
INVASION GENETICS OF EMERALD ASH BORER (*AGRILUS PLANIPENNIS FAIRMAIRE*) IN NORTH AMERICA

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ABSTRACT

Emerald ash borer (EAB) was first detected in Michigan and Canada in 2002. Efforts to eradicate this destructive pest by federal and state regulatory agencies continue. 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. Genetic techniques, such as mtDNA gene sequencing, amplified fragment length polymorphisms (AFLP), nuclear gene sequencing, and microsatellite analysis will help determine the geographic origin of EAB in its native range throughout eastern Asia.

To date, we have obtained approx. 2,100 EAB individuals, mainly from 32 localities in Michigan, but also from three localities in Ohio, one locality each in Indiana and Canada, seven localities in China, and four localities in South Korea (kindly loaned to us by Dr. Dave Williams, USDA-APHIS). We also have obtained one adult from Shiroishi, Japan (kindly loaned to us by Dr. Paul Schaefer, USDA-ARS). Mitochondrial cytochrome oxidase I (COI) sequences (485 bp) from all North American EAB (Michigan: 76, Ohio: 2, Indiana: 4, and Canada: 6), all EAB from China (Dagong: 5, Hangu: 1, Heilongjiang Province: 4, Hebei: 2, Jilin: 2, and Liaoning: 2), and six EAB individuals from three localities in South Korea were identical. However, mitochondrial COI sequences from five individuals in two populations in South Korea differed from this common haplotype by two to four nucleotides, and the Japanese sample differed from the common EAB mtDNA haplotype by 3.7%. Therefore, the mtDNA COI sequence of the Japanese sample is very different from any other individual sampled, and there is COI haplotype variation in two of the three localities in South Korea. We have also obtained AFLP profiles from EAB individuals from Michigan (46), Ohio (2), Ontario, Canada (6), South Korea (4), Dagong (4), Heilongjiang Province (3), Liaoning (2), Hebei (2), Jilin (2), and one individual from Japan (four selective AFLP primer pairs; 139 scoreable loci).

We have observed differences in AFLP profiles both within populations from the same location as well as between all populations. Neighbor-joining analysis of the 139-band AFLP data set indicates that individuals from Michigan cluster more often with individuals from China, while the Japan individual fell into a separate, more distantly related group. However, we cannot rule out South Korea as the geographic origin of North American EAB. Despite the observed COI haplotypes diversity in South Korea, the common haplotypes that is shared by all Chinese and North American EAB individuals exists in each of the Korean populations sampled. Thus, it will be necessary to increase our sampling of Asian populations if we hope to make valid inferences about the geographic location(s) of source populations that gave rise to the North American EAB infestations.

We are continuing to expand our AFLP data set to include data from a fifth and sixth selective primer pair. We are also working to obtain DNA sequences from the nuclear genes wingless (*Wg*), phosphoenolpyruvate carboxykinase (*PepCK*), cytochrome *c* (*Cytc*), and elongation factor-1 α (*EF-1 α*). Finally, microsatellite markers are being developed for EAB to incorporate these highly polymorphic markers into the data set. We expect that analysis of the expanded data set will improve resolution of the EAB populations and allow us to determine which populations are most closely related to each other and if there was a single introduction or multiple introductions of this pest.