Genetic Diversity, Gene Flow, and the Persistence of Long-Lived Tree Species in an Era of Rapid Environmental Change: Lessons for *Sequoiadendron giganteum*.

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During this century, climate warming and altered precipitation patterns will lead to habitat changes that may be beneficial to some long-lived tree species and detrimental to others. Paleoendemics, with limited and disjunct distributions will face the greatest challenges as, migration rates will be too slow to keep pace with rapid environmental change and populations at the receding edges are eroded through maladaptation. Giant sequoia (*Sequoiadendron giganteum*) is an iconic Sierra Nevada tree species with populations that tend to be small and highly fragmented (particularly in the northern range), making them especially vulnerable to environmental change. Thus, attention needs to be paid to mechanisms that can mitigate population extirpation. Important determinants of within-range persistence for giant sequoia include the existence of genetic variation that is suited to future conditions and the spread of these “pre-adapted” genotypes within current range boundaries by gene flow. Our ongoing research addresses 1) the levels and distribution of genetic diversity (adaptive and non-adaptive) throughout the range of giant sequoia, and 2) the dispersal distances of pollen and seed and consequent rates of gene flow across a highly fragmented habitat.

We utilize microsatellite markers and Restriction site Associated DNA sequencing (RAD-seq) to assess genetic diversity. Gene flow is assessed with DNA from germinated seeds, using multilocus genotypes to characterize parentage and estimate dispersal distance.

Preliminary findings show that current levels of genetic diversity are determined, in large part, by population size. We anticipate that proximity to other giant sequoia populations, that is more important in the southern range of the species, is also an important driver of genetic diversity through genetic exchange among groves. Our research will show the spatial scale and limits to gene flow among geographically proximate populations and isolated groves. Also, we anticipate that smaller populations will draw pollen from a larger area due to a more limited local pollen pool. This research is essential for land managers with giant sequoia on their lands, as it will help them to prioritize giant sequoia conservation efforts by highlighting areas of high and low genetic diversity. Moreover, this research has the potential to improve tree-planting strategies by identifying gene pools as seed sources and planting strategies that promote maximum genetic diversity over future generations.