

GENETIC ANALYSIS OF EMERALD ASH BORER (*AGRILUS PLANIPENNIS* FAIRMAIRE) TO DETERMINE POINT OF ORIGIN IN NORTH AMERICAN INFESTATIONS

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ABSTRACT

The objective of this project is to estimate the geographic origin of emerald ash borer (EAB) populations in Asia that gave rise to EAB in North America. Knowledge of EAB genetics will be useful in understanding the invasion dynamics of the beetle, and to help identify geographic localities of potential biocontrol agents. EAB naturally ranges from Mongolia, northeastern China, and the Russian Far East to Korea, Japan, and Taiwan. We are sampling populations of EAB in Asia and comparing them genetically with introduced populations in North America (Michigan, Ohio, and southwestern Ontario) using mitochondrial DNA sequences and amplified fragment length polymorphism (AFLP) fingerprints. Genetic data will be analyzed by phylogenetic analysis and population assignment tests.

Our EAB collection from spring 2003 included 20 adults and 20 larvae from SE Michigan, 4 adults and 3 larvae from Harbin, Heilongjiang Province, China, and 21 adults (dried or pinned) from Dagong and Hangu (Tianjin Province, China). Initial analysis of mitochondrial cytochrome oxidase subunit I (COI) sequences placed an EAB individual from Michigan in a group with the other buprestid in the taxon sample. Subsequent analysis of COI sequences (500 nucleotides) from three adult EAB from Michigan, one adult EAB from Dagong, and one adult EAB from Hangu indicated that these sequences were identical. The insects obtained from Heilongjiang Province did not yield DNA that could be used for mtDNA analysis. In addition, EAB has not yet yielded analyzable AFLP profiles. Work in these areas is continuing. In fall 2004, we received samples of larval EAB from China including Jilin, Liaoning, Hebei, and additional sites in Tianjin and Heilongjiang Provinces (collections by H. Liu and T. Petrice).