CAP Analysis of the Distribution of the Introduced *Bemisia tabaci* (Hemiptera: Aleyrodidae) Species Complex in Xinjiang, China and the Southerly Expansion of the Mediterranean Species

Zunzun Jia,1,* Kaiyun Fu,2,* Wenchao Guo,3,5 Weihua Jiang,4 Tursun Ahmat,2 Xinhua Ding,2 Jiang He,2 and Xiaowu Wang3

1College of Agriculture, Xinjiang Agricultural University, Xinjiang, China, 2Institute of Plant Protection, Xinjiang Academy of Agricultural Sciences/Key Laboratory of Integrated Pest Management on Crops in Northwestern Oasis, Ministry of Agriculture/Scientific Observing and Experimental Station of Korla, Ministry of Agriculture, Xinjiang, China, 3Institute of Microbial Application, Xinjiang Academy of Agricultural Sciences, Xinjiang, China, 4College of Plant Protection, Nanjing Agricultural University, Nanjing, China, and 5Corresponding author, e-mail: gwc1966@163.com

*Z.J. and K.F. are the first two authors of this article.

Received 28 July 2020; Editorial decision 21 December 2020

**Abstract**

*Bemisia tabaci* (Gennadius) cryptic complex has invaded Xinjiang, China, since 1998. The distribution of Mediterranean (MED) and Middle East-Asia Minor 1 (MEAM1) *B. tabaci* substrains has been gradually identified due to the development of molecular technology. In this study, the distribution of MED and MEAM1 in Xinjiang was determined by cleaved amplified polymorphic sequence (CAPs). Results showed that MED dominated in northern Xinjiang (84%), whereas MEAM1 was dominant in southern Xinjiang (72%). Five pairs of simple sequence repeat (SSR) primers were used to analyze the genetic diversity of *B. tabaci* among 36 geographic populations. The genetic diversity of MED and MEAM1 was low and varied little among populations in Xinjiang (0.09 ± 0.14 and 0.09 ± 0.13, respectively). Based on ∆K statistic, 13 populations of MEAM1 could be classified into two subgroups at K = 2, whereas the 23 populations of MED could be classified into four subgroups at K = 4. However, Mantel t-test demonstrated no correlation between geographical and genetic distances among *B. tabaci* complex (R = 0.42, P = 1.00). Neighbor-joining and principal coordinate analysis showed that geographical isolation and interspecific differences were the main causes of the genetic variation. Gene flow predicted that MEAM1 was most likely introduced from Urumqi to the southern Xinjiang. Meanwhile, a large proportion of MED in Kashi region came from Changji and Yining. To block ongoing dispersal, strict detection and flower quarantine regulations need to be enforced.

**Key words:** *Bemisia tabaci*, cryptic species, invasive species, genetic diversity

The whitefly, *Bemisia tabaci* (Gennadius), is a rapidly evolving cryptic species complex (Perring 2001), composed of at least 34 cryptic species (Boykin and De Barro 2012, Alemandri et al. 2015, Götz and Winter 2016). Among the complex members, Middle East-Asia Minor 1 (MEAM1, previously known as B biotype) and Mediterranean (MED, previously known as Q biotype) are the most adaptive whitefly cryptic species in the world. Both cause severe damage to feeding crops and horticultural plants, e.g., nectar secretion leading to sooty mold, and transmission of various viruses (Judith and Czosnek 2002, Paul and Barro 2012, Navas-Castillo 2014, Gilbertson et al. 2015, Wainaina et al. 2018), including cotton leaf curl Multan virus (CLCuMuV), which causes a significant reduction in yield (Nur and Abu Salih 1970, Briddon and Markham 2000, Tahir et al. 2011, Chatzivassiliou et al. 2007).

As an important invasive pest, *B. tabaci* first invaded China in 1949 (Zhou 1949). In the 1990s, *B. tabaci* brought serious damage to various regions (Zhang 2000, Chu et al. 2010, Wang et al. 2010, Guo et al. 2014). In 1998, *B. tabaci* first settled in the flower market in Urumqi, and it soon spread to Shihezi, Hami, Korla, Karamay, and Turpan (Zhao et al. 2000). Before 2010, MEAM1 was the sole species identified in Xinjiang (Zhao et al. 2000). Using sequence characterized amplified regions (SCAR) and COI (cytochrome oxidase
I) barcoding, Cao et al. (2011) found out that MED had invaded Xinjiang.

Recently, molecular markers such as COI barcoding and simple sequence repeat (SSR) have been widely used to identify species of whiteflies. These tools help in understanding genetic diversity, gene flow, and even the replacement of populations (David 1998, Götz and Winter 2016). Boykin et al. (2007) used the whole COI sequence to analyze the genetic diversity of the B. tabaci, and he unveiled 12 members of the species complex. With the discovery of MED B. tabaci’s invasion, it was then known that Xinjiang harbored at least two cryptic species: MED and MEAM1 (Duan et al. 2011).

SSR is widely used in identification and in investigations related to the genetic evolution, genetic mapping, phylogenetic, and genetic diversity of animal and plant species. For example, Colorado potato beetles, Leptinotarsa decemlineata (Say) (Coleoptera: chrysomelidae), was a notoriously invasive species. Zhang et al. (2013) analyzed its genetic diversity among 10 geographical populations in Xinjiang and the mode of the beetle diffusion from the border to inner Xinjiang. Previous report on B. tabaci showed that SSR may not distinguish cryptic species in the complex unless there was an appropriate method to study population structure and the mechanism of invasion and diffusion (Chu et al. 2012). Thus, cleaved amplified polymorphic sequence (CAPs) was used to detect cryptic species within the B. tabaci species complex. Previous COI barcoding studies showed that only MEAM1 and MED of B. tabaci were found in Xinjiang (Asfah et al. 2015).

With the expansion of greenhouses and the increasing frequency of flower trade, whiteflies have invaded most areas in Xinjiang (Jia et al. 2017). As the largest cotton-producing area in China, Xinjiang is facing great threats from the whitefly-transmitted cotton leaf curl Multan virus. Despite of this, the distribution of MED and MEAM1 B. tabaci remains unclear. Meanwhile, the ecological conditions of the unique desert oasis agriculture in Xinjiang may impose certain limitations on the spread of whitefly. In this study, we aimed to uncover the distribution patterns of MEAM1 and MED from 2015 to 2017 to provide insights into the invasion and diffusion of the B. tabaci complex in Xinjiang.

Materials and Methods

Samples

Bemisia tabaci samples were collected from 54 sites in Xinjiang from June 2015 to December 2017 (Table 1). At least 200 adults per site were collected, placed in tubes containing 95% ethanol, and stored at −20°C. Thirty to 50 samples were randomly selected for identification. In total, 1,768 adults were identified as MEAM1 or MED cryptic species. We chose samples for SSR by initially, randomly sampling the sites, and then by the individuals coming from the chosen sites (Table 1).

Cleaved Amplified Polymorphic Sequence

Total genomic DNA was extracted from each adult according to Frohlich et al. (2010). Briefly, each adult was laid on clean paraffin and homogenized in DNase-free Eppendorf tube (Thermo Fisher Scientific) containing 5-µl lysis buffer (5 mM Tris [pH 8.0], 0.5 mM EDTA, 0.5% NP40, and 1 mg/ml protein K; Beijing Solarbio Science & Technology Co., Ltd.). The homogenate was then transferred to tubes with 30-µl lysis buffer and incubated at 65°C for 15 min and then at 95°C for 10 min. The products were stored at −20°C. A 13-µl reaction system containing 2.6-µl DNA, 6.5-µl 2× Taq PCR Master Mix (Tiangen Biotech Co., Ltd. Beijing), and 0.52-µl primer (20 µM, Nanjing Jinsirui Biotechnology Co., Ltd.) was pre-denatured at 95°C for 5 min, followed by 40 cycles of denaturation at 95°C for 30 s. After annealing at 52°C for 30 s and extension at 72°C for 30 s, samples went through a final extension at 72°C for 5 min. All PCR products were stored at −20°C. The forward and reverse primers were C1-J-2195 (5′-TTGAT TTTTTGGCTATCCAGAGT-3′) and R-BQ-2819 (5′-CTGAGATATACGRCGAGGCATTCC-3′), respectively (Simon et al. 1994, Chu 2010).

Enzyme digestion method followed Horowitz et al. (2005) and Chu (2010). Seven microliters of VspI Digestion Mix (0.5 µl VspI, 4.5 µl H2O, 2 µl buffer 0; Thermo Fisher Scientific) was added to each of the 20-µl PCR products, and the final mixture was incubated at 37°C for 2 h. Digestion products were electrophoresed on 1% agarose gel under 120 V for 45 min and visually inspected under BIO-RAD Gel Doc XR+. MEAM1 individuals were identified by the presence of a unique 620-bp band, whereas MED individuals exhibited 498- and 122-bp bands.

Simple Sequence Repeat

Five microsatellite markers were selected according to previous studies of De Barro et al. (2003) and Valle et al. (2012; Table 2). The 25-µl PCR system contained 2-µl DNA, 12.5 µl 2× Taq PCR MaserMix (Tiangen Biotech [Beijing] Co., Ltd.), and 1 µl of each primer (20 µM). The PCR program was set to the following conditions: initiation at 95°C for 5 min, followed by 45 cycles of denaturation at 95°C for 30 s, annealing for 30 s, extension at 72°C for 30 s, then final extension at 72°C for 5 min. Annealing temperatures for each primer are provided in Table 2. The PCR products were analyzed by capillary electrophoresis following the directions of DNF-905 kiton Fragment Analyzer TM (Advanced Analytic Service). Fragment detailed data were extracted using Agilent PROSize 2.0.

Genetic Diversity

PopGenec32 was used to analyze genetic diversity parameters such as the number of alleles (N_a), number of effective alleles (N_e), average diversity index (H), and the Shannon diversity index (I). The inbreeding coefficients (F_is) were also calculated to reflect the inbreeding status of the populations. Genetic differences among populations were evaluated by pairwise Fst values, with 10 000 permutations to assess significance (Weir and Cockerman 1984; FSTAT v.2.9.3.2, Goudet 2002).

Population Relationships

Group and population clusters were generated using STRUCTURE v.2.3.3 based on Bayesian methods (STRUCTURE v.2.3.3, Pritchard et al. 2000). AK method was used to estimate the optimum number of genetic groups (Evanno et al. 2005). We chose the admixture model with correlated allele frequencies and set the K from 1 to 10 for MED group and from 1 to 20 for MEAM1 group. We ran three replicates of each run and set a burn-in period of 50 000 Markov chain Monte Carlo generations followed by 5 × 10^6 iterations. To confirm the existence of population structure, analysis of molecular variance (AMOVA) was performed to assess the genetic variance partitioned into four levels (among groups, among populations, within groups, within populations, and within individuals) based on structure output, with 10 000 permutations to test for significance (Arlequin v.3.11, Excoffier et al. 2005). Correlation between geographical and genetic distances (Slatkin’s linear covariance) was performed to assess the genetic distance among populations using the Admixture model and correlated allele frequencies.
| Area                              | No. | Population | Time  | Longitude and latitude                  | Host                  | No. | No. of SSR |
|----------------------------------|-----|------------|-------|----------------------------------------|-----------------------|-----|------------|
|                                  |     |            |       |                                        |                       |     |            |
|                                 | 1   | Urumqi-1   | 2016.5| (43°48′49″N, 87°34′37″W)               | Pharbitis nil         | 28  | 0          |
|                                 | 2   | Urumqi-2   | 2016.8| (43°48′21″N, 87°33′22″W)               | Cucumis sativus       | 50  | 49         |
|                                  | 3   | Karamay    | 2016.5| (45°29′26″N, 84°57′23″W)               | Solanum lycopersicum  | 78  | 49         |
|                                  |     |            |       |                                        |                       |     |            |
|                                 | 4   | Hami-1     | 2016.4| (42°50′32″N, 93°27′18″W)               | Solanum lycopersicum  | 30  | 16         |
|                                  | 5   | Hami-2     | 2016.4| (43°0′35″N, 93°35′58″W)               | Solanum lycopersicum  | 30  | 24         |
|                                 | 6   | Changji-1  | 2016.5| (44°0′40″N, 87°18′29″W)               | Phaseolus vulgaris    | 60  | 40         |
|                                 | 7   | Changji-2  | 2017.3| (44°3′32″N, 88°1′22″W)               | Hydrocleys tetraphylla| 60  | 41         |
|                                 | 8   | Changji-3  | 2017.3| (44°3′32″N, 87°58′45″W)               | Hibiscus rosasinensis | 15  | 0          |
|                                 |     |            |       |                                        |                       |     |            |
|                                 | 9   | Alashankou | 2016.9| (45°10′12″N, 82°33′36″W)               | Hibiscus rosasinensis | 50  | 50         |
|                                 | 10  | Bazhou-1   | 2015.8| (38°7′4″N, 85°34′46″W)                | Vigna angularis       | 30  | 28         |
|                                 | 11  | Bazhou-2   | 2015.8| (38°8′3″N, 85°30′42″W)                | Vigna angularis       | 30  | 0          |
|                                 | 12  | Bazhou-3   | 2015.8| (38°6′10″N, 85°31′9″W)                | Cucurbita moschata    | 30  | 19         |
|                                 | 13  | Korla      | 2016.3| (41°46′12″N, 86°8′57″W)               | Hibiscus rosasinensis | 30  | 0          |
|                                 |     |            |       |                                        |                       |     |            |
|                                 | 14  | Aksu       | 2017.3| (40°32′19″N, 81°17′53″W)               | Hibiscus rosasinensis | 30  | 0          |
|                                 | 15  | Kashi-1    | 2015.9| (38°24′44″N, 77°17′3″W)               | Gossypium spp         | 50  | 33         |
|                                 | 16  | Kashi-2    | 2015.7| (39°24′0″N, 75°54′0″W)                | Solanum lycopersicum  | 30  | 11         |
|                                 | 17  | Kashi-3    | 2015.8| (38°21′22″N, 77°10′56″W)               | Gossypium spp         | 30  | 11         |
|                                 | 18  | Kashi-4    | 2015.8| (38°17′9″N, 77°11′49″W)               | Gossypium spp         | 30  | 6          |
|                                 | 19  | Kashi-5    | 2015.8| (38°19′20″N, 77°12′10″W)              | Gossypium spp         | 30  | 9          |
|                                 | 20  | Kashi-6    | 2015.8| (38°20′44″N, 77°09′26″W)              | Gossypium spp         | 30  | 4          |
|                                 | 21  | Kashi-7    | 2015.9| (38°24′3″N, 76°8′1″W)                | Solanum melongena     | 30  | 5          |
|                                 | 22  | Kashi-8    | 2015.9| (39°24′2″N, 76°5′3″W)                | solanum melongena     | 30  | 10         |
|                                 | 23  | Kashi-9    | 2015.9| (39°14′3″N, 76°2′35″W)               | Vigna angularis       | 30  | 0          |
|                                 | 24  | Kashi-10   | 2015.9| (38°55′41″N, 76°8′13″W)               | Cucumis sativus       | 30  | 0          |
|                                 | 25  | Kashi-11   | 2015.9| (39°47′0″N, 78°31′46″W)               | Solanum lycopersicum  | 30  | 0          |
|                                 | 26  | Kashi-12   | 2015.9| (39°47′41″N, 78°34′18″W)              | Solanum melongena     | 30  | 0          |
|                                 | 27  | Kashi-13   | 2016.4| (38°18′28″N, 77°56′42″W)              | Solanum lycopersicum  | 30  | 0          |
|                                 |     |            |       |                                        |                       |     |            |
|                                 | 28  | Hetian-1   | 2015.6| (37°2′47″N, 79°52′29″W)               | Solanum lycopersicum  | 30  | 60         |
|                                 | 29  | Hetian-2   | 2015.8| (37°4′4″N, 82°42′55″W)               | Vigna angularis       | 30  | 10         |
|                                 | 30  | Hetian-3   | 2015.8| (37°4′6″N, 82°40′11″W)               | Canavalia gladiata    | 30  | 0          |
|                                 | 31  | Hetian-4   | 2015.8| (37°3′29″N, 82°41′41″W)               | Solanum lycopersicum  | 30  | 6          |
|                                 | 32  | Hetian-5   | 2015.8| (36°50′16″N, 81°38′51″W)              | Solanum lycopersicum  | 30  | 14         |
| Area                      | No. | Population | Time   | Longitude and latitude                  | Host                              | No. | No. of SSR |
|---------------------------|-----|------------|--------|----------------------------------------|-----------------------------------|-----|-----------|
| Ili Kazak Autonomous Prefecture |     |            |        |                                        |                                    |     |           |
| 34 Hetian-7               | 30  | 5          |        | (36°50′58″N, 81°37′8″W)                | Solanum lycopersicum              | 30  | 5         |
| 35 Hetian-8               | 30  | 6          |        | (36°59′55″N, 81°4′12″W)               | Capsicum annuum                   | 30  | 0         |
| 36 Hetian-9               | 30  | 12         |        | (36°59′49″N, 80°5′8″51″W)             | Brassica rapa                     | 30  | 0         |
| 37 Hetian-10              | 30  | 0          |        | (37°14′14″N, 79°4′1″34″W)             | Solanum lycopersicum              | 30  | 5         |
| 38 Hetian-11              | 30  | 27         |        | (37°14′18″N, 79°4′4″19″W)             | Solanum lycopersicum              | 30  | 0         |
| 39 Hetian-12              | 30  | 5          |        | (37°17′32″N, 79°3′95″43″W)            | Capsicum annuum                   | 30  | 0         |
| 40 Hetian-13              | 50  | 90         |        | (37°15′7″N, 80°5′12″W)               | Solanum lycopersicum              | 30  | 27        |
| Turpan                   |     |            |        |                                        |                                    |     |           |
| 43 Tulupan-1              | 30  | 0          |        | (42°59′59″N, 89°9′58″W)               | Solanum lycopersicum              | 30  | 0         |
| 44 Tulupan-2              | 30  | 10         |        | (42°57′56″N, 89°6′16″W)               | Cucumber                          | 30  | 0         |
| 45 Tulupan-3              | 30  | 50         |        | (42°48′40″N, 88°27′17″W)              | Gossypiumspmar                    | 30  | 0         |
| 46 Tulupan-4              | 30  | 13         |        | (42°46′54″N, 88°41′56″W)              | Solanum lycopersicum              | 30  | 18        |
| 47 Tulupan-5              | 30  | 18         |        | (42°79′37″N, 88°38′24″W)              | Solanum lycopersicum              | 30  | 14        |
| 48 Tulupan-6              | 30  | 18         |        | (42°57′6″N, 89°5′22″W)               | Solanum lycopersicum              | 30  | 11        |
| 49 Tulupan-7              | 30  | 18         |        | (42°46′39″N, 89°3′31″W)              | Solanum lycopersicum              | 30  | 8         |
| 50 Tulupan-8              | 30  | 11         |        | (42°47′14″N, 89°43′18″W)              | Solanum lycopersicum              | 30  | 8         |
| 51 Tulupan-9              | 30  | 8          |        | (42°43′21″N, 89°41′43″ W)             | Pharbitis nil                      | 30  | 8         |
| Shihnez                 |     |            |        |                                        |                                    |     |           |
| 52 Shihnez               | 30  | 92         |        | (44°18′22″N, 86°4′48″W)               | Euphorbia pulcherrima             | 30  | 43        |
| Alaer                     |     |            |        |                                        |                                    |     |           |
| 54 Alaer                 | 30  | 0          |        | (40°32′42″N, 81°16′41″W)             | Hibiscus rosa-sinensis            | 30  | 0         |

**Table 1.** Continued
Table 2. The information of simple sequence repeat molecular marker primer

| Microsatellite locus | Direction | Primer sequences | Annealing temperature (°C) | References          |
|---------------------|-----------|------------------|----------------------------|---------------------|
| bem31               | F         | GTCATTTCGGATTCTTCAGCA | 57            | De Barro et al. (2003) |
|                     | R         | AAGAACCTAGCCAGGGGACCAAC |               |                     |
| bem40               | F         | GAAAGTGAGAGGTTAGGTGA  | 57            | De Barro et al. (2003) |
|                     | R         | TGGAGAAGGTATATAAAGTGGA |               |                     |
| BEM06               | F         | GATGGCTTATGTATATATCTA | 52            | De Barro et al. (2003) |
|                     | R         | TTACACTTAACACCAGAATCT |               |                     |
| bta4                | F         | CGGCAGTCAGGGTTATT    | 56            | Valle et al. (2012)  |
|                     | R         | CGCTCCTCAAAGTTTCGTTT |               |                     |
| bta5                | F         | GGTCAGAGGATTTGGAATGC  | 60            | Valle et al. (2012)  |
|                     | R         | TATACCTGGGCGATCTAGC   |               |                     |

Fig. 1. Sampling for *Bemisia tabaci* collected in Xinjiang.
We used a neighbor-joining cluster method in MEGA 3.01 to generate a circle phylogenetic tree based on $D^*$ distance which was calculated using Popgene32. To assess the genetic associations of individuals among various groups representing cryptic species and population, a pairwise similarity matrix was generated using simple matching coefficient (Sokal and Michener 1958), with 10,000 permutations. Random, this was converted to Euclidean distance matrix as the square root of 1 minus element-wise similarity for a principal coordinate analysis (PCoA) using NTSYS-pc 2.01 (Rohlf 1987). Top 2 components were plotted for MED, MEAM1, MED, and MEAM1 complex. Direction of gene flow was inferred by a partial Bayesian method from GENECLASS 2.0, and assignment probabilities of individuals were tested from geographical populations with a threshold probability value of 0.01. Assigned probability data of MED to MED, MED to MEAM1, MEAM1 to MED, MEAM1 to MEAM1 groups were arcsin-square root transformed to normal distribution. Significant levels ($P < 0.05$) were tested using Tukey’s multiple comparisons test of ANOVA in Graphpad Prism 6.0 (Ramalai and Mountain 1997) and GeneClass v.2.0 (Paetkau et al. 2004, Piry et al. 2004).

Results

The Distribution of B. tabaci Cryptic Species

The distribution of B. tabaci cryptic species were identified in 54 sampling sites during 2015 and 2017 by CAPs. The randomly chosen 631 samples for SSR were also sequenced to verify these results (data not shown). Results showed that there was a large percentage difference between northern and southern Xinjiang (Fig. 1). The MED was the dominant cryptic species in northern Xinjiang, accounting for 84% of the samples. Apart from Urumqi (26%), it dominated in Changji Hui Autonomous Prefecture (87%), Shihezi City (100%), Karamay City (100%), Yili District (100%), Bortala Mongolian Autonomous Prefecture (100%), Turpan Region (100%), and Hami Region (97%). Meanwhile, the MEAM1 was the dominant cryptic species in southern Xinjiang, accounting for 73% of the samples. It dominated in Hotan (95%), Bazhou (91%), Kashgar (38%), and Aksu (100%). No species were present in Alar (0%; Fig. 2).

Genetic Diversity

Five pairs of SSR primers were used to analyze the genetic diversity of 631 samples belonging to 36 randomly selected B. tabaci populations (Table 1). Polymorphism position and polymorphism information content, ranging from 15 to 48 and 0.92 to 0.95, respectively, showed high loci polymorphism in each population. The results also showed that the primers used were applicable for genetic diversity analysis of B. tabaci. The MEAM1 and MED population’s diversity indices including number of alleles per locus ($n_a$), effective number of alleles ($n_e$), gene diversity ($h$), and Shannon’s Information index ($I$) averaged at 1.77 ± 0.42 and 1.92 ± 0.27 (range 1.15–1.48), 1.13 ± 0.25 and 1.13 ± 0.25 (range 1.07–1.13), 0.09 ± 0.14 and 0.09 ± 0.13 (range from 0.04 to 0.15).

Fig. 2. Distribution of 54 populations of Bemisia tabaci cryptic species in Xinjiang. Sampling sites: 1. Hetian Prefecture; 2. Kashgar Prefecture; 3. Mongolian Autonomous Prefecture of Bayingolin; 4. Alaer; 5. Aksu Prefecture; 6. Hami City; 7. Turpan; 8. Bortala Mongol Autonomous Prefecture; 9. III Kazak Autonomous Prefecture; 10. Karamay; 11. Shihezi; 12. Changji hui autonomous prefecture; 13. Urumqi.
### Table 3. Proportion of membership of each predefined population in MEAM1 or MED groups

| Population       | $K = 2, P = 13$ |          |          |          |          | $K = 4, P = 23$ |          |          |          |          |
|------------------|-----------------|----------|----------|----------|----------|-----------------|----------|----------|----------|----------|
|                  | MEAM1           | MEAM1    | MEAM1    | MEAM1    | MEAM1    | MED             | MED      | MED      | MED      | MED      |
| Urumqi-2-MEAM1   | 0.25            | 0.75     |          |          |          | 0.05            | 0.02     | 0.88     | 0.05     |          |
| Hetian-13-MEAM1  | 0.04            | 0.96     |          |          |          | 0.32            | 0.02     | 0.57     | 0.09     |          |
| Hetian-2-MEAM1   | 0.05            | 0.96     |          |          |          | 0.03            | 0.08     | 0.85     | 0.04     |          |
| Hetian-4-MEAM1   | 0.04            | 0.96     |          |          |          | 0.03            | 0.03     | 0.90     | 0.05     |          |
| Hetian-3-MEAM1   | 0.03            | 0.97     |          |          |          | 0.03            | 0.02     | 0.93     | 0.01     |          |
| Hetian-6-MEAM1   | 0.04            | 0.96     |          |          |          | 0.02            | 0.03     | 0.94     | 0.02     |          |
| Hetian-8-MEAM1   | 0.02            | 0.98     |          |          |          | 0.08            | 0.06     | 0.76     | 0.1      |          |
| Hetian-9-MEAM1   | 0.07            | 0.93     |          |          |          | 0.01            | 0.24     | 0.74     | 0.01     |          |
| Hetian-11-MEAM1  | 0.12            | 0.88     |          |          |          | 0.02            | 0.02     | 0.95     | 0.01     |          |
| Hetian-12-MEAM1  | 0.03            | 0.97     |          |          |          | 0.04            | 0.02     | 0.92     | 0.02     |          |
| Kashi-8-MEAM1    | 0.14            | 0.86     |          |          |          | 0.64            | 0.17     | 0.02     | 0.18     |          |
| Bazhou-1-MEAM1   | 0.96            | 0.04     |          |          |          | 0.65            | 0.12     | 0.14     | 0.1      |          |
| Bazhou-3-MEAM1   | 0.96            | 0.04     |          |          |          | 0.8             | 0.04     | 0.08     | 0.09     |          |
| Tula-pan-5-MED   | 0.63            | 0.06     |          |          |          | 0.63            | 0.06     | 0.11     | 0.2      |          |
| Tula-pan-6-MED   | 0.89            | 0.05     |          |          |          | 0.89            | 0.05     | 0.03     | 0.03     |          |
| Tula-pan-8-MED   | 0.51            | 0.1      |          |          |          | 0.51            | 0.1      | 0.16     | 0.23     |          |
| Tula-pan-9-MED   | 0.45            | 0.1      |          |          |          | 0.45            | 0.1      | 0.05     | 0.4      |          |
| Changji-MED      | 0.11            | 0.74     |          |          |          | 0.11            | 0.74     | 0.1      | 0.04     |          |
| Yining-MED       | 0.14            | 0.75     |          |          |          | 0.14            | 0.75     | 0.02     | 0.08     |          |
| Alashankou-MED   | 0.09            | 0.35     |          |          |          | 0.09            | 0.35     | 0.03     | 0.54     |          |
| Shihezi-MED      | 0.14            | 0.39     |          |          |          | 0.14            | 0.39     | 0.02     | 0.45     |          |
| Hami-1-MED       | 0.21            | 0.32     |          |          |          | 0.21            | 0.32     | 0.02     | 0.46     |          |
| Hami-2-MED       | 0.11            | 0.13     |          |          |          | 0.11            | 0.13     | 0.01     | 0.74     |          |

**Bold** indicate the proportion of each population assigned to the most reliable group. $K$, the number of inferred population groups; $P$, the number of populations.
to 0.08), and 0.15 ± 0.20 and 0.15 ± 0.20 (range 0.07–0.13), respectively. These indicates low genetic diversity and little variation among populations (Table 2). Fis values were all negative in 36 SSR analyzed sites with 12 and 20 populations reaching P < 0.05 and P < 0.001 significant departure levels. These results indicate that the genetic diversity of B. tabaci in Xinjiang is low and the genetic differentiation is high.

Genetic Relationship

ΔK Statistic

Based on ΔK statistic, 13 populations of MEAM1 could be divided into two subgroups at K = 2, whereas the 23 populations of MED could be divided into four subgroups at K = 4 (Table 3). In MEAM1, one group Kashi-1, Kashi-2, Kashi-3 included those from Tulupan; the third group included those from Changji and Yining; and finally, the fourth group included those from Alashankou, Shihezi, and Hami.

Analysis of Molecular Variance

Basing on the subdivision by ΔK, AMOVA demonstrated that most of the variation came from within individuals (100.89%, 115.31%; Table 4), with K = 2 in MEAM1 group and K = 4 in MED group. Fixation indices of within populations (Fis) were negative (−0.23, −0.23). It demonstrated that there was a strong disassortative mating, which was consistent with the Fis in each population (Table 5). Variation among population and groups in MEAM1 and MED population was low but significant (df = 11, F = 0.06, P = 0.00; df = 19, F = 0.04, P = 0.00; df = 1, F = 0.12, P = 0.00, df = 3, F = 0.03, P = 0.00; Table 4), which supported the groupings.

Mantel t-Test

Mantel test analysis of the matrix (Ln Ks) based on ΔK subdivision showed that there was no correlation between geographical and genetic distances among B. tabaci complex (R = 0.42, P = 1.00), or in MED (R = 0.49, P = 1.00) and MEAM1 (R = 0.44, P = 1.00) group or subgroup (Table 6). MEAM1-group2 and MED-group3’s data were not available as there were only two populations in these groups.

Neighbor-Joining Tree

The neighbor-joining tree (Fig. 3A) showed that most of the MED and MEAM1 population were clustered separately, except for the Kashi, Kelamayi, and Urumqi population. The Kashi-5-MED and Urumqi-MEAM1 population were clustered with Kashi-8-MEAM1 and Urumqi-MED. The rest of the Kashi-MED population (Kashi-1, Kashi-2, Kashi-3, Kashi-4, Kashi-6, Kashi-7, and Kashi-13), Kelamayi-MED in northern-Xinjiang, and Hetian-MEAM1 in Southern Xinjiang converged into one branch. Nei’s genetic clustering results showed that there was no significant correlation between genetic relationship and the regional distribution of B. tabaci in Xinjiang.

Principal Coordinate Analysis

The phylogenetic tree has shown that most of MED and MEAM1 populations could be clearly separated according to geographic clustering. Thus, we verified the relationships between MED and MEAM1 samples with a PCoA plot. Based on 99 alleles of five SSR primers, the top three principle components accounted for 55.9, 67.9, and 70.2% of the SSR variation in MED, MEAM1, MED, and MEAM1 complex. There were no clear boundaries between MED and MEAM1 samples. However, the MED samples from Southern
Table 5. Summary data of genetic diversity among groups and populations in Xinjiang, China

| Population | N     | n_a  | n_e  | h    | I     | PP       | PIC     | F_is | P-value |
|------------|-------|------|------|------|-------|----------|---------|------|---------|
| All        | 631   | 2.00 | 1.13 | 0.09 | 0.15 | 99       | 0.96    | 0.96 |         |
| MEAM1      | 174   | 1.77 | 1.13 | 0.09 | 0.15 | 76       | 0.96    | 0.96 |         |
| MED        | 457   | 1.92 | 1.13 | 0.09 | 0.15 |          |         |      |         |
| MEAM1      |       |      |      |      |      |          |         |      |         |
| Urumqi-2-MEAM1 | 33  | 1.45 | 1.12 | 0.13 | 0.08 | 45       | 0.95    | 0.05 |         |
| Bazhou-1-MEAM1 | 19  | 1.27 | 1.10 | 0.07 | 0.06 | 30       | 0.92    | -0.24 | 0.0003 |
| Hetian-13-MEAM1 | 38  | 1.28 | 1.13 | 0.12 | 0.12 | 28       | 0.95    | -0.28 | 0.0008 |
| Hetian-11-MEAM1 | 10  | 1.23 | 1.12 | 0.06 | 0.09 | 19       | 0.95    | -0.31 | 0.0003 |
| Hetian-12-MEAM1 | 5   | 1.21 | 1.11 | 0.07 | 0.10 | 21       | 0.95    | -0.26 | 0.0003 |
| Hetian-13-MEAM1 | 6   | 1.19 | 1.10 | 0.06 | 0.10 | 18       | 0.95    | -0.29 | 0.0003 |
| Hetian-11-MEAM1 | 14  | 1.24 | 1.09 | 0.07 | 0.10 | 24       | 0.95    | -0.34 | 0.0003 |
| Hetian-12-MEAM1 | 5   | 1.22 | 1.10 | 0.06 | 0.10 | 22       | 0.95    | -0.25 | 0.0003 |
| Hetian-2-MEAM1 | 10   | 1.28 | 1.12 | 0.12 | 0.12 | 27       | 0.94    | -0.24 | 0.0003 |
| Hetian-3-MEAM1 | 19  | 1.27 | 1.11 | 0.12 | 0.12 | 20       | 0.93    | -0.17 | 0.0053 |
| Hetian-8-MEAM1 | 10   | 1.19 | 1.12 | 0.06 | 0.13 | 21       | 0.93    | -0.32 | 0.0003 |
| Hetian-9-MEAM1 | 45  | 1.45 | 1.12 | 0.13 | 0.09 | 38       | 0.94    | -0.29 | 0.0003 |
| Hetian-1-MEAM1 | 10   | 1.28 | 1.12 | 0.12 | 0.12 | 29       | 0.94    | -0.22 | 0.0003 |
| Hetian-12-MEAM1 | 5   | 1.21 | 1.10 | 0.07 | 0.10 | 21       | 0.94    | -0.26 | 0.0003 |

N, sample size; n_a, observed number of alleles; n_e, effective number of alleles (Kimura and Crow 1964); h, Nei's (1973) gene diversity; I, Shannon's Information index (Lewontin 1972); F_is, inbreeding coefficient; PP, polymorphism position; PIC, polymorphism information content.
Xinjiang were mainly located at the right side of the coordinate axis, whereas the MEAM1 samples from Northern Xinjiang were mainly located at the bottom (Fig. 2B). We further tested whether MED and MEAM1 samples could be separated by geographic isolation. Results show that MED samples that grouped by sampling sites were highly highly dispersed but can be partially separated into Northern and Southern Xinjiang, with the large Tianshan Mountain potentially serving as a geographical barrier for the two groups (Fig. 2C). MEAM1 samples were clearly separated, especially those from Southern Xinjiang. Interestingly, MEAM1 in Northern Xinjiang occupied the center which separated the samples of Bayingol from those of Hotan and Kashgar.

MEAM1 B. tabaci in northern Xinjiang showed clear separation from those in Hotan, Bazhou, and Kashgar area. MED B. tabaci from northern Xinjiang was intersected by those from Bazhou and Hotan areas. The results showed further that MED B. tabaci individuals and MED B. tabaci from southern Xinjiang were clearly clustered, whereas those from northern Xinjiang were more dispersed. The range of MED from northern Xinjiang overlaps with that of MED B. tabaci from southern Xinjiang.

Gene Flow
The GENECLASS 2.0 assigned individual probabilities to evaluate the degree of migration and the migration direction of MED or MEAM1 groups based on $\Delta K$ (Fig. 4). The results indicate that individuals migrated between MED and MEAM1 B. tabaci populations. Most of the highest probabilities were self-assigned in each subdivision or even in local areas. However, probabilities of migration from Urumqi-MEAM1 to Urumqi-MED (0.47), Hetian-11-MEAM1 to Hetian-13-MED (0.44), Changji-MED to Hetian-6-MEAM1 (0.23), Changji-MED to Alashankou-MED (0.32), Changji-MED to Hami-MED (0.28), and Hetian-13-MED to Hetian-11-MEAM1 (0.41) were higher than self-assigned probabilities in their subdivisions.

To predict the immigrant origins, we calculated the means of migration probabilities in each column (Fig. 4). Interestingly, we found that populations of Kashi-3-MED (0.22), Kashi-4-MED (0.22), Kashi-3-MED (0.21), Kashi-3-MED (0.20), Hetian-13-MED (0.21), Turpan-5-MED (0.21), Hetian-11-MEAM1 (0.26), and Hetian-11-MEAM1 (0.20) had a relatively high value. Migration assigned probabilities from MED to MED, MED to MEAM1, MEAM1 to MED, and MEAM1 to MEAM1 are also depicted as box diagrams (Fig. 5). Results showed that there was no difference between migration assigned probabilities from MED to MED (mean ± SE = 0.174 ± 0.007) and MEAM1 to MEAM1 (0.206 ± 0.015; $F = 0.007$, $P = 0.977$), but there were significant differences between MED to MED and MED to MEAM1 (0.065 ± 0.005; $F = 0.184$, $P < 0.001$), MED to MED and MEAM1 to MED (0.119 ± 0.006; $F = 0.077$, $P < 0.001$), MEAM1 to MEAM1 and MED to MEAM1 ($F = 0.184$, $P < 0.001$), and finally, MEAM1 to MEAM1 and MEAM1 to MED ($F = 0.083$, $P < 0.001$).

To further analyze the gene flow between MED and MEAM1 populations in local regions, Kashi and Hetian populations were selected since they were coexisting populations and there were plenty of sampling points. Kashi-8-MEAM1 was the only MEAM1 population chosen for the SSR analysis out of six randomly selected Kashi populations. Hetian-13-MED was the only population chosen out of 10 randomly selected Hetian populations. MED and MEAM1 showed different migration patterns. For Kashi-8-MEAM1 population, the assigned probability was self-assigned (0.44) and the rest of the Kashi-MED populations were mainly migrants from Kashi-2-MED (0.35–0.67). As
Fig. 3. Genetic relationship analyzed by a unrooted neighbor-joining (NJ) phylogenetic tree (A) and principal coordinate analysis (PCoA) plot of *Bemisia tabaci* complex (B), MED (C), and MEAM1 (D) population in Xinjiang. For NJ trees, green and blue branches indicate population from Southern and Northern Xinjiang, respectively.

Fig. 4. Means of individual assignment probabilities from (rows) and into (columns) each population of *Bemisia tabaci* in Xinjiang. Populations with immigrating individuals are given in rows; populations with emigrating individuals in columns. Note: Highest assignment probability in rows and means of migration probabilities in each column > 0.20 were red. The green background color deepened as the probability got higher. Subdivision of MED and MEAM1 groups were framed, respectively.
for Hetian-13-MED, the gene flows from Hetian-11-MEAM1 (0.44), Hetian-12-MEAM1 (0.38), Hetian-13-MEAM1 (0.36), Hetian-6-MEAM1 (0.34) were higher than the self-assigned (0.28). The gene flow from Hetian-13-MED population to other populations was high (0.39–0.52), except for Hetian-6-MEAM1 population, which received migrants mainly from Changji-MED. Apart from Hetian-6-MEAM1 and Hetian-11-MEAM1, the Hetian-MEAM1 populations received gene flows mainly from Hetian-11-MEAM1 (0.47–0.67) and Hetian-13-MEAM1 (0.69–0.79).

**Discussion**

MED *B. tabaci* has spread and gradually replaced the ecological niche of MEAM1 as a dominant cryptic species in many provinces since it was first found in Yunnan in 2004 (Chu et al. 2005). After 22 yr of *B. tabaci* invasion in Xinjiang, CAPs were used to identify MED and MEAM1 cryptic species in this study, and the randomly chosen SSR samples were also used for sequencing COI gene (data not shown) to verify CAP-based identification. Based on the results of CAPs, we found that MED *B. tabaci* was mainly distributed in northern Xinjiang and was in agreement with Cao et al. (2013). We also found that in southern Xinjiang, a higher proportion of MEAM1 existed, there was a wide percentage difference between northern (MED: 84%) and southern (MED: 28%) Xinjiang. The investigation revealed that the most serious damage occurred in Turpan area and the MED was the dominant crop pest. This was attributed to local climatic conditions, planting patterns, and field management. The samples from Shihezi, Alashankou, Changji, and Aler were collected in flowers and were identified and confirmed as MED-byrelated studies. The spread of MED *B. tabaci* is related to the introduction of flowers (Chu et al. 2005). MEAM1 was the main cryptic species in southern Xinjiang including western part of Bazhou, parts of Hotan and Kashgar. This phenomenon could be attributed to the adjacent planting of local vegetable greenhouses, cotton fields, and with frequent flower transport and trade.

We were interested in the invasion pathways of MEAM1 and MED *B. tabaci* and the effect of substitutions on the internal genetic diversity of *B. tabaci*. We used five microsatellite primers to analyze the genetic relationship between MED and MEAM1 populations. There was low genetic diversity in *B. tabaci* in Xinjiang and low genetic variation between populations. The main sources of genetic variation between MED and MEAM1 *B. tabaci* were interspecific genetic differences and geographical isolation. There was no correlation between the geographical and genetic distances in *B. tabaci*. The reason is that the man-made transmission factor of *B. tabaci* is larger than that of the natural transmission. To block ongoing dispersal, strict detection and flower quarantine regulations need to be enforced. Based on the AMOVA and the $F_{ST}$ value, *B. tabaci* populations in Xinjiang had highly significant differentiation. The correlation between the geographical distance (LN Km) and the genetic distance of the whitefly populations was analyzed using Mantel test. Mantel's *t*-test demonstrated that there was no relationship between geographical distance and
genetic distance (Table 6). ΔK statistic divides MEAM1 into two subgroups and into four subgroups for MED. As the provincial capital, Urumqi may be the main source of MED whitely transmission, while MEAM1 invasion pathways may be more varied. NJ-tree and PCoA could neither distinguish MED and MEAM1 nor separate the northern and southern Xinjiang into two clusters well (Fig. 3). This may be explained by the gene flow between a few MED and MEAM1 populations, such as Hetian-13-MED, Urumqi-2-MEAM1, and Changji-MED (Fig. 4). The unique characteristics of irrigation agriculture and oasis agriculture in Xinjiang, at the same time, the large desert areas surrounding cities, provide geographical barrier for whitely transmission. Thus, human-based transmission becomes the main mode of transmission for B. tabaci. MED populations had a stronger gene flow toward MEAM1 populations. The probabilities in MEAM1 were mainly self-assigned, indicating that the MEAM1 had a reproductive disadvantage to MED. This can result from pesticide resistance (Roditakis et al. 2009, Wu et al. 2010) or asymmetric mating interaction (Liu et al. 2007).

Acknowledgments
We thank Sheng Han (Xinjiang Academy of Agricultural Sciences, Xinjiang, China) for the experimental assistance. This work was supported by grants from the Key Cultivation Projects for Scientific and Technological Innovation of Xinjiang Academy of Agricultural Sciences (no. sjkpy-002); Science and Technology Program under the Xinjiang project, ‘Molecular detection technology study of resistance of Bemisia tabaci’ (no. 201591140); and the National Key Research Project, ‘The dynamic distribution and resource database construction of the main invading organisms’ (no. 2016YFC1202100).

Author contributions
Z.J., K.F., and W.G. conceived and designed the experiments. Z.J., K.F., W.G., T.A., X.D., J.H., X.W. collected samples, performed the experiments and analyzed the data. Z.J., K.F., W.J. and W.G. wrote the paper. All authors read and approved the manuscript.

References Cited
Ashfaq, M., P. D. Hebert, M. S. Mirza, A. M. Khan, S. Mansoor, G. S. Shah, and Y. Zafar. 2015. DNA barcoding of Bemisia tabaci complex (Hemiptera: Aleyrodidae) reveals southerly expansion of the dominant whitely species of cotton in Pakistan. PLoS One 9: e104485.
Alemandri, V., C. G. Vaghi Medina, A. D. Dumon, E. B. Argiliero Caro, M. F. Mattio, S. Garcia Medina, P. M. Lopez Lambertini, and G. Truel. 2015. Three Members of the Bemisia tabaci (Hemiptera: Aleyrodidae) Cryptic Species Complex Occur Sympatrically in Argentine Horticultural Crops. J. Econ. Entomol. 2: 405–413.
Boykin, L. M., and P. J. De Barro. 2012. A practical guide to identifying members of the Bemisia tabaci species complex: and other morphologically identical species. Front. Ecol. Evol. 2: 1–5. doi:10.3389/fevo.2014.00045
Boykin, L. M., R. G. Shatters, R. C. Rosell, C. L. McKenzie, R. A. Bagnall, P. J. D. Barro, and D. R. Frohlich. 2007. Global relationships of Bemisia tabaci (Hemiptera: Aleyrodidae) revealed using Bayesian analysis of mitochondrial COI DNA sequences. Mol. Phylogenet. Evol. 44: 1306–1319.
Bridgen, R. W., and P. G. Markham. 2000. Cotton leaf curl virus disease. Virus Res. 71: 151–159.
Cao, Q.-J., L. Li, K. Mairemuguli, H. Q. Wang, G. Z. Li, and D. Y. Ma. 2013. Biotype distribution and infection status of tomato yellow leaf curl virus (TYLCV) in Bemisia tabaci (Hemiptera: Aleyrodidae) in Xinjiang, northwestern China. Acta Entomol. Sin. 56: 652–664.
Chatzivassiliou, E. K., D. Peters, and P. Lolas. 2007. Occurrence of tomato spotted wilt virus in Stevia rebaudiana and Solanum tuberosum in Northern Greece. Plant Dis. 91: 1205.
Chu, D., Y. J. Zhang, B. Cong, B. Y. Xu, Q. J. Wu, and G. R. Zhu. 2005. Sequence Analysis of mtDNA COI Gene and Molecular Phylogeny of Different Geographical Populations of Bemisia tabaci (Gennadius). Agri. Sci. Ch. 4: 533–541.
Chu, D., F. H. Wan, Y. J. Zhang, and J. K. Brown. 2010. Change in the biotype composition of Bemisia tabaci in Shandong Province of China from 2005 to 2008. Environ. Entomol. 39: 1028–1036.
Chu, D., X. C. Li, and Y. J. Zhang. 2012. Microsatellite analyses reveal the sources and genetic diversity of the first-introduced Q-biotype population and the well-established B-biotype populations of Bemisia tabaci in China. Acta Entomol. Sin. 55: 1376–1385.
David, P. 1998. Heterozygosity-fitness correlations: new perspectives on old problems. Heredity (Edinb). 80 (Pt 5): 531–537.
De Barro, P. J., K. D. Scott, G. C. Graham, C. L. Lange, and M. K. Schutte. 2003. Isolation and characterization of microsatellite loci in Bemisia tabaci. Mol. Ecol. Res., 3: 40–43.
Duan, X. D., L. J. Ma, Z. P. Yao, Q. Cao, C. L. Leng, and D. Y. Ma. 2011. Sequence analysis of mtDNA COI gene in the invasive insect, Bemisia tabaci (Gennadius) in Xinjiang, North-western China. J. Biosaf. 20: 50–55.
Evanno, G., S. Regnaut, and J. Goudet. 2005. Detecting the number of clusters of individuals using the software STRUCTURE: a simulation study. Mol. Ecol. 14: 2611–2620.
Excoffier, L., G. Laval, and S. Schneider. 2005. Allelquin (version 3.0): an integrated software package for population genetics data analysis. Evol. Bioinform. Online 1: 47–50.
Frohlich, D. R., I. TorresJeríz, I. D. Bedford, P. G. Markham, and J. K. Brown. 2010. A phylogeographical analysis of the Bemisia tabaci species complex based on mitochondrial DNA markers. Mol. Ecol. 8: 1683–1691.
Gilbertson, R. L., O. Batuman, C. G. Webster, and S. Adkins. 2015. Role of the insect supervisor, Bemisia tabaci and, Frankliniella occidentalis, in the emergence and global spread of plant viruses. Ann. Rev. Virol. 2: 67–93.
Götz, M., and S. Winter. 2016. Diversity of Bemisia tabaci, in Thailand and Vietnam and indications of species replacement. J. Asia Pac. Entomol. 19: 537–543.
Guo, L. T., W. Xie, S. L. Wang, Q. Wu, R. Li, N. Yang, X. Yang, H. Pan, and Y. Zhang. 2014. Detoxification enzymes of Bemisia tabaci B and Q: Biochemical characteristics and gene expression profiles. Pest Manag. Sci. 70, 1588–1594.
Goudet, J. 2002. Fstat v. 2.9.3.2: a computer program to calculate f-statistics. J. Hered. 86.
Horowitz, A. R., S. Kuntsedalov, V. Khasdan, and I. Ishaya. 2005. B and Q of Bemisia tabaci and their relevance to neonicotinoid and pyrethroid resistance. Arch. Insect Biochem. Physiol. 58: 216–225.
Jia, Z., K. Fu, X. Din, W. C. Guo, A. Tuerxun, W. H. Jiang, and A. S. Kader. 2017. Biotype identification and resistance status of Bemisia tabaci from Xinjiang Agriculture areas. Xinjiang Agric. Sci. 2: 114–122.
Judith, K. B., and H. Czosnek. 2002. Whityle transmission of plant viruses. Adv. Bot. Res. 36: 65–76.
Kim, M. S., and J. F. Crow. 1964. The number of alleles that can be maintained in a finite population. Genetics 49: 725–738.
Lewontin, R. C. 1972. The apportionment of human diversity, pp. 381–398. In Evolutionary biology. Springer, New York, NY.
Liu, S. S., P. J. De Barro, J. Xu, J. B. Luan, L. S. Zang, Y. M. Ruan, and G. R. Zhu. 2008. Sequence Analysis of mtDNA COI Gene and Molecular Phylogeny of Different Geographical Populations of Bemisia tabaci (Gennadius). Agri. Sci. Ch. 4: 533–541.
Nur, E. E., and H. S. Abu Salih. 1970. Cotton leaf curl virus disease. Trop. Pest Manag. 16: 121–131.
Paul, J., and D. Barro. 2012. The Bemisia tabaci species complex: questions to guide future research. J. Agric. Sci. 11: 187–196.
Paetkau, D., R. Slade, M. Burden, A. Estoup, D. Paetkau, R. Slade, M. Burden, and A. Estoup. 2004. Direct real-time estimation of migration rate using assignment methods: a simulation-based exploration of accuracy and power. Mol. Ecol. 13: 55–65.
Peakall, R., and P. E. Smouse. 2006. Genalex & genetic analysis in Excel. Population genetic software for teaching and research. Mol. Ecol. Resour. 6: 288–295.
Perring, T. M. 2001. The _Bemisia tabaci_ species complex. Crop Prot. 20: 725–737.
Piry, S., A. Alapetite, J.-M. Cornuet, D. Paetkau, L. Baudouin, and A. Estoup. 2004. GeneClass2: a software for genetic assignment and first generation migrants detection. J. Hered. 95: 536–539.
Pritchard, J. K., M. Stephens, and P. Donnelly. 2000. Inference of population structure using multilocus genotype data. Genetics. 155: 945–959.
Rannala, B., and J. L. Mountain. 1997. Detecting immigration by using multilocus genotypes. Proc. Nat. Acad. Sci. USA. 94: 9197–201.
Roditakis, E., M. Grispou, E. Morou, J. B. Kristoffersen, N. Roditakis, R. Nauen, J. Vontas, and A. Tsagkarakou. 2009. Current status of insecticide resistance in _Q_ biotype _Bemisia tabaci_ populations from Crete. Pest Manag. Sci. 65: 313–322.
Rohlf, F. J. 1987. NTSYS-pc: microcomputer programs for numerical taxonomy and multivariate analysis. Am. Statis. 41: 330.
Simon, C., F. Frati, A. Beckenbach, B. Crespi, H. Liu, and P. Flook. 1994. Evolution, weighting, and phylogenetic utility of mitochondrial gene sequences and compilation of conserved polymerase chain reaction primers. Ann. Entomol. Soc. Am. 87: 651–701.
Sokal, R., and C. D. Michener. 1958. A statistical method for evaluating systematic relationships. Uni. Kansas sci. Bulletin. 38: 1409–1438.
Tahir, M. N., I. Amin, R. W. Briddon, and S. Mansoor. 2011. The merging of two dynasties – identification of an African cotton leaf curl disease-associated begomovirus with cotton in Pakistan. PLoS One 6: e20366.
Valle, G. E., A. Lourenço, M. I. Zucchi, and J. B. Pinheiro. 2012. Low polymorphism revealed in new microsatellite markers for _Bemisia tabaci_ (hemiptera: aleyrodidae). Genet. Mol. Res. 11: 3899.
Wainaina, J. M., P. De Barro, L. Kubatko, M. A. Kehoe, J. Harvey, D. Karanja, and L. M. Boykin. 2018. Global phylogenetic relationships, population structure and gene flow estimation of _Trialeurodes vaporariorum_ (greenhouse whitefly). Bull. Entomol. Res. 108: 5–13.
Wang, Z. Y., H. F. Yan, Y. H. Yang, and Y. Wu. 2010. Biotype and insecticide resistance status of the whitefly _Bemisia tabaci_ from China. Pest Manag. Sci. 66: 1360–1366.
Weir, B. S., and C. C. Cockerham. 1984. Estimating F-statistics for the analysis of population structure. Evolution 38: 1358–1370.
Wu, S., Z. Wang, and Y. Wu. 2010. Competition between the _B_ and _Q_ biotypes of _Bemisia tabaci_ and its relevance to insecticide resistance. Chin. Bull. Entomol. 47: 1118–1121.
Zhang, Z. 2000. Some thoughts on the outbreaks of tobacco whitefly. Beijing Agric. Sci. (Suppl. _Bemisia tabaci_ Special) 1–3.
Zhang, J. J., J. Yang, Y. C. Li, L. Ning, and R. Z. Zhang. 2013. Genetic relationships of introduced Colorado potato beetle _Leptinotarsa decemlineata_ populations in Xinjiang, China. Insect Sci. 5: 643–654.
Zhao, L., R. Zhang, X. Yang, Y. Cui, and W. Huang. 2000. The important damage insect to cotton found in Xinjiang. Xinjiang Agric. Sci. 1: 27–28.
Zhou, Y. 1949. Records of whitefly in China. Chin. J. Entomol. 3: 1–18.