



MtDNA variability in whitefly (*Bemisia tabaci*) populations in Brazil

G.E. Valle¹, A.L. Lourenção¹, M.I. Zucchi², J.B. Pinheiro³ and A.G. Abreu²

¹Centro de Fitossanidade, Instituto Agrônomo de Campinas, Campinas, SP, Brasil

²Agência Paulista de Tecnologia dos Agronegócios, Piracicaba, SP, Brasil

³Departamento de Genética, Escola Superior de Agronomia “Luiz de Queiroz”, Universidade de São Paulo, Piracicaba, SP, Brasil

Corresponding author: G.E. Valle

E-mail: gevalle@yahoo.com.br

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ABSTRACT. *Bemisia tabaci* (Hemiptera: Aleyrodidae) consists of a complex of morphologically indistinct biotypes that vary mainly in their capacity to transmit plant viruses and to induce physiological disorders in plants of economic importance. The adaptability of *B. tabaci* to many regions of the world has fostered the appearance of various biotypes and has resulted in a broad spectrum of host plants. Our goal was to identify which biotypes were present in four *B. tabaci* populations in Brazil. We quantified genetic variability between and within populations. Three individuals were collected from three host plant species: two populations on soybean (Campinas and Rondonópolis), one on pumpkin (Barreiras) and one on tomato (Cruz das Almas) in three States of Brazil (São Paulo, Mato Grosso, and Bahia). We chose one sequence of the B biotype, obtained from GenBank; the Campinas population, which had been previously characterized as biotype B, was used as a control for this biotype. We also included one sequence of the Q biotype, obtained from GenBank, as an outgroup. The COI region of the mtDNA gene was partially amplified with the CI-J-2195 and L2-N-3014 pair of primers, and the reaction products were sequenced. Based on distance-

based algorithm analyses, we found that all haplotypes belong to biotype B, which was confirmed by the haplotype network. Genetic structure analyses showed that the host plant species does not influence population structuring of this pest; only the geographic location mattered.

Key words: Insecta; Aleyrodidae; Whitefly; Genetic diversity; Molecular characterization