

Further Spread of and Domination by *Bemisia tabaci* (Hemiptera: Aleyrodidae) Biotype Q on Field Crops in China

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ABSTRACT The sweetpotato whitefly, *Bemisia tabaci* (Gennadius) (Hemiptera: Aleyrodidae), causes severe crop losses to many crops. The worst of these losses are often associated with the invasion and establishment of biotypes B and Q of this pest. Previous research in 2007 showed that biotype Q occurred with other biotypes in most field populations in China. To determine the current status of the biotype composition in the field, an extensive survey covering mainly eastern parts of China was conducted in 2009. Using polymerase chain reaction primers specific for the mitochondrial cytochrome oxidase I of biotypes B and Q and gene sequencing, we determined the biotypes composition in 61 whitefly populations and their distribution across 19 provinces in China. Our research revealed that only biotypes B and Q have been found in the field in 2009 in China. Among them, biotype Q was dominant in 44 locations (100.0%) and biotype B was dominant in 17 locations (100.0%). The current survey indicates that biotype Q has rapidly displaced biotype B in most locations in China.

KEY WORDS *Bemisia tabaci*, biotype Q, biotype B, displacement, China

The sweetpotato whitefly, *Bemisia tabaci* (Gennadius) (Hemiptera: Aleyrodidae), is one of the most invasive and damaging pests of protected crops and field crops worldwide. This polyphagous whitefly damages plants directly through its feeding and indirectly by vectoring 111 plant viruses (Jones 2003, Inbar and Gerling 2007). *B. tabaci* is recognized as a species complex that comprises a large number of genetically distinct sibling species and/or biotypes (Brown et al. 1995). These biotypes differ genetically as well as in host range, fecundity, insecticide resistance, capacity to cause plant disorders, and ability to transmit viral diseases and the symbionts they harbor (Brown et al. 1995, Jones 2003, Chiel et al. 2007). New biotypes are continually being described in different parts of the world (Brown et al. 1995, Perring 2001). Among them, there are two biotypes termed biotypes B and Q that are now regarded as the two most invasive and widely distributed biotypes worldwide. Based on the recent genetic grouping of *B. tabaci* (Dinsdale et al. 2010, Xu et al. 2010), biotypes B and Q belong to the Middle East-Asia Minor 1 and Mediterranean group, respectively (Dinsdale et al. 2010).

Over the past 20 yr, biotype B has been introduced into many regions where it subsequently caused se-

vere crop damage (Brown et al. 1995, Perring 2001), and biotype Q has caused substantial crop damage in the Mediterranean Basin (Brown et al. 2000, Horowitz et al. 2003, Simón et al. 2007, Papayiannis et al. 2009). More recently, biotype Q has been found in the non-Mediterranean countries such as China (Chu et al. 2006), Japan (Ueda and Brown 2006), the United States (Brown et al. 2005), Mexico (Martinez-Carrillo and Brown 2007), and Guatemala (Bethke et al. 2009).

In China, *B. tabaci* was first recorded in the late 1940s (Zhou 1949) but did not cause significant and recognized damage until the 1990s (Luo et al. 2002). Biotype B was introduced into China in the mid-1990s (Luo et al. 2002), rapidly established, and has since caused serious losses in many crops (Zhang et al. 2005, Chu et al. 2006, Qiu et al. 2007). The first recorded occurrence of biotype Q in China was on poinsettias in Yunnan Province in 2003 (Chu et al. 2006). Since then, biotype Q has been found in Henan, Beijing, Zhejiang, and Shandong provinces (Chu et al. 2006, 2007; Xu et al. 2006). Teng et al. (2010) revealed that biotype Q was present and occurred with other biotypes in most provinces of China in 2007. Within the mixed *B. tabaci* populations, it represented variable proportions of the different populations (7.5–94.5%). Chu et al. (2010a,b) showed that biotype Q could displace B within 3–4 yr in some regions in China. However, whether biotype Q could displace the other biotypes including biotype B in the field populations

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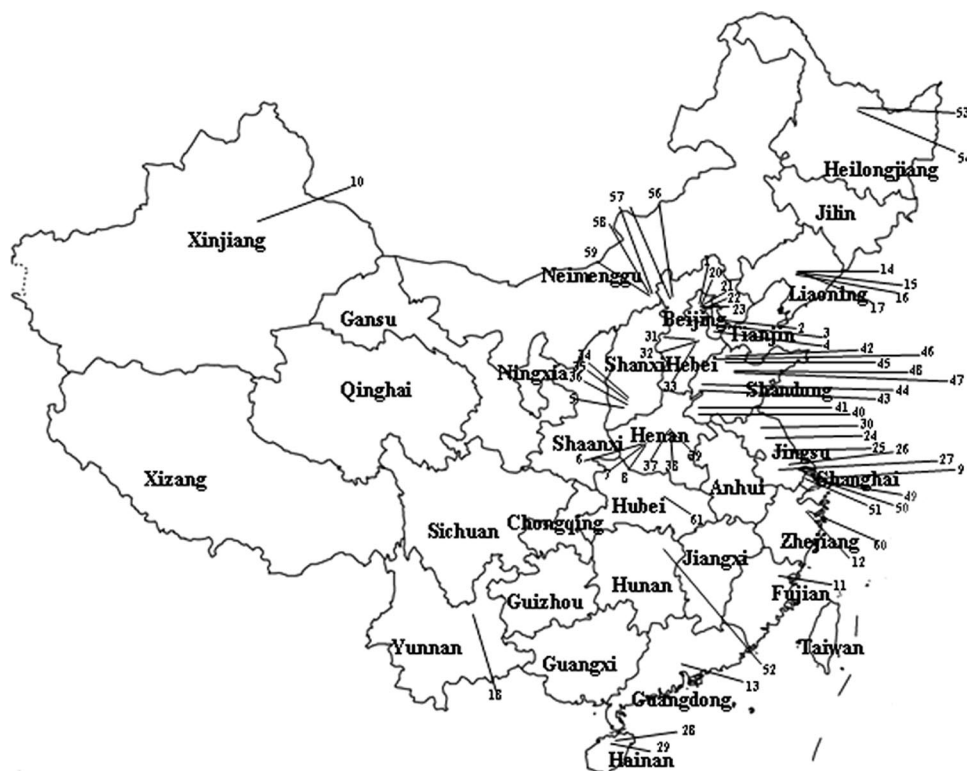


Fig. 1. Sampling locations for *B. tabaci* biotypes in China in 2009. Numbers on the map correspond to population numbers in Table 1.

in the whole country during the past several years is not known yet.

Management of *B. tabaci* requires the adjustment of control methods to match the target biotype(s) because biotypes differ in their susceptibility to different controls and because the proportion of different biotypes in a field is not constant. For example, biotype Q is more resistant than other biotypes to neonictinoid and growth regulator insecticides (Nauen et al. 2002, Rauch and Nauen 2003). These differences among *B. tabaci* populations highlight the importance of correct biotype identification for effective and sustainable pest control.

The composition of *B. tabaci* biotypes on field crops in China has not been determined since 2007. The objective of this study was to determine the current composition of *B. tabaci* biotypes and especially the two invasive biotypes, B and Q, in China.

Materials and Methods

Whitefly Collection. In 2009, populations of *B. tabaci* were sampled at 61 agricultural locations in China (Fig. 1). The 61 locations cover an area stretching from Hainan Province (19° 86' N, 110° 47' E) in the south to Heilongjiang Province (45° 83' N, 126° 53' E) in the north and from Xinjiang Province (43° 78' N, 87° 58' E) in the west to Shanghai City (31° 18' N, 126° 46'

E) in the East. Background information on these locations is provided in Table 1.

At each location, three subsamples of whiteflies were collected, with at least 500–1,000 m between subsamples by using the five-spot-sampling method. The whiteflies in the three subsamples were combined to obtain one sample per location. The whiteflies were preserved in 95% ethanol and stored at –20°C before DNA extraction. There were at least 100 *B. tabaci* individuals in each sample, and ≈24 specimens in each sample were analyzed.

Biotype Determination by Using Sequence-Characterized Amplified Region Markers. After total DNA was extracted from individual whiteflies by using the methods of Luo et al. (2002). The DNA samples were stored at –20°C until used for polymerase chain reaction (PCR) analysis. For determination of biotype, the DNA of 1,533 individuals of *B. tabaci* from China was subjected to PCR. The biotype of individuals was determined based on the specific mitochondrial cytochrome oxidase I (mtCOI) primers (forward primer, 5'-CTAGGGTTTATTGTTTGAGGTCATCATATATTC-3' and reverse primer, 5'-AATATCGACGAGGCATTC-CCCCT-3' for the B biotype and forward primer, 5'-CTTGGAACCTCTTCTGTAGATGTGTGTT-3' and reverse primer, 5'-CCTTCCCGCAGAAGAAATTTTGTTC-3' for the Q biotype) (Shatters et al. 2009). The PCR parameters were as follows: denaturation at 94°C for 2 min,

Table 1. *B. tabaci* sampling information and biotype composition based on PCR of sequence-characterized amplified region markers

Pop no.	Location	Host plant	Collection time (month in 2009)	No. individuals	% biotype	
					Q	B
1	Haidian, Beijing	Cucumber	July	48	0.0	100.0
2	Xiqing, Tianjin	Cotton	July	48	0.0	100.0
3	Xiqing, Tianjin	Cucumber	Sept.	24	0.0	100.0
4	Xiqing, Tianjin	Cabbage	Sept.	24	0.0	100.0
5	Yucheng, Shanxi	Tomato	Aug.	24	0.0	100.0
6	Luoyang, Henan	Cotton	Aug.	24	0.0	100.0
7	Luoyang, Henan	Cucumber	Aug.	24	0.0	100.0
8	Luoyang, Henan	Cabbage	Aug.	24	0.0	100.0
9	Shanghai	Cabbage	Aug.	24	0.0	100.0
10	Urumchi, Xinjiang	Cotton	Sept.	24	0.0	100.0
11	Fuzhou, Fujian	Sweet potato	Sept.	24	0.0	100.0
12	Hangzhou, Zhejiang	Tomato	Sept.	24	0.0	100.0
13	Guangzhou, Guangdong	Poinsettia	Sept.	24	0.0	100.0
14	Shenyang, Liaoning	Cucumber	Sept.	24	0.0	100.0
15	Shenyang, Liaoning	Tomato	Sept.	24	0.0	100.0
16	Shenyang, Liaoning	Beans	Sept.	24	0.0	100.0
17	Shenyang, Liaoning	Cabbage	Sept.	24	0.0	100.0
18	Kunming, Yunnan	Poinsettia	July	24	100.0	0.0
19	Haidian, Beijing	Capsicum	July	24	100.0	0.0
20	Haidian, Beijing	Pimiento	July	24	100.0	0.0
21	Changping, Beijing	Cucumber	July	22	100.0	0.0
22	Haidian, Beijing	Tomato	July	24	100.0	0.0
23	Haidian, Beijing	Eggplant	July	48	100.0	0.0
24	Yangzhou, Jiangsu	Capsicum	July	24	100.0	0.0
25	Yangzhou, Jiangsu	Eggplant	July	24	100.0	0.0
26	Yangzhou, Jiangsu	Gerbera	July	24	100.0	0.0
27	Wuxi, Jiangsu	Cucumber	July	24	100.0	0.0
28	Haikou, Hainan	Eggplant	July	24	100.0	0.0
29	Haikou, Hainan	Towel Gourd	July	23	100.0	0.0
30	Dongtai, Jiangsu	Eggplant	July	24	100.0	0.0
31	Langfang, Hebei	Capsicum	July	24	100.0	0.0
32	Langfang, Hebei	Eggplant	July	24	100.0	0.0
33	Langfang, Hebei	Cucumber	July	24	100.0	0.0
34	Yucheng, Shanxi	Cucumber	Aug.	24	100.0	0.0
35	Yucheng, Shanxi	Eggplant	Aug.	24	100.0	0.0
36	Yucheng, Shanxi	Cotton	Aug.	24	100.0	0.0
37	Zhengzhou, Henan	Cucumber	Aug.	24	100.0	0.0
38	Zhengzhou, Henan	Cotton	Aug.	24	100.0	0.0
39	Zhengzhou, Henan	Eggplant	Aug.	24	100.0	0.0
40	Heze, Shandong	Cotton	Aug.	24	100.0	0.0
41	Heze, Shandong	Eggplant	Aug.	24	100.0	0.0
42	Dezhou, Shandong	Eggplant	Aug.	24	100.0	0.0
43	Liaocheng, Shandong	Eggplant	Aug.	24	100.0	0.0
44	Liaocheng, Shandong	Japanese hop	Aug.	24	100.0	0.0
45	Dezhou, Shandong	Cotton	Aug.	24	100.0	0.0
46	Dezhou, Shandong	Japanese hop	Aug.	24	100.0	0.0
47	Jinan, Shandong	Japanese hop	Aug.	24	100.0	0.0
48	Jinan, Shandong	Cotton	Aug.	24	100.0	0.0
49	Shanghai	Tomato	Aug.	24	100.0	0.0
50	Shanghai	Eggplant	Aug.	24	100.0	0.0
51	Shanghai	Cucumber	Aug.	24	100.0	0.0
52	Changsha, Hunan	Cotton	Aug.	24	100.0	0.0
53	Haerbin, Heilongjiang	Cucumber	Aug.	24	100.0	0.0
54	Haerbin, Heilongjiang	Tomato	Aug.	24	100.0	0.0
55	Zhangjiakou, Hebei	Cucumber	Sept.	24	100.0	0.0
56	Zhangjiakou, Hebei	Eggplant	Sept.	24	100.0	0.0
57	Huhehaote, Neimeng	Cucumber	Sept.	24	100.0	0.0
58	Huhehaote, Neimeng	Squash	Sept.	24	100.0	0.0
59	Huhehaote, Neimeng	Beans	Sept.	24	100.0	0.0
60	Hangzhou, Zhejiang	Eggplant	Sept.	24	100.0	0.0
61	Wuhan, Hubei	Cotton	Sept.	24	100.0	0.0

followed by 35 cycles (94°C for 30 s, 64°C for 1 min, 72°C for 1 min), and a final extension at 72°C for 10 min. The two primers were used to determine biotype status in conjunction with analysis of mtCOI DNA sequence.

mtCOI Sequencing and Phylogenetic Analysis. To confirm that the results obtained using PCR of sequence-characterized amplified region markers

correctly identified the *B. tabaci* biotypes, an ≈620-bp DNA fragment of the mtCOI was amplified, sequenced, and analyzed for two individuals in each sample from China. The fragment was amplified using the previously published PCR primers C1-J-2195 and TL2-N-2819 of Zhang et al. (2005). The PCR parameters were as follows: denaturation

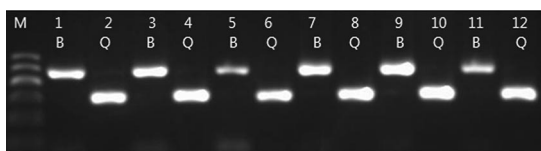


Fig. 2. Amplification of *B. tabaci* mtCOI with biotype-specific primers to distinguish the B and Q biotypes. M, marker; Templates in the PCR reactions were as follows: 1) Haidian, Beijing; 2) Kunming, Yunnan; 3) Xiqing, Tianjin; 4) Haidian, Beijing; 5) Yuncheng, Shanxi; 6) Yangzhou, Jiangsu; 7) Luoyang, Henan; 8) Haikou, Hainan; 9) Urumchi, Xinjiang; 10) Zhengzhou, Henan; 11) Hangzhou, Zhejiang; and 12) Liaocheng, Shandong.

at 94°C for 5 min, followed by 34 cycles (94°C for 1 min, 50°C for 1 min, 72°C for 1 min), and a final extension at 72°C for 5 min.

All sequences were aligned, and the biotypes were determined according to the methods of Dinsdale et al. (2010). The neighbor-joining algorithms available in MEGA 4 (Kumar et al. 2008) were used to infer phylogenetic relationships. The consensus sequences of 24 species (Dinsdale et al. 2010) were used. One thousand bootstrap replications were performed for each analysis.

Results

Biotype Determination of *B. tabaci*. Specific PCR amplification was performed using the sequence-characterized amplified region primers with DNA isolated from individual whiteflies. Examples of the amplification profiles are shown in Fig. 2. The amplification profiles using DNA from 1,533 individuals showed that, for each individual, the two sequence-characterized amplified region primers set supported the amplification of a single DNA product of the expected size (478 bp for the B biotype and 303 bp for the Q biotype). Biotypes B and Q were the only biotypes found in this survey.

Phylogenetic analysis based on mtCOI sequences (Fig. 3) from specimens from China indicated that the whiteflies belonged to the Mediterranean group (biotype Q) or Middle East-Asia Minor 1 group (biotype B). These results were consistent with the results obtained with the sequence-characterized amplified region method and therefore indicated that the B- and Q-sequence-characterized amplified region markers in Shatters et al. (2009) could be used to determine the biotypes B and Q in China.

Distribution of Biotypes B and Q in China. PCR indicated that biotype Q was dominant in 44 locations (across 14 provinces), whereas biotype B was dominant in 17 locations (across nine provinces) in China (Table 1; Fig. 4). None of the 61 locations in China contained mixed biotypes, i.e., the samples were 100.0% Q or B biotype. In addition, both B and Q biotypes were collected in Beijing, Shanxi, Zhejiang, Shanghai, and Henan provinces of the 19 provinces that were sampled.

Discussion

Changes in Relative Frequency of *B. tabaci* Biotypes B and Q in China. Our results represent the largest number of field-sampled *B. tabaci* screened to date for the distribution of *B. tabaci* biotypes B and Q in China. Based on this study and earlier studies, the invasion of China by biotype Q can be divided into three phases. In the first phase (during or before 2003), biotype Q was introduced to the country. During this period of initial introduction, biotype Q occurred only sporadically in or around the flower markets of Yunnan Province, Henan Province, and Beijing, whereas biotype B was distributed in most parts of China (Chu et al. 2006).

In the second phase (2004–2006), biotype Q established and spread but still represented only a low proportion of the *B. tabaci* in field populations. Between 2004 and 2006, however, the Q biotype spread quickly in China. In Zhejiang Province in 2005, biotype Q caused substantial crop damage and began displacing biotype B in many locations (Xu et al. 2006). In addition, the Q biotype represented only a small proportion of field populations in Shandong and Hubei provinces in 2005. In 2006, however, biotype Q increased dramatically on many crops in many cities in Shandong and Hubei provinces (Chu et al. 2010a,b; Rao et al. 2010).

In the third phase (from 2007 to present), biotype Q became the dominant *B. tabaci* biotype in China. In 2007, biotype Q was found in 19 collections from 13 provinces in China, including Shandong, Gansu, Shaanxi, Guangxi, Zhejiang, Guizhou, Tianjin, Shanxi, Hunan, Henan, Hubei, Jiangsu, and Hainan provinces. Among the 19 collections, 10 were dominated (>50.0%) by biotype Q (Teng et al. 2010). Other studies based on data for 2007 also reported that biotype Q had displaced biotype B and become the dominant biotype in the field in Shandong and Hubei provinces (Chu et al. 2010a,b; Rao et al. 2010).

The current study, based on specimens collected in 2009, revealed that biotype Q has continued to spread and displace the other *B. tabaci* biotypes (including the invasive biotype B that was previously dominant) throughout China. Of the 61 populations in China examined in this study, biotype Q represented 100.0% of 44 populations from 14 provinces. In 2007, biotype Q represented from 6.4 to 95.2% of 19 populations (Teng et al. 2010). However, no any indigenous biotype were found in these collections, even if the two specimens in Zhejiang. From previous literatures, indigenous biotypes were found in 2007 (Teng et al. 2010) and have not been reported in the main cropping systems since then. It seems likely that the indigenous biotypes have been displaced by the B and Q biotypes within the latest two years. Extensive field surveys in Zhejiang Province also have revealed such rapid displacement of the indigenous ZHJ1, ZHJ2 biotype whiteflies by the invasive B and Q biotypes (Liu et al. 2007, Xu, 2009). Until recently, Hu et al. (2011) convinced that again, by 2009, the indigenous species mostly disappeared from extensive agricultural areas

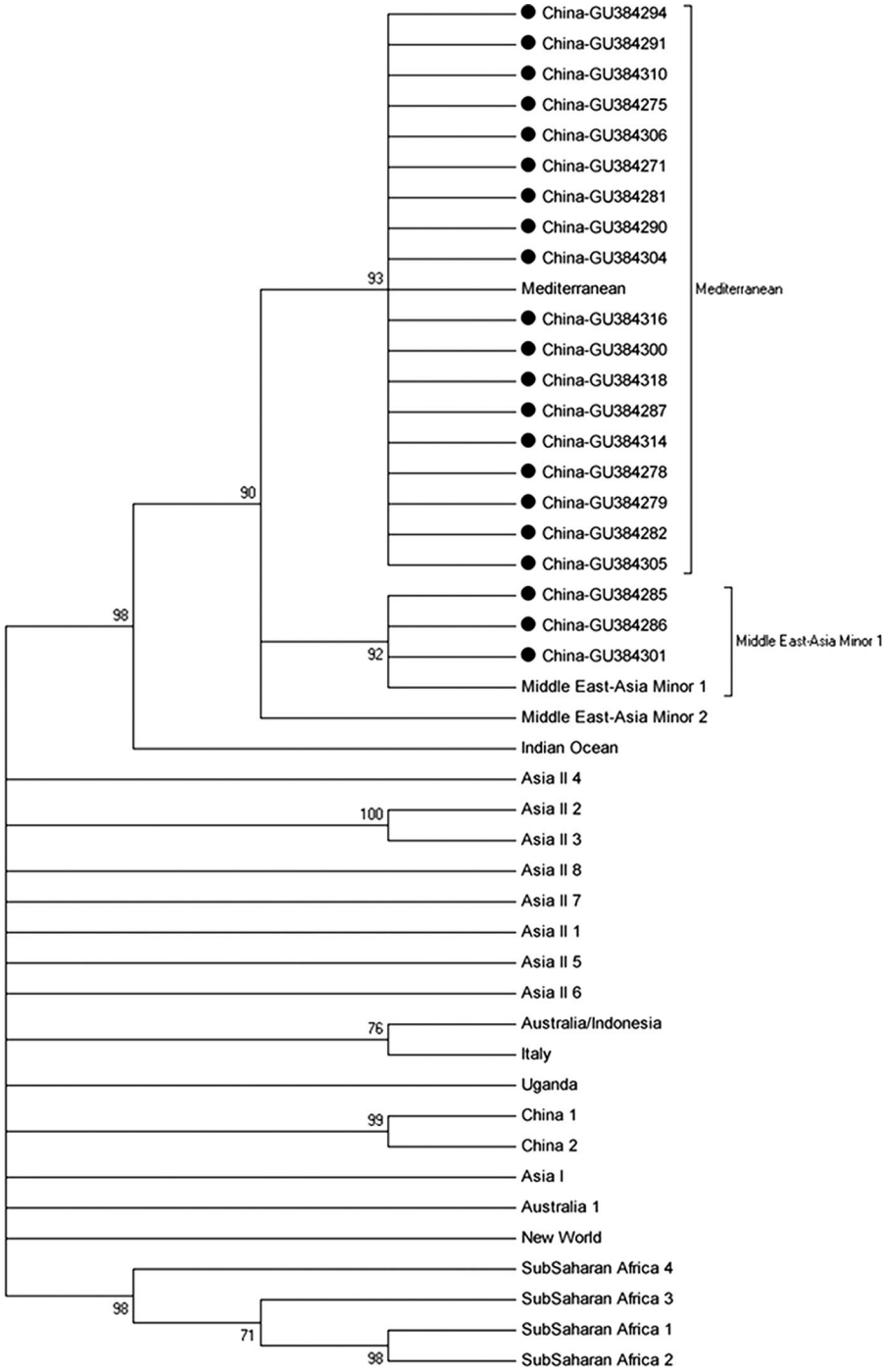


Fig. 3. Phylogenetic tree based on the mtCO1 sequences. ● indicates the mtCO1 haplotypes of *B. tabaci* from China in 2009.

in China; meanwhile, they showed that the indigenous species were mainly existed in remote mountainous areas. The whiteflies in this study were mainly collected in the main cropping field, which is one of the possible reasons why there were only B and Q biotypes, not any indigenous species identified.

In this study, many *B. tabaci* populations from Xinjiang, Shanxi, Tianjin, Fujian, and Guangdong provinces were still composed of biotype B. Additional studies are required to determine whether biotype Q will continue to spread and displace biotype B in those regions of China.

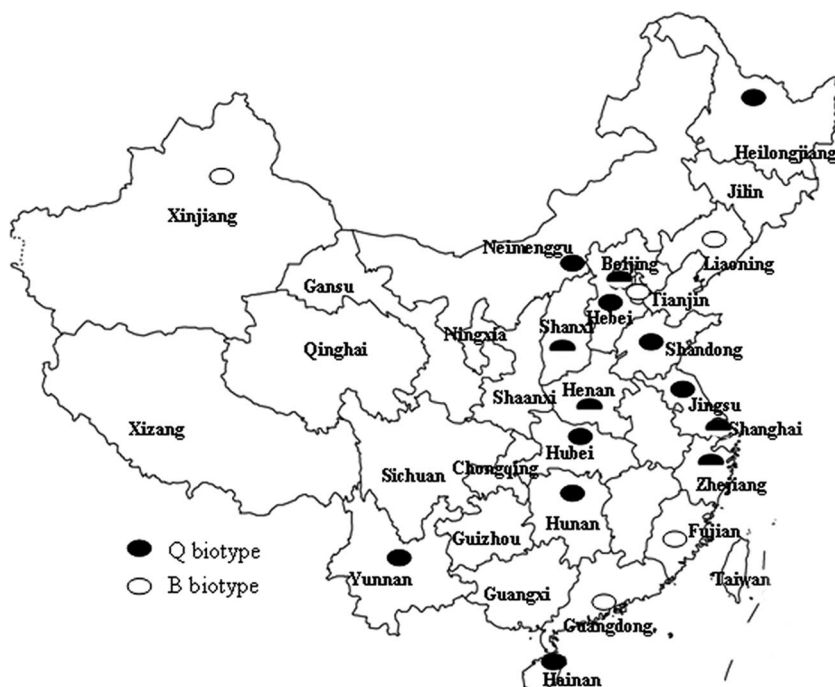


Fig. 4. Distribution of *B. tabaci* biotypes B and Q in China in 2009. For each black and/or white oval it represents different sampling locations from each province. The black oval for *B. tabaci* populations in Heilongjiang represents two sampling locations, in Neimenggu two sampling locations, in Hebei five sampling locations, in Shandong nine sampling locations, in Jiangsu five sampling locations, in Hubei one sampling location, in Hunan one sampling location, in Yunnan one sampling location, and in Hainan two sampling locations; the white oval for *B. tabaci* populations in Liaoning represents four sampling locations, in Xinjiang one sampling location, in Tianjin three sampling locations, in Fujian one sampling location, in Guangdong one sampling location; and the mixed black and white oval for *B. tabaci* populations in Beijing represents six sampling locations, in Shanxi four sampling locations, in Henan six sampling locations, in Shanghai four sampling locations, and in Zhejiang two sampling locations.

Potential Mechanisms for Displacement of Biotype B by Q. Little is known about why biotype Q is able to displace established populations of biotype B during the past several years in China. Previous studies showed that the species exclusion or coexistence between *B. tabaci* species include life-history traits (Byrne and Miller 1990, Muniz 2000, Nombela et al. 2001, Pascual and Callejas 2004, Pascual 2006, Zang et al. 2006, Crowder et al. 2010a), asymmetric mating interactions (Liu et al. 2007, Crowder et al. 2010b), an indirect vector-virus mutualism (Jiu et al. 2007), ovipositional host choice (De Barro and Bourne 2010), and age-based differential host acceptability and human-mediated disturbance (De Barro et al. 2010).

The displacement of B by Q in China might involve many factors. One possible explanation for the displacement of B by Q in China is the differential sensitivity to pesticides (Luo et al. 2010, Wang et al. 2010). How species respond to pesticide pressure can strongly influence population demographics and patterns of species exclusion or coexistence (Reitz and Trumble 2002). The manufacture of imidacloprid in China began in 1992, and then other neonicotinoids insecticides, including acetamiprid, thiamethoxam, and nitenpyram, have become standard treatments for many sucking pests, including whiteflies, on a variety

of crops (<http://www.chinapesticide.gov.cn>). In recent comparisons of B and Q biotypes from China (Luo et al. 2010), the B strains remained largely susceptible to acetamiprid, imidacloprid, and thiamethoxam, whereas the Q biotype strains expressed 20- to 170-fold resistance to these insecticide. Wang et al. (2010) discovered that the Q biotype collected from the city of Yancheng in Jiangsu Province, China displayed extremely high resistance to imidacloprid (1900-fold) and thiamethoxam (1200-fold) than the B biotype. The Q population from Yunnan Province, China, had high levels of resistance to imidacloprid and thiamethoxam (450- and 300-fold) over the B biotype. The hypothesis also was supported by the previous studies in the other countries (Guirao et al. 1997, Nauen et al. 2002, Rauch and Nauen 2003, Horowitz et al. 2005). In southern Spain, biotype Q almost completely displaced biotype B within a few years (Guirao et al. 1997) and exhibited high resistance and cross-resistance to neonicotinoids (Nauen et al. 2002, Rauch and Nauen 2003) at a time when the use of neonicotinoids for control of *Bemisia* had increased. In Israel, application of neonicotinoids to a mixed population containing both biotypes B and Q resulted in dominance by biotype Q (Horowitz et al. 2005). It is therefore reasonable to hypothesize that

the use of neonicotinoid insecticides may explain, at least in part, the displacement of biotype B by biotype Q in China.

Another possible explanation for the displacement of B by Q in China is their differential host plant adaptability (Iida et al. 2009). In one recent study, the effects of host plants on the hatching rate, survival rate, and development time in B and Q biotypes were investigated in Japan, clear and interesting differences between the two biotypes were recognized (Iida et al. 2009). A particularly important difference was that the B biotype successfully developed to adults on only one of the five cultivars of kidney bean (*Phaseolus vulgaris* L.), whereas the Q biotype was able to use all the test plants as hosts regardless of the cultivar (Iida et al. 2009).

In conclusion, our research revealed that only biotypes B and Q have been found in the crop fields in 2009 in China. The current survey indicates that biotype Q has rapidly displaced biotype B in most agricultural systems in China. The potential mechanisms for displacement of biotype B by Q in China might be the differential sensitivity to pesticides or the differential adaptability to host plants and should be further studied in the future researches.

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