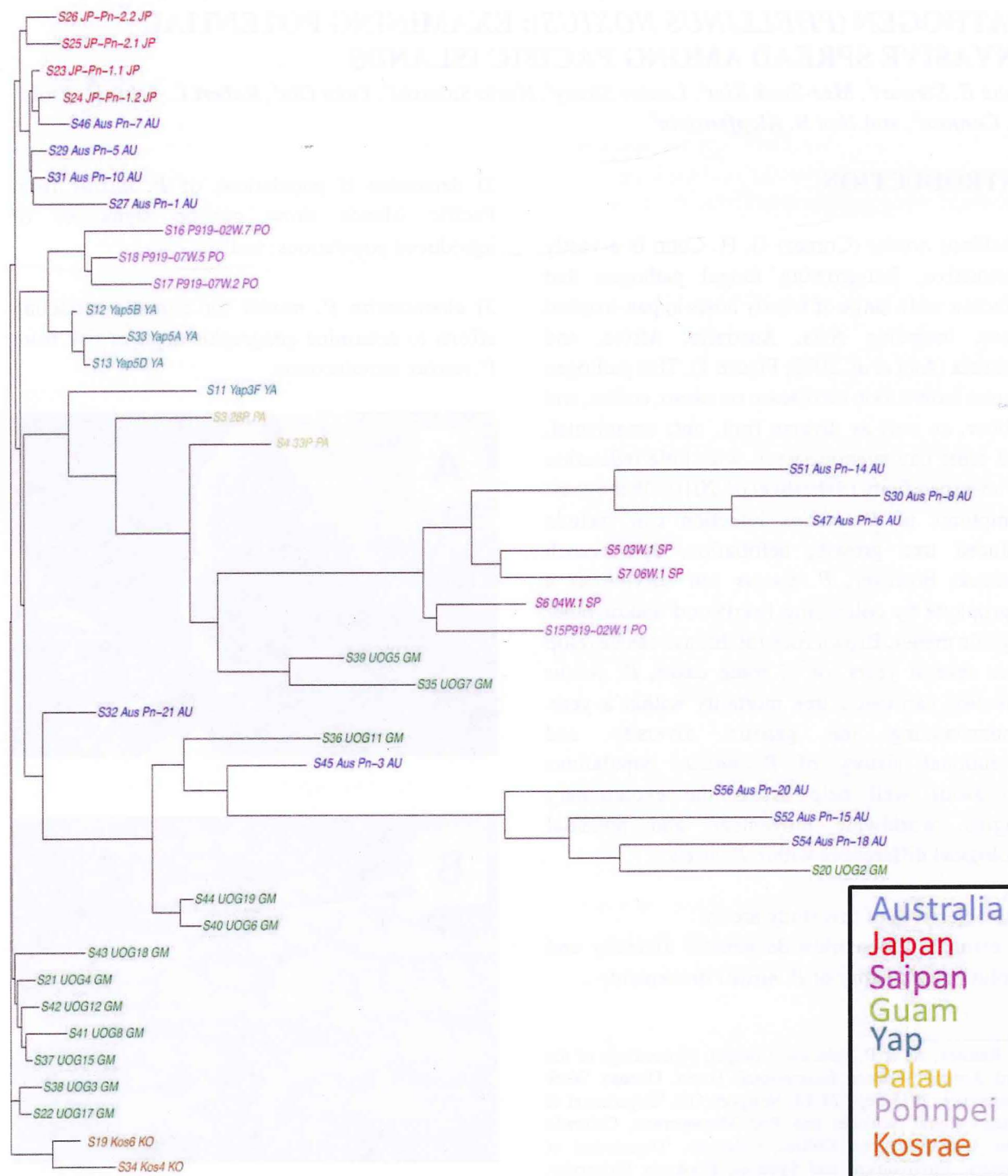


Figure 2. Preliminary results: Neighbor-joining of 1,449 SNPs within 396 loci. Isolates are color-coded by location.

METHODS

Isolates

A total of 56 isolates were included from Japan (4 isolates), Australia (19), and the Pacific islands including Saipan (5), Guam (10), Palau (4), Pohnpei (5), Kosrae (2).

Molecular characterization and analyses of molecular data

Sequence data were generated by Illumina sequencing of double-digest, reduced representation libraries (ddRAD). Restriction site associated DNA markers (RADseq), 3RAD design - Enzymes: *Bam*HI, *Cla*I, *Msp*I. RADseq loci were *de-novo* assembled, cataloged and analyzed in STACKS (Catchen *et al.* 2013). Pegas (Paradis 2010) (implemented in R) was used for neighbor-joining analyses (Figure 2).

RESULTS

Reads were assembled *de-novo* and grouped using STACKS (Catchen *et al.* 2013). A total of 24,142 total RAD loci were catalogued with 12,000 RAD loci per individual. The average depth per locus was 14x. Of the total RAD loci, 396 loci were used for analyses. These loci were found in 80% of the total 44 samples at a depth greater than 5x. We had a total of 50% missing data across the 396 loci for the 44 individuals. We recovered a total of 1,449 SNPs within the sampled population.

DISCUSSION AND FUTURE WORK

Preliminary results of the ddRAD single nucleotide polymorphism data show multiple genotypes of *P. noxius* that are structured geographically (Figure 2). Isolates from Pacific islands showed reduced levels of genetic diversity, which supports the hypothesis of potential introductions to some Pacific islands. Future research will include more populations from diverse geographic areas. Continued analyses will examine levels of gene

flow among populations, examine potential pathways of spread, and predict the potential spread of specific genotypes related to the current and changing climates. This study is aimed toward performing a wide-scale, population-genetic study of *P. noxius* isolates from eastern Asia, Pacific islands, and Australia to determine the regional population structure, estimate diversity in recently observed populations, and assess the potential suitable climate space for specific genotypes.

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