Development of Species-Specific Markers and Molecular Differences in Mitochondrial and Nuclear Dna Sequences of Aphis Gossypii and Myzus Persicae (Hemiptera: Aphididae)

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DEVELOPMENT OF SPECIES-SPECIFIC MARKERS AND MOLECULAR DIFFERENCES IN MITOCHONDRIAL AND NUCLEAR DNA SEQUENCES OF APHIS GOSSYPII AND MYZUS PERSICAЕ (HEMIPTERA: APHIDIDAE)

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ABSTRACT
Aphids are one of the major challenges in the agricultural pest management programmes. A reliable, quick, accurate and life stage-independent method of identification of vectors such as Aphis gossypii Glover and Myzus persicae (Sulzer) is important with respect to virus transmission, insecticide resistance and biological control. The complex life cycles, significant polymorphism, immature taxonomy and absence of trained manpower make the identification of these pests difficult. On the other hand, molecular identification is not limited by the above factors and can be easily executed by a non-specialist with a little training. Since the mitochondrial cytochrome oxidase-1 (COI) exhibits maternal inherited characteristics and reliable inter-specific variation as compared to other molecular markers, species-specific markers have been developed using existing nucleotide differences in the COI partial sequences of both A. gossypii and M. persicae. These species-specific markers have proved to be adequate for the molecular identification of these species, and to corroborate their morphological identification. Molecular diversity analyses using both mitochondrial and nuclear markers showed that neither A. gossypii nor M. persicae has as much genetic variability as expected. An outcome of this investigation is the development of a technique that is useful for the quick identification of A. gossypii and M. persicae, a critical factor in understanding the epidemiology and management of the potyviruses, and also in facilitating quarantines of these 2 pests.

Key words: Aphis gossypii, Myzus persicae, species-specific marker, COI

RESUMEN
Los áfidos son uno de los retos más grandes en los programas de manejo de plagas agrícolas. Un método de identificación de vectores como Aphis gossypii Glover y Myzus persicae (Sulzer) que es confiable, rápido, preciso e independiente del estadio de la vida presente es importante con respecto a la transmisión de enfermedades por vectores, resistencia a los insecticidas y control biológico. El complicado ciclo de vida el grado de polimorfismo, taxonomía de los inmaduros y la falta de mano de obra calificada hace difícil la identificación de estas plagas. Por otro lado, la identificación molecular no está limitada por los factores mencionados anteriormente y puede ser ejecutada fácilmente por un no-especialista con un poco de entrenamiento. Puesto que la oxidasa mitocondrial citocromo-1 (COI), exhibe características heredadas maternas y variación inter-específica confiable de en comparación con los otros marcadores moleculares, se han desarrollado marcadores específicos para las especies utilizando las diferencias que existen en los nucleótidos de las secuencias de COI parciales de A. gossypii y M. persicae. Se han demostrado que estos marcadores específicos son adecuados para la identificación molecular de estas especies, y para corroborar su identificación morfológica. Los análisis de la diversidad molecular utilizando los marcadores mitocondriales y nucleares, demostró que A. gossypii y M. persicae no tienen mucha variabilidad genética a como se esperaba. Uno de los resultados de esta investigación es el desarrollo de una técnica que es útil para la identificación rápida de A. gossypii y M. persicae, un factor
Predominant among the many challenges in sustaining productivity of food and nutritional security are the direct and indirect damages caused by insect pests. Management of the plant pathogens vectored by insect pest is all the more complex because of the insect factors influencing the epidemiology of the disease. Aphid transmitted viruses are numerous and predominant among the many plant viruses transmitted by insects. Aphids transmit only plant viruses, and mostly in a non-persistent manner. However, some plant viruses are transmitted in semi-persistent and persistent way. Among the aphid vectors of viruses, themelon aphid or cotton aphid, *Aphis gossypii* Glover, and the green peach aphid, *Myzus persicae* (Sulzer) are predominant. While hundreds of aphid species infest plants, only a few are predominant vectors; and it is still not clear why species, such as *Aphis gossypii* and *Myzus persicae*, are effective vectors of many potyviruses transmitted in a non-persistent way, nor what factors determine these species’ competence to transmit a virus.

The complex life cycles and significant polymorphism makes the identification of *A. gossypii* and *M. persicae* difficult. Their rapid and parthenogenetic reproduction and feeding behavior of aphids results inconsiderable crop damage. Their feeding can cause the induction of premature leaf senescence (Shah et al. 2005), secondary pathogen infection through fungal growth on aphid honeydew and the transmission of plant viruses, which remains the greatest threat for agricultural crops. *Aphis gossypii* and *M. persicae* are known to be capable of transmitting more than 75 plant viruses, and they are most versatile of insect vectors of plant viruses (Blackman & Eastop, 2000). In India *Papaya ringspot virus* (PRSV) is transmitted by both *A. gossypii* and *M. persicae* (Kalleshwaraswamy et al. 2007). Accurate and timely identification not limited by life stage of aphid vectors is important in elucidating the epidemiology of potyviruses, their management and also in quarantine.

Various molecular markers have been employed by researchers for species identification and molecular phylogeny studies, viz., Cytochrome b (Raboudi et al. 2005), 16S rRNA (von Dohlen & Moran 2000), 18S rRNA, 28S rRNA, 5.8S rRNA (Ji et al. 2003), internal transcribed spacers, elongation factor-1α (Jernaes & Arngaad 2006; Ji et al. 2003), mitochondrial cytochrome oxidase (mtCOI) (von Dohlen et al. 2006), etc., in aphids. Mitochondrial genes, because of maternal inheritance and reliable inter-specific variation as compared to other markers (Savolainen et al. 2005), have been widely employed in studying the molecular systematics of insects (Simon et al. 1994). In our study molecular diversity analyses were carried out using both mitochondrial (mitochondrial cytochrome oxidase-I) and nuclear (elongation factor-1α) genes.

The present investigation was carried out to develop the species-specific markers for *A. gossypii* and *M. persicae* based on COI for life-stage independent identification, and also to carry out phylogenetic analyses based on mitochondrial cytochrome oxidase I and II (COI and COII) and elongation factor-1α (EF1α).

**Materials and Methods**

**Maintenance of Stock Culture and Morphological Identification**

For developing species-specific markers, the *A. gossypii* and *M. persicae*, were collected on cotton (*Gossypium hirsutum* L.; Malvales; Malvaceae), and brinjal (*Solanum melongena* L.; Solanales; Solanaceae) respectively, at the experimental farm of the Indian Institute of Horticultural Research (IIHR), Bangalore, India. Pure cultures of both species were maintained on cotton and on brinjal at room temperature (30-32 °C) and 70-90% RH. In addition to these two species, 33 different species of aphids viz. *Aphis fabae* (Theobald), *Aphis punicae* Passerini, *Aphis craccivora* Koch, *Aphis nerri* (Boyer de Fonscolombe), *Aphis spireaca* Patch, *Melanaphis sacchari* (Zehntner), *Melanaphis donacis* (Passerini), *Acrystosiphon pismum* (Harris), and *Macrosiphum rosea* (L.), etc. were collected from the Division of Entomology, National Bureau of Agriculturally Important Insects (NBAII), Bangalore for testing the species-specific primers, which were developed in the present study. In molecular diversity studies, *A. gossypii* and *M. persicae* were collected from different host plants from different geographical locations in India (Tables 1 and 2) samples preserved in ethyl alcohol (100%) and stored at -20 °C until further use. Morphological identifications of *A. gossypii* and *M. persicae* were carried out according to Blackman (2010) prior to molecular studies.

**DNA Isolation and Polymerase Chain Reaction**

Total DNA was isolated from individual *A. gossypii* and *M. persicae* from the stock culture using
the ‘salting out’ procedure adapted from Rugman Jones et al. (2006). Individual aphid specimens were pierced through one side of the abdomen by using a sterilized minute pin and placed in 0.5 mL PCR tubes containing 100 μL of TNES (10 mM Tris-HCl, pH 7.5, 1 mM EDTA, 100 mM NaCl, 5% Sucrose). Tubes were incubated at 37 °C for 24 h, and somewhat later, proteins were precipitated with the addition of 5 M NaCl and vigorous shaking for 30 s. Proteins were pelleted in a microfuge at 13,000 rpm for 5 min, and the supernatant was transferred to a new microfuge tube. DNA was

Table 1. Analyzed samples of *Aphis gossypii* with description of the host plant, site of collection and NCBI-GenBank accession numbers.

| Sl. No. | Species  | Host plant   | Site of collection | NCBI-GenBank accessions |
|---------|----------|--------------|--------------------|-------------------------|
| 1       | *A. gossypii* | Sweet orange | Nagpur (NRCC-1)    | JQ67095 JQ67109 JQ690307 |
| 2       | *A. gossypii* | Sweet orange | Nagpur (NRCC-2)    | JQ67096 JQ67110 JQ690308 |
| 3       | *A. gossypii* | Sweet orange | Nagpur (1)         | JQ67097 JQ67111 JQ690309 |
| 4       | *A. gossypii* | Sweet orange | Nagpur (2)         | JQ67098 JQ67112 JQ690310 |
| 5       | *A. gossypii* | Cotton      | Bangalore          | JQ67099 JQ67113 JQ690311 |
| 6       | *A. gossypii* | Watermelon  | Bangalore          | JQ67100 JQ67114 JQ690312 |
| 7       | *A. gossypii* | Cotton      | Shimoga            | JQ67101 JQ67115 JQ690313 |
| 8       | *A. gossypii* | Watermelon  | Calicut (IISR)     | JQ67102 JQ67116 JQ690314 |
| 9       | *A. gossypii* | Watermelon  | Cochin             | JQ67103 JQ67117 JQ690315 |
| 10      | *A. gossypii* | Watermelon  | Kasaragod (CPCRI)  | JQ67104 JQ67118 JQ690316 |
| 11      | *A. gossypii* | Watermelon  | Calicut (Balussery)| JQ67105 JQ67119 JQ690317 |
| 12      | *A. gossypii* | Hibiscus    | Calicut (Balussery)| JQ67106 JQ67120 JQ690318 |
| 13      | *A. gossypii* | Cotton      | Pune               | JQ67107 JQ67121 JQ690319 |
| 14      | *A. gossypii* | Cotton      | Gujarath           | JQ67108 JQ67122 JQ690320 |
| 15      | *A. gossypii* | Cotton      | Kolar              | JQ690329 JQ690299 JQ690315 |
| 16      | *A. gossypii* | Cotton      | Coimbatore (TNAU)  | JQ690330 JQ690300 JQ690322 |
| 17      | *A. gossypii* | Cotton      | Akola, Maharashtra | JQ690331 JQ690301 JQ690323 |
| 18      | *A. gossypii* | Sponge guard | Jaipur, Rajasthan  | JQ690332 JQ690302 JQ690324 |
| 19      | *A. gossypii* | Brinjal     | Jaipur, Rajasthan  | JQ690333 JQ690303 JQ690325 |
| 20      | *A. gossypii* | Pumpkin     | Jaipur, Rajasthan  | JQ690334 JQ690304 JQ690326 |
| 21      | *A. gossypii* | Cotton      | Kaurol, Rajasthan  | JQ690335 JQ690305 JQ690327 |
| 22      | *A. gossypii* | Cotton      | Dausa, Rajasthan   | JQ690336 JQ690306 JQ690328 |

Table 2. Analyzed samples of *Myzus persicae* with description of the host plant, site of collection and the NCBI-GenBank accession numbers.

| Sl No. | Species  | Host plant | Site of collection | NCBI-GenBank accessions |
|--------|----------|------------|--------------------|-------------------------|
| 1      | *M. persicae* | Egg plant  | Nagpur             | JQ808454 JQ808469 JQ808484 |
| 2      | *M. persicae* | Okra       | Nagpur             | JQ808455 JQ808470 JQ808485 |
| 3      | *M. persicae* | Egg plant  | Bangalore (IIHR)   | JQ808456 JQ808471 JQ808486 |
| 4      | *M. persicae* | Okra       | Bangalore (IIHR)   | JQ808457 JQ808472 JQ808487 |
| 5      | *M. persicae* | Watermelon | Bangalore          | JQ808458 JQ808473 JQ808488 |
| 6      | *M. persicae* | Watermelon | Bangalore (IIHR)   | JQ808459 JQ808474 JQ808489 |
| 7      | *M. persicae* | Egg plant  | Shimoga           | JQ808460 JQ808475 JQ808490 |
| 8      | *M. persicae* | Egg plant  | Calicut (IISR)     | JQ808461 JQ808476 JQ808491 |
| 9      | *M. persicae* | Egg plant  | Calicut (Balussery)| JQ808462 JQ808477 JQ808492 |
| 10     | *M. persicae* | Okra       | Gujarath           | JQ808463 JQ808478 JQ808493 |
| 11     | *M. persicae* | Egg plant  | Jaipur             | JQ808464 JQ808479 JQ808494 |
| 12     | *M. persicae* | Egg plant  | Coimbatore (TNAU)  | JQ808465 JQ808480 JQ808495 |
| 13     | *M. persicae* | Okra       | Maharashatra (Akola)| JQ808466 JQ808481 JQ808496 |
| 14     | *M. persicae* | Okra       | Kolar (Karnataka)  | JQ808467 JQ808482 JQ808497 |
| 15     | *M. persicae* | Egg plant  | Kasaragod (CPCRI)  | JQ808468 JQ808483 JQ808498 |
precipitated from the supernatant by adding of one volume of ice-cold 100% ethanol and incubation for 1 h at -20 °C. DNA was then pelleted by centrifugation, washed in ice-cold 70% ethanol, air-dried, and finally dissolved in 30 μL of sterile distilled water. The original specimens were preserved as specimen vouchers in Entomology Division, Indian Institute of Horticultural Research.

For molecular diversity analyses, we used both mitochondrial (mitochondrial cytochrome oxidase-I and II) and nuclear (elongation factor-1) genes (primer details in Table 3). The species-specific markers were developed using the mitochondrial cytochrome oxidase I (COI) gene, which resulted in the amplification of 658 bp fragment. PCR was carried out in a thermal cycler (ABI-Applied Biosystems, Veriti, USA) with the following cycling parameters; 94 °C for 4 min as initial denaturation followed by 35 cycles of 94 °C 30 s, (46 °C-54 °C) for 40 s, 72 °C for 40 s and 72 °C for 20 min as final extension. PCR was performed in 25 μL total reaction volume containing 20 picomoles of each primer, 10 mM Tris HCl (pH-8.3), 50 mM KCl, 2.5 mM MgCl₂, 0.25 mM of each dNTP and 0.5U of Taq DNA polymerase (Fermentas Life Sciences, Maryland, USA). The amplified products were resolved in 1.0% agarose gel, stained with ethidium bromide (10μg/mL) and visualized in a gel documentation system (UVP). For the species-specific primers mentioned in Table 4, PCR mix and PCR cycling parameters were the same except for the annealing temperature viz., 64 °C for 45 s for both A. gossypii and M. persicae.

**Molecular Cloning and Sequencing**

The PCR amplified fragments were eluted using Nucleospin® Extract II according to the manufacturer’s protocol (Macherey-Nagel, Düren, Germany) and ligated into the general purpose-cloning vector, InsT/Aclone (Fermentas GmbH, St. Leon-Rot, Germany) according to the manufacturer’s protocol. Blue/white selection was carried out and all the white colonies were maintained on LBA containing ampicillin (100 mg/ml), incubated at 37 °C overnight and stored at 4 °C until further use. Plasmids were prepared from the overnight culture of the positive colonies cultured in LB broth (enzymatic casein- 10 g, yeast extract-5 g, NaCl-5 g in 1000 mL of water, pH-7.0) using GeneJET™ Plasmid Miniprep Kit (Fermentas GmBH, St. Leon-Rot, Germany) according to manufacturer’s protocol, from the over-night cultures of the 5 randomly selected clones grown in LB broth. Sequencing was carried out in an automated sequencer (ABI Prism® 3730 XL DNA Analyzer; Applied Biosystems, Maryland, USA) using M13 universal primers both in forward and reverse directions.

**Development of Species-Specific Markers and Molecular Diversity**

Homology search was carried out using BLAST (http://www.ncbi.nlm.nih.gov), and the differences in COI sequences of A. gossypii and M. persicae were determined using the sequence alignment editor BioEdit version 7.0.5.3 (Hall 1999). Sequences for A. gossypii and M. persicae

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**Table 3. Primers employed in the current study.**

| Region      | Gene Location | Primer Name       | Sequence                  | Reference                      |
|-------------|---------------|-------------------|---------------------------|--------------------------------|
| Mitochondria | COI           | LCO1490           | 5’-GGTCAACAAATCATATAAGATATTGG-3’   | Hebert et al. 2003a,b         |
|             |               | HCO2198           | 5’-TAAACTTCAAGGGTGACCCAAAAATCA-3’ |                                |
| Mitochondria | tRNA/COII     | 2993+             | 5’-CATTCATATTCAGAATTACC-3’    | Stern 1994                     |
|             |               | A3772             | 5’-GAGACCATTACTGCTTCAGTCACT-3’ | Normark 1996                   |
| Nuclear DNA | EF1α          | EF3               | 5’-GAGCTGGAACGTGGATAC-3’      | von Dohlen et al. 2002        |
|             |               | EF6               | 5’-TGACCAGGGTGGTTC-3’         |                                |

**Table 4. Species specific molecular markers developed for Aphis gossypii and Myzus persicae.**

| Species     | Primer       | Binding Region (bp) | Product size (bp) |
|-------------|--------------|---------------------|-------------------|
| A. gossypii | KBR(AG)-F    | 5’- TTCTTCTTTGAAATTATCCGATTA -3’ | 43-70             |
|             | KBR(AG)-R    | 5’- AAGATAGGGTTCTCCCCACCT -3’ | 616-643           |
| M. persicae | KBR(MP)-F    | 5’- ATCATACCTAGATCTTTAATCCGATTA -3’ | 43-70             |
|             | KBR(MP)-R    | 5’- TGGATTATATTTAAGATTGTACAAATA -3’ | 445-472           |
were deposited with the NCBI database, and the accession numbers are recorded in Tables 1 and 2. To develop the species-specific markers for \( A. \) gossypii and \( M. \) persicae, 5 sets of forward and reverse primers were synthesized based on the variable regions in the aligned sequences of the same (Fig. 1). The primers thus designed were validated both on identified \( A. \) gossypii and \( M. \) persicae (8 specimens each) and 5 each of the unidentified test specimens collected on cotton and brinjal. The PCR amplified fragments resulting from species-specific markers for \( A. \) gossypii and \( M. \) persicae were further cloned, sequenced and analyzed as above. In order to validate the species-specific primer specificity, we tried cross amplification through PCR for both the primer sets developed in the present study with 33 different species of aphids viz. \( Aphis \) fabae (Theobald), \( Aphis \) punicae Passerini, \( Aphis \) craccivora Koch, \( Aphis \) nerii Boyer de Fonscolombe, \( Aphis \) spiraeola Patch, \( Melanaphis \) sacchari (Zehntner), \( Melanaphis \) donacis (Passerini), \( Acyrthosiphon \) pisum (Harris), and \( Macrosiphum \) rosea (L.), etc., which were morphologically identified and collected from National Bureau Agriculturally Important Insects, Bangalore (DNA barcodes for all these 35 species were developed and submitted to both iBOL and NCBI, unpublished data).

**Sequence Analysis**

All the sequences generated in the present study, corresponding to COI, COII and EF1\( \alpha \) was aligned using BioEdit. The alignment was further analyzed using MEGA 4.0 (Kumar et al. 1993). Maximum Parsimony (MP) and Neighbour-Joining (NJ) trees were constructed using the Kimura-2-parameter (K2P) distance model (Kimura 1980; Saitou & Nei 1987). All the corresponding sequences for different mitochondrial and nuclear markers of \( A. \) gossypii and \( M. \) persicae were deposited in the NCBI-GenBank. Phylogenetic analyses were carried out by Maximum Parsimony (MP) and Bayesian approach using PAUP v4b10 (Swofford, 1998).

**RESULTS AND DISCUSSION**

The PCR amplicon of the same size (approx.700 bp) was amplified for both \( A. \) gossypii and \( M. \) persicae and the sequences showed that the total nucleotide length obtained was 709 bp for both \( A. \) gossypii and \( M. \) persicae. The BLAST search for all of the sequences generated in the present study showed that the sequences had the similarity for the respective species. Alignment of the COI sequences for \( A. \) gossypii (HM237329) and \( M. \) persicae (HM237331) in BioEdit v.7.0 showed that there were variations in 60 nucleotides out of 658 amounting to 9% difference between \( A. \) gossypii and \( M. \) persicae (Fig. 1). Species-specific markers require only customary PCR which is readily available, rapid and inexpensive. Out of 5 primer sets identified each for \( A. \) gossypii and \( M. \) persicae, 1 primer set, viz., KBR(AG)-F & KBR(AG)-R and KBR(MP)-F & KBR(MP)-R, could successfully identify \( A. \) gossypii and \( M. \) persicae, respectively (Table 4, Fig. 2). These species-specific markers amplified an expected fragment size of 600 bp and 429 bp.

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![Fig 1](https://example.com/fig1.png)

**Fig 1.** Consensus sequence of 658 bp from the mitochondrial cytochrome oxidase I (COI) gene for the Bangalore strain of \( A. \) gossypii and \( M. \) persicae.
for *A. gossypii* and *M. persicae*, respectively. The same fragments were cloned, sequenced and the BLAST search of these sequences obtained using species-specific markers showed the similarity for the respective species. Similar amplicon sizes were obtained from test specimens of aphids collected on cotton and brinjal.

The validation of the species specific primers, which were developed in the present study, were carried out, by employing PCR using both these primers and genomic DNA isolated from 33 different species of aphids, which were morphologically identified and collected from NBAII. No PCR reactions produced amplification, including non-specific amplicons, where the PCR mix and PCR cycling conditions were kept the same, including the annealing temperature, viz., 64°C for 45 s for all the reactions. However the applicability of these primers on other populations of *A. gossypii* and *M. persicae* within and outside India will depend on variations in the nucleotide sequences both in forward (43-70 for both *A. gossypii* and *M. persicae*) and reverse primer binding regions (613-643 and 441-472 for *A. gossypii* and *M. persicae* respectively).

Comparison of forward primer binding regions for *A. gossypii* (HM237329) with other 129 existing COI sequences (sequences generated in the present study and from NCBI-GenBank database) showed that there were variations at the 622nd position. One accession had T instead of A at the 623rd position. One accession had A instead of G at the 633rd position. Two accessions had T instead of A in all the other sequences.

A comparison of the forward primer binding region for *M. persicae* with 35 existing COI sequences (sequences generated in the present study and from NCBI-GenBank database) showed that there were no variations in any of the nucleotide positions; whereas in the reverse primer binding region such comparison showed that there were variations in the 451st position. Two accessions had C instead of T in all sequences. In this regard, development of degenerate primers would be a valuable tool in identifying the other populations of *A. gossypii* and *M. persicae* throughout the world independent of life stages and sex (Asokan et al. 2011). Other criteria to be taken into consideration while developing a species-specific marker for aphid species are intra- and inter-specific variations (Footitt et al. 2008; Shufran et al. 2004). Molecular identification using a species-specific marker is an advantage where there is polymorphism in the target species. Development of species-specific markers for *A. gossypii* and *M. persicae* would be of immense value to identify these vectors at any of the developmental stages (egg, nymph or adult). Previously Shufran & Putterka (2011) demonstrated the utility of COI in identification of aphid eggs and undescribed morphs found in wheat (*Triticum* spp.) or barley (*Hordeum vulgare* L.), but here the additional cost was that of sequencing. The species-specific markers that have been identified in this study will enable even a non-specialist to identify the target species, *A. gossypii* and *M. persicae* at any developmental stage without the aid of sequencing.

The intraspecific variations associated with host utilization is the most frequent and familiar phenomenon shown by phytophagous insects (Mopper & Strauss 1997; Margaritopoulos et al. 2006). Massutti & Chavigny (1998) reported host associated genetic differentiation in *A. gossypii* using Random Amplified Polymorphic DNA (RAPD) markers. In our present study, we targeted *A. gossypii*, a species in which there is already evidence of intraspecific variation with respect to host associated reproductive performance and related traits i.e., on chrysanthemum, cucumber (*Cucumis sativus* L.) and cotton (*Margaritopoulos* et al. 2006). Using morphological traits Margaritopoulos et al. (2006) proved the existence of the taxonomic status of the Compositae and Non-Compositae forms of *A. gossypii*, and they suggested the molecular work for the confirmation of the same. In this regard, it is necessary to analyze the molecular diversity in *A. gossypii* and *M. persicae* considering the fact that they are major vectors of many plant viruses. Comparison of the
COI, COII and EF1α sequences of 22 populations of *A. gossypii* and 15 populations of *M. persicae*, collected from various geographical locations in India and on various host plants showed that there were very few nucleotide variations among them, and the phylogram (Figs. 3 and 4) suggested that there are neither cryptic (sub) species nor biotypes existing in India.

The datasets for COI, COII and EF1α were combined based on the ILD test performed using PAUP 4.0. The Maximum Composite Likelihood Estimate of the Pattern of Nucleotide Substitution for *A. gossypii* sequences was performed using MEGA 4.0 (Tamura et al. 2007). The reliability of the clustering pattern in the trees was determined by the bootstrap test, with 1000 replications. The *A. gossypii* nucleotide frequencies were 0.343 (A), 0.359 (T), 0.164 (C) and 0.133 (G). The base composition of these 3 gene fragments was biased toward Adenine (A) and Thymine (T), which together constituted 70.2% of the total. The overall transition (ti)/transversion (tv) bias of *A. gossypii* nucleotide sequence was $R = \frac{[A] + [G]}{[T] + [C]}$, where $R = \frac{\sum [A] + [G] + [C] + [T]}{\sum [T] + [C]}$. Codon positions included were 1st + 2nd + 3rd + Noncoding. For *M. persicae*, the nucleotide frequencies were 0.34 4 (A), 0.361 (T), 0.155 (C) and 0.14 (G). As in the previous case the base composition of 3 gene sequences were biased towards Adenine and Thymine, with an estimated frequency of 70.5% of the total. The overall transition/transversion ratio was 0.3. Summary statistics for the different substitutional changes are shown in Tables 5 and 6.

Further analysis carried out using the acquired sequences from NCBI-GenBank corresponding to COI for both *A. gossypii* and *M. persicae*, revealed that there are very few sequence variations. This suggests that genetic structuring in terms of sub (cryptic) species, biotypes or host-associated genetic differences etc., associated with both *A. gossypii* and *M. persicae* were not evidenced using COI sequences of the world population. Both *A. gossypii* and *M. persicae* can exhibit phenotypic plasticity (Rosenheim et al. 1994; Blackman & Spence 1994) in response to the morphology of the
host plants of the samples; and also temperature can affect both isometric and allometric growth in aphids (Blackman & Spence 1994). Our study undoubtedly proved that these morphological variations of *A. gossypii* and *M. persicae* are not reflected in their genetic structure, and can be the result of host plant morphology and environmental factors affecting aphid growth and development.

**CONCLUSION**

In the present study, we showed the utility of species-specific markers which can be used for reliable species identification of *A. gossypii* and *M. persicae* amongst many other aphid species, which are morphologically and genetically close.

Thus, our work will help in rapid, accurate, life stage and color morph independent identification of these aphid vectors, which in turn will help in further elucidating the epidemiology of potyviruses, their management and be of value in the operation of quarantines. Also we showed that both *A. gossypii* and *M. persicae* are individual cosmopolitan and polyphagous species, which do not have any cryptic (sub) species or biotypes.

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**Fig 4.** Maximum-Parsimony (MP) tree with bootstrap support (1000 replicates) showing clustering of *Myzus persicae* (collected from different geographical locations and on different host plants) for both nuclear and mitochondrial datasets. *Aphis craccivora* used as an out group.

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**Table 5.** Maximum composite likelihood estimate of the pattern of nucleotide substitution from 22 populations of *Aphis gossypii*.

|   | A   | T   | C   | G   |
|---|-----|-----|-----|-----|
| A | —   | 6.69| 3.06| **9.95** |
| T | 6.39| —   | **8.5** | 2.47 |
| C | 6.39| **18.58** | — | 2.47 |
| G | **25.74** | 6.69| 3.06| — |

Each entry shows the probability of substitution from one base (row) to another base (column) instantaneously. Only entries within a row should be compared. Rates of different transitional substitutions are shown in bold and those of transversional substitutions are shown in italics.

**Table 6.** Maximum composite likelihood estimate of the pattern of nucleotide substitution from 15 populations of *Myzus persicae*.

|   | A   | T   | C   | G   |
|---|-----|-----|-----|-----|
| A | —   | 12.03| 5.18| **4.66** |
| T | **11.46** | —   | **5.18** | **4.66** |
| C | 11.46| **12.03** | — | **4.66** |
| G | **11.46** | **12.03** | 5.18| — |

Each entry shows the probability of substitution from one base (row) to another base (column) instantaneously. Only entries within a row should be compared. Rates of different transitional substitutions are shown in bold and those of transversional substitutions are shown in italics.
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