

RANGEWIDE PATTERNS OF GENETIC DIVERSITY IN TABLE MOUNTAIN PINE  
(*PINUS PUNGENS*), AN APPALACHIAN ENDEMIC

Kevin M. Potter <sup>1</sup>, Robert M. Jetton <sup>2</sup>, Barbara S. Crane <sup>3</sup>, Valerie D. Hipkins <sup>4</sup>, Craig Echt <sup>5</sup>, W. Andrew Whittier <sup>6</sup>, and Gary Hodge <sup>7</sup>

<sup>1</sup> Research Professor, Department of Forestry and Environmental Resources, North Carolina State University, Research Triangle Park, NC, USA 27719 (kpotter@ncsu.edu);

<sup>2</sup> Associate Professor, Camcore, North Carolina State University, Raleigh, NC, USA 27695;

<sup>3</sup> Regional Geneticist (retired), Southern Region, USDA Forest Service, Atlanta, GA, USA 30309;

<sup>4</sup> Director (former), National Forest Genetics Laboratory, USDA Forest Service, Placerville, CA, USA 95667;

<sup>5</sup> Research Geneticist (retired), Southern Institute of Forest Genetics, USDA Forest Service, Saucier, MS, USA 39574;

<sup>6</sup> Research Associate, Camcore, North Carolina State University, Raleigh, NC, USA 27695;

<sup>7</sup> Professor, Camcore, North Carolina State University, Raleigh, NC, USA 27695

Table Mountain pine (*Pinus pungens*) is an imperiled tree species endemic to the Appalachian Mountains from Georgia to Pennsylvania. Generally reliant on fire for regeneration, its formerly fragmented but widespread distribution has dwindled to fewer than 30,000 acres. It typically occurs in small and geographically isolated populations at elevations of 1,000-4,000 feet in rocky soils on south- and west-facing ridgelines. The suppression of wildfire has allowed hardwoods to take over many sites formerly dominated by Table Mountain pine. We quantified the genetic diversity of 346 trees in 32 populations across the range of the species using data from seven highly polymorphic simple sequence repeat (SSR) loci. The species is relatively inbred ( $F_{IS} = 0.208$ ) while differentiation among populations was relatively low ( $F_{ST} = 0.029$ ). Areas with high genetic diversity included the Blue Ridge Mountains of west-central Virginia and of southwest Virginia and northwestern North Carolina, and the Great Smoky Mountains along the Tennessee-North Carolina border. Populations with unique alleles were scattered throughout the species range. We found a strong negative correlation between population isolation and heterozygosity and a strong positive correlation between population isolation and genetic differentiation. Few significant differences in genetic diversity metrics existed among the seed collection zones proposed for Table Mountain pine, except that populations in the most northern seed zone had lower heterozygosity than the southern seed zones, and that central seed zone populations are less genetically differentiated than the northern and southern seed zones. Genetic structure analysis suggested the existence of six to eight genetic clusters in Table Mountain pine. Some of these genetic clusters were associated with different parts of the species distribution. These results add to our limited knowledge of genetic variation across the distribution of this rare and threatened conifer.