

Genetic structure of spotted alfalfa aphid *Theroaphis trifolii* (Hemiptera: Aphididae) populations in China inferred from complete mitochondrial genomes

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Abstract

Biological invasions represent a natural rapid evolutionary process in contemporary time scale, and the invasive species may present a major threat to biodiversity and ecosystem integrity. Analyzing the genetic structure and demographic history of invasive populations is critical for the effective management of invasive species. The spotted alfalfa aphid (SAA) *Theroaphis trifolii* is indigenous in the Mediterranean region of Europe and Africa and has invaded other continents, causing severe damages to the alfalfa industry; however, little is known about its genetic structure and invasion history. In this study, we obtained 167 complete mitochondrial genome sequences from 23 SAA populations across China based on high-throughput sequencing and performed population genetic and phylogenomic analyses. High haplotype diversity and low nucleotide diversity were found in SAA populations in China with distinct genetic structures, i.e., all population samples diverged into three phylogenetic lineages with possible different invasion sources. Demographic history analyses showed a recent expansion of the SAA population, consistent with the rapid invasion history. Our study supported that SAA populations in China were possibly derived from multiple introduction events through commercial trades of alfalfa.

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