

BEMISIA TABACI BIOTYPE Q DOMINATES OTHER BIOTYPES ACROSS CHINAXI TENG¹, FANG-HAO WAN¹ AND DONG CHU^{2,*}¹State Key Laboratory for Biology of Plant Diseases and Insect Pests, Institute of Plant Protection, Chinese Academy of Agricultural Science, Beijing 100094, China

E-mail for Xi Teng: tengxi123@163.com; Corresponding author; E-mail for Fang-Hao Wan: wanfh@mail.caas.net.cn

²High-tech Research Center, Shandong Academy of Agricultural Sciences, Jinan 250100, China
E-mail: chinachudong@sina.com

*Contributed equally as first author

ABSTRACT

Bemisia tabaci (Gennadius) biotype Q was first reported as an invasive species in 2005 in China. The present study is the first with this serious pest to determine the distribution and proportion with *B. tabaci* Q-SCAR (sequence characterized amplified region) marker, and to identify the distribution of the biotype Q through extensive survey and systematic sampling in most regions of China. We made 22 collections from 15 provinces in Sep-Oct, 2007. The results showed that *B. tabaci* biotype Q was found in 19 collections from Shangdong, Gansu, Shaanxi, Guangxi, Zhejiang, Guizhou, Tianjin, Shanxi, Hunan, Henan, Hubei, Jiangsu, and Hainan provinces. The proportion (%) of *B. tabaci* biotype Q occurrence varied from 6.4% to 95.2% in these 19 collections, and it dominated (>50%) in 10 collections. The genetic divergence analysis based on mitochondrial *cytochrome oxidase I* (mtCOI) gene revealed that Q-SCAR marker was specific to biotype Q, and the non-Q biotypes mainly consisted of biotype B. The present results revealed that the biotype Q has become dominant across the country, and suggested that the displacement of non-Q biotypes by biotype Q has occurred in many regions. Furthermore, the introduction of the biotype Q might have mainly occurred through human activities rather than natural sources.

Key Words: biological invasion, *Bemisia tabaci* biotype Q, displacement, mitochondrial *cytochrome oxidase I*, systematic survey, China

RESUMEN

El biotipo Q de *Bemisia tabaci* (Gennadius) fue reportado por primera vez como una especie invasora en 2005 en China. El presente estudio es el primero de esta seria plaga para determinar su distribución y proporción con el marcador, *B. tabaci* Q-SCAR (region amplificada caracterizada por la secuencia [RACS]), y para identificar la distribución del biotipo Q con una evaluación extensiva y muestreo sistemático de la mayoría de las regiones de China. Hicimos 22 colecciones en 15 provincias en septiembre y octubre del 2007. Los resultados mostraron que el biotipo Q de *B. tabaci* fue encontrado en 19 de las colecciones de las provincias: Shangdong, Gansu, Shaanxi, Guangxi, Zhejiang, Guizhou, Tianjin, Shanxi, Hunan, Henan, Hubei, Jiangsu, y Hainan. La proporción (%) de la ocurrencia del biotipo B de *B. tabaci* varia de 6.4% a 95.2% en estas 19 colecciones, y fue el biotipo dominante (>50%) en 10 colecciones. El análisis de divergencia genética basado en la subunidad I del gen citocromo oxidase del ADN mitocondrial (mtCOI) reveló que el marcador Q-RACS fue específico para el biotipo Q, y los biotipos no Q consistieron principalmente de biotipo B. Los resultados revelaron que el biotipo Q ahora es el biotipo dominante en todo el país, y sugiere que el desplazamiento de los biotipos no-Q por el biotipo Q ha sucedido en varias regiones. Además, la introducción de biotipo Q ha sucedido por actividades humanas y no por fuentes naturales.

The sweet potato whitefly, *Bemisia tabaci* (Gennadius), is a serious pest of agricultural crops worldwide (Jones 2003). This species complex includes many biotypes such as A, B, Q and Ms (Perring 2001), which can be morphologically indistinguishable (Liu et al. 2007). Biotype B is one of the most invasive biotypes that has caused serious economic losses. Biotype Q, another invasive biotype, has caused even greater damage, and is more adaptable than biotype B on some

host plant species (Muniz et al. 2000; Nombela et al. 2001). Biotype Q may have originated in the Mediterranean/North Africa based on phylogenetic analysis (Boykin et al. 2007). It was first recorded in the Iberian Peninsula (Guirao et al. 1997; Moya et al. 2001) and is now reported from many non-Mediterranean countries (Chu et al. 2006; Ueda & Brown 2006; Brown 2007).

In China, *B. tabaci* has become a serious economic pest of many agricultural crops, and has

All of the 145 sequences of partial *mtCOI* gene from the 22 collections were used to perform genetic divergence analysis. All sequences were aligned with Clustal W (Thompson et al. 1994) and the ends trimmed. All sequences were checked for the gaps, idels, numts, and pseudogenes. The sequences which have no the gaps, idels, or numts were compared against the consensus sequences for Mediterranean clade according to the methods of Dinsdale et al. (2010). The Q sequences were to have Mediterranean as their best match. Each unknown sequence was associated to the consensus sequence with which it had the lowest divergence match difference. In addition, we used the Bayesian Inference (BI) in PAUP* 4.0b10 (Swofford 2000) to analyze the phylogenetic relationship of the sequences.

RESULTS

Geographic Distribution of *B. tabaci* Biotype Q

Biotype Q was found in 19 collections by the SCAR marker from Jingzhou, Xiangfan, and Wuhan (Hubei Province), Laiyang and Taian (Shandong Province), Sanya (Hainan Province), Guilin and Nanning (Guangxi Autonomous Region), Guiyang (Guizhou Province), Hangzhou and Ningbo (Zhejiang Province), Xiangtan and Yueyang (Hunan Province), Yangzhou (Jiangsu Province), Xinxiang (Henan Province), Baoji (Shaanxi Province), Jiuquan (Gansu Province), Yuncheng (Shanxi Province) and Tianjin (Table 1 and Fig. 1). Biotype Q was not found in 3 collections from Langfang and Chengde (Hebei Province) and Tulufan (Xinjiang Province).

Genetic Divergence Analysis Based on MtCOI and Biotype Determination

A fragment of partial mtCOI gene (about 680 bases) from 145 *B. tabaci* individuals was sequenced and the representative sequences of the collections were deposited in the Gene Bank (accession numbers: FJ375346-FJ375358, FJ594428-FJ594434, and FJ647195-FJ647217). In the present study, gaps, idels, and numts were not found in these sequences, and all sequences

should not be pseudogenes. Forty-nine sequences were identified as biotype Q because the genetic divergence between these sequences and the consensus sequences within the Mediterranean clade (Dinsdale et al. 2010) was close to zero. Ninety-two sequences (non-Q biotype based on SCAR) were determined as biotype B because the genetic divergence between these sequences and the consensus sequences within the Middle East-Asia Minor 1 clade (Dinsdale et al. 2010) was close to zero. Four sequences (non-Q biotype based on SCAR) were non-B/Q biotype, which might be indigenous haplotypes in China (tree not shown). These results were consistent with the ones based on the SCAR marker.

Proportion of Biotype Q in the *B. tabaci* Biotypes

Biotype Q was found in 19 collections made from across the country ranging from 6.4% (Taian, Shandong Province) to 95.2% (Xiangfan, Hubei Province) occurrence (Table 1 and Fig. 1). Biotype Q dominated (>50%) the other biotypes in 10 collections from Yuncheng (Shanxi Province), Yueyang and Xiangtan (Hunan Province), Hangzhou (Zhejiang Province), Xinxiang (Henan Province), Jingzhou, Xiangfan, and Wuhan (Hubei Province), and Yangzhou (Jiangsu Province), Sanya (Hainan Province), while it ranged from 30%-50% in the other 4 collections, i.e., Ningbo

TABLE 1. PERCENTAGE OF BIOTYPE Q AMONG THE DIFFERENT *B. TABACI* COLLECTIONS IN 2007.

Code	Location	Number of individuals	Number of biotype Q	Percentage biotype Q
1	Tulufan, Xinjiang	56	0	0.0
2	Langfang, Hebei	53	0	0.0
3	Chengde, Hebei	63	0	0.0
4	Jiuquan, Gansu	80	6	7.5
5	Baoji, Shaanxi	78	7	9.0
6	Taian, Shandong	78	5	6.4
7	Guilin, Guangxi	85	21	24.7
8	Nanning, Guangxi	83	10	12.0
9	Tianjin	59	27	45.8
10	Laiyang, Shandong	55	20	36.4
11	Ningbo, Zhejiang	76	24	31.6
12	Guiyang, Guizhou	30	13	43.3
13	Yuncheng, Shanxi	80	49	61.3
14	Xinxiang, Henan	61	56	91.8
15	Xiangfan, Hubei	84	80	95.2
16	Yangzhou, Jiangsu	47	43	91.5
17	Hangzhou, Zhejiang	58	49	84.5
18	Wuhan, Hubei	49	45	91.8
19	Jingzhou, Hubei	67	61	91.0
20	Yueyang, Hunan	49	40	81.6
21	Xiangtan, Hunan	66	61	92.4
22	Sanya, Hainan	79	75	94.9
Total		1439	692	48.2 (mean)

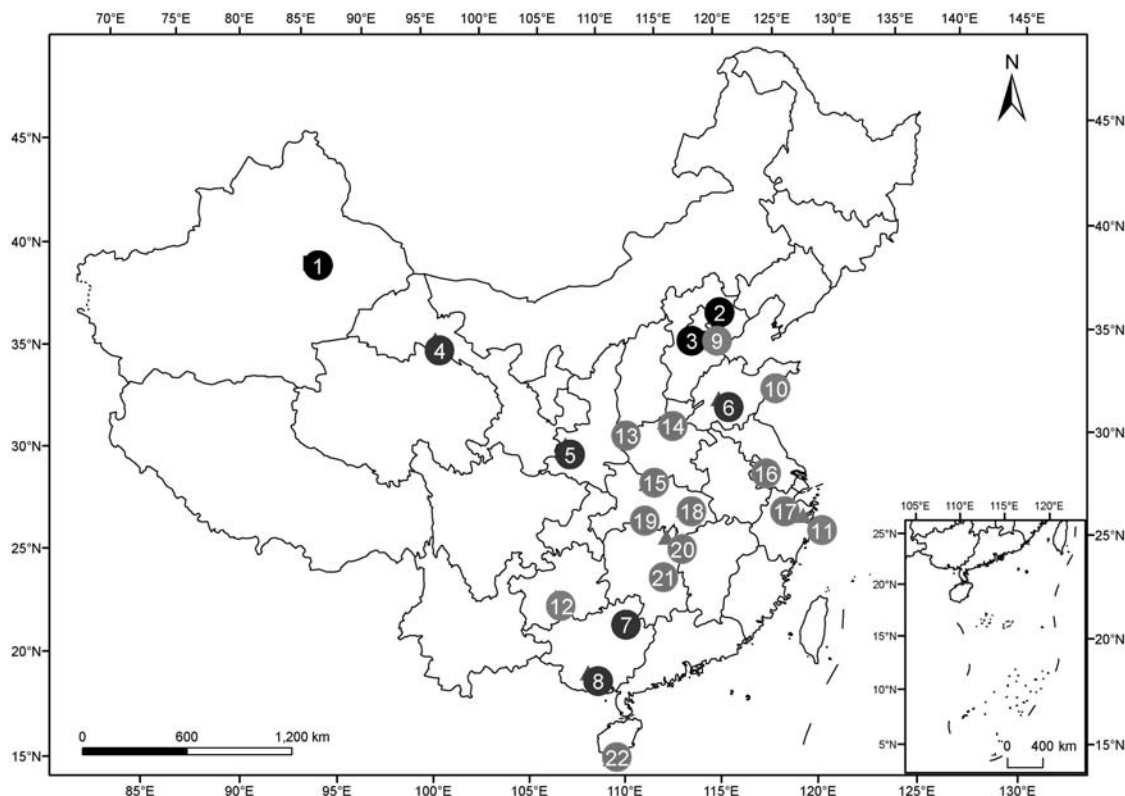


Fig. 1. Distribution and proportion of *B. tabaci* biotype Q in China in 2007. The codes for each sample are as in Table 1. Circles 1, 2, and 3 indicate no biotype Q; Circles 4-8 indicate less than 30% biotype Q; Circles 9-12 indicate between 30% and 50% of biotype Q; and Circles 13-22 indicate more than 50% biotype Q.

(Zhejiang Province), Laiyang (Shandong Province), Guiyang (Guizhou Province), and Tianjin. The proportion of biotype Q was below 30% in only 5 collections, i.e., Taian (Shandong Province), Jiuquan (Gansu Province), Baoji (Shaanxi Province), and Nanning and Guilin (Guangxi Autonomous Region).

DISCUSSION

Biotype Q has greater survival ability than biotype B under low as well as high temperature conditions (Bonato et al. 2007), and has shown greater resistance to neonicotinoides and pyriproxyfen insecticides than biotype B (Horowitz et al. 2005), perhaps contributing to the displacement of biotype B by Q (Pascual 2006). Biotype Q has successfully invaded and dominated (>50%) the other *B. tabaci* biotypes in most of the south-eastern provinces of China, and is distributed in several under-developed western provinces. Biotype Q was not found in Langfang and Chengde (Hebei Province), but detected in the collections from Beijing and Tianjin. Our samples may not be large enough to thoroughly cover these regions.

Our data suggest that more than 1 factor is responsible for the current distribution and high proportion of the biotype Q in China. Furthermore, transportation and human activities in the developed south-eastern provinces of the country are more than in the under-developed western provinces, and these factors might have affected the introduction, spread, and abundance of the biotype Q in these provinces.

Our study provided evidence that the 2 biotypes B and Q prevailed in the same collections. Based on mtCOI sequencing, biotype Q was detected in 19 collections in which biotype B was also found. The co-existence of biotypes B and Q has also been detected in other countries, e.g., Spain (Guirao et al. 1997), Japan (Ueda & Brown 2006) and Southern France (Dalmon et al. 2008). In USA, biotype B has displaced the previously established biotype A (Brown et al. 1995). In Spain, biotype B could not displace the established biotype Q, which might be due to the greater insecticide resistance of the latter biotype (Pascual 2006). During 2005-2008, the displacement of biotype B by Q in several regions of the Shandong Province was observed (Chu et al.

2010). For example, in 2005, biotype Q comprised zero of the *B. tabaci* population on cotton in Jinan of Shandong Province. In 2006, biotype Q comprised 15.2% of the *B. tabaci* population on cotton. In 2007, biotype Q comprised 60.9% of the *B. tabaci* population on cotton and finally, in 2008, biotype Q comprised 96.7% of the *B. tabaci* population on cotton. Similar results have been observed in other regions (Chu et al. 2010). Based on the results of the present study, it was assumed that partial displacement of biotype B by biotype Q has occurred in many regions of the country. There is a high probability that biotype Q, due to its greater tolerance to extreme temperature and resistance to insecticides, will continue to spread, displace, and dominate biotype B and other indigenous biotypes in other regions of the country. In the displacement of biotype B by Q, the application of insecticides in the main agricultural cropping systems of the country might play an important role. The present results might help understand the displacement mechanism of the *B. tabaci* biotypes and provide a theoretical basis for prophylaxis and control of this invasive pest in China.

ACKNOWLEDGMENTS

We thank Dr. Dan L. Johnson (Professor of Environmental Science, Canada Research Chair in Sustainable Grassland Ecosystems) and Dr. Imtiaz Ali Khan (Department of Entomology, NWFP Agricultural University Peshawar, NWFP, Pakistan) for reviewing and editing the original manuscript. We thank Dr. De Barro P.J. (CSIRO Entomology 120 Meiers Road Indooroopilly, Qld 4068, Australia) for providing the consensus sequences in the genetic divergence analysis. This work was funded by the Key Project of Chinese National Programs for Fundamental Research and Development (2009CB119200), Key Program of National Natural Science Foundation of China (30930062) and Outstanding Youth Science Foundation of Shandong Province (JQ200811).

REFERENCES CITED

- BONATO, O., LURETTE, A., VIDAL, C., AND FARGUES, J. 2007. Modelling temperature-dependent bionomics of *Bemisia tabaci* (Q biotype). *Physiol. Entomol.* 32: 50-55.
- BOYKIN, L. M., SHATTERS, R. G., ROSELL, R. C., MCKENZIE, C. L., BAGNALL, R. A., DE BARRO, P. J., AND FROHLICH, D. R. 2007. Global relationships of *Bemisia tabaci* (Hemiptera: Aleyrodidae) revealed using Bayesian analysis of mitochondrial COI DNA sequences. *Mol. Phyl. Evol.* 144: 1306-1319.
- BROWN, J. K. 2007. The *Bemisia tabaci* complex: genetic and phenotypic variability drives begomovirus spread and virus diversification. <http://www.aps-net.org/online/feature/btabaci/>.
- BROWN, J. K., FROHLICH, D. R., AND ROSELL, R. C. 1995. The sweet potato or silver leaf whiteflies: biotypes of *Bemisia tabaci* or a species complex? *Annu. Rev. Entomol.* 40: 511-534.
- CHU, D., JIANG, T., LIU, G. X., JIANG, D. F., TAO, Y. L., FAN, Z. X., ZHOU, H. X., AND BI, Y. P. 2007. Biotype status and distribution of *Bemisia tabaci* (Hemiptera: Aleyrodidae) in Shandong Province of China based on mitochondrial DNA markers. *Environ. Entomol.* 36: 1290-1295.
- CHU, D., WAN, F. H., ZHANG, Y. J., AND BROWN, J. K. 2010. Change in the biotype composition of *Bemisia tabaci* in Shandong Province of China from 2005 to 2008. *Environ. Entomol.* 39(3). DOI: 10.1603/EN09161.
- CHU, D., ZHANG, Y. J., BROWN, J. K., CONG, B., XU, B. Y., WU, Q. J., AND ZHU, G. R. 2006. The introduction of the exotic Q biotype of *Bemisia tabaci* (Gennadius) from the Mediterranean region into China on ornamental crops. *Florida Entomol.* 89: 168-174.
- CHU, D., ZHANG, Y. J., CONG, B., XU, B. Y., AND WU, Q. J. 2005. Identification for Yunan Q-biotype *Bemisia tabaci* population. *Entomological Knowledge* 42: 59-62. (in Chinese)
- DALMON, A., HALKETT, F., GRANIER, M., DELATTE, H., AND PETERSCHMITT, M. 2008. Genetic structure of the invasive pest *Bemisia tabaci*: evidence of limited but persistent genetic differentiation in glasshouse populations. *Heredity* 100: 316-325.
- DINSDALE, A., COOK, L., RIGINOS, C., BUCKLEY, Y., AND DE BARRO, P. J. 2010. Refined global analysis of *Bemisia tabaci* (Hemiptera: Sternorrhyncha: Aleyrodoidea: Aleyrodidae) mitochondrial cytochrome oxidase 1 to identify species level genetic boundaries. *Ann. Entomol. Soc. America* 103(2). DOI: 10.1603/AN09061
- HOROWITZ, A. R., KONTSEDALOV, S., KHASDAN, V., AND ISHAAYA, I. 2005. Biotypes B and Q of *Bemisia tabaci* and their relevance to neonicotinoid and pyriproxyfen resistance. *Arch. Insect Biochem. Physiol.* 58: 216-225.
- JONES, D. 2003. Plant viruses transmitted by whiteflies. *European J. Plant Pathol.* 109: 195-219.
- LIU, S. S., DE BARRO, P. J., XU, J., LUAN, J. B., ZANG, L. S., RUAN, Y. M., AND WAN, F. H. 2007. Asymmetric mating interactions drive widespread invasion and displacement in a whitefly. *Science* 259: 74-77.
- MA, D. Y., GORMAN, K., DEVINE, G., LUO, W. C., AND DENHOLM, I. 2007. The biotype and insecticide-resistance status of whiteflies, *Bemisia tabaci* (Hemiptera: Aleyrodidae), invading cropping systems in Xinjiang Uygur Autonomous Region, northwestern China. *Crop Protection* 26: 612-617.
- MOYA, A., GUIRAO, P., CIFUENTES, D., BEITIA, F., AND CENIS, J. L. 2001. Genetic diversity of Iberian populations of *Bemisia tabaci* (Hemiptera: Aleyrodidae) based on random amplified polymorphic DNA-polymerase chain reaction. *Mol. Ecol.* 10: 891-897.
- MUNIZ, M. 2000. Host suitability of two biotypes of *Bemisia tabaci* on some common weeds. *Ent. Exp. et Appl.* 95: 63-70.
- NOMBELA, G., BEITIA, F., AND MUNIZ, M. 2001. A differential interaction study of *Bemisia tabaci* Q-biotype on commercial tomato varieties with or without the Mi resistance gene, and comparative host responses with the B-biotype. *Ent. Exp. et Appl.* 3: 339-344.
- PASCUAL, S. 2006. Mechanisms in competition, under laboratory conditions, between Spanish biotypes B and Q of *Bemisia tabaci* (Gennadius). *Spanish J. Agr. Res.* 4: 351-354.
- PERRING, T. M. 2001. The *Bemisia tabaci* species complex. *Crop Prot.* 20: 725-737.

- QIU, B. L., COATS, S. A., REN, S. X., IDRIS, A. M., XU, C. X., AND BROWN, J. K. 2007. Phylogenetic relationships of native and introduced *Bemisia tabaci* (Homoptera: Aleyrodidae) from China and India based on mtCOI DNA sequencing and host plant comparisons. *Prog. Nat. Sci.* 17(6): 645-654.
- SIMON, C., FRATI, F., BECKENBACH, A., CRESPI, B., LIU, H., AND FLOOK, P. 1994. Evolution, weighting, and phylogenetic utility of mitochondrial gene sequences and a compilation of conserved polymerase chain reaction primers. *Ann. Entomol. Soc. America* 6: 651-701.
- SWOFFORD, D. L. 2000. PAUP*: Phylogenetic analysis using parsimony (*and other methods), Ver. 4. Sinauer, Sunderland, MA.
- THOMPSON, J. D., HIGGINS, D. G., AND GIBSON, T. J. 1994. CLUSTAL W: Improving the sensitivity of progressive multiple sequence alignment through sequence weighting, position specific gap penalties and weight matrix choice. *Nucl. Acid Res.* 22: 4673-4680.
- UEDA, S., AND BROWN, J. K. 2006. First report of the Q biotype of *Bemisia tabaci* in Japan by mitochondrial oxidase I sequence analysis. *Phytoparasitica* 34: 405-411.
- WAN, F. H., ZHENG, X. B., AND GUO, J. Y. 2005. *Biology and Management of Invasive Alien Species in Agriculture and Forestry*. Science Press, Beijing, China. 71 pp.

Reproduced with permission of the copyright owner. Further reproduction prohibited without permission.