

Geographic Origin of North America's Emerald Ash Borer in Asia Second-quarter report

Cooperator

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Objective

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. We are sampling populations of EAB in Asia and North America (Michigan, Ohio, and southwestern Ontario), and characterizing them 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 through spring 2005 includes 623 individuals from 19 locations in southeastern Michigan, 24 individuals from 2 locations in Ohio, 27 individuals from Indiana, 1 adult from Maryland, 100 adults and 622 larvae from Canada, 1 adult from Shiroishi City, Japan (kindly loaned to us by Dr. Paul Schaefer, USDA-ARS), 1 adult from South Korea (kindly loaned to us by Dr. Dave Williams, USDA-APHIS), 4 adults and 3 larvae from Harbin, Heilongjiang Province, China, and 21 adults (dried or pinned) from Dagong and Hangu (Tianjin Province, China).

What preliminary data suggest

Analysis of mitochondrial COI sequences from 60 individuals from Michigan, 4 individuals from Dagong, 3 individuals from Heilongjiang Province, and 1 individual from Hangu indicated that these sequences were identical in >500 nucleotides. On the other hand, the mtDNA sequence from the Japanese sample differed from the other EAB mtDNA sequence by 3.7%. Therefore, the mtDNA COI sequence of the Japanese sample is very different from any other individual sampled. AFLP profiles from 46 individuals from Michigan, 2 individuals from Ohio, 6 individuals from Ontario Canada, 1 individual from Japan, and 4 individuals from Dagong and 3 individuals from Heilongjiang Province using four selective AFLP primer pairs have thus far yielded 139 scoreable bands. We have observed slight differences between all populations as well as among populations from the same locations.

Neighbor-joining analysis of the 98-band AFLP data set indicates that individuals from MI cluster with individuals from Dagong and Hangu (Tianjin City) while EAB individuals from Harbin (Heilongjiang Province) and Japan fell into a separate, more distantly related group. We are currently working to expand our data set to include data from a fourth AFLP primer pair and to expand our taxon sample by increasing the number of North American locations represented. 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. It will be necessary to increase our sampling of Asian populations if we hope to make valid inferences about the geographic location of source populations that gave rise to our North American EAB infestations. Towards this end, in late spring 2005, we expect to receive larval EAB samples from China that will expand our collection to include samples from Jilin, Liaoning, Hebei, and additional sites in Tianjin and Heilongjiang Provinces (collections by H. Liu and T. Petrice). Japan and Korea remain problematic.

Work is continuing on increasing sample collection, DNA extraction and analysis in Michigan, Indiana, Ohio, and Canadian populations. We have identified four nuclear genes, wingless, elongation factor 1 α , cytochrome C, and pepCK, that have been used for other beetle species and are in the process of evaluating all individuals in the study with these gene segments.