

## SUSTAINABILITY GENETICS FOR AMERICAN WHITE OAK (*QUERCUS ALBA*)

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White oak (*Q. alba*) is a keystone forest tree species distributed over much of the eastern US. The species is important ecologically for watershed and wildlife health, and economically for lumber, veneer, and specialty products such as barrel staves. Because of the species importance, there are sustainability concerns primarily driven by forest mesophication, limiting regenerated seedlings' recruitment into the canopy, and climate change. The recently formed White Oak Initiative speaks to these concerns and looks to partner on key research themes encompassing white oak's biological potential in forest management. An important determinant in biological potential is a species' genetic diversity and how this diversity might be characterized and utilized in forest management. Our stakeholder-supported research program is addressing white oak genetics in three ways— (1) germplasm collection, conservation, and improvement; (2) genomic, transcriptomic and metabolomic assessment of genetic diversity; and (3) characterization of adaptive genes through analysis of genotype-phenotype associations. Initial work has resulted in two years of range-wide acorn collections, including a first-year nursery crop with subsequent field test plantings, and completion of a diversity study of white oak stands in the Daniel Boone National Forest. We are currently developing a high-quality, white oak genome sequence and comprehensive transcriptome and metabolome resources. Subsequent work will continue range-wide acorn collections and field test plantings, as well as finalizing and annotating the genome and initiating trait phenotyping and genotyping.