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Genetic signals of past demographic changes and the history of oak populations in California

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A retrospective view of species' demographic changes can inform on population stability through times of climatic change and the origins and spatial structure of genetic diversity in contemporary populations. The former provides the means to predict responses to future climatic change, while the latter allows us to infer the ability of populations to buffer the effects of reductions in population size and fragmentation. The approximately 1.8 my of the Pleistocene is believed to have had a significant impact on diversity through high rates of extinction during early glacial cycles and population expansions and contractions during the later cycles. In the Mediterranean basin, early emphasis on taxa with wide latitudinal ranges led to models of refugial sites and subsequent recolonization routes that could explain geographic patterns in genetic diversity, with a trend towards reduced genetic diversity in the north. More recently, the study of strictly Mediterranean taxa has revealed relictual sites that have persisted over very long periods of time, commonly relatively poor in diversity, but populations well differentiated from one site to another. In California, relatively little is known of the population dynamics of plant taxa during the Pleistocene glacial cycles, or to what extent differentiation today is a result of pre-Pleistocene events. For several animal taxa, differentiation between Coastal and Sierran taxa are believed to date to the Pliocene. Major demographic changes resulting in population isolation, bottlenecks, founder events and population expansions leave a genetic signal that can be detected through appropriate genetic markers and analyses. Such signals help to infer whether past climate fluctuations have had important effects on population demographics. Here, I will focus on key oak species of the California mediterranean climate zone. I will explore the likely effects of the last glacial maximum on oak populations using palaeoclimate and niche modeling together with analyses of population genetic structure. One of the major questions that will be addressed is whether populations have persisted over long periods of time and if the contemporary population structure has derived from events earlier than the Pleistocene. Population genetic structure will then be used to propose strategies that will optimize conservation of genetic resources.