

Editorial

# Quercus Genetics: Insights into the Past, Present, and Future of Oaks

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The genus *Quercus* comprises over 400 species found across the Northern Hemisphere. Oaks provide important ecosystem services to a multitude of species, including humans, and have shown remarkable resilience and an ability to adapt to variations in climate and geography over the past 56 million years. The tools of genetics and genomics have been important in understanding *Quercus* evolutionary history and distributions, as well as current species delineations, population structure, conservation needs, and the genetic mechanisms that have allowed oaks to adapt to challenging environments. As climate change accelerates, oaks will need to adapt at an even greater pace. Genetics/genomics helps conservationists understand the adaptive mechanisms of oak, and will be valuable for planning management strategies.

In this Special Issue of *Forests*, we have gathered articles describing a range of genetic methods and how they are being applied to the genus *Quercus*. They include investigations into oak evolutionary history, population diversity, gene flow, effects of human disturbance, gaps in genetic research of threatened species, and epigenetic modification effects on phenotype variation.

Rapid climate change and anthropogenic disturbances challenge many oak species. The Red List of Oaks 2020 estimates that 41% of oaks are ‘species of conservation concern’. A review article identifies threatened *Quercus* species and geographical areas that have gaps in genetic research and delineates genetic methods that would address those gaps [1]. A population study of *Q. ruber* in Lithuania using chloroplast DNA provides insight into postglacial migration of the species and raises the hypothesis that human logging over the last few centuries has reduced existing genetic diversity [2]. A review and synthesis of recent work using RAD-seq-based phylogenies reconstructs the timing and biogeography of North American oak diversification, clarifying relationships and providing new insight into evolutionary radiations [3]. One study used reduced-representation bisulfite sequencing to examine the relationship between genomic and epigenomic variation and observed phenotypic traits. The findings indicate that epigenetic methylation may be a valid marker of phenotype variation, but more research needs to be conducted to determine if it drives variation [4]. Two articles describe studies into genetic variation in and among species, with an emphasis on conservation genetics. One study examines a uniquely adapted desert oak with a disjunct distribution using genetic, morphometric and environmental datasets. The authors present conservation and taxonomic implications of their findings [5]. A second paper examines the genetic diversity of three threatened oaks, comparing levels of diversity to that of common oaks and testing for correlations with range size, population size, and abiotic variations. They also characterize genetic diversity in ex situ collections and demonstrate a need for more extensive geographic sampling [6]. Two papers look at gene flow in oaks. One reviews recent genomic research into oaks’ environment-driven adaptive divergence while maintaining species integrity given rates of gene flow, introgression, and hybridization propensity [7]. The second paper reviews studies in *Quercus* pollination using microsatellites and paternity analysis. The paper looks at what has been learned, what questions remain, and how these findings can inform forest management in a rapidly changing world [8].



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