

MOLECULAR ECOLOGY OF HEMLOCK WOOLLY ADELGID, ITS HOSTS, AND ITS NATURAL ENEMIES

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ABSTRACT

Molecular analyses show that the hemlock woolly adelgid (HWA) has distinct native lineages in western North America, Japan, China, and Taiwan, while in eastern North America, HWA is not native and was introduced from Japan some time before 1951 (Havill et al. 2006 and 2007). The typical holocyclic lifecycle in the family Adelgidae involves primary hosts in the genus *Picea* and secondary hosts in other conifer genera (Havill and Footitt 2007). It is therefore feasible that in the regions where it is native, HWA alternates between *Tsuga* and *Picea* species. A database of DNA barcodes (approximately 650 base pairs from the COI gene) being compiled at the Canadian Centre for DNA Barcodes (Guelph, Ontario) includes HWA as well as adelgid samples collected from various Asian *Picea* species. We found an exact match between Chinese HWA and adelgids from galls on *Picea likiangensis* (Franch.) Pritzel and between Japanese HWA and adelgids from galls on *Picea torano* (K. Koch) Koehne. This confirms that HWA host alternates in at least part of its ranges in China and Japan. We are currently working to further understand HWA lifecycles and the relationships between HWA and its hosts with population genetic methods using microsatellites.

The beetle *Laricobius nigrinus* Fender (Derodontidae) is native to western North America and has been released throughout the range of introduced HWA in eastern North America. There are three additional *Laricobius* species reported to be present in North America: *L. laticollis* Fall is native to western North America, *L. rubidus* LeConte is native to eastern North America and is routinely collected from HWA-infested eastern hemlock, and *L. erichsonii* Rosenhauer was introduced from Europe in the 1950s and 1960s as a biological control of balsam woolly adelgid, but to our knowledge it has not been collected in North America in recent decades. A molecular phylogeny using mitochondrial and nuclear DNA sequence data shows that *L. nigrinus* and *L. rubidus* are closely related. A restriction fragment length polymorphism (RFLP) assay was developed based on nucleotide differences in the COI gene that are fixed for each species. This assay provides rapid and inexpensive identification of *Laricobius* larvae to aid post-release monitoring of establishment and spread of *L. nigrinus*. It should be noted, however, that since mitochondria are strictly maternally inherited, that

this assay only identifies the maternal genealogy of the beetles and is not useful for detecting potential hybrids. While there is currently no evidence that *L. nigrinus* and *L. rubidus* can successfully produce hybrid offspring, this possibility should be addressed given the close relationship of the two species.

KEYWORDS

DNA barcoding, lifecycle, *Laricobius*, *Tsuga*, *Picea*

ACKNOWLEDGEMENTS

Many people have graciously contributed to these projects both intellectually and by providing samples. We wish to especially thank Gisella Caccone, Steve Cook, Gina Davis, David Mausel, Shigehiko Shiyake, Carol von Dohlen, Guoye Yu, and Gabriella Zilahi-Balogh for their contributions.

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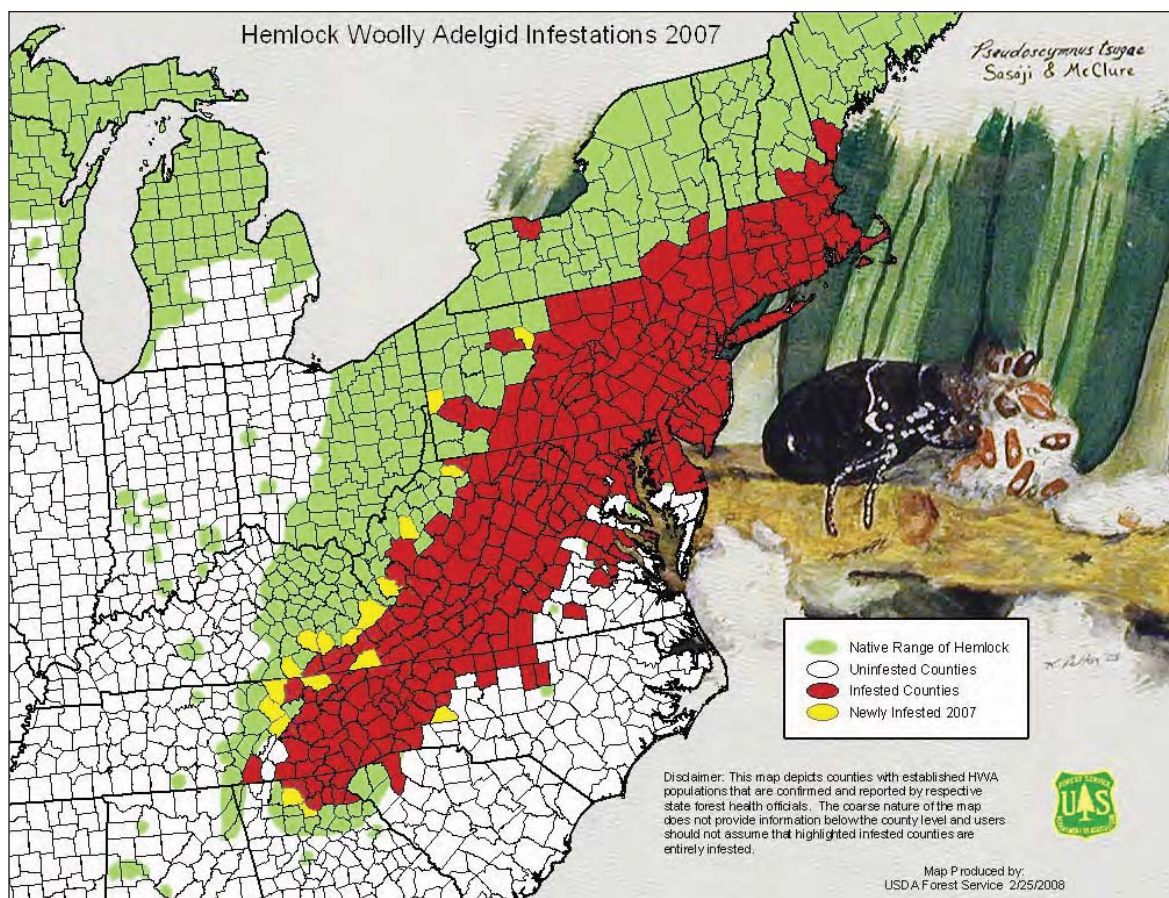
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*Hemlock Woolly
Adelgid*

FOURTH SYMPOSIUM ON HEMLOCK WOOLLY ADELGID IN THE EASTERN UNITED STATES

HARTFORD, CONNECTICUT
FEBRUARY 12-14, 2008



Brad Onken and Richard Reardon, Compilers



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