PHYLOGEOGRAPHIC ANALYSES AND EVALUATION OF SHORTLEAF PINE POPULATION STRUCTURE IN MISSOURI

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EXTENDED ABSTRACT

A great expanse of shortleaf pine in Missouri was logged before the mid-20th century, and since that time, seedlings of the species have been planted. Due to large-scale decline in oak trees occupying previous shortleaf pine range, restoration of the shortleaf pine is a priority in Missouri. Restoration can be enhanced through the use of locally adapted trees that have the genetic background to endure the nutrient- and water-limited environment of the Ozark hillsides of southern Missouri. This study's objective was to document the distribution of genetic diversity and population structure in natural, remnant shortleaf pine stands. Based on the geographic level of genetic structuring, the results will be used in combination with ecological and silvicultural results to formulate a conservation-oriented seed management strategy for effective restoration of the species.

Genetic diversity in the form of SSR (microsatellite) allelic variation was documented for shortleaf pine growing in four stands in east-central and southern Missouri. Those stands were selected because (1) they possessed a high abundance of large shortleaf pine trees, and hence were assumed to be natural rather than planted; and (2) they represented the extent of geographic distribution of the species in Missouri. Results from the first 10 polyallelic loci examined showed large amounts of diversity, although results for five of the loci were not sufficient (< 80 percent of individuals resolved) to be included in population diversity analyses. From the second five loci, sample size per site averaged 39 and results were obtained for an average of 36 trees per site. We observed a mean of 8.1 alleles per locus and direct-count heterozygosity of 0.56. At individual loci, stand genotype proportions ranged from 40 to 100, with an average of 58, meaning that more than half of the trees in the stand had unique genotypes.

Fixation index (FST) among the stands was low at all loci due to the great amount of among-tree (total) diversity. To improve our ability to diagnose relationships between the old native stands, the next stage of analyses will include adding five more loci that are not as polymorphic as those in the first stage. In addition, the stands will be resampled, expanding their geographic limits and focusing on larger trees (>18 in DBH) to help ensure native origins. Geographically intermediate stands will also be selected for sampling to refine geneflow limits, although the relationship between genetic diversity and geographic distance will likely prove to be on a scale that excludes all but the most distant remaining sites (Fig. 1).

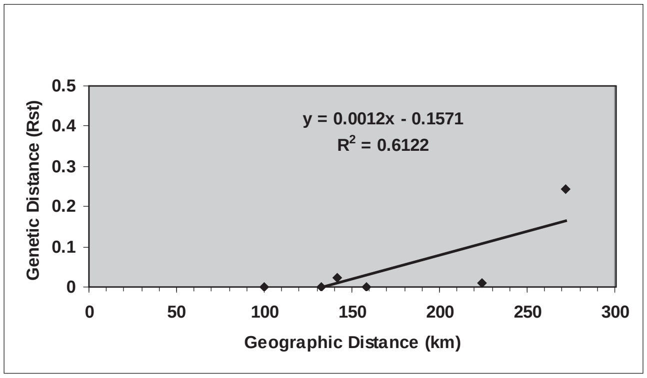

Figure 1.—The relationship between genetic distance and geographic distancefor four stands of native shortleaf pine representing range extremes for the species in Missouri.

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