

First Report of the Q Biotype of *Bemisia tabaci* in Japan by Mitochondrial Cytochrome Oxidase I Sequence Analysis

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Nucleotide sequences reported are available in the DDBJ/EMBL/GenBank databases under accession numbers AB204577, AB204578, AB204579, AB204580, AB204581, AB204582, AB204583, AB204584, AB204585, AB204586, AB204587 and AB204588.

The recent upsurge of *Bemisia tabaci* (Genn.) as an important insect pest and vector of *Tomato yellow leaf curl virus* (TYLCV) is directly linked to serious damage to tomato crops grown throughout Japan. The molecular genetic identification and phylogenetic relationships of 12 *B. tabaci* populations collected from representative locations in Japan were determined based on the mitochondrial cytochrome oxidase I (mtCOI) sequence. Phylogenetic analysis of the whitefly mtCOI sequence indicated that both the invasive B and Q biotypes now occur in Japan. The Q biotype was found at four locations: Mihara in Hiroshima, Nishigoshi in Kumamoto, Miyanojo and Okuchi in Kagoshima prefectures; the remaining eight collections were identified as the B biotype. This is the first report of the introduction of Q biotype in Japan.

KEY WORDS: Aleyrodidae; invasive species; sweet potato whitefly; vegetable crops; whitefly pest; whitefly vector.

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