

## Genetic Hitch-hiking Extends the Range of Coast Live Oak

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The northernmost range of coast live oak (*Quercus agrifolia*) is reported from the Ukiah Valley (Mendocino Co., 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 using two sets of molecular marker (chloroplast and nuclear SSRs or microsatellites). 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 and historical signals. The nuclear genome is bi-parentally inherited and provides an excellent system for observing gene flow.

We have 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 are 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 nuclear microsatellite data confirm that hybrid origin is important in all populations north of the San Francisco Bay.

Ecologists and pathologists working in California’s coastal oak woodlands should recognize that they are not dealing with a single well-defined species and should take into account that “pure” species’ habitat preferences are not necessarily appropriate in these mixed populations.