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ScienceDirect
Crop Protection 26 (2007) 612–617
Crop Protection
www.elsevier.com/locate/cropro

The biotype and insecticide-resistance status of whiteflies, *Bemisia tabaci* (Hemiptera: Aleyrodidae), invading cropping systems in Xinjiang Uygur Autonomous Region, northwestern China

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Received 4 January 2006; received in revised form 20 April 2006; accepted 27 April 2006

Abstract

Xinjiang Uygur Autonomous Region in northwestern China is undergoing rapid development of its agricultural industries. Areas planted with cotton, grapes and vegetables have expanded dramatically in recent years. The tobacco whitefly, *Bemisia tabaci*, was first found in Xinjiang in 1998 on poinsettias (*Euphorbia pulcherrima*) and may have been imported to the region on that crop. Analysis of non-specific esterases using native polyacrylamide gel electrophoresis showed six samples of *B. tabaci* collected within a 200 km radius of Urumqi (Xinjiang's capital city) to belong to the highly invasive B biotype. The samples showed very similar profiles of insecticide resistance with very strong (>1000-fold) resistance to pyrethroids, low to moderate resistance to imidacloprid and pyriproxyfen, and no resistance to abamectin. The implications for resistance management and contending with further invasions of aggressive *B. tabaci* biotypes are discussed.

Keywords: *Bemisia tabaci*; Biotype; Insecticide resistance; Cotton; Xinjiang; China

1. Introduction

Over the last 30 years, the whitefly *Bemisia tabaci* has risen from relative obscurity to become one of the primary insect pests of agriculture worldwide. A major reason for its expansion in importance and geographical range appears to have been the replacement of native races or biotypes by ones of far greater economic significance capable of invading new cropping systems, developing on a broad range of cultivated and non-crop species, transmitting a large number of plant viruses, and rapidly evolving resistance to chemical control agents (Byrne and Bellows, 1991; Brown et al., 1995a; Denholm et al., 1996; Perring, 2001). The biotype of greatest notoriety in this respect is the so-called 'B' biotype (synonym *B. argentifolii*) that has spread to and become established in cotton and vegetable-growing systems in many regions including the USA, Central America, India and Australia (Costa et al., 1993; De Barro and Hart, 2000; Banks et al., 2001).

The history of *B. tabaci* in China is rather poorly documented but it was included in a list of whitefly species recorded from that country by 1949 (Zhou, 1949). However, it is now very widely distributed and has assumed primary pest status on several vegetable crops (especially cucurbits and solanaceous species) as well as cotton (Luo et al., 2000; Luo and Zhang, 2000). A study of the genetic diversity of *B. tabaci* in China, based on mitochondrial cytochrome oxidase I (mtDNA COI) sequences, identified four genotypic clusters with the one showing close homology to B-type populations elsewhere in the world being the most widespread and prevalent (Zhang et al., 2005). A second group of samples from

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0261-2194/$ - see front matter © 2006 Elsevier Ltd. All rights reserved.
doi:10.1016/j.cropro.2006.04.027

Beijing and Yunnan province were associated with known populations of the 'Q' biotype, formerly only recorded from the Mediterranean Basin (De la Rua et al., 2006). The other two genetic groups did not associate clearly with named biotypes and may represent indigenous Chinese populations (Zhang et al., 2005), potentially in the process of being competitively displaced by B- (and possibly Q-) type whiteflies imported recently to China from other areas.

Threats posed by *B. tabaci* to agriculture in China (and elsewhere in the world) are exemplified well by developments in Xinjiang Uygur Autonomous Region (henceforth termed Xinjiang) in the northwest of the country. Xinjiang comprises approximately one-sixth of the total land area of China and is undergoing rapid economic development including an expansion and diversification of its agricultural industries. Most notably, cotton production has increased from 0.08 million tons of lint cotton in 1980 to 1.3 million tons in 1998, and now equals at least 30% of China's total output (Wang, 1998). This move was precipitated in part by a need to overcome increasing problems with controlling insecticide-resistant bollworms, *Helicoverpa armigera*, in traditional cotton-growing regions in eastern China (Wang, 1998). The production of grapes, vegetables and ornamentals is also expanding rapidly to satisfy growing domestic and export markets, with an increasing proportion of crops being cultivated under plastic or glass to prolong the growing season despite harsh winter conditions. These developments seem ideal for favouring the invasion, establishment and resistance of the most aggressive and polyphagous whitefly biotypes.

B. tabaci was first found in Xinjiang on poinsettias (*Euphorbia pulcherrima*) in 1998 (Zhao et al., 2000), and may have been introduced initially on that crop. It has subsequently been found causing damage to cotton and grapes near the city of Turfan, with the affected area exceeding 500 ha in 2004 (unpublished report by the Xinjiang Turfan Agricultural Technology Promotion Centre). Using a PCR-based diagnostic, samples of *B. tabaci* from eggplant and hemp near Shihezi in Xinjiang were assigned to the B biotype (Wu et al., 2002). However, the biotype status of whiteflies on other crops including cotton have not been determined, nor is there any information on levels of resistance to insecticides available for controlling whitefly outbreaks. We report here on a study of six samples of *B. tabaci* collected over the last 2 years from Xinjiang, and discuss implications for the design and sustainability of strategies for managing *B. tabaci* and coexisting crop pests.

2. Materials and methods

2.1. Whitefly strains

Six strains of *B. tabaci* (XJ1-XJ6) were collected in 2004 and 2005 from sites within a 200 km radius of Urumqi, the capital of Xinjiang (Table 1). Two of these (XJ1 and XJ2) came from poinsettia (*E. pulcherrima*) crops in greenhouses, and the others from field crops of cotton (*Gossypium* spp.), grape (*Vitis vinifera*) or melon (*Cucumis melo*). Samples comprised at least 100 individuals and were transferred to Rothamsted within 10 days of collection. The study also included two strains (CHLORAKA and PIRGOS) collected in 2003 from Cyprus that served as standard strains representing the Q and B biotypes, respectively. A long established laboratory strain (SUD-S), susceptible to all insecticide groups (Cahill et al., 1995), provided baseline data for establishing the resistance status of Chinese samples. At Rothamsted, all strains were maintained on cotton plants (*Gossypium hirsutum* L. var. '*Deltapine* 16') without exposure to insecticides, under a 16 h photoperiod at 26 °C. All adult insects used for biotype determinations and bioassays were within 7 days of emergence.

Table 1
Details of field and reference strains of *B.tabaci*

Strain[a]	Year	Origin	Host plant
XJ1	2004	Urumqi, Xinjiang	Poinsettia
XJ2	2004	Changji, Xinjiang	Poinsettia
XJ3	2004	Turfan, Xinjaing	Cotton
XJ4	2004	Turfan, Xinjiang	Grape
XJ5	2005	Shanshan, Xinjiang	Cotton
XJ6	2005	Shanshan, Xinjiang	Melon
CHLORAKA Q	2003	Cyprus	Cucumber
PIRGOS B	2003	Cyprus	Various
SUD-S	1978	Sudan	Cotton

[a]Samples from poinsettia came from greenhouses in urban areas. Samples from cotton were collected within 5–10 km of towns that could have provided over-wintering sites for *B. tabaci*.

2.2. Biotype determination

To determine the biotype of *B. tabaci* strains from Xinjiang, non-specific esterases were analysed by native polyacrylamide gel electrophoresis (PAGE), and banding patterns were compared to reference ones for the Q (CHLORAKA) and B (PIRGOS) biotypes (Costa and Brown, 1991; Byrne and Devonshire, 1993; Brown et al., 1995b; Horowitz et al., 2003b). Single adults were homogenised in wells of a 96-well microplate containing 5 µl of 1.6% TX-100 (pH 7.5), and the volume was adjusted to 20 µl using 1.6% TX-100 (pH 7.5) containing 10% sucrose and 0.01% bromocresol purple. Fifteen microlitres of this homogenate was added to each well of a gel, which was run at 250 v for 1.5 h in a tank containing barbitone buffer made up from 27.6 g barbitone and 5.0 g Tris base in 5 l distilled water. Gels were stained by immersion in 50 ml phosphate buffer (pH6) containing 100 mg Fast Blue RR salt and 0.25 ml of 100 mM a-napthyl butyrate. The first two and last two lanes of each gel contained standard Q-type and B- type whiteflies, respectively. The remaining 10 wells contained individuals from one of the six strains from