

# INVASION GENETICS OF EMERALD ASH BORER (*AGRILUS PLANIPENNIS* FAIRMAIRE)

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## ABSTRACT

Emerald ash borer (EAB), *Agrilus planipennis* Fairmaire (Coleoptera: Buprestidae), is a devastating invasive pest of North American ash trees (*Fraxinus* spp.) that was first discovered outside of its native range of northeastern Asia in 2002 (Haack et al. 2002). With unintended assistance from human movement of infested ash material, EAB spread swiftly from its initial zone(s) of discovery in the Detroit, MI/Windsor, ON, metropolitan area and now can be found in 13 states in the United States and 2 provinces in Canada. Characterizing the structure of EAB populations could provide valuable information on EAB geographic origin (and thus the location of possible effective biological control agents) and host range potential, and it could provide evidence of the main mode of spread. This study thus had two main goals: (1) to obtain samples from throughout the native and introduced ranges of EAB and (2) to characterize the genetic population structure of EAB in its native and introduced range using mitochondrial partial gene sequencing and DNA fingerprinting using amplified fragment length polymorphisms. To accomplish the first goal, a network of collaborators was established to obtain samples from the native range of EAB in China, South Korea, and Japan, and its introduced ranges in the United States, Canada, and western Russia. This effort yielded a collection of 1,799 EAB specimens from 7 states in the United States, 114 specimens from Ontario, Canada, 12 from Moscow, Russia, 274 from China, 17 from South Korea, and 3 from Japan. To accomplish the second goal, eight Asian and seven North American populations were characterized with

partial mtDNA cytochrome oxidase subunit I sequence (481 bp) and four AFLP primer pair combinations (108 loci). Analysis of COI sequences revealed one common haplotype in China, South Korea, and all samples from N. America, as well as three unique haplotypes in China and four haplotypes from South Korea, which differed from the common haplotype by 1 to 2 nucleotides. A haplotype from a single EAB individual from Japan differed by 22 nucleotide changes (3.7 percent). Very weak genetic structure was detected, and most of the AFLP genetic variability was within populations (87 percent) and not among populations (13 percent). Average pairwise  $\Phi_{pt}$  between North American EAB (considered as a single population) and Asian EAB populations revealed the lowest population differentiation between North America and Dagong and Tangshan, China ( $\Phi_{pt} = 0.0877$  and  $0.0848$ , respectively). Further, population assignment tests assigned more than 67 percent of the individual beetles from North America to either Dagong or Tangshan, China. AFLP analysis also revealed local isolation by distance but did not reveal long-range isolation by geographic distance. This suggests that EAB, while dispersing at a local scale, is moving longer distances primarily due to human-mediated transport.

## Literature Cited

Haack, R.A.; Jendek, E.; Liu, H.; Marchant, K.; Petrice, T.; Poland, T.; He, H. 2002. **The emerald ash borer: a new exotic pest in North America.** Newsletter of the Michigan Entomological Society. (5-4): 1-5.