

Does Stand Density Affect Mating System and Population Genetic Structure in Coast Live Oak (*Quercus agrifolia*)?

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Coast Live Oak, (*Quercus agrifolia*) is a major species at risk in the current *Phytophthora ramorum* epidemic in California's oak woodlands. To search effectively for resistant genotypes, it is imperative to have an understanding of the host population genetic structure that exists in these forests now, and how its reproductive capacity may be affected by major losses. The purpose of our study is to quantify genetic variation, and to examine and compare the current mating system in relatively dense, mixed species coastal populations, and in open woodland populations near to the interior limit of the species range.

To inventory the existing genetic structure, we sampled adult trees from five large, contiguous coastal and interior populations in central California. Spatial locations of the trees were mapped, and their multilocus genotypes were identified using 13 neutral microsatellite markers.

Over this range in central California, Wright's F-statistics and Hardy-Weinberg tests revealed these adult populations to be in panmictic equilibrium with a global F_{st} of 0.037, suggesting high outcrossing that is typical of oaks. We detected heterozygote deficiency in all populations when a stepwise mutational model for microsatellite alleles is assumed, suggesting that these populations have been expanding over recent generations. Our findings show that 96% of the molecular variance in Coast Live Oak occurs within populations, and therefore the genetic structure is fairly uniform throughout this range. In light of this information, searches for *Phytophthora*-resistant genotypes could be limited to smaller areas of the species' distribution. Individual F_{is} estimates for each population suggest slightly more outcrossing in the interior populations, and more inbreeding in the coastal populations, where pollen flow may be restricted due to stand structure.

Current work addresses the recent mating within these populations. We have collected acorns from the adult study trees and are using the same 13 loci to determine their paternity. Using the spatial locations of the parent trees, we will estimate the average distance of pollen dispersal within a stand, and identify the proportion of effective pollen donors in each population. The parent trees are being genotyped using 5 maternally inherited chloroplast primers, which will indicate how genes are being spread through the dispersal of acorns as well as through pollen flow. Evaluating the current mating system of Coast Live Oak during the *Phytophthora* outbreak will help to assess the impact of adult tree mortality on the future genetic diversity of these populations.