

## **Amplified Fragment Length Polymorphism Assessment of Population Diversity in California Bay (*Umbellularia californica*)**

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*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 are investigating 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 primers pairs have been surveyed, resulting in six pairs providing 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 (45-82), percent polymorphism (60-75%), total diversity ( $H_T$ : 0.096-0.131), and between population diversity ( $G_{ST}$ : 0.071-0.105). One combination of three primers (186 loci) gave very similar diversity values when compared to all six primers (340 loci). This study produces a solid basis for conducting a population genetics study of an estimated 6000 *U. californica* trees in the study area's plots and generating useful data for modeling the spread of *P. ramorum*.