

Population Structure of the Emerging Plant Pathogen *Phytophthora ramorum* on the West Coast of the United States¹

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Abstract

Phytophthora ramorum is a devastating pathogen in native forests in California and southwestern Oregon and in nursery crops in California, Oregon and Washington. In this study we analyzed the population structure of *P. ramorum* in the west coast (CA, OR, and WA) of the United States by screening 579 isolates recovered from 2001 to 2005 at 10 microsatellite loci.

The overall *P. ramorum* population was composed of 73 multilocus genotypes. Based on allele patterns, 72 genotypes belonged to the North American clonal lineages NA1 or NA2 (both A2 mating type) and one nursery genotype (OR and WA) belonged to the European clonal lineage (EU1, A1 mating type). Within the North American types, 71 genotypes clustered into the same clonal lineage (NA1), while one nursery genotype (CA and WA) belonged to NA2. None of the genotypes detected shared alleles of NA1 or NA2 and EU1, indicating that sexual reproduction is currently not occurring in the west coast population. Twenty out of 73 genotypes were present in more than one population. The lowest incidence of genotypes shared among populations was observed in the OR-forest population (7 out of 30), which was dominated by a genotype not found elsewhere. Using assignment tests, a high percentage of the genotypes could not be assigned to the population from where they originated. The number of genotypes shared between two populations was not correlated with the minimal geographic distance between the two populations. The overall estimated F_{ST} -value among the four populations was 0.183 (95 percent confidence interval: 0-0.377). When using clone-corrected data sets, pairwise differentiation was significant only between the OR-forest and the three other populations. Accordingly, genetic distances among OR-nursery, CA, and WA populations were very small.

Our study demonstrates how the spread and the population structure of an invasive plant pathogen can be strongly affected by human activity. Accepting the hypothesis of a recent introduction of *P. ramorum* into western United States, the movement of infected nursery stock has probably played a major role in the rapid expansion of the geographical range of the pathogen over long distances. Thus, the current *P. ramorum* NA1 population is genetically similar from California to Washington. The dominance in southwestern Oregon of a genotype not found elsewhere may account for the significant differentiation between the OR-forest and the other three populations.

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