

Molecular Phylogenetic Analysis Reveals at Least Five Genetic Races of *Bemisia tabaci* in China

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Phylogenetic analysis using ITS1 and CO1 nucleotide sequences has revealed six major races of *Bemisia tabaci* in the world, including three major indigenous races in the Asia-Pacific region, viz., *B. tabaci* (Asia), *B. tabaci* (Bali) and *B. tabaci* (Australia), but the status of a large collection of genotypes in this region remains unresolved. The ITS1 sequences of representative whitefly samples collected from around China were determined in this study. These sequences and other homologous sequences retrieved from GenBank were then used to conduct a phylogenetic analysis. The results demonstrated that the whiteflies collected in China were split genetically into four groups, where at least five genetic races were revealed, i.e., B biotype (SDLe, XJEp, XJAt, HNNt, BJlb, GDEp, XJGh, GDHrs, XJSm and SHEp), Bali group (ZJGh), M biotype (Hainan1), G biotype (GXCm) and Asian H/K group (FJlb, GDCv), although the Asian H/K group with low bootstrap score remains unresolved. Of all genetic races, the B biotype is the most extensively distributed. In the dendrogram, the J biotype, L biotype and Q biotype cluster together and form a sister clade to the B biotype. The data indicate that extensive migration of *B. tabaci* has taken place in Asian countries. The populations ZJGh, FJlb, GDCv, GXCm and Hainan1 collected in China might have originated there, but the possibility that they were introduced from elsewhere cannot be excluded at this point. Using PyR from Israel as a reference Q biotype, the random amplified polymorphic DNA banding patterns of SDLe, XJEp, XJAt and HNNt were shown to be consistent with that of the Q biotype, which indicated that the four local whitefly populations identified as the B biotype based on ITS1 sequences were closely related to the Q biotype. KEY WORDS: *Bemisia tabaci*; internal transcribed spacer 1, ITS1; phylogenetic analysis; genetic race.

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