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Dynamic monitoring (B versus Q) and further resistance status of Q-type *Bemisia tabaci* in China

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ABSTRACT

Bemisia tabaci (Gennadius) (Hemiptera: Aleyrodidae) causes serious economic losses in many countries and has developed substantial resistance to commonly used insecticides. To determine whether the ratio of *B. tabaci* B to *B. tabaci* Q has continued to change in China, we collected specimens in 2013 and 2014 from most provinces in the country. Resistance to insecticides was also assessed in Q-type *B. tabaci*. *B. tabaci* Q remained much more abundant than *B. tabaci* B throughout China in 2013 and 2014, representing 82% of the specimens in 2013 and 88% in 2014. *B. tabaci* B was mainly found in the southeast coast and Yangtze river basin. Abamectin remained highly toxic to *B. tabaci* adults, with LC_{50} values <0.2 mg/l in 2013 and 2014. Thiamethoxam showed lower toxicity to HN and HB strains, with LC_{50} values >500 mg/l in 2014. Although cyantraniliprole also remained highly toxic to pre-adults of *B. tabaci*, the resistance ratio (relative to the sensitive Lab-Q strain) increased to 27.80 for eggs and to 35.79 for larvae. *B. tabaci* Q continues to dominate in China. As of 2014, abamectin, cyantraniliprole, and pyriproxyfen were still effective against *B. tabaci* based on our laboratory bioassays but moderate resistance to cyantraniliprole and pyriproxyfen was detected in some areas.

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1. Introduction

The sweet potato whitefly, *Bemisia tabaci* (Gennadius) (Hemiptera: Aleyrodidae), is one of the most damaging pests of vegetable and field crops worldwide. *B. tabaci* causes damage by direct feeding, excreting honeydew and transmitting more than 100 plant viruses (Oliveira et al., 2001; Jones, 2003; Brown et al., 2015).

Recent studies indicate that *B. tabaci* is a complex of more than 36 reproductively isolated but morphologically indistinguishable species (Dinsdale et al., 2010; De Barro et al., 2011; Liu et al., 2012; Esterhuizen et al., 2013; Barbosa et al., 2014; Boykin and De Barro, 2014). These cryptic species differ in host range, life history traits, insecticide resistance, transmission competency for begomoviruses, and the symbionts that they harbor (Perring, 2001; De Barro et al., 2011; Liu et al., 2012; Brown et al., 1995; Pan et al., 2012). The two most invasive and destructive species are *B. tabaci* B and *B. tabaci* Q. *B. tabaci* B belongs to the Middle East-Minor Asia 1 (MEAM1) genetic group, and *B. tabaci* Q belongs to the Mediterranean (MED) genetic group (Dinsdale et al., 2010). *B. tabaci* B and Q have invaded nearly 60 countries and caused massive agricultural losses in the past two decades (De Barro et al., 2011; Wan and Yang, 2016). After *B. tabaci* B invaded China in the 1990s, it rapidly spread (Luo et al., 2002) and caused serious agricultural losses. *B. tabaci* Q was first found in Yunnan Province, China, in 2003 (Chu et al., 2006), and has now displaced the well-established populations of B in most parts of China (Chu et al., 2010a; Teng et al., 2010; Pan et al., 2011; Hu et al., 2011, 2014). According to Pan et al. (2011), the invasion of China by *B. tabaci* Q can be divided into three phases: in the first phase (during or before 2003), *B. tabaci* Q was introduced to the country; in the second phase (2004–2006), *B. tabaci* Q rapidly spread; and in the third phase (after 2007), Q became the dominant *B. tabaci* in China (Pan et al., 2015).

Chemical insecticides have been the main tools used to control *B. tabaci*. Because of overuse and/or misuse, however, *B. tabaci* has developed high resistance to some commonly used insecticides,

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especially the neonicotinoids and insect growth regulators (IGRs) (Denholm, 1988; Nauen and Denholm, 2005; Roditaki et al., 2005; Erdogan et al., 2008). In Spain, Israel, and the USA, for example, *B. tabaci* has developed high resistance to pyriproxyfen and neonicotinoids (Elbert and Nauen, 2000; Nauen et al., 2002; Rauch and Nauen, 2003; Dennehy et al., 2007; Ma et al., 2010; Horowitz et al., 2004, 2005). *B. tabaci* in China also has high resistance to neonicotinoid insecticides (Luo et al., 2010; Wang et al., 2010). One insecticide resistance management (IRM) strategy involves the use of novel insecticides, such as chlorantraniliprole and cyantraniliprole (Li et al., 2012; Caballero et al., 2013; Grávalos et al., 2015).

In the current study, we monitored the distributions of *B. tabaci* B and Q in 2013 and 2014 in China, and determined whether the resistance of Q-type *B. tabaci* strains from Beijing, Shandong, Shanxi, Hubei, and Hunan to cyantraniliprole, pyriproxyfen, thiamethoxam and abamectin had changed since the earlier report by Xie et al. (2014).

2. Materials and methods

2.1. Field populations

Ninety-six populations of *B. tabaci* in 2013 and 93 populations in 2014 were collected from different host plants across 22 provinces in China (Figs. 1 and 2). Populations in the same locations were separated by at least 500 m. Population number, location, host plant, and collection date are listed in Table 1. For each population, approximately 150 adult whiteflies were randomly collected, placed in a 1.5-ml centrifuge tube with 95% ethanol, and stored at −20 °C for later identification.

Field populations were collected alive from six host plants (cucumber (Cucumis sativus L.), pepper (Capsicum annuum L.), eggplant (Solanum melongena L.), cotton (Gossypium hirsutum L.), tomato (Lycopersicon esculentum), and melon (Cucumis melo L.)) in five localities (Beijing, Shandong, Shanxi, Hunan, and Hubei) in 2013 and again in 2014. These specimens were collected from the same five field areas from which *B. tabaci* adults had been collected in 2012 by Xie et al. (2014). The specimens from each locality were considered to represent one population. The collected specimens were identified (as described in the next section) and assessed for insecticide resistance using the same insecticides and methods reported by Xie et al. (2014) and as described in section 2.3.

2.2. B. tabaci identification

B. tabaci specimens were identified based on the cleaved amplified polymorphic sequence (CAPS) of the mtCOI fragment according to Chu et al. (2010b). In brief, the total DNA was extracted from individual adults according to Luo et al. (2002), and was PCR amplified with the primers C1-J-2195 and TL2-N-2819 to obtain the mtCOI fragment (about 620 bp) (Chu et al., 2010a; Zhang et al.,

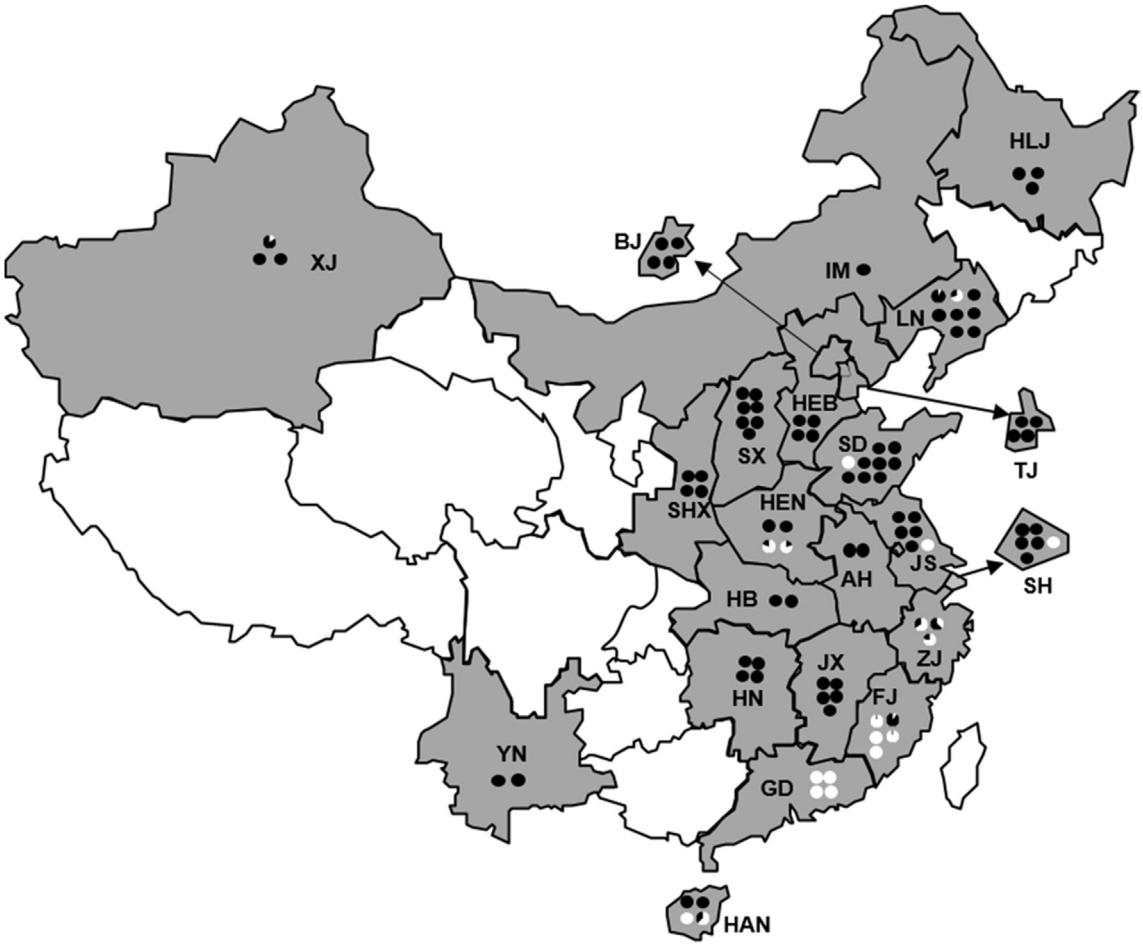

Fig. 1. Detection of *B. tabaci* B and Q in 96 populations in China in 2013. Surveyed provinces are shaded in grey. Field populations with 100% *B. tabaci* B are indicated by white dots, 100% *B. tabaci* Q are indicated by black dots, and mixed populations are indicated by dots with white and dark parts that reflect the proportion of each species.

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