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RESEARCH ARTICLE

First report of field resistance to cyantraniliprole, a new anthranilic diamide insecticide, on *Bemisia tabaci* MED in China



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Abstract

The *Bemisia tabaci* (Gennadius) cryptic species complex comprises important insect pests that cause devastating damage to agricultural crops worldwide. In China, the *B. tabaci* Mediterranean (MED) (or biotype Q) species is threatening agricultural production all over the country as resistance to commonly used insecticides has increased. This situation highlights the need for alternative pest control measures. Cyantraniliprole, a novel anthranilic diamide insecticide, has been widely employed to control Hemipteran pests. To monitor the levels of resistance to cyantraniliprole in *B. tabaci* field populations in China, bioassays were conducted for 18 field samples from nine provinces over two years. Compared with median lethal concentration (LC₅₀) for the MED susceptible strain, all field samples had significantly higher resistance to cyantraniliprole. Furthermore, resistance factors (RFs) increased significantly in samples from Shanxi (from 5.62 in 2015 to 25.81 in 2016), Hunan (3.30 in 2015 to 20.97 in 2016) and Hubei (from 9.81 in 2015 to 23.91 in 2016) provinces. This study indicates a considerable decrease in the efficacy of cyantraniliprole against *B. tabaci* and establishes a baseline of susceptibility that could serve as a reference for future monitoring and management of *B. tabaci* resistance to cyantraniliprole.

Keywords: *Bemisia tabaci*, cyantraniliprole, anthranilic diamides, baseline susceptibility, resistance development

1. Introduction

The tobacco whitefly *Bemisia tabaci* (Gennadius), also known as cotton whitefly or sweet potato whitefly, is a cryptic

species complex of small insects with sucking mouthparts. This species complex is distributed globally in tropical, subtropical, and low-latitude temperate regions. *B. tabaci* has been recorded feeding on more than 600 plants (De Barro *et al.* 2011; Wang *et al.* 2014) including cotton, tomato, tobacco, cassava, sweet potato, and many other flower and vegetable crops. In addition, *B. tabaci* is an important disease vector, transmitting more than 200 species of plant viruses (Hogenhout *et al.* 2008). The two most invasive and destructive cryptic species of *B. tabaci* are Middle East-Asia Minor I (MEAM1 or biotype B) and Mediterranean (MED or biotype Q). MEAM1 is widely distributed in China on vegetable and cotton crops (Luo *et al.* 2002; Wang *et al.* 2010), and MED was first detected in China in 2003 following suspected importation on poinsettia (Chu *et al.* 2006). Recently, MED

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has displaced MEAM1 and is now the dominant species in most regions of China (Zheng *et al.* 2017). Insecticides such as organophosphates, pyrethroids, carbamates and insect growth regulator (IGR) used to be applied as the primary means of controlling *B. tabaci*. However, a strong reduction in the efficacy of these insecticides has been reported in some populations of *B. tabaci* due to rapid evolution of insecticide resistance (Ahmad *et al.* 2010; Wang *et al.* 2010; Basit *et al.* 2012; Zheng *et al.* 2017). Additionally, a relatively high toxicity of these insecticides has been observed in non-target organisms, including arthropods and even humans (David *et al.* 2007; Androne *et al.* 2016; Cook *et al.* 2016). As a result, it is not an appropriate choice to extensively employ above insecticides with low pesticide residues for producing agricultural products.

In the 1990s, a number of neonicotinoids such as imidacloprid, nitenpyram, acetamiprid, thiamethoxam, clothianidin and dinotefuran were developed and used to control Hemipteran pests around the globe (Bass *et al.* 2015). Currently, *B. tabaci* MED is dominant in China and has been threatening agricultural production throughout the country (Pan *et al.* 2011, 2015). More importantly, MED has developed resistance to several different insecticides, especially neonicotinoids (Pan *et al.* 2015; Zheng *et al.* 2017). Anthranilic diamide insecticides have been shown to effectively control a large number of insect pest species from different orders such as Diptera (Peck *et al.* 2008), Thysanoptera (Jacobson and Kennedy 2011), Lepidoptera (Wakil *et al.* 2013), Isoptera (Barwary *et al.* 2015), Hemiptera (Grávalos *et al.* 2015) and Coleoptera (Lanka *et al.* 2015). Following the commercial success of chlorantraniliprole, the first anthranilic diamide, cyantraniliprole, the second systemic anthranilic diamide, has been used to control Hemipteran pests (Sattelle *et al.* 2008). Cyantraniliprole is a powerful tool for managing adult and immature stages of whitefly, and for reducing transmission of plant viruses (Lahm *et al.* 2007; Grávalos *et al.* 2015;

Wang *et al.* 2017; Zheng *et al.* 2017). Cyantraniliprole has provided a promising alternative to existing insecticides, as it exhibits novel modes of action and acute toxicological profiles against insect pests.

Before the initial application of any new insecticide, it is important to determine baseline susceptibility to confirm the current resistance situation in the field. Studies of baseline susceptibility of cyantraniliprole in *B. tabaci* from the United States and Spain demonstrated no cross-resistance to commonly used insecticides, and proved to be an effective way to mitigate resistance of *B. tabaci* to other insecticides (Li *et al.* 2012; Grávalos *et al.* 2015). In the present study, we determined the baseline susceptibility of cyantraniliprole and assessed the development of resistance to cyantraniliprole in *B. tabaci* from nine provinces in China.

2. Materials and methods

2.1. *B. tabaci* strains

B. tabaci MED susceptible strain (MED-S) was originally collected from damaged poinsettia in Beijing, China in 2009 (Pan *et al.* 2012). The insects were fed on cotton plants (*Gossypium hirsutum* L. var. Shiyuan 321) free of any insecticides under a 16 h L:8 h D photoperiod at (27±1)°C and (60±10)% relative humidity (RH). Nine samples of *B. tabaci* were collected in 2015 and 2016 from different host plants across nine provinces in China. Sampling site, date and host plant are listed in Table 1. More than 3 000 adults were collected randomly from crop leaves to obtain F₁ progeny. In addition, at least 200 individuals of each sample were collected at random, and then placed in a 1.5-mL centrifuge tube with 95% ethanol and stored at –20°C for later species identification. All samples were identified as MED according to nucleotide sequences of a fragment of the mitochondrial *COI* gene (Luo *et al.* 2002).

Table 1 Sampling site, date and host plant of *Bemisia tabaci* Mediterranean (MED) from the fields in China

Sample name ¹⁾	Site of collection	Date of collection	Host plant
MED-S	39.90°N, 116.30°E	July in 2009	Poinsettia
BJ	39.56°N, 116.20°E	August in 2015 and 2016	Cucumber
TJ	39.39°N, 117.05°E	October in 2015 and 2016	Tomato
HB	38.05°N, 114.52°E	September in 2015 and 2016	Tomato
SD	36.68°N, 116.99°E	July in 2015 and 2016	Cotton
SX	37.88°N, 112.56°E	October in 2015 and 2016	Eggplant
ZJ	30.26°N, 120.19°E	September in 2015 and 2016	Pepper
HuB	30.59°N, 114.31°E	September in 2015 and 2016	Tomato
HuN	28.23°N, 112.95°E	September in 2015 and 2016	Melon
HaiN	20.05°N, 110.21°E	April in 2015 and 2016	Melon

¹⁾ MED-S is the susceptible strain in lab which was collected from Beijing in 2009; BJ collected from Beijing; TJ collected from Tianjin; HB collected from Shijiazhuang, Hebei; SD collected from Ji'nan, Shandong; SX collected from Taiyuan, Shanxi; ZJ collected from Hangzhou, Zhejiang; HuB collected from Wuhan, Hubei; HuN collected from Changsha, Hunan; HaiN collected from Haikou, Hainan.

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