

EVOLUTIONARY ORIGINS OF THE HEMLOCK WOOLLY ADELGID RESISTANCE-DISPARITY BETWEEN ASIAN AND NORTH AMERICAN HEMLOCKS (*TSUGA* SP.)

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Evolutionary theory provides a framework for understanding population and species level variation, which, when translated into a context for understanding the scope and magnitude of a conservation problem, can provide novel solutions. The hemlock woolly adelgid (HWA, *Adelges tsugae*) is a sap-feeding pest evolved in eastern Asia and introduced into Eastern North America in the 1950's that has nearly extirpated local populations of the eastern hemlock (*Tsuga canadensis*) across the central and southern portions of its range. The Chinese hemlock (*T. chinensis*), in contrast, has a long evolutionary history of exposure to the HWA and is largely resistant. Here, we seek to use evolutionary theory to understand the origins of the disparity of resistance to HWA by focusing on patterns of allele frequency variation in terpenoid biosynthesis pathway genes. Terpenoids are generally thought to be stress avoidance or tolerance mechanisms in gymnosperms, and are likely candidates to explain patterns of resistance to the HWA within *Tsuga*. We employ neutrality tests in gene coding regions to understand patterns of sequence evolution. This study will provide an important context for understanding the origin of epidemics after the introduction of novel pests as well as provide important genomic resources for an understudied and imperiled tree of North American forests.