

USING MITOCHONDRIAL DNA TO DETERMINE THE NATIVE RANGE OF THE HEMLOCK WOOLLY ADELGID

Nathan P. Havill

Department of Ecology and Evolutionary Biology,
Yale University, New Haven, CT 06520

ABSTRACT

The history of the introduction and spread of the hemlock woolly adelgid (HWA), *Adelges tsugae* (Hemiptera: Adelgidae), is well known for eastern North America where it is causing serious decline of eastern and Carolina hemlocks. However, while it is assumed that these insects were introduced from somewhere in Asia, we do not know their precise geographic origin. Adelgids can also be found on other hemlock species in western North America and east Asia, but these trees are not significantly damaged, suggesting the existence of different varieties of HWA.

The purpose of this study is to use molecular methods to clarify the relationship among hemlock adelgids worldwide, and therefore determine the geographic origin of the introduction to eastern North America. Three mitochondrial genes (COII, ND1, and cytB), providing a total of over 1,500 base pairs of DNA, were sequenced for adelgid samples collected from hemlock in multiple locations in eastern and western North America, China, and Japan to identify their differences.

Phylogenetic analyses indicate that the source of *A. tsugae* in eastern North America was a population of adelgids living on *Tsuga seiboldii* that occurs in the south and at lower elevations in Japan. Adelgids collected in China appear to represent a separate lineage, as do adelgids collected from the other Japanese hemlock species, *T. diversifolia*. It is unclear whether adelgids collected on *T. heterophylla* in western North America represent a native population, or were introduced from an un-sampled population in Japan.

These results indicate that molecular methods can be used to successfully pinpoint the origin of introduced insect pests. In addition, these results can be used to facilitate quarantine efforts by helping to prevent the introduction of other non-native adelgid genotypes, and can help direct resistance breeding and biological control programs.

KEYWORDS

Mitochondrial DNA, phylogeny, native range.