EMERALD ASH BORER GENETICS: AN UPDATE

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

[1]Department of Entomology, Michigan State University
243 Natural Science Building, East Lansing, MI 48824
kingalic@msu.edu

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

[3]Lyman Briggs College, Michigan State University
East Holmes Hall, East Lansing, MI 48825

ABSTRACT

Emerald ash borer (EAB), *Agrilus planipennis* Fairmaire, samples were collected from introduced sites in Michigan, Ohio, Indiana, Pennsylvania, Illinois, and Ontario, Canada, as well as native sites in China, Japan, and South Korea with the help of a network of collaborators. The beetles were analyzed using DNA sequences from mitochondrial cytochrome oxidase I (COI) and amplified fragment length polymorphism (AFLP) DNA fingerprinting.

EAB individuals from introduced sites in North America all had a mitochondrial COI haplotype identical in more than 450 nucleotides to the haplotype found in most individuals from our collection sites in China and in six individuals from three sites in South Korea. However, haplotypes from individuals from two collection sites in Liaoning Province, China, differed from this main haplotype by one base pair; five individuals from two populations in South Korea differed from the main haplotype by two to four base pairs; and a Japanese sample differed from the main haplotype by 22 base pairs. Interestingly, one individual from Ontario, Canada, differed from all other North American samples by three base pairs.

Two individuals collected in Moscow, Russia, were also analyzed by mtDNA COI and were found to be identical to the main haplotype. EAB is only native to Russia in the Far East north of North Korea; therefore, the population in Moscow was the result of an introduction from the beetles' native range.

AFLP analyses have been carried out using four selective primer pairs, which yielded 139 scoreable bands (loci). In neighbor-joining analysis, samples from throughout the introduced range in North America grouped more often with individuals from China than with individuals from South Korea and the individual from Japan. However, support for hypothesized AFLP relationships was weak. Therefore, microsatellite markers are being developed that we hope will provide the information necessary to identify the geographic origin of the North American EAB populations (and possibly the Moscow, Russia, population) and enabled us to reconstruct the invasion history of EAB in North America (including the separate introductions).

EAB from Lansing, Michigan, were used to develop 96 clones for evaluation. Forty-one primer pairs have been designed and tested for amplification, with 32 of these providing successful amplification. These primers are currently being tested for variability in EAB populations.