



Identification of three major *Bemisia tabaci* biotypes in China based on morphological and DNA polymorphisms

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<https://doi.org/10.1016/j.pnsc.2008.08.013> 

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Abstract

The sweet potato whitefly, *Bemisia tabaci*, is a complex species, and many of its biotypes are important agricultural pests. The B and Q biotypes are invasive and coexist with the native Cv biotype on vegetable and ornamental crops in China. In this study, these three biotypes were identified based on their morphological characteristics, RAPD–PCR analysis, and DNA sequences of the COI gene. The anterior and posterior wax fringes of the B, Q, and Cv biotypes significantly differed from each other. Based on this morphological characteristic, the three biotypes can easily be distinguished in greenhouses and fields. Genomic DNA RAPD–PCR band patterns also revealed differences between these biotypes using the H₁₆ primer. The B biotype has three bright DNA bands between 250 and 600bp, the Q biotype only has one bright band at ~300bp, while the Cv biotype has no band between 250 and 500bp. Both the Cv and Q biotypes have two bright bands at ~750 and 1000bp while the B biotype has only one band at ~1000bp. Based on the COI gene, the genetic identity between B and Cv, B and Q, and Q and CV was 85.8%, 94.7%, and 86.0%, respectively. The MP tree indicated that the phylogenetic relationship between the B and Q biotypes is much closer than that between the B and Cv or the Q and Cv biotypes. The uses of the morphological,