

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

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Investigating the population genetics of *Phytophthora ramorum*, 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* were 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 within 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 European and US nursery isolates, although no variation was identified among isolates from the wild in the US. This information provided insight regarding the amounts of genetic variation within populations, identified new genotypes, and separated isolates into two distinct lineages correlated with continental provenance.