

Molecular Genetics of Asian Longhorned Beetles: Introduction, Invasion, and Spread in North America

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Abstract

We have used molecular techniques to study the genetic structure of Asian longhorned beetle (ALB) populations in North America, allowing us to assess the dispersal behavior of the adult beetles, the extent to which populations have spread in urban areas, and the potential for future spread. We have extracted and sequenced DNA from individuals of six populations; four from China, one from New York and one from Chicago. Three regions of the mitochondrial genome have been assessed for variation among populations. Sequenced gene regions include cytochrome oxidase I and II, and a portion of the large ribosomal subunit of the 16S rRNA. Unfortunately, screens of over 500 base pairs of sequence from each of these gene regions either showed little variation (telling us little about population structure) or were unreadable when sequenced.

We have begun examining population structure using Random Amplified Polymorphic DNA (RAPD) analysis. We screened 20 RAPD primers for variation among the six populations, scored eleven loci from 2 primer sets, and subjected these data to discriminant function analysis. We found that the Gansu population from China shares a significant portion of its band variation with Illinois and New York, and Illinois and New York populations share some similarities among individuals. Results from sequencing the mitochondrial sodium dehydrogenase 4 (ND4) gene corroborated the RAPD data. Sequence data from 242 base pairs of ND4 for beetles from the six sites identified 12 informative sites. Preliminary phylogenetic analyses using neighbor-joining methods indicate that the Illinois and New York populations are related to the Gansu population.

Our findings confirm that there is considerable genetic variability among ALB populations, and this variation can be used for continuing our search for populations in China that were the origin of North American infestations. This information will be critical for evaluating international quarantine practices and preventing introduction of other invasive pest species.