# DNA FINGERPRINTING RESULTS FOR THE FOREST SERVICE LONGLEAF PINE AND SHORTLEAF PINE SEED ORCHARDS AND SEED BANK

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USDA Forest Service National Forest System (NFS) in the Southern Region provides oversight for the management of approximately 800,000 acres of longleaf pine (*Pinus palustris*) and 1,440,000 acres of shortleaf pine (*Pinus echinata* Mill.). About 97% of the longleaf pine ecosystem and 53% of the shortleaf pine ecosystem have been lost over the past century. Consequently, longleaf and shortleaf pines are priority species targeted for increased restoration on the thirteen national forests in the Southern Region (R8). Quality seed is needed to support successful artificial regeneration of these species. And the genetic integrity of a species is important to ensure adaptation, survival and resilience of future forests. Recently, the question has arisen about potential increased hybridization between pine species. Currently, longleaf x loblolly pine hybrids (*Pinus sondereggeri*) and shortleaf x loblolly pine hybrids are known to occur in the general forests, but at a very low rate of 5% or less. Climate variability can trigger extreme fluctuations in temperatures, which could influence flower receptivity and pollen flight windows between species, potentially resulting in increased inter-species hybridization. Hybridization may degrade the inherent genetic adaptive traits of a species and present challenges to successful restoration. To assess the genetic purity of R8’s germplasm, the National Forest System Genetics program chose to DNA fingerprint longleaf and shortleaf pine families and seed bank samples from the regional seed orchards. Simple sequence repeats (SSRs) were the DNA markers used to fingerprint the orchard trees and seed bank samples. Three markers were developed from GenBank chloroplast DNA sequences that together identify species-specific profiles (haplotypes) among longleaf, shortleaf and loblolly pines. Because chloroplast DNA is only inherited through the pollen in pines, loblolly pine chloroplast DNA was the differential indicator for detecting hybrids in the samples. Approximately 250 longleaf pine clones and 619 shortleaf pine clones were tested. Seed samples, spanning 1981 – 2017 were also tested. Source locations for the clones and seed represented Alabama, Arkansas, Florida, Georgia, Kentucky, Louisiana, Mississippi, Missouri, North Carolina, South Carolina, Tennessee, Texas and Virginia.