

## Determining the origin of the emerging pathogen, *Phytophthora multivora*

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*Phytophthora multivora* is widespread in Western Australia (WA); it has a wide host range and considerably variability in the sequence of the mitochondrial gene *cox1* led to the hypothesis that it may be endemic to the region. To test this hypothesis, four nuclear (ITS, enolase, HSP90 and *ras*) and three mitochondrial (*cox1*, *cox1GS* and *nadh1*) loci were sequenced for 60 isolates of *P. multivora* isolated from Australia, South Africa (RSA) and Europe and the data were subjected to phylogenetic, coalescent-based and population genetic analyses. Isolates from RSA possess greater nucleotide diversity and a greater number of alleles at three of the nuclear loci and at all three mitochondrial loci than those from WA. In addition, the RSA population had more unique multilocus genotypes than the WA population. While *P. multivora* is widely distributed in natural ecosystems in WA and RSA, it is usually isolated from nurseries or horticulture elsewhere in the world. Additionally, *P. multivora* is consistently isolated from cankers and dead and dying plants of numerous endemic hosts in WA, but is predominantly isolated from soil associated with asymptomatic plants in RSA. Based on this evidence it is proposed that *P. multivora* is endemic to RSA and has been introduced to Western Australia.

## Four phenotypically distinct lineages identified within *Phytophthora lateralis*

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Until recently *Phytophthora lateralis* was known only as the cause of dieback and mortality of *Chamaecyparis lawsoniana* in its native range in the Pacific Northwest [1]. Since the 1990s however disease outbreaks have occurred increasingly on ornamental *C. lawsoniana* in Europe; and in 2007 the pathogen was discovered in soil around old growth *C. obtusa* in Taiwan, where it may be endemic [2]. When the phenotypes of over 150 isolates of *Phytophthora lateralis* from Taiwan; across the Pacific Northwest (British Columbia to California); and from France, the Netherlands and the UK were compared three well separated growth rate groups were resolved: one from Taiwan, one from the Pacific Northwest and Europe and one from a small area of the UK. Among these groups nine distinct types were identified based on colony patterns and spore metrics and discriminated in a multivariate analysis. The assumption that the three main growth rate groups represented distinct phylogenetic units was tested by comparative sequencing of two mitochondrial and three nuclear genes. This assumption was confirmed. In addition two phenotype clusters within the Taiwan growth group were also shown to be separate lineages. The characteristics and distribution of the four *P. lateralis* lineages will be presented and their evolutionary, taxonomic and plant health significance discussed.

[1] Hansen E.M., Goheen D.J., Jules E.S. and Ullian B. Managing Port-Orford-Cedar and the introduced pathogen *Phytophthora lateralis*. *Plant Disease* **84** 4-14 (2000).

[2] Brasier C.M., Vettraino A.M., Chang T.T. and Vannini A. *Phytophthora lateralis* discovered in an old growth *Chamaecyparis* forest in Taiwan. *Plant Pathology* **59** 595-603 (2010).



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