

Genetic Variation Sampled in Three California Oaks¹

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Abstract: As a first step in acquiring genetic information about oak species indigenous to California's hardwood rangelands we drew on experience from both forest regeneration and species conservation and applied biochemical techniques for rapidly assaying patterns of genetic variation. In a study sponsored by the California Integrated Hardwood Range Management Program we sampled 860 trees from 29 populations of three species of oaks spanning their distribution in California. Using leaf tissue collected from each tree we performed starch gel electrophoresis to assay allozymic variation within and among populations and species. Our findings included some surprises and confirmed certain interpretations made by previous taxonomic work. We found large genetic differences between all pairs of species, including blue and valley oaks, with many unique genes distinguishing each species. Our allozyme results support assigning blue oak to the white oak group. At the population level we found little variation within populations of coast live oak and valley oak. Blue oak was about twice as variable within populations as the other two species. Differences between populations within species were small. We could detect no geographic pattern in allozyme variation in any of the species and no indication of racial or subspecific variation.

Experience in both production forestry and species conservation has demonstrated the importance of knowledge about genetic variation and its distribution within and among populations. Until recently, little has been known about natural genetic variation in any of California's oak species. With land conversion and more intensive land use diminishing the ranges of several species and unsuccessful regeneration becoming a matter of concern, genetic approaches may help us to understand possible causes and remedies for population declines. To begin acquiring the genetic information needed as background for answering management questions, we undertook a survey of allozyme variation in three species of California oaks. We chose allozyme techniques as a first step to describing patterns of genetic variation because they are well established, relatively quick and inexpensive, and have been shown to yield useful information in most cases.

We directed our study toward describing genetic variation in two endemic California oak species that appear to be particularly affected by land conversion and regeneration failure: valley oak (*Quercus lobata*) and blue oak (*Quercus douglasii*) of the subgenus *Quercus*. As an ecological and taxonomic "control" on our findings we included coast live oak (*Quercus agrifolia*) of the subgenus *Erythrobalanus* in our survey.

METHODS

We sampled 15 stands of coast live oak and seven stands each of blue oak and valley oak representing the full range of each species in California. Twenty trees were selected from each of 15 stands of coast live oak. After discovering that levels of genetic variation were lower than we initially expected, we elected to sample a larger number of trees (40) from fewer populations (seven) in order to improve our chances of detecting meaningful patterns of variation among stands. With all species, foliage (10-15 leaves) was collected from mature trees of varying sizes spaced 50-100 meters apart. Trees at most sites were marked or mapped to facilitate repeat collections and possible use by other investigators.

Leaf tissue extracts were prepared from foliage samples using techniques described by Mitton and others (1979). Extracts were electrophoresed on starch gels using established techniques (Conkle and others 1982; Millar, 1985), and gel systems (Strauss and Conkle 1986). Eighteen loci resolved in coast live oak and 21 loci in valley oak and blue oak.

FINDINGS

Our findings are reported in detail elsewhere (Millar and others, unpublished draft). A general overview is provided here. Those interested in more detail should contact the authors for information.

In contrast to our initial expectations based on life history traits, we found little variation within coast live oak and valley oak populations relative to what has been found for conifers and other oak species that have been studied in the eastern United States. Blue oak populations were markedly more variable than those of either of the other two species—about twice as variable

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as coast live oak with respect to the percent of loci polymorphic.

A major finding of our study was the striking allozymic differences among the three species, attributable to both the occurrence of unique alleles and distinguishing allele frequencies. Genetic distance measures show valley oak and blue oak to be very distinct but about equally separated from the even more distinct coast live oak. These results support the taxonomic assignment of blue oak to the subgenus *Quercus* and previous expectations about the magnitude of allozymic differences expected between subgenera (coast live oak is in the subgenus *Erythobalanus*). The large genetic distance between the congeners valley oak and blue oak and the relatively small distances among populations within each species contrasts with some previous findings and suggests an explanation based on the paleobotanical record (Millar and others unpublished draft).

Genetic differences among populations were small as expected on the basis of life history traits (Hamrick and Godt 1990) but especially so for valley oak and blue oak. We expected to find differences among populations that might reveal patterns of local adaptation or historical isolation and origin. We found no detectable geographic pattern in allozyme variation in any of the species and no indication of racial or subspecific variation.

MANAGEMENT IMPLICATIONS

The study reported here has generated a basic description of how one component of genetic diversity (allozymic variation) is distributed within and among populations. With this fundamental knowledge we can proceed to compare our interpretations with those generated by other kinds of population data. We can also begin to recognize which of various applied problems can be addressed using allozyme assays and which may be better served by other approaches. It now seems apparent that allozyme markers will not be very useful for rapid assessment of population identity or provenance. Analysis of DNA restriction fragment variation or of variation in specific DNA sequences may prove more useful in this regard. However, allozyme markers may

provide a relatively simple and inexpensive way to identify and characterize hybrid populations or individuals and to help determine whether interspecific gene flow should be actively encouraged or discouraged in particular management situations.

Another management implication of this study is that we should not jump to the common conclusion that low levels of allozymic variation are indicative of 'genetic trouble' for a population. Successfully regenerating coast live oak populations typically exhibited lower levels of variation than even the most isolated valley oak or blue oak populations that we examined in this study. Observed levels, and patterns of variation will have to be interpreted in the context of the evolutionary background and life history of each species. Within species, however, there are indications that a comparative use of variability indices may help focus attention on populations that should be evaluated more closely using a suite of demographic, ecological, and genetic approaches. Continuing work by one of us (Riggs) is addressing these possibilities.

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