

Population Genetic Analysis Reveals Ancient Evolution and Recent Migration of *P. ramorum*¹

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Abstract

Phytophthora ramorum populations in North America and Europe are comprised of three clonal lineages based on several different genetic marker systems (Ivors and others 2006, Martin 2008). Whether these lineages are ancient or a recent artifact of introduction has been unclear. We analyzed DNA sequence variation at five nuclear loci in order to better understand the evolutionary history of the three lineages and the relationships among them (Goss and others 2009). We did not see differences among isolates within each lineage, therefore the observed genetic divergence among lineages precedes introduction. Analysis with coalescent-based methods revealed that the lineages have been diverged for an evolutionarily significant period of time, roughly 165,000 to 500,000 years. Genes contained signatures of historical recombination between the lineages, indicating that ancestors of the *P. ramorum* lineages reproduced sexually. The large genetic differences among lineages suggest that they were not introduced from a single interbreeding population. Instead, the three lineages likely originated from three different geographic locations such that they evolved in isolation from each other prior to introduction to North America and Europe.

Within the *P. ramorum* lineages, highly variable microsatellite markers have proved useful for examining population structure (Ivors and others 2006, Prospero and others 2007, Mascheretti and others 2008, Prospero and others 2009). *P. ramorum* has been moved via the nursery trade from source populations on the West Coast to locations across the U.S. (Frankel 2008). We investigated whether we could infer *P. ramorum* migration patterns in the U.S. nursery trade using existing microsatellites markers. We genotyped 279 isolates collected from infested nurseries in 19 states between 2004 and 2007 (Goss and others, unpublished data). This resulted in 53 multilocus genotypes in 228 NA1 isolates, 2 multilocus genotypes in 17 NA2 isolates, and 2 multilocus genotypes in 34 EU1 isolates. Our analysis focused on isolates in the NA1 lineage because of the limited distributions and low genetic diversities of the EU1 and NA2 clonal lineages in U.S. nurseries. A single NA1 genotype was shared among the majority of states and isolates clustered into two genetic groups, one mainly containing isolates from Connecticut, Oregon, and Washington and the other isolates largely from California and the remaining states. From this pattern we inferred two predominant eastward migration routes for NA1 individuals originating either in California or the Pacific Northwest. This is consistent with U.S. Department of Agriculture, Animal and Plant Health Inspection Service (USDA APHIS) trace-forward and trace-back investigations, which indicate large shipments to 39 states from California and smaller shipments from Oregon in

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2004. Genotyping of North American nursery isolates is ongoing. The clonal lineage of each *P. ramorum* isolate genotyped is posted to a public website as soon as permission is obtained from the providing institution or agency (fig. 1).

Phytophthora ramorum Multilocus Genotyping Database

Home | About the Project | Database

Welcome

This site provides information on multilocus microsatellite genotypes of *P. ramorum* currently found in North America. Access the database: [P. ramorum multilocus genotyping database](#).

Isolates of *P. ramorum* are currently placed in one of the following three clonal lineages currently recognized for *P. ramorum* worldwide (Grunwald et al. 2008, 2009):

Lineage	Current distribution	Habitat	Mating type
EU1	Europe, North America	Gardens, Woodlands, Nurseries	A1 (see #)
NA1	North America	Forests, Nurseries	A2
NA2	North America	Nurseries	A2

Lineage EU1 is predominantly of A1 mating type with rare findings of A2 isolates in Belgium (Verres and De Merlier 2003).

Current distribution of clonal lineages in the US is shown in figure 1.

Figure 1. Current distribution of clonal lineages of *P. ramorum* in the US. Color coding identifying clonal lineages is identical to that in table above.

Figure 1—*P. ramorum* multilocus genotyping database webpage (<http://oregonstate.edu/~grunwaln/index.htm>).

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