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# OF MICROSATELLITES, HEMLOCK WOOLLY ADELGID AND CLIMATE CHANGE: ASSESSING GENETIC DIVERSITY, AND THREATS TO IT, ACROSS THE RANGE OF EASTERN HEMLOCK

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## ABSTRACT

Eastern hemlock (*Tsuga canadensis* [L.] Carr.) is an ecologically important species facing two serious threats: extensive mortality caused by the invasive hemlock woolly adelgid (HWA) (*Adelges tsugae* Annand), and changing climatic conditions that could render much of its current habitat unsuitable. We are conducting the first rangewide population diversity study of eastern hemlock, using highly variable molecular markers, to (1) help guide gene conservation efforts for the species, (2) assess the genetic effects of isolation on peripheral disjunct populations, and (3) assess regional differences in genetic variation to better understand the biogeographical processes that have shaped the genetic architecture of the species. This study encompasses 61 eastern hemlock populations, of which 9 are peripheral disjuncts, half are from areas north of the maximum extent of the Wisconsinian glaciations, and 17 have been infested with HWA. We selected 13 highly polymorphic and consistent nuclear microsatellite loci to include in the analysis after screening 42 loci that were previously isolated from eastern hemlock, Carolina hemlock (*Tsuga caroliniana* Engelm.) and western hemlock (*Tsuga heterophylla* [Raf.] Sarg.). We have conducted a preliminary analysis using eight of the 13 loci.

We found moderate levels of genetic differentiation among populations, with approximately 6 percent of the variation among, rather than within, populations ( $F_{ST} = 0.063$ ). Overall

observed heterozygosity was less than expected heterozygosity (0.619 and 0.532, respectively), and most populations throughout the range of the species had relatively high levels of inbreeding, with the exception of some populations in the southern Appalachian mountains and the Northeast. Based on measures of allelic richness and heterozygosity, the species appears to have two main centers of genetic variation, in the southern Appalachians and New England. Unique alleles, however, were present in the highest numbers in western populations, including disjuncts in Indiana and Kentucky. Northern populations, on average, had more unique alleles than southern populations, while southern populations had slightly higher allelic richness and heterozygosity. Interior populations were more diverse than disjunct populations by nearly every measure. Disjuncts, however, had more private alleles on average, and were much more inbred. Populations uninfested by HWA had slightly higher levels of allelic richness and heterozygosity, and more unique alleles on average, than infested populations.

Using a standard population clustering approach, eastern hemlock populations appear to cluster weakly into regional groups. A Bayesian clustering analysis of individual trees using the program InStruct, meanwhile, suggested that the species contains eight gene pools. Strong geographic patterns were apparent in the arrangement of these gene pools, with all eight gene pools dominant in southern populations, only four dominant in the Northeast, and only one dominant in the Great Lakes region. These findings may offer clues into the location of glacial refugia and patterns of post-Pleistocene movement of the species. Specifically, a glacial refuge may have existed in the South, with a main post-glacial movement into the Northeast, and from there into the Great Lakes region. A separate migratory path may have existed to the populations west of the southern Appalachian crest and south of the Great Lakes.

We are incorporating these results into a genetic risk assessment that takes into account patterns of HWA infestation and potential climate change pressures. We are using the Multivariate Spatio-Temporal Clustering approach to generate maps of currently acceptable habitat for eastern hemlock, and then projecting future suitable habitat in 2050 and 2100 under two scenarios (high and low emissions) for each of two global climate models (Hadley and Parallel Climate Model [PCM]). To quantify the risk of climate change pressure to eastern hemlock populations, we identified currently acceptable habitat that might not be acceptable in 2050 by overlaying the species' current habitat with habitat projected under the Hadley low emissions scenario. While newly acceptable habitat may be available to eastern hemlock north of its current range in Canada, large areas west of the southern Appalachians and in New England may no longer be suitable. These areas contain high levels of genetic variation: higher heterozygosity and allelic richness in New England and unique alleles west of the Appalachians.

The preliminary results of this work suggest the following: (1) Efforts to conserve the genetic variation of eastern hemlock should focus on the areas with the highest allelic richness and heterozygosity (the southern Appalachians and New England) and on areas elsewhere in the range with high numbers of unique alleles. (2) Gene conservation activities also should target disjunct populations. While these appear to be more inbred and less genetically diverse than interior populations, several also contain high numbers of unique alleles. (3) It is not too late to conserve eastern hemlock genetic variation, given that much genetic variation exists in locations that have not yet been impacted by HWA. (4) The potential impacts of climate change should be considered alongside risk of HWA infestation when determining gene conservation strategies for eastern hemlock.

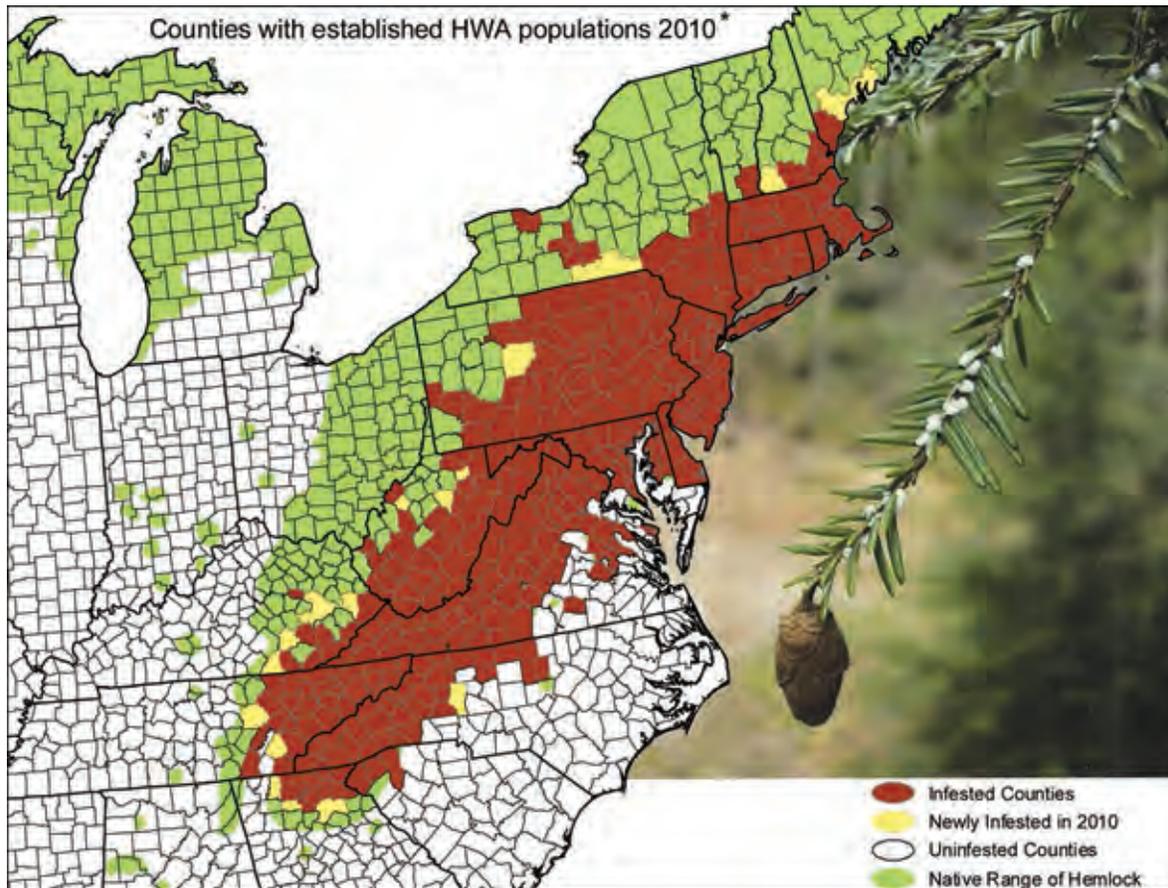
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*Hemlock Woolly  
Adelgid*

## Fifth Symposium on Hemlock Woolly Adelgid in the Eastern United States

Asheville, North Carolina  
August 17-19, 2010



\*See inside cover.

Compiled by Brad Onken and Richard Reardon



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**\*Cover map:** Produced by USDA Forest Service, 2010. The map depicts counties with established populations of hemlock woolly adelgid (HWA) that have been confirmed by state forest-health officials. The coarse nature (scale) of the map does not provide information below the county level; highlighted counties are not necessarily entirely infested with HWA.

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