

Hybridization and Management of Oak Populations¹

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Abstract

Hybridization can result in the transfer of adaptations among species and may contribute to speciation processes. On the other hand, hybridization can also result in a loss of species diversity due to asymmetric gene flow between species (genetic swamping) and in low hybrid fitness. An understanding of the outcomes of interspecific hybridization is crucial for the management and conservation of tree populations. As a result of warming climates, it is expected that distribution ranges of species will shift, resulting in new zones between species and potentially new or increased hybridization.

Oaks (*Quercus* spp.) are the dominant species in many hardwood forests of North America. Hybridization is common in oaks and species boundaries are fuzzy as a result of large within-species variation, phenotypic plasticity and interspecific gene flow. While morphological identification of species can be difficult, DNA markers such as nuclear and genic microsatellites can be used to assign individuals to species and hybrids. We have developed a set of 44 microsatellite markers that distinguishes between closely related red oak species with different adaptations to drought. While most markers in the set showed low to moderate interspecific differentiation, one genic microsatellite marker showed pronounced interspecific differentiation as result of strong divergent selection and may be associated with adaptive species differences. By using these new microsatellite markers, we will be able to assess interspecific gene flow and introgression of adaptive alleles. Results on the frequency of hybridization and hybrid fitness will be important for the management of oak populations in the face of climate change.

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