# EFFECTS OF THINNING REGIMES ON GENETIC VARIATION OF WHITE OAK (*QUERCUS ALBA* L.*)* IN EASTERN HARDWOOD FORESTS

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Artificial selection due to management practices and industry demands can produce significant effects on the nature and extent of genetic diversity in natural tree populations. White oak (*Quercus alba* L.), a keystone species of economic importance to eastern hardwood forests, is potentially subject to genetic degradation due to selective harvest of timber-type trees (i.e., phenotypes) by the forest industry. This research project assesses the effects of silvicultural thinnings on the allelic variation of white oak utilizing microsatellite DNA analysis, specifically genomic and transcriptomic simple sequence repeat (SSR) markers. Our research objectives are to: (1) understand if silvicultural thinnings significantly change the degree of allelic variation in white oak stands, leading to a loss in population diversity and (2) discover the spatial attributes of genetic variation of white oak within stands in light of past silvicultural practices. Existing long-term thinning experiments of a white oak dominated study site established by the USDA Forest Service, in 1961 and 1962 on the Daniel Boone National Forest (Jackson County, KY, USA), provided eight half-acre plots varying in thinning intensity and timing. Leaf tissue samples were collected for DNA isolation and SSR marker analysis from all mature white oaks within the study plots for a spatial analysis of genetic variation. Differences in heterozygosity (observed and expected), total and effective allele numbers, Hardy-Weinberg deviations, linkage disequilibrium (LD), mean repeat number, variance of repeat number, inbreeding coefficient (F) and Fst (total genetic variance) were calculated using GenAlEx, and spatial analyses were conducted with R Studio and Arc GIS. We will present the results of this study and discuss its implications for white oak sustainability and conservation.

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