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Adaptation of *Bemisia tabaci* biotype B (Gennadius) to cassava, *Manihot esculenta* (Crantz)☆

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Abstract

Bemisia tabaci is a recognized pest in cassava (*Manihot esculenta*) crops in Asia and Africa, where it transmits the cassava mosaic geminiviruses (CMGs) (family: *Geminiviridae*, genus: *Begomovirus*). A general consensus exists that *B. tabaci* is a complex of morphologically indistinguishable populations with different biological biotypes. In the Americas, though the polyphagous *B. tabaci* biotype B appears to feed on cassava, it is postulated that the absence of CMGs is related to the inability of this biotype to colonize this crop effectively. However, its potential adaptation is considered a threat for cassava production in the Neotropics. This study was initiated to verify whether *B. tabaci* can become gradually adapted to *M. esculenta*. Trials in rearing chambers were carried out measuring population development of whitefly individuals passed through a series of intermediate hosts, previously selected and based on phylogenetic closeness to *Manihot*. The capacity of biotype B to adapt gradually to cassava, started on a legume (*Phaseolus vulgaris*), followed on two Euphorbiaceae (*Euphorbia pulcherrima* and *Jatropha gossypiifolia*) until, finally reaching a commercial cassava variety. *B. tabaci* female mean longevity on cassava, coming from *P. vulgaris*, *E. pulcherrima* and *J. gossypiifolia* was 3.1, 5.6 and 3.3 days, respectively. The highest oviposition rate (2.6 eggs/female/2 days), the shortest development time (44.4 days) and the highest value of r_m (0.48 day^{-1}) were for populations coming from *J. gossypiifolia*, where 27.5% of the individuals coming from this host survived and reproduced on cassava. The importance and potential impact of phylogenetically close plants as intermediate hosts faciliting the adaptation of *B. tabaci* biotype B to cassava is discussed.

Keywords: *Bemisia tabaci*; Biotype B; *Manihot esculenta*; Adaptation; Hosts

1. Introduction

Bemisia tabaci (Homoptera: Aleyrodidae) is considered one of the most important pests in tropical and subtropical agriculture, as well as in production systems in glasshouses in temperate zones (Byrne and Bellows, 1991; Byrne et al., 1990). Since the 1980s, it has caused considerable economic losses in the southern United States, Mexico, Venezuela, the Eastern Caribbean Basin, and Central and South America due to its proven efficiency as a virus vector, together with damage caused by direct feeding and excretion of honeydew (Brown et al., 1995; Oliveira et al., 2001). Many biotypes have been identified in different regions of the world, which suggests that *B. tabaci* may be a complex of species and biotypes (Perring, 2001; Abdullahi et al., 2003) undergoing continuous evolutionary changes.

In the Americas there are complex associations between some hosts and various *B. tabaci* biotypes. In Puerto Rico, for example, the *Sida* biotype, which colonizes many species of plants including the genus *Sida*, to which it transmits several geminiviruses (family Geminiviridae: genus *Begomovirus*), and the *Jatropha* biotype, monophagous only on *Jatropha gossypiifolia* L., to which it specifically transmits

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☆Recent evidence suggests that *B. tabaci* represents a species complex with numerous biotypes and two described cryptic species. The binomial *B. tabaci* is used here in the broadest sense to include all members of the species complex.

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the *Jatropha mosaic virus* (Brown et al., 1995), co-exist in the same geographic area but in different niches.

After its first report and identification in the USA, the *B. tabaci* biotype B has become important due to its unique biochemical and biological characteristics. *B. tabaci* species complex adapts easily to new hosts and geographic regions. With the exception of Antarctica, it has been reported throughout the world (Martin et al., 2000) associated with almost 600 species of plants (Mound and Halsey, 1978; Secker et al., 1998). These include many cultivated and noncultivated species, annuals and perennials, which act as host plants, favoring its feeding and/or reproduction (Bedford et al., 1992; Brown et al., 1995; Butler and Henneberry, 1986). The families with the highest number of host species are Fabaceae, Asteraceae, Malvaceae, Solanaceae and Euphorbiaceae (Mound and Halsey, 1978). The introduced biotype B displays one of the broadest host range known among *Bemisia* whiteflies (Brown et al., 1995). However, unlike its West African counterpart the biotype B exhibits a wide polyphagous habit but cassava appears to be a nonsuitable host. Further, it had been speculated that the absence of cassava-infecting begomoviruses in South America is in part related to the inability of *B. tabaci* to colonize cassava (Bellotti and Arias, 2001; Costa and Russell, 1975). Nevertheless, *B. tabaci* was found feeding on cassava in Cuba (Vásquez et al., 1995) and specifically the biotype B in the Dominican Republic (Brown et al., 1995). These facts, together with the economic impact that affected southern USA, were attributed to the introduction and establishment of this highly invasive biotype B and its association to viral diseases (Brown et al., 1995; Brown and Bird, 1995). These examples indicate a potentially serious threat of the possible introduction of cassava mosaic geminiviruses (CMGs) to the Americas, especially because most traditional cassava cultivars in the Neotropics are highly susceptible to the disease. In addition, the *B. tabaci* species complex is the vector of viruses on several other crops often grown in association with or in proximity to cassava (e.g. beans, cowpea, sweet potatoes, string beans, tomatoes, cotton, soy bean) (Bellotti and Arias, 2001; Costa and Russell, 1975). The possibility of viral diseases moving among these crops or the appearance of new viruses represents a potential threat, e.g. tomato-yellow leaf curl virus infecting common bean (Navas-Castillo et al., 1999).

In order to anticipate these events and as a prerequisite for developing any control measure (especially one that entails quarantine), research was initiated to evaluate the adaptative capacity of *B. tabaci* biotype B. The main goal of the present study was to verify, experimentally, the capacity of the biotype B to adapt on cassava. Specifically, it was evaluated, in a hypothetical but quantifiable manner (through life tables), possible ways in which this adaptation could occur in Colombia.

2. Materials and methods

2.1. Biotype B of Bemisia tabaci

A strain of *B. tabaci*[1] biotype B was obtained from individuals of a colony established at CIAT by the Bean Project in 1997, originating from Dapa County (Cauca Valley, Colombia). The strain was reared for five generations on *Phaseolus vulgaris* plants (variety ICA-Pijao) in cages made of tulle and wood (1 × 1 × 1 m) under controlled conditions (25 ± 2 °C, 70 ± 5% RH and a 12-h photophase) according to methodology proposed by Eichelkraut and Cardona (1989). Periodically, the purity of adult biotype B specimens in the colony was checked using RAPD-PCR (CIAT, 1999).

2.2. Adaptation of B. tabaci from P. vulgaris to M. esculenta (MCol 2063)

The experimental hypothesis was that *B. tabaci* could become gradually adapted to *M. esculenta* by passing firstly through a series of intermediate hosts, previously selected based on phylogenetic closeness to *Manihot* (Burkill, 1994) and susceptibility to whiteflies. The adaptation process was initiated on a highly susceptible host (*P. vulgaris* L.), phylogenetically distant from *M. esculenta*; passing through two Euphorbiaceae (*Euphorbia pulcherrima* Willd. ex. Klotzch "poinsettia" and *Jatropha gossypiifolia* L. "jatropha"), both intermediate hosts to *B. tabaci*, being relatively familiar and phyllogenetically close to *Manihot.* As the final host, the cassava cultivar MCol 2063 "var. Secundina" was selected for its known susceptibility to the whiteflies *Aleurotrachelus socialis* Bondar and *B. tuberculata* Bondar (Bellotti et al., 1999).

Eight, 40 days old *E. pulcherrima* plants, divided into two cages (1 m × 1 m × 1 m) were each infested with an average of 4400 *B. tabaci* pupae on *P. vulgaris* leaves. These individuals had passed through five generations on the latter host. Later, young leaves of *E. pulcherrima* infested with an average of 5880 fifth generation *B. tabaci* pupae, were used to infest 8, 40 days old plants, of *J. gossypiifolia* using the above described methodology. Lastly, young *J. gossypiifolia* leaves containing an average of 7600 fifth generation *B. tabaci* pupae were used to infest 8, 35 days old *M. esculenta* (var MCol 2063) plants (Fig. 1).

2.3. Biology and demographic parameters of B. tabaci on M. esculenta with individuals coming from host sequence: P. vulgaris, E. pulcherrima and J. gossypiifolia

In order to determine the relative importance of each host involved in the sequence to reach the adaptation of

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[1] Unless a more specific designation is indicated, for practical reasons, the binomial *B. tabaci* is used here thereafter to refer to its Biotype B, which is so far the only one reported in Colombia.