

MOLECULAR GENETIC PATHWAY ANALYSIS OF ASIAN LONGHORNED BEETLE

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ABSTRACT

The Asian longhorned beetle, *Anoplophora glabripennis*, is a destructive pest of hardwood trees. Historically, *A. glabripennis* was geographically restricted within China and Korea and not of economic importance. However, as a result of massive reforestation programs designed to combat desertification, the species emerged as a pest and rapidly spread throughout China.

The presence of multiple outbreak populations of *A. glabripennis* within the U.S. raises questions about its movement. Did the species invade the U.S. once, subsequently spawning additional populations, or did multiple invasions occur undetected until populations established? In either case, can we trace the pathways of invasion and thereby limit future threats?

We set about to address these questions by amplifying and sequencing 1,300 bases of the Cytochrome Oxidase I gene in the mitochondrial genome. The resulting 43 unique DNA sequences (haplotypes) indicate that a minimum of 33 female beetles have

invaded the U.S. (excluding foreign haplotypes). Most of these haplotypes are rare, having been sampled from a single beetle each, indicating a need for further sampling.

Using statistical parsimony, we traced the ancestry and inferred patterns of relationship among the observed haplotypes. This analysis found that the sole post-eradication beetle found in Chicago, after 5 beetle-free years, was genetically divergent from pre-eradication samples taken from the Chicago infestation. Conversely, the recently discovered Worcester, MA, population shares most haplotypes with New York beetles. Jersey City beetles are genetically identical to New York beetles, suggesting the population originated from New York migrants.

Confirming movement within the U.S., as well as detecting the direction and frequency of movement, will require additional samples to assess the genetic variation present as well as additional genetic markers to make the most use of that genetic variation.