

# Amplified Fragment Length Polymorphism Assessment of Population Diversity in California Bay Laurel (*Umbellularia californica*)<sup>1</sup>

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## Abstract

*Umbellularia californica* is a major foliar host for *Phytophthora ramorum*. The population genetics of a host influences the spread of pathogens through the host population, however no information is available on the population genetics of *U. californica*. We investigated the population genetics of *U. californica* using Amplified Fragment Length Polymorphism (AFLP) in a study of the factors underlying the spread of *P. ramorum* through the Sonoma Valley. Genomic DNA was extracted from leaves from 97 populations of *U. californica*, representing 1293 adults and 2119 juveniles. Forty-six AFLP primer pairs have been surveyed, resulting in six pairs providing a strong signal. We surveyed two geographically proximate populations to find a combination of markers that provides representative genetic diversity. Comparing individual primers, noticeable variation was seen in the number of scorable loci (45 to 82), percent polymorphism (60 to 75 percent), total diversity (HT: 0.096 to 0.131), and between population diversity (GST: 0.071 to 0.105). One combination of three primers (186 loci) gave very similar diversity values when compared to all six primers (340 loci). This study produced a solid basis for conducting a population genetics study of an estimated 6000 *U. californica* trees in the study area and generating useful data for modeling the spread of *P. ramorum*.

*Key words:* AFLP markers, population genetics, *Umbellularia californica*

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