# MOLECULAR GENETICS AND THE EFFORT TO CONSERVE SOUTHERN HEMLOCKS DECIMATED BY HEMLOCK WOOLLY ADELGID

Kevin M. Potter[1], Robert M. Jetton[2], Lia Campbell[1], John M. Hastings[1], Sedley A. Josserand[3], Valerie D. Hipkins[4], C. Dana Nelson[5], William S. Dvorak[2]

[1]Department of Forestry and Environmental Resources, North Carolina State University, Research Triangle Park, NC; [2]Camcore, Department of Forestry and Environmental Resources, North Carolina State University, Raleigh, NC; [3] Biological Technician, Southern Research Station, USDA, Forest Service, Saucier, MS, USA, 39574; [4]Pacific Southwest Research Station, USDA Forest Service, Placerville, CA; [5]Forest Health Research and Education Center, Southern Research Station, USDA Forest Service, Lexington, KY

An exotic insect is decimating populations of the two hemlock species native to the eastern United States, eastern hemlock (*Tsuga canadensis*), a widespread and ecologically important tree species, and Carolina hemlock (*T. caroliniana*), a rare species endemic to the Southern Appalachian Mountains. The insect pest is hemlock woolly adelgid (*Adelges tsugae*), which was brought to the eastern United States from southern Japan in the early to mid-twentieth century. Both hemlock species have been the focus of long-term cooperative efforts between the United States Forest Service and the Camcore conservation cooperative at North Carolina State University to conserve representative seed collections. To help guide these *ex situ* gene conservation efforts, we employed rangewide microsatellite molecular marker studies of both species to identify locations of high and low genetic variation, evaluate genetic variation in peripheral disjunct and core range populations, and assess regional patterns in genetic diversity to better understand their phylogeographic history. The results for eastern hemlock demonstrated widespread inbreeding and found that peripheral disjunct populations are less genetically diverse than main-range populations, but that some are highly genetically differentiated or contain unique alleles. Bayesian clustering analyses suggested that three or four Pleistocene glacial refuges may have existed in the Southeastern United States, with a main postglacial movement from one of those refuges into the North. The results for Carolina hemlock discovered that its populations are extremely inbred and surprisingly highly differentiated from each other, with most populations containing at least one unique allele. This level of differentiation, most likely the result of very low interpopulation gene flow, is unprecedented for a North American conifer. These findings have been employed in analyses to prioritize populations for additional conservation seed collections from both eastern hemlock and Carolina hemlock.