

Population Isolation Results in Low Genetic Variation and High Differentiation in Carolina Hemlock (*Tsuga caroliniana*), an Imperiled Southern Appalachian Conifer¹

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Carolina hemlock (*Tsuga caroliniana*) is a rare conifer species that grows in small, isolated populations in the southern Appalachian Mountains of Virginia, North Carolina, South Carolina, Tennessee, and Georgia. The species is additionally imperiled by the hemlock woolly adelgid (*Adelges tsugae*), an invasive insect that can kill the trees in as few as 4 years. We conducted the first range-wide genetic diversity study of Carolina hemlock, using 16 highly polymorphic nuclear microsatellite loci to quantify genetic variation across 439 trees from 29 populations, representing a comprehensive range-wide sampling of most known populations. The results demonstrate that this southern Appalachian endemic has low genetic diversity, is highly inbred, and consists of populations that are highly differentiated from each other. Populations outside the core of the species range are characterized by particularly low variation and high differentiation. Most populations contained at least one unique allele. Clearly, Carolina hemlock exists primarily as a limited set of small populations with restricted inter-population gene flow. Knowledge about the population genetic structure of the species will inform ongoing management and conservation efforts, including prioritizing regions and populations for protection and seed collections. The fact that nearly all Carolina hemlock populations are highly inbred emphasizes the necessity of quickly and effectively preserving the genetic diversity of the species. The high levels of differentiation among Carolina hemlock populations, and the commonness of alleles unique to populations, underscore the importance of ensuring that ongoing gene conservation efforts represent as many populations as possible.

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