

Genetic Hitch-Hiking Extends the Range of Coast Live Oak ¹

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Abstract

The northernmost range of coast live oak (*Quercus agrifolia*) is reported from the Ukiah Valley (Mendocino County, California). Here, field observations suggest that hybridization with interior live oak (*Q. wislizeni*) is important. Elsewhere in northern California, morphology of coast live oak can be highly variable (particularly foliar form) and this has commonly been attributed to “noise” from a polymorphic species belonging to a genus renowned for its variability. This variability can be worrisome to scientists working on sudden oak death, since it may result in confounding species in ecological and pathogenicity studies.

To better understand the causes of this variability, within and among the major red oak species of the coastal oak woodlands of California, we have been studying population structure and differentiation by comparing nuclear and chloroplast DNA. The nuclear genome is bi-parentally inherited and provides important information on population demographic processes, such as gene flow and historical fluctuations in population size. The chloroplast genome in oaks is maternally inherited and is therefore passed on clonally through seed from mother tree to progeny. The heavy seeds of oaks are not likely to be widely dispersed resulting in strong population structure in chloroplast DNA that provides historical signals of population lineages in time and space.

Our nuclear DNA studies have shown important interspecific gene flow among the three evergreen red oaks of California (*Q. agrifolia*, *Q. wislizeni* and *Q. parvula*) and minor gene flow between these species and the deciduous red oak, *Q. kelloggii* (Dodd and Afzal-Rafii 2004). In populations morphologically assigned to *Q. wislizeni*, genetic admixture from up to three of the other red oak species can be detected in an individual’s genotype. We have shown that admixture proportions at a population level are well correlated with environmental conditions at that site suggesting that introgression among species can produce genotypes that may be better adapted to the local habitat than are pure parental genotypes. Since introgression among red oaks is important in northern California, in the region of heavy infection from *Phytophthora ramorum*, we compared chloroplast DNA to investigate possible cyto-nuclear disequilibrium that would suggest differences in the relative success of one species as maternal or paternal parent.

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Chloroplast DNA diversity based on six microsatellite loci was documented for 28 populations of *Q. agrifolia*, including 12 from northern California (north of San Francisco Bay), eight from central California and eight from southern California and Baja California, Mexico. As the chloroplast genome is non-recombining, the six loci are inherited together as a single locus that we refer to as a haplotype. A total of 27 different haplotypes were detected, including six haplotypes in northern California, seven in central California and 14 in southern California. This higher haplotype diversity in the south, suggests this to be a region in which coast live oaks have a longer history than in the north and may be a refugium during the last glacial advance. We found that chloroplast haplotypes may be shared among species, where populations occupy the same geographic range. This is particularly true for coast live oak in northern California. The northernmost populations of coast live oak, including hybrid populations at Hopland and Yorkville, were characterized by a single haplotype. Interestingly, this haplotype is the only one found in interior live oak over a broad zone north from Ukiah. We conclude that these northernmost populations of coast live oak must have an interior live oak maternal lineage. This suggests that coast live oak has colonized this region through pollen hybridizing with interior live oak, followed by generations of backcrossing to “regenerate” the coast live oak morphotype. Further south, including the well-studied populations of Marin County, two or three chloroplast haplotypes were detected including the northern interior live oak haplotype and two coast live oak haplotypes. This indicates that these populations are of mixed species lineages through seed and pollen dispersal. We hypothesize that coast live oak has been advancing northwards through pollen “hitchhiking” on interior live oak and that, once established, occasional seed dispersal from more southerly populations of coast live oak produces a population of mixed maternal lines.

Our findings on population structure of California red oaks indicate that these are not well-defined species genetically. Ecological studies and studies of pathogenicity may need to take account of this and that “pure” species’ habitat preferences are not necessarily appropriate in these mixed populations.

References

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