

# Phylogenetic Analysis and Rapid Identification of the Whitefly, Bemisia afer, in China

Authors: Chu, Dong, Liu, Guoxia, Wan, Fanghao, Tao, Yunli, and Gill, Ray J

Source: Journal of Insect Science, 10(86): 1-9

Published By: Entomological Society of America

URL: https://doi.org/10.1673/031.010.8601

The BioOne Digital Library (<u>https://bioone.org/</u>) provides worldwide distribution for more than 580 journals and eBooks from BioOne's community of over 150 nonprofit societies, research institutions, and university presses in the biological, ecological, and environmental sciences. The BioOne Digital Library encompasses the flagship aggregation BioOne Complete (<u>https://bioone.org/subscribe</u>), the BioOne Complete Archive (<u>https://bioone.org/archive</u>), and the BioOne eBooks program offerings ESA eBook Collection (<u>https://bioone.org/esa-ebooks</u>) and CSIRO Publishing BioSelect Collection (<u>https://bioone.org/csiro-ebooks</u>).

Your use of this PDF, the BioOne Digital Library, and all posted and associated content indicates your acceptance of BioOne's Terms of Use, available at <u>www.bioone.org/terms-of-use</u>.

Usage of BioOne Digital Library content is strictly limited to personal, educational, and non-commercial use. Commercial inquiries or rights and permissions requests should be directed to the individual publisher as copyright holder.

BioOne is an innovative nonprofit that sees sustainable scholarly publishing as an inherently collaborative enterprise connecting authors, nonprofit publishers, academic institutions, research libraries, and research funders in the common goal of maximizing access to critical research.



### Phylogenetic analysis and rapid identification of the whitefly, Bemisia afer, in China

Dong Chu<sup>1a</sup>, Guoxia Liu<sup>1</sup>, Fanghao Wan<sup>2</sup>, Yunli Tao<sup>1</sup>, Ray J Gill<sup>3b</sup>

<sup>1</sup>High-tech Research Center, Shandong Academy of Agricultural Sciences, Jinan 250100, Shandong, China <sup>2</sup>State Key Laboratory for Biology of Plant Diseases and Insect Pests, Institute of Plant Protection (South Campus), Chinese Academy of Agricultural Sciences, Beijing, 100081, China <sup>3</sup>Plant Pest Diagnostic Center, 3294 Meadowview Road, Sacramento, California, 95832 USA

### Abstract

The phylogenetic relationship between the whitefly *Bemisia afer* (Priesner & Hosny) (Hemiptera: Aleyrodidae) from China and other populations among the world were analyzed based on the mitochondrial cytochrome oxidase I (mtCOI) gene. Phylogenetic analysis of mtCOI sequences and those of reference *B. afer* sequences showed that the populations of the species could be separated into 5 clades (I-V). There were at least two clades of the species from China (IV and V). These data suggested that *B. afer* might be a species complex. The Chinese *B. afer* populations were most divergent with *B. afer* from the United Kingdom and African countries. The distance between the Chinese *B. afer* (IV and V) and clades I, II, and III is more than 32%, while the distance among clades I, II, III is lower than 7.7%. A new set of primers specific to *B. afer* was designed to amplify a region of approximately 400 bp to discriminate *B. afer* from other *Bemisia* species in China based on mtCOI sequences.

Keywords: mitochondrial cytochrome oxidase I, molecular markers Abbreviations: mtCOI, mitochondrial cytochrome oxidase I gene Correspondence: a chudong1977@hotmail.com, b rgill@cdfa.ca.gov Received: 2 July 2008, Accepted: 24 November 2008 Copyright : This is an open access paper. We use the Creative Commons Attribution 3.0 license that permits unrestricted use, provided that the paper is properly attributed. ISSN: 1536-2442 | Vol. 10, Number 86

#### Cite this paper as:

Chu D, Liu G, Wan F, Tao Y, Gill RJ. 2010. Phylogenetic analysis and rapid identification of the whitefly, *Bemisia afer*, in China. *Journal of Insect Science* 10:86 available online: insectscience.org/10.86

#### Introduction

During recent years, the outbreak of Bemisia tabaci (Priesner & Hosny) (Hemiptera: Aleyrodidae) and the serious damage caused by this whitefly pest in many countries have required researchers to study the biological and ecological characteristics of and effective control strategies against it (Brown et al. 2000; Brown 2007; De Barro et al. 2000, 2003). The identification of species in the genus Bemisia is the basis of this research, but the taxonomy of whiteflies has long been problematic because of similarities in the morphology of pupae and adults. Pupae of Bemisia species exhibit phenotypic variation in response to differences in leaf surface topology and to environmental and physical factors (Maruthi et al. 2007).

In China, *B. tabaci* became the major pest of the fiber crops, ornamental plants and vegetables (Chu et al. 2006, 2007, 2008). During field research, a Bemisia species, which was difficult to distinguish from B. tabaci, was discovered on Broussonetia (Linn.) Vent. (Urticales: papyrifera Moraceae). Based on the morphological characteristics of pupae and adults, the species was identified as B. afer. As B. tabaci has several close relatives and numerous biotypes, B. afer also is likely to have many forms and cryptic species. Earlier studies indicated that B. afer exhibits much greater morphological variation than does B. tabaci and its variants (Anderson et al. 2001; Maruthi et al. 2007). The Chinese B. afer has slightly different morphology compared to B. afer from other geographical locations, and it is expected that these differences would be reflected at the molecular level.

The mitochondrial cytochrome oxidase I (mtCOI) gene has been used extensively as a molecular marker to identify B. tabaci variants that exhibit rich biological differences (Frohlich et al. 1999; Hsieh et al. 2007) but lack distinguishing morphological features. Previous studies have shown that mtCOI sequences also are informative for identifying B. afer variants, which lack distinguishing morphological features (Maruthi et al. 2007). In this study, the mtCOI gene of *B. afer* was sequenced using the primer set (C1-J-2195 and L2-N-3014) that has been used extensively on *B. tabaci*, and the fragments were also sequenced. The phylogenetic relationships among the world populations were analyzed. The infection status of an endosymbiont Wolbachia of Chinese B. afer studied it often was because causes reproductive incompatibilities between infected and uninfected hosts, which can affect the divergence of mtDNA and can facilitate or even cause host speciation (Werren 1997; Ballard et al. 2004; Shoemaker et al. 2004). Finally, the specific primers to Chinese B. afer were designed based on the sequences of the mtCOI gene of Chinese B. afer and B. tabaci biotypes B and Q.

The objectives of the paper are: 1) to further analyze the phylogenetic relationships, based on the mitochondria COI gene, between Chinese populations of *B. afer* on *B. papyrifera* with other populations of *B. afer* from the United Kingdom and African countries and to discuss the relationship between the divergence of *B. afer* and the endosymbiont, *Wolbachia*; 2) to develop a rapid molecular marker based on the mtCOI gene to distinguish *B. afer* from *B. tabaci* biotypes B and Q, which are the predominate biotypes in China, especially the biotypes in the Shandong province. The aim is to

contribute to the understanding of the systematic status of B. *afer* populations in China and the genetic differentiation of B. *afer* worldwide.

#### **Materials and Methods**

## Collection of the samples and species identification

During 2006 and 2007, pupae and adults of *Bemisia* species on *B. papyrifera* were collected alive and placed singly into tubes containing 95% ethanol. The species were identified based on the pupae and adults.

#### **DNA extraction and PCR**

Genomic DNA was extracted from individual adults according to the method described previously by Frohlich et al. (1999). Polymerase chain reaction (PCR) was employed to amplify fragments of the *B. afer* mitochondrial COI gene (800-820 bp), using parameters and PCR primers (C1-J-2195 and L2-N-3014) as described by Frohlich et al. (1999).

PCR assays were conducted using 2  $\mu$ l of each template DNA in a total reaction volume of 25  $\mu$ l. PCR conditions follow Frohlich et al. (1999), with 1 unit of Taq DNA polymerase. PCR products were separated on 1.0% agarose gel. The bands were visualized by ethidium bromide staining and viewed with a UV light source.

# Cytochrome oxidase I sequencing and phylogenetic analysis

PCR products were purified using an EZ Spin Column DNA Gel Extraction Kit (Sangon Technology Company, www.sangon.com/ index.htm) according to the manufacturer's instructions. The DNA sequence for each PCR product was determined from the 5'end at the Sangon Technology Company. The mtCOI sequences determined were deposited in GenBank.

Phylogenetic analysis included all available mtCOI sequences from GenBank and sequences from this study, with the sequences of Bemisia tabaci (mainly including the biotypes indigenous from China), В. tuberculata, B. berbericola, Trialeurodes vaporariorum, and Trialeurodes abutilonea as the outgroup (Table 1). The mtCOI sequences were aligned using the CLUSTAL W algorithm (Thompson et al. 1994). The aligned mtCOI sequences of ~ 600 bp are presented. Distances based on the mtCOI sequences of ~600 bp were calculated based on the Kimura 2-parameter model using MEGA 4.1 (Tamura et al. 2007). The ME (Molecular Evolution) and MP (Maximum Parsimony) algorithms available in MEGA were used to infer phylogenetic 4.1 relationships from the sequences. One thousand Bootstrap replicates were performed for each analysis.

On the basis of the results of phylogenetic analysis, the *B. afer* specimens were separated into five subclades. The sequences in the subclades were selected to further calculate distances within and between group average calculations using MEGA 4.1.

#### Wolbachia detection of Chinese B. afer

All *B. afer* were also screened for *Wolbachia* infection by PCR, employing the primers wsp81F and wsp691R (Zhou et al. 1998), which amplify part of the *Wolbachia* surface protein gene (*wsp*). The study included 15 Chinese *B. afer* individuals, and the PCR was repeated three times.

#### Development of the specific diagnostic test

Experiments showed that the primers C1-J-2195 and L2-N-3014 did not always amplify

products of the expected size, although the DNA was useful. A set of primers specific to the *B. afer* mtCOI gene was designed, which included the newly designed forward primer Bafer-J2 (5'-GTTAGTTTTGGGGATTAGTC-3') by aligning in CLUSTAL W (Thompson et al. 1994) and the reverse primer L2-N-3014 (5'-TCCAATGCACTAATCTGCCATATTA-

3'). The other whitefly species (Table 2) were used in PCR reactions to test the specificity of primers to *B. afer*. The PCR reaction mix followed the method previously described by Frohlich et al. (1999). Reactions used the following PCR program: 94!"# for 2 min; followed by 30 cycles of 94!"# "for 1 min, 54!" # for 1 min, and 72!"# for 1 min; and ending

Whitefly	Acronym	GenBank	Location	Cladea
species	,	accession No.		
B afer	Al8420377anzibarTan	AI842037	Africa	1
	Al842039ZanzibarTan	A1842039	Africa	
	Al8420427anzibarTan	A1842042	Africa	
	Al842043ZanzibarTan	A1842043	Africa	
	Al842034KibabaTan	A1842034	Africa	
	Al842024KibabaTan	A1842024	Africa	
	AF418673Namulongl lg	ΔF418673	Africa	
	Al842022NamulongeTan	A1842022	Africa	1
		Δ1842047	Africa	
	Al842045ChenikaTan	Δ1842045	Africa	
	Alga2029KibabaTan	A1942073	Africa	
	AJ042027KibahaTan	A1942027	Africa	
	AJ042030KibahaTan	A1942030	Africa	
		AJ842031	Africa	
		AJ042032	Africa	
		AJ042033	Africa	
	AJ842048Malawi	AJ842048	Africa	
		AJ842049	Africa	
	AJ842050Malawi	AJ842050	Africa	
	AJ842023NamulongeUg	AJ842023	Africa	
	AJ842044Chenika I an	AJ842044	Africa	
	AJ842052Surrey	AJ842052	UK	
	AJ784260Xinjiang	AJ784260	China	
	B.afer I to B.afer8	EU825776-EU825783	China	
	AY057218	AY057218	-	
B .tuberculata	AY057220B.tuberculata	AY057220	-	
B . berbericola	AY057219B.berbericola	AY057219	-	
B. tabaci	UgandaAF418665	AF418665	Uganda	
	CyprusDQ365877	DQ365877	Cyprus	
	SpainQDQ365875	DQ365875	SpainQ	
	ZimbabweAF344285	AF344285	Zimbabwe	
	CameroonAF344258	AF344258	Cameroon	
	SeychellesAJ550182Ms	AJ550182	Seychelles	
	TurkeyAY827616M	AY827616	Turkey	
	DQ174542USAA	DQ174542	USA	
	TaiwanAY686075NB	AY686075	Taiwan	
	ChinaHeNAY686090B	AY686090	Henan,China	
	ChinaHNAY686085NB	AY686085	Hunan, China	
	ChinaAY686089NB	AY686089	Hubei, China	
	ChinaCQAY686091NB	AY686091	Chongging, China	
	ChinaGDAY686072NB	AY686072	Guangdong,China	
	ChinaGDAY686064NB	AY686064	Guangdong.China	
	ChinaZIAY867557NB	AY867557	Zhejiang, China	
	ChinalSAY686088NB	AY686088	liangsu.China	
	ChinaZIAI867556NB	AI867556	Zheijang China	
	ChinaGDAY686083NB	AY686083	Guangdong China	
т	AFLI0708T vaporariorum	AFI10708	-	
vaborariorum	AI550183T vaporariorum	AI550183	Reunion	
	Aj5501051.vap0rari0fulli	7,550105	Realiton	

-, indicates unknown

Journal of Insect Science | www.insectscience.org

with 72!"# for 5 min. PCR products were separated on 1.0% agarose gel. The bands were visualized by ethidium bromide staining and viewed with a UV light source.

#### Results

#### Morphology of *B. afer*

Adults of New World specimens of B. afer have the upper and lower eyes completely separate in both sexes, as contrasted with B. tabaci adults, which have one ommatidium connection. Some afer В. from the Macaronesian Islands have the male eyes connected by one ommatidium but separated in the female, while others from different hosts have both eyes separate as in the North American forms (RJ Gill, unpublished data). In the specimens for this study, the female had a one ommatidium connection, while the male had both eyes connected positively with one ommatidium, but also another ommatidium almost but not touching. In the adults, there were clear morphological differences.

#### Phylogenetic analysis of *B.afer*

A total of 8 *B. afer* mtCOI gene sequences of about 600 bases were obtained from populations in Shandong, China during 2006

and 2007. The GenBank accession numbers EU825776 EU825783. are to The phylogenetic tree generated with the Minimum Evolution (ME) method is shown in Figure 1. The tree generated with MP (Maximum Parsimony) method (not shown) is similar to Figure 1. The tree that was generated by heuristic research had 65% confidence level. Based on the trees, B. afer could be separated into 5 clades. The populations from Xinjiang, China (AJ784260Xinjiang) and Shandong, China (Bafer1-Bafer8) were grouped in clade IV and V, respectively. The Chinese B. afer populations (clade IV and V) were most divergent with clades I, II, and III.

## Genetic differentiation of the *B.afer* in China and *Wolbachia* infection

Average distances within and between clades based on mtCOI of whiteflies are summarized in Table 3. The Chinese *B. afer* populations were most divergent with *B.afer* from the United Kingdom and African countries. The distance between the Chinese *B. afer* (clade IV and V) and clades I, II, and III was more than 32%, while the distance among clades I, II, and III were lower than 7.7%. No *Wolbachia* could be detected in Chinese

Whitefly species or biotype	Geographical origin	Host plant orgin	Collection year	
Bemisia tabaci biotype B	Shandong, China	Lycopersicon esculeutum	2007	
	Shandong, China	Euphorbia pulcherrima	2007	
	Shandong, China	Gossypium herbaceum	2007	
	Shandong, China	Solanum melongena	2007	
Bemisia tabaci biotype QIª	Shandong, China	Lycopersicon esculeutum	2007	
	Shandong, China	Euphorbia pulcherrima	2007	
	Shandong, China	Gossypium herbaceum	2007	
	Shandong, China	Solanum melongena	2007	
	Shandong, China	Capsicum frutescens	2007	
Bemisia tabaci biotype Q2 ª	Cyprus	Gossypium herbaceum	2006	
Bemisia tabaci biotype Nauru <sup>b</sup>	Taiwan	Euphorbia pulcherrima	2007	

<sup>b</sup> Described in Hsieh et al.(2007)

Journal of Insect Science | www.insectscience.org



High quality figures are available online.

Journal of Insect Science | www.insectscience.org

populations of *B.afer* (clade V).

#### Specific primers for the *B*. *afer* in China

Figure 2 shows the PCR products generated from the DNA of several whitefly species using Bafer-J2 and L2-N-3014 primers. A band of approx 400 bp was obtained from DNA of *B. afer* from Shandong, China. No specific PCR products were obtained from DNA of *B. tabaci* biotype B, Q1, Q2, or Nauru.

#### Discussion

The phylogenetic analysis based on the mtCOI sequences suggested that the *B. afer* is a species complex that includes many genetically divergent clades. The result based on the molecular marker is consistent with the analysis based on the morphological characteristics.

This study revealed the presence of at least 5 clades in *B. afer* worldwide. The

 Table 3. Average distance within and between clades of whiteflies based on mtCOI. The genetic distance among the haplotypes within each clade is presented along the diagonal.

•	B. afer								-	-
	Clade I	Clade II	Clade III	Clade IV	Clade V	B. tabaci	в. tuberculata	в. berbericola	ı. vaporariorum	ı. abutilonea
B. afer Clade	0.002									
B. afer Clade	0.013	0.01								
B. afer Clade	0.077	0.073	n/c							
B. afer Clade IV	0.33	0.325	0.323	n/c						
B. afer Clade V	0.334	0.328	0.323	0.01	0					
B. tabaci	0.445	0.44	0.455	0.372	0.37	0.175				
B. tuberculata	0.375	0.378	0.381	0.333	0.338	0.314	n/c			
B. berbericola	0.442	0.428	0.426	0.331	0.324	0.366	0.288	n/c		
T. vaporariorum	0.577	0.581	0.626	0.62	0.62	0.641	0.533	0.608	0	
T. abutilonea	0.772	0.777	0.893	0.736	0.736	0.765	0.644	0.682	0.516	n/c

n/c, not calculated.



**Figure 2.** PCR products generated using the *Bemisia afer* specific primers (Bafer-J2 and L2-N-3014) (lanes 1-3); *Bemisia tabaci* biotype B (lanes 4-5), biotype Q1 (lanes 6-7), biotype Q2 (lane 8-9), biotype Naura (lane 10). M: 100 bp molecular weight marker, the sizes of which are shown on the left. High quality figures are available online.

endosymbiont *Wolbachia* was not detected in *B. afer* and may not have affected the evolution of the Chinese *B. afer* (clade V). Studies with higher sample sizes are required and detailed examinations of morphological and molecular characters are necessary to understand the *B. afer* species complex.

In China, there are at least two clades of B. *afer* based on the mtCOI sequences. Although this study confirmed the presence of B. *afer* in China, the biology of the Chinese species, including host ranges, is still unknown and should be further studied. This study shows that a simple, PCR-based technique is sufficient for the reliable identification of B. *afer* using a new primer pair designed to amplify a portion of the mtCOI gene, which has been shown to be specific to the Chinese B. *afer* (clade V).

#### Acknowledgements

We would like to acknowledge Dr. Ian Denholm (Rothamsted Experimental Station) and Chia-Hung Hsieh (National Taiwan University Taiwan University) for providing whitefly samples for the experiments. This work was funded by the Outstanding Youth Science Foundation of Shandong Province (JQ200811), the Key Project of Chinese National Programs for Fundamental Research and Development (2009CB119200), the National Natural Science Foundation of China (30771410).

#### References

Anderson PK, Martin JH, Hernandez P, Lagnaout A. 2001. *Bemisia afer sens. lat.* (Homoptera: Aleyrodidae) outbreak in the Americas. *Florida Entomologist* 84: 316-317. Ballard JWO, Whitlock MC. 2004. The incomplete natural history of mitochondria. *Molecular Ecology* 13: 729-744.

Brown JK. 2007. The *Bemisia tabaci* complex: Genetic and phenotypic variability drives begomovirus spread and virus diversification. *Plant Disease APSNet*. Available from: http://www.apsnet. org/online/feature/btabaci/

Brown JK, Frohlich DR, Rosell RC. 1995. The sweetpotato or silverleaf whiteflies: Biotypes of *Bemisia tabaci* or a species complex. *Annual Review of Entomology* 40: 511-534.

Chu D, Jiang T, Liu GX, Jiang DF, Tao YL, Fan ZX, Zhou HX, Bi YP. 2007. Biotype status and distribution of *Bemisia tabaci* (Hemiptera: Aleyrodidae) in Shandong province of China based on mitochondrial DNA markers. *Environmental Entomology* 36: 1290-1295.

Chu D, Wan FH, Tao YL, Liu GX, Fan ZX, Bi YP. 2008. Genetic differentiation of *Bemisia tabaci* (Hemiptera: Aleyrodidae) biotype Q based on mitochondrial DNA markers. *Insect Science* 15: 115-123.

Chu D, Zhang YJ, Brown JK, Cong B, Xu BY, Wu QJ, Zhu GR. 2006. The introduction of the exotic Q biotype of *Bemisia tabaci* (Gennadius) from the Mediterranean region into China on ornamental crops. *Florida Entomologist* 89: 168-174.

De Barro PJ, Driver F, Trueman JWH, Curran J. 2000. Phylogenetic relationships of world populations of *Bemisia tabaci* (Gennadius) using ribosomal ITS1. *Molecular Phylogenetics and Evolution* 16: 29-36.

De Barro PJ, Scott KD, Graham GC, Lange CL, Schutze MK. 2003. Isolation and

characterization of microsatellite loci in *Bemisia tabaci. Molecular Ecology Notes* 3: 42-43.

Frohlich DR, Torres-Jerez I, Bedford ID, Markham PG, Brown JK. 1999. A phylogeographical analysis of *Bemisia tabaci* species complex based on mitochondrial DNA markers. *Molecular Ecology* 8: 1683-1691.

Hsieh CH, Wang CH, Ko CC. 2007. Evidence from molecular markers and population genetic analyses suggest recent invasions of the Western North Pacific region by biotypes B and Q of *Bemisia tabaci* (Gennadius). *Environmental Entomology* 36: 952-961.

Maruthi MN, Rekha AR, Sseruwagi P, Hillocks RJ. 2007. Mitochondrial DNA variability and development of a PCR diagnostic test for populations of the whitefly *Bemisia afer* (Priesner and Hosny). *Molecular Biotechnology* 35: 31-40.

Shoemaker DD, Dyer KA, Ahrens M, McAbee K, Jaenike J. 2004. Decreased diversity but increased substitution rate in host mtDNA as a consequence of a *Wolbachia* endosymbiont infection. *Genetics* 168: 2049-2058.

Tamura K, Dudley J, Nei M, Kumar S. 2007. MEGA4: Molecular Evolutionary Genetics Analysis (MEGA) software version 4.0. *Molecular Biology and Evolution* 24:1596-1599.

Thompson JD, Higgins DG, Gibson TJ. 1994. CLUSTAL W: Improving the sensitivity of progressive multiple sequence alignment through sequence weighting, positionsspecific gap penalties and weight matrix choice. *Nucleic Acids Research* 22: 4673-4680. Werren JH. 1997. Biology of *Wolbachia*. *Annual Review of Entomology* 42: 587-609.

Zhou W, Rousset F, O'Neill S. 1998. Phylogeny and PCR-based classification of *Wolbachia* strains using *wsp* gene sequences. *Proceedings of the Royal Society B: Biological Sciences* 265: 509-515.