

# Approaching the origins of *Phytophthora taxon Agathis*<sup>1</sup>



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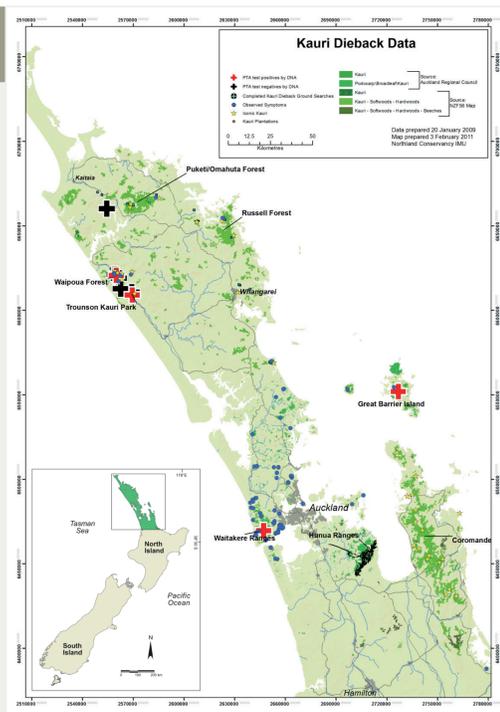
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<sup>1</sup> In memory of Dr Ross E. Beever

## INTRODUCTION

Kauri dieback is an increasing problem affecting kauri (*Agathis australis*) in Auckland and Northland (Fig. 1). *Phytophthora taxon Agathis* (PTA) has been identified (by Ross Beever<sup>A</sup>) as a causal agent of kauri dieback, but we do not know if PTA is a new endemic species or whether it has been described elsewhere and was introduced to New Zealand.

Figure 1: Distribution of kauri (*Agathis australis*) and kauri dieback symptoms



## MISTAKEN IDENTITY?

- PTA was originally misidentified as the morphologically similar *P. heveae*.<sup>B</sup>
- PTA shares a place in *Phytophthora* Clade 5<sup>C</sup> with *P. heveae* and *P. katsurae* but has different oospore morphology (Fig. 2). The morphospecies are distinguished largely on basis of spore ornament.



Figure 2: Comparable-sized oospores (approx 35–37 µm) from within *Phytophthora* Clade 5<sup>C</sup>, but note the markedly different ornamentation, L–R: *P. katsurae* – ‘bullate protuberances’, PTA – ‘slightly raised protuberances’, *P. heveae* – smooth-walled.

- Clade 5 morphospecies (i.e. *P. katsurae* and *P. heveae*) are known from ‘indigenous’ communities in tropical forests in Australia, Papua New Guinea, and Taiwan.
- Perhaps PTA will be matched by isolates from these areas?
- A new morpho-molecular study of this clade is warranted.

## MULTI-GENE ANALYSIS

Preliminary studies showed small genetic differences between the species in Clade 5<sup>C</sup> using the ITS region of the nuclear ribosomal DNA. More recently, researchers are using multiple loci from both the nuclear and mitochondrial genomes to resolve species boundaries within *Phytophthora*.<sup>D–F</sup> We have commenced a multi-gene phylogenetic study to better understand the relationship between these members of Clade 5<sup>C</sup>. Although relationships within Clade 5 remain uncertain, PTA is consistently differentiated from the other two species in Clade 5, based on the three gene regions sampled to date, Translation Elongation factor 1 alpha, Beta-tubulin, and the mitochondrial gene NADH dehydrogenase.

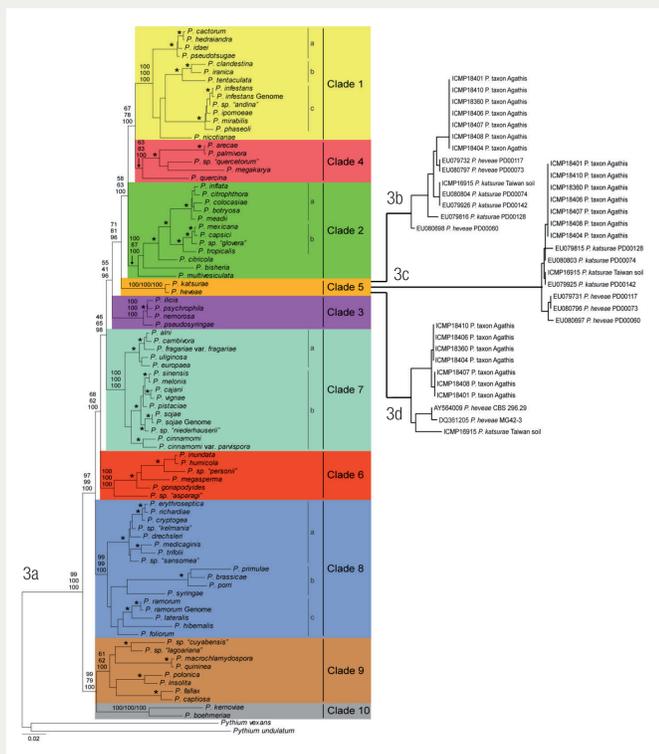


Figure 3a: A genus-wide phylogeny for *Phytophthora* downloaded from the www.phytophthora.org website, based on the 7 gene analysis in Blair et al. 2008.

Figures 3b–d: Detailed phylogeny showing relationship of PTA to other Clade 5 species, based on Translation Elongation factor 1 alpha, Beta-tubulin, and NADH dehydrogenase respectively. Data for ICMP isolates unpublished.

## SPECIES CONCEPT FOR PTA

- The genus *Agathis* consists of 21 species.<sup>G</sup>
- Its range extends west to Sumatra; north to the Philippines; east to Fiji; and south to New Zealand (Fig. 4).<sup>H</sup>
- The greatest representation of the genus (five species) occurs in New Caledonia.<sup>I</sup>
- *Agathis australis* is restricted to New Zealand.

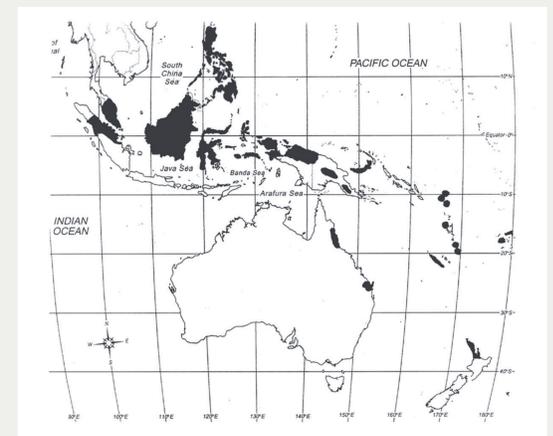


Figure 4: Distribution of the genus *Agathis*, including New Zealand (North Island), Australia (Queensland), New Caledonia, Solomon Islands, Vanuatu and Fiji.

- Preliminary evidence suggests that *A. robusta* – native to south-eastern Queensland – is resistant to PTA.
- We will seek Clade 5 morphospecies (i.e. *P. katsurae* and *P. heveae*) known from ‘indigenous’ communities in tropical forests in Australia, Papua New Guinea, Sumatra; Philippines; Vanuatu, New Caledonia and Fiji for comparative purposes.
- Once we have collected isolates of PTA from the range of infested kauri throughout the North Island we will compare:
  - Colony morphology on V8 juice, MEA, and PDA
  - Morphologic and morphometric variation of sporangia, oogonia, oospores and antheridia
  - Pathogenicity
  - Host range of PTA on other *Agathis* spp. (Fig. 4).
- By combining phylogenetic analysis with examination of all other morphological and physiological data we will be able to infer whether this taxon is unique and not previously described.

## MICROSATELLITE ANALYSIS TO RESOLVE ORIGINS AND QUESTIONS AROUND TIME OF EXOTIC INCURSION

- Founder populations typically contain only a small fraction of the genetic variation found in the original source populations.<sup>K</sup> Because founder populations are usually small, genetic drift can occur during the founder event and in subsequent generations until the population size increases. Therefore the genetic structure of founder populations is often very different from the original source populations.

- *Phytophthora* population dynamics research in Oregon over the last four years has focused on understanding the evolution of the three clonal lineages of the exotic sudden oak death pathogen *Phytophthora ramorum*.<sup>L, M</sup>
- We aim to screen a ‘population-sample’ of PTA isolates for alleles at 10 microsatellite loci to derive an estimate of the genetic diversity of the sample, and decide whether it is indicative of an introduced organism, i.e. whether the population structure reflects characteristics of a founder population.

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