GENETIC ANALYSIS OF EMERALD ASH BORER TO DETERMINE THE POINT OF ORIGIN OF MICHIGAN INFESTATIONS

Alicia M. Bray [1], Leah S. Bauer [1,2],
Robert A. Haack [1,2], and James J. Smith [1,3]

[1] Department of Entomology, Michigan State University,
243 Natural Science Building,
East Lansing, MI 48824

[2] USDA Forest Service, North Central Research Station,
220 Nisbet Building, 1407 S. Harrison Rd.,
East Lansing, MI 48823

[3] Departments of Zoology and Lyman Briggs School of Science, Michigan State University,
203 Natural Science Building,
East Lansing, MI 48824

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 and amplified fragment length polymorphisms (AFLP) will help determine the geographic origin of EAB in its native range throughout eastern Asia.

In an initial analysis, we collected EAB individuals from several localities in Michigan and three populations in China. Analysis of mtDNA cytochrome oxidase subunit I (COI) sequences from 20 individuals from Michigan, three individuals from Dagong (Tianjin City), one individual from Hangu (Tianjin City), and three individuals from Harbin (Heilongjiang Province) indicated that all COI sequences (~500 nucleotides) were identical. However, differences between individuals were observed using AFLPs. AFLP analysis using three primer pairs yielded fingerprints from EAB individuals from Michigan (19), Dagong (2) and Hangu (1) (Tianjin City), and Harbin (4) (Heilongjiang Province). Eighty-two scoreable bands, coded as binary characters (presence/absence), were analyzed in a neighbor-joining (NJ) analysis. The NJ tree showed that individuals from MI cluster with individuals from Dagong and Hangu (Tianjin City), while EAB individuals from Harbin (Heilongjiang Province) fell into a separate, more distantly related group. Therefore, with this limited sample, AFLP appears to reveal population-level differences between EAB populations, and the Michigan populations appear more closely related to EAB from Tianjin Province than to EAB from Heilongjiang Province. Nonetheless, more thorough sampling in China is necessary to better characterize the relationships of the Michigan and Chinese EAB populations. Due to the rarity of EAB in Korea, Japan, Mongolia, Taiwan, and Russia, no samples have yet been found for genetics. We now

plan more intensive sampling of EAB populations within Michigan to provide information on invasion genetics and possible age of infestation. We also plan more extensive sampling in North America including EAB from Ohio, Maryland, Virginia, Indiana, and Ontario, Canada, to determine if there was a single or multiple introductions of EAB into North America. Overall, mtDNA sequences appear to be a good positive control that ensures all individuals in our analyses are indeed EAB. AFLP fingerprints detected differences between EAB populations, important when locating potential biological control agents.