

Geographic isolation and habitat differences as drivers of genetic differentiation in the Mediterranean and the Middle East Asia Minor 1 *Bemisia tabaci* (Gennadius) populations of Xinjiang, China

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Abstract

Invasive alien species are generally highly fertile and adaptable and can pose a severe threat to the ecological security of invaded localities. *Bemisia tabaci* (Gennadius) is a rapidly evolving cryptic complex. Among them, Mediterranean (MED) and Middle East-Asia Minor 1 (MEAM1) is the most invasive and widely distributed. To clarify the invasion source, population structure, and genetic differentiation drivers of whitefly populations in Xinjiang, China, we collected *B. tabaci* from 14 host crops in Xinjiang, China. A total of 453 sequenced cytochrome c oxidase subunit I(COI) fragments were analysed. We used common methods and parameters of genetic analysis, such as phylogenetic analysis, haplotype diversity, and nucleotide diversity, neutrality testing, and mismatch distribution chart analysis to determine the genetic structure and genetic differentiation and explore the origin of the invasion of *B. tabaci* populations in Xinjiang. The results have shown that global MED and MEAM1 populations are genetically differentiated, and MED has a significant geographical lineage structure at the Xinjiang and global spatial scales. This was the same for the MEAM1 population at the Xinjiang spatial scale. There have been multiple local expansions and founder effects in the MED populations. The MEAM1 population has retained a stable population size with a bottleneck effect. Based on the phylogenetic tree for MED and MEAM1, it has been demonstrated that there have been multiple points and pathways of invasion of *B. tabaci* and the sources in Xinjiang, China were complex. The sources of MED invasion of MED are likely to be Zhejiang, Hebei, or Shanxi. The source for MEAM1 is complex, and Zhejiang is one of the main invasion sources. This study has shown that host plant differences in open habitats, geographic isolation, and habitat differences were the driving factors for genetic differentiation of *B. tabaci* populations in Xinjiang, China

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