

Use of Microsatellite Markers Derived From Whole Genome Sequence Data for Identifying Polymorphism in *Phytophthora ramorum*¹

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Abstract

Investigating the population genetics of *Phytophthora ramorum*, the causal agent of sudden oak death (SOD), is critical to understanding the biology and epidemiology of this important phytopathogen. Raw sequence data (445,000 reads) of *P. ramorum* was provided by the Joint Genome Institute. Our objective was to develop and utilize Simple Sequence Repeat (SSR) techniques for fingerprinting large numbers of *P. ramorum* isolates originating from different host species within Europe and the United States. Using a computer program developed at Plant Research International, 1334 potential microsatellite loci were identified. Primers were selected from over 110 flanking regions of SSRs and tested in PCR reactions to amplify repeats. Thirty-one polymorphic loci were identified and 14 primer sets were optimized for isolate genotyping. Three loci showed variation among nursery isolates from Europe and the United States, although no variation was identified among isolates from forests in the United States. This information provided insight regarding genetic variation within populations, identified new genotypes, and separated isolates into two distinct lineages correlated with continental provenances.

Key words: microsatellites, *Phytophthora ramorum*, polymorphism

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