

Genetic Uniformity of *Phytophthora ramorum* in North American Forests Revealed by Microsatellite Markers

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Phytophthora ramorum causes an emerging forest disease in California and Oregon. The geographic origin of the pathogen remains unknown but its clonal population structure in North America revealed by AFLP analysis suggests a recent introduction. In this study we investigated the population structure of *P. ramorum* in Northwestern American forests using microsatellite markers.

After constructing a microsatellite enriched library for *P. ramorum*, we isolated 24 loci containing di- or tri-nucleotide microsatellites, for which we designed specific primers. Initial testing of the primer sets showed that 14 loci successfully amplified products of the expected size. Seven of them discriminated European (mating type A1) and North American (mating type A2) isolates and were used for population analysis.

We have screened more than 200 isolates of *P. ramorum* for alleles at the seven loci. Most of these isolates were recovered from infected tanoak, coast live oak, evergreen huckleberry, rhododendron, and Oregon myrtle in forests of Oregon and California. Some isolates were obtained from soil samples and from stream baits. Twenty-six isolates were previously tested for mating type and all were A2. Our results show that all the screened isolates have an identical microsatellite genotype. This strongly supports the hypothesis of a recent introduction of the pathogen into North America.