

AFLP Analysis of *Phytophthora nemorosa* and *P. pseudosyringae* Genetic Structure in North America

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In California and Oregon, *Phytophthora ramorum* has an overlapping host and geographic range with two newly described *Phytophthora*, *P. nemorosa* and *P. pseudosyringae*. *P. nemorosa* alone causes symptoms similar to those of *P. ramorum*, including lethal tanoak cankers, and *P. pseudosyringae* is associated with oak decline in Europe. However, epidemiological observations, namely broader geographic distribution and reduced virulence, suggest the other two are endemic in this region, while *P. ramorum* is hypothesized to have been introduced. Though molecular evidence suggests that *P. nemorosa* and *P. pseudosyringae* are each other's closest known relatives, both are rather distantly related to *P. ramorum*. In order to study patterns of genetic variability within *P. nemorosa* and *P. pseudosyringae* and to shed light on the hypothesis of endemism, we use amplified fragment length polymorphism (AFLP) analysis to generate DNA fingerprints for isolates of the two species. 41 isolates of *P. nemorosa* and 30 isolates of *P. pseudosyringae* are analyzed, and isolates were chosen from throughout the known geographic and host ranges of the two taxa in North America. From AFLP fingerprint data, we calculate a distance cladogram with *P. ilicis*, the closest known phylogenetic relative to *P. nemorosa* and *P. pseudosyringae* as an outgroup. The degree of genetic variability and structure within each species will be shown and implications for the history of these taxa in North America will be discussed.