

The Genetic Architecture of Local Adaptation and the Genomic Exploration of Rugged Evolutionary Landscapes Within Species of *Pinus* Subgenus *Strobus*

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Naturally occurring genetic diversity is the material upon which much of the biodiversity we attribute to forested ecosystems is based. The structuring of genetic diversity within natural populations of forest trees results from the interplay of numerous evolutionary forces, such as genetic drift, migration, and natural selection. Landscape genomics is concerned with testing hypotheses about how these interacting evolutionary forces change over geographical space and time to shape naturally occurring patterns of this diversity. Here, I will use a landscape genomic approach to illustrate how genetic drift, migration, and natural selection interact to determine patterns of genetic diversity, including the genetic diversity underlying fitness-related phenotypes, at multiple spatial scales within natural populations of forest trees.

I will accomplish this task by arguing that populations of sugar pine (*Pinus lambertiana*), western white pine (*P. monticola*), and whitebark pine (*P. albicaulis*) are adapted to local site conditions within the Lake Tahoe Basin of California and Nevada, USA. More

specifically, I will test the hypothesis that local adaptation is apparent at local spatial scales (~600 km²), despite large amounts of pollen-mediated gene flow among local populations. I will also highlight, however, several instances where clearly adaptive patterns of genetic diversity have been influenced by local demographic events. Building upon these results, I will then illustrate how the observed patterns of molecular genetic diversity for a varied set of functional genes are organized relative to the phenotypic variation used to highlight local adaptation. The drivers of these patterns are very likely the multilocus aspects of molecular genetic diversity as it contributes to local adaptation at fine spatial scales. Last, I will draw upon emerging examples from eastern white pine (*P. strobus*) and foxtail pine (*P. balfouriana*) to illustrate the promising role that species of *Pinus* subgenus *Strobus* will play in our understanding of the genetic architecture of local adaptation and the ability of this architecture to rapidly respond to environmental change within natural populations of forest trees.

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