GENETIC IMPROVEMENT IN WHITE OAK (*QUERCUS ALBA*): CONNECTIONS TO FOREST HEALTH, CLIMATE CHANGE, AND FOREST PRODUCT INDUSTRIES

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White oak influences ecosystem processes throughout eastern US forests and is thus critical to forest health. The species is also highly valued for forest product industries (e.g., cooperage industry). The long-term sustainability of white oak is uncertain and there are few long-term improvement programs for the species. To address these problems, we are developing a white oak genetic improvement program in the Forest Health Research and Education Center (University of Kentucky) focused on growth, yield, and health related to improving forest health and forest products. Our program will complement other white oak improvement programs to provide a range-wide effort. The improved white oak will be grown in managed, natural forests, thus genetic structure and adaptation to local and future climate conditions must be conserved. Therefore, program development is occurring concomitant with genomic, silvicultural and health research. Field identification of superior white oaks is particularly challenging given the large portion of private ownership in eastern forests, and thus a variety of partners and methods including TreeSnap are being used. Additionally, little genetic information exists to guide tree improvement in terms of how white oak responds to stressors, or how adaptive and non-adaptive traits such as wood organoleptic characteristics vary genetically. Limited studies indicate that despite extensive gene flow, species coherence is strong, there is high within-population genetic variation, and high phenotypic plasticity. Genotypes are correlated with environmental variation, population density, and site productivity. Some functional genes critical to environmental variation have been characterized and can be used to predict risk of non-adaptedness. Molecular information can maximize genetic gain per time by rapidly improving output quality of seed orchards. The superior trees being field selected serve as in-situ genetic reserves and they provide material for ex-situ seed orchards that can be used to uncover genetic variation patterns in traits of interest.