

HEMLOCK WOOLLY ADELGID POPULATION GENETICS

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ABSTRACT

The hemlock woolly adelgid, *Adelges tsugae* (Hemiptera: Adelgidae), was first reported in eastern North America over 50 years ago. Efforts to control the impacts of the adelgids are focusing on classical biological control and tree resistance. The success of these strategies relies on knowledge of the ecological and evolutionary context uniting the pest, its host plants, and its natural enemies.

We report preliminary results of a project using 14 microsatellite markers to further understand the genetic structure of *A. tsugae*. Adelgid samples were collected from 27 sites throughout the range of hemlock in Japan, from Ullung Island, South Korea, and from eastern and western North America. A total of 553 individual adelgids have been genotyped to date. Principal component analysis of all genotypes resulted in three clusters. Samples from western North America show no evidence of recombination and are distinct from those in Japan and eastern North America. This agrees

with previous assertions of a separate, endemic lineage in western North America. There was also a clear distinction between samples collected from *T. diversifolia* and *T. sieboldii* in Japan. Samples collected from *Picea polita* grouped with those from *T. sieboldii* indicating that alternation between *T. sieboldii* and *P. polita* is common while alternation between *T. diversifolia* and *P. polita* is absent or rare. There appears to be a patchwork of entirely parthenogenetic and cyclically parthenogenetic populations in Japan with varying levels of recombination depending on the proximity of primary and secondary hosts.

The results of this project will be used to clarify hemlock adelgid taxonomy, to predict the adaptive potential of *A. tsugae* in its introduced range, to target exploration for biological controls, and to aid development of resistant hemlock genotypes.