

Molecular identification and phylogenetic analysis of spiralling whitefly, *Aleurodicus dispersus* Russell (Hemiptera, Aleyrodidae) from different agroecological zones of Kerala, India

Drisya Pavithran*, J.V. Siji#, C.A. Jayaprakas and B.G. Sangeetha

ICAR-Central Tuber Crops Research Institute, Sreekariyam, Thiruvananthapuram 695017, Kerala, India.

#NSS College, Nilamel, Thiruvananthapuram, 691535, Kerala, India.

Email: drisyaedat@gmail.com

ABSTRACT: This study represents the first investigation into the genetic diversity and phylogenetic analysis of *Aleurodicus dispersus* Russell, populations collected from various agroecological zones of Kerala. The analysis, based on the mitochondrial cytochrome oxidase I (mtCOI) gene, demonstrated a significant amount of genetic divergence among *A. dispersus* populations from different agroecological regions of Kerala. Samples of spiralling whitefly collected from the Palakkad plains were genetically more distinct than those collected from other agroecological zones. Isolates from coastal sandy and red loam soils exhibited 100 per cent similarity with accession no. OQ844129.1 available in the GenBank. This study facilitates rapid diagnosis of the diversity in spiralling whiteflies attacking plants of economic importance in Kerala. © 2025 Association for Advancement of Entomology

KEY WORDS: Genetic diversity, mitochondrial cytochrome oxidase I, rapid diagnosis, phylogenetic tree

INTRODUCTION

Aleurodicus dispersus Russell (Hemiptera, Aleyrodidae) is a highly polyphagous pest native to the Caribbean region and Central America (Russell, 1965), where it is known to inhabit a wide range of host plants without being considered a pest (Waterhouse and Norris, 1989). Globally, it is more commonly known as a 'spiralling whitefly' due to its characteristic egg-laying pattern, which forms a spiral shape (Kumashiro *et al.*, 1983). This pest exhibits a broad host range, affecting 481 plant species from 295 genera across 90 families of

vegetables, fruits, and ornamental trees (Srinivasa, 2000). In India, it was first documented on cassava in 1993 in Thiruvananthapuram, Kerala (Palaniswami *et al.*, 1995). Subsequently, it was reported from several parts of Kerala (David and Regu, 1995; Ranjith *et al.*, 1996), Tamil Nadu (David and Regu, 1995), Karnataka (Mani *et al.*, 2000), Andhra Pradesh, Maharashtra (Charati *et al.*, 2003), Orissa (CABI/EPPO, 2006) and Mizoram (Boopathi, 2008). Since its first report in 1993, the species has spread throughout Southern and North-Eastern India, establishing itself as a significant pest of agricultural and horticultural crops (Boopathi and

* Author for correspondence

Karuppuchamy, 2013; Boopathi *et al.*, 2013a). Feeding damage was caused by the piercing and sucking of sap from foliage by immature and adult stages of whiteflies (Boopathi *et al.*, 2013b). High-density populations of this polyphagous pest can lead to pre mature leaf drop and the production of abundant honeydew, serving as a substrate for sooty mold growth, resulting in the abandonment of cassava fields by farmers (Akinlosotu *et al.*, 1993). Sooty mold formation blackens the leaves, reduces photosynthetic activity, and diminishes host vigour, often resulting in disfigurement (Kumashiro *et al.*, 1983; John *et al.*, 2007).

Mitochondrial DNA (mtDNA) has been extensively used in phylogenetic studies of animals, because it evolves much more rapidly than nuclear DNA, favouring the accumulation of nucleotide differences (i.e., polymorphisms) among closely related species (Brown *et al.*, 1979; Lunt *et al.*, 1996). Accumulation of these polymorphisms is primarily attributed to the loss or gain of restriction sites without a detectable change in genome size (Hebert *et al.*, 2003a). Sequence changes within the mitochondrial cytochrome oxidase I (COI) gene, make it an ideal candidate for use as a DNA barcode system (Hebert *et al.*, 2003b; Kress and Erickson, 2008). Generally, sequencing of the polymerase chain reaction fragment amplified from the COI gene is used for mitochondrial haplotype identification, which can then be associated with specific species (Shatters *et al.*, 2009). A molecular technique based on polymerase chain reaction is widely used in applied entomology (Harry *et al.*, 1998). Relatively little attention has been given to *A. dispersus*, including genetic studies particularly in India (Callejas *et al.*, 2005; Boopathi *et al.*, 2014). Despite the economic importance of *A. dispersus*, understanding of the level and patterns of genetic variability within its populations remains limited. Therefore, this study employed a molecular technique focusing on the mitochondrial genome to investigate the genetic variability of *A. dispersus* populations in Kerala.

MATERIALS AND METHODS

Surveys were conducted in 13 different

agroecological zones of Kerala, where cassava is grown (Table 1) and samples of whiteflies were collected using an aspirator and preserved in 90 per cent ethanol. Adult whiteflies were identified based on the taxonomic description (Russell, 1965). Total genomic DNA was obtained from spiralling whiteflies using the acetyl trimethyl ammonium bromide method (CTAB) adopted by Gawel and Jarrett (1991). The DNA barcode region was amplified from all whitefly species using 101M of universal DNA primers LCO1490 (50-GGTCAACAAATCATAAAGATATTGG-30) and HCO 2198 (50-TAAACTTCAGGGTGACCAAA AAATCA-30) for the amplification of mitochondrial cytochrome c oxidase subunit I -COI (Folmer *et al.*, 1994). PCR was conducted in a thermal cycler (AB-Applied Biosystems, Veriti 96 wells) with the following cycles; Initial denaturation at 94°C for 5 min. followed by 35 cycles (45 sec at 94°C, 45 sec at 47°C, and 45 sec at 72°C) with a final extension period of 72°C for 10 min. PCR products were tested on one per cent agarose gel. DNA ladders (1.0 kb plus) were used to measure the size of the obtained DNA fragments. The electrophoresis was followed by documentation under ultraviolet light and photographed by a Gel Documentation System (BioRad XR+).

DNA Sequences were edited to the spiralling whitefly species-specific COI sequence by eliminating the vector and universal primer sequence. DNA sequences were compared with those in the NCBI databases using the Basic Local Alignment Search Tool (<http://www.ncbi.nlm.nih.gov/BLAST>). From the aligned sequences phylogenetic tree was constructed using MEGA 11 software (Tamura *et al.*, 2013). The Mt (COX-1) gene sequences have been deposited in the NCBI Gen Bank, public databases.

RESULTS AND DISCUSSION

Initially, the mtDNA COI universal primers LCO1490 and HCO2198 were employed to amplify the COI region of thirteen *A. dispersus* populations collected from various geographic regions of Kerala. The COI gene (COX1) is one of 3 coding protein genes in the mitochondrial genome. The

Table 1. Locations of survey in Kerala

No	Zone	Place (Code)	Location
1	Onattukara	Kayamkulam (KYM)	9.1504°N; 76.3223°E
2	Coastal sandy	Chavakkad (CHA)	9.2243°N; 76.2145°E
3	Southern midlands	Sreekariyam (SKM)	8.3247°N; 76.5500°E
4	Central midlands	Perumbavoor (PBR)	10.0651°N; 76.2838°E
5	Northern midlands	Payyanur (PNR)	12.0550°N; 75.1137°E
6	Malappuram type	Kozhikode (KZH)	11.1536°N; 75.4649°E
7	Malayoram	Konni (KON)	9.1337°N; 76.5057°E
8	Palakkad plains	Palakkad (PKD)	10.4714°N; 76.3916°E
9	Red loam	Neyyatinkara (NYT)	8.2412°N; 77.0512°E
10	Chittoor black soil	Chittur (CTR)	10.3650°N; 76.4125°E
11	Kuttanad	Champakulam (CBK)	9.2439°N; 76.2437°E
12	Riverbank alluvium	Muvattupuzha (MVP)	9.5922°N; 76.3442°E
13	High ranges	SulthanBathery (SRY)	11.4805°N; 76.00176°E

amplification of the COX-1 gene of spiralling whitefly isolate was carried out and the amplicon product size was 658 bp. Gel images of PCR amplification (Fig.1). All the sequences obtained were aligned using BioEdit software. BLAST analysis of spiralling whitefly isolates showed 100 per cent similarity to *A. dispersus* sequences available in the GenBank. The sequence data generated were deposited in the GenBank nucleotide database (NCBI). The simple matching, Neighbour joining dendrogram of *A. dispersus* populations from 13 agroecological zones of Kerala revealed two major clusters with a few out-group individuals (Fig. 2). The cluster analysis revealed that *A. dispersus* populations are generally distributed independently across the sampled localities. However, certain clusters were evident, joining populations according to the regions. This pattern suggests that population differentiation has already occurred, likely influenced by regional factors. Heterogeneous grouping of the population may be attributed to variations in nutritional resources and behavioural traits. Additionally, the observed differentiation could be a result of multiple introductions of *A. dispersus* into different regions of India (Boopathi *et al.*, 2014) from diverse sources

rather than a single founding population. COI sequence analysis has proven to be a good molecular marker for intra- and interspecific variation in whitefly species (Thao and Baumann, 2004; Boykin *et al.*, 2007; Shoorcheh *et al.*, 2008; Chu *et al.*, 2012; Henri *et al.*, 2013).

The spiralling whitefly isolates from various agroecological regions of Kerala were matched with existing sequences in the GenBank database, revealing 100 per cent similarity with *A. dispersus* sequences (Table 2). All isolates showed 100 per

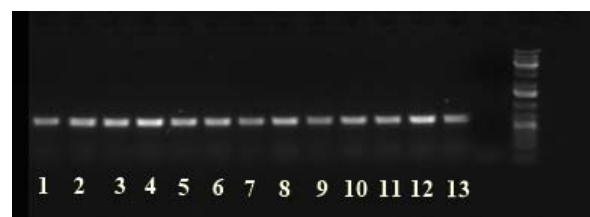


Fig.1 Gel images of PCR amplification of insect DNA *Aleurodicus dispersus* from different agro-ecological zones of Kerala (lane 1- CHA, lane 2- SKM, lane 3- PBR, lane 4- PNR, lane 5- KZH, lane 6- KON, lane 7- PKD, lane 8 - NYT, lane 9- CTR, lane 10- CBK, lane 11 - MVP, lane 12- SBY, lane 13- KYM), NTC- Non template control, L: 100 bp molecular weight marker

cent similarity with *Aleurodicus dispersus* sequences, confirming their molecular identity. The matching sequences correspond to various genes, including cytochrome c oxidase subunit I (COX1) and cytochrome oxidase subunit I (COI), and were retrieved from different isolates and clones. Despite the geographic spread, there is no apparent sequence variation among the isolates. Some isolates (e.g. CHA, NYT) match the same sequence (OQ844129.1) indicating possible genetic similarity or shared origin. The isolates from KYM, SKM, PBR, PNR, KZH, KON, PKD, CTR, CBK, MVP, and SRY regions were matched with existing sequences, confirming their identity as *A. dispersus*. This high degree of sequence identity

was observed across various genetic markers, including the cytochrome c oxidase subunit I (COX1) and cytochrome oxidase subunit I (COI) genes.

The uniformity in sequences suggests a recent common ancestry among the isolates, implying a high level of gene flow and genetic exchange within the population. Furthermore, the absence of significant genetic variation among the isolates implies a lack of geographic structuring, suggesting that the spiralling whitefly population is genetically homogeneous across the sampled regions. These findings have important implications for understanding the ecology, behaviour, and



Fig. 2 Phylogenetic tree of *Aleurodicus dispersus* mitochondrial cytochrome oxidase (COX-1) sequences from 13 different agroecological zones of Kerala

Table 2. Identification of *Aleurodicus dispersus* from different agroecological zones of Kerala

Isolates with acc No.	Identification – <i>A. dispersus</i>	Acc No. (reference)	Similarity
KYM - OP968041.1	mitochondrion, partial genome	KR063274.1	100%
MVP - PP133062.1			
CHA - OQ028271.1	Isolate; Pundibari cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial	OQ844129.1	100%
NYT - PP133051.1			
SKM - OQ061321.1	Isolate; ADC cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial	OP303313.1	100%
PBR - OQ073870.1	Isolate; ADB cytochrome oxidase subunit I(CO1) gene, partial cds; mitochondrial.	MK543950	100%
PNR - OQ073874.1	Isolate; CHI cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial	OR672939.1	100%
KZH - ON150855.1	Isolate; 411NdubWalg cytochrome oxidase subunit I (COI) gene, partial cds; mitochondrial	MN022652.1	100%
KON - ON150772.1			
PKD - ON171232.1	Clone; WFG1KT1 cytochrome oxidase subunit I (coxI) gene, partial cds; mitochondrial	KY574540.1	100%
SRY - OP641807.1			
CTR - ON171233.1	Isolate; 131_KtnKab cytochrome oxidase subunit I (COI) gene, partial cds; mitochondrial	MN022643.1	100%
CBK - PP133087.1	Clone; WFG1AL1 cytochrome oxidase subunit I (coxI) gene, partial cds; mitochondrial	KY574539.1	100%

management of this economically important pest species. However, more advanced molecular tools have recently been used to understand the population dynamics of whiteflies. For example, *Elfekih et al.* (2018) reported that the genetic mixing between populations of the same invasive species within the *B. tabaci* complex from various geographical localities worldwide using a dense array of genome-wide SNPs.

Earlier studies indicated that this species was first reported in 1993 on cassava (Palaniswami *et al.*, 1995), which means that this species had 30 years to adapt to the environment on the Indian subcontinent. Therefore, it is speculated that the populations were pre-diverged and from multiple sources. The very low level of heterozygosity indicates little gene flow between host-specific spiralling whiteflies. Low gene flow might be the result of restricted outcrossing between populations. Similar results are reported in earlier studies on whitefly populations from distant geographic

locations in India (Boopathi *et al.*, 2014) and 18 districts in Tamil Nadu, India (Boopathi *et al.*, 2017). The large-scale spread from neighbouring countries such as Sri Lanka (Ranjith *et al.*, 1996) and Myanmar (Boopathi, 2008) may have further contributed to genetic variations and changes in allele frequencies across regions.

The primer sequences for around 10 SSR markers are publicly available for studying the genome of the spiralling whitefly (Ma *et al.*, 2011). SSR markers are used in the analysis of genetic divergence and geographical distribution of *A. dispersus* (Boopathi *et al.*, 2014, 2017b). Earlier, the SSR markers were utilized for studying the genetic diversity of *B. tabaci* differentiating the variants and determining the genetic relationships of closely related populations (Gawel and Jarrett, 1991; De Barro *et al.*, 2003; Palaniswami, 2004; De Barro, 2005; Delatte *et al.*, 2006; Tsagkarakou *et al.*, 2007; Gauthier *et al.*, 2008; Palaniswami and Henneberry, 2011; Diaz *et al.*, 2015). Elfekih *et al.*

(2018) have developed a useful molecular diagnostic toolkit for detecting invasive *B. tabaci* via sequence characterization of mtDNA haplotypes.

Furthermore, molecular protocols also play a crucial role in studying predator communities that prey on whiteflies (Lundgren *et al.*, 2013). Through molecular gut content analysis, the predators linked to a specific whitefly species can be identified, that provide valuable insights for developing effective biological control programs to managing these pests (Kheirodin *et al.*, 2020). Additionally, it has been observed that endosymbiotic bacteria found in *A. dispersus* contribute to the protection of their host insects against natural enemies such as predators and pathogens, and may even be involved in mechanisms of insecticide resistance (Zindel *et al.*, 2011; Drisy *et al.*, 2022). The present study highlights the potential of molecular approaches in understanding *A. dispersus* ecology, in accurate species identification and genetic diversity. Future research could therefore focus on utilizing molecular gut content analysis to identify key natural enemies of *A. dispersus* across different agroecological zones of Kerala, similarly molecular characterization of endosymbionts in geographically distinct populations could reveal their role in shaping host adaptation, survival, and resistance mechanisms.

ACKNOWLEDGEMENTS

The authors express their gratitude to the Director, ICAR-Central Tuber Crops Research Institute, Thiruvananthapuram for the facilities provided. The first author thankfully acknowledges CSIR-UGC for granting financial support.

REFERENCES

- Akinlosotu T.A., Jackal L.E.N., Ntonifor N.N., Hassan A.T., Agyakwa C.W., Odebiyi J.A., Akingbohunge A.E and Russel H.W. (1993) Spiralling whitefly, *Aleurodicus dispersus* in Nigeria. *FAO plant protection bulletin* 41(2): 127–129.
- Boopathi T. (2008) Monitoring and management of pest complex of fruits, vegetables, and spices in Mizoram. In: Annual Report of ICAR Research Complex for NEH Region 2008–2009. ICAR Research Complex for NEH Region, Umiam, Meghalaya. 289pp.
- Boopathi T. and Karuppuchamy P. (2013a) Evaluation of Ecofriendly Agents against Spiralling Whitefly, *Aleurodicus dispersus* Russell on Brinjal. *Madras Agricultural Journal* 100(4-6): 559–661.
- Boopathi T., Karuppuchamy P., Kalyanasundaram M., Mohankumar S and Ravi M. (2013b) Pathogenicity, ovicidal action, and median lethal concentrations (LC_{50}) of entomopathogenic fungi against exotic spiralling whitefly, *Aleurodicus dispersus* Russell. *Journal of Pathology* 2013: 393787. 7pp. doi: org/10.1155/2013/393787. Epub 2013.
- Boopathi T., Mohankumar S., Karuppuchamy P., Kalyanasundaram M., Ravi M., Preetha B and Aravindraj R. (2014) Genetic evidence for diversity of spiralling whitefly, *Aleurodicus dispersus* (Hemiptera: Aleyrodidae) populations in India. *Florida Entomologist* 97: 1115–1122.
- Boopathi T., Mohankumar S., Karuppuchamy P., Singh S.B., Ravi M., Preetha B., Aravindraj R and Manju T. (2017) SSR markers-based identification of genetic variability of spiralling whitefly, *Aleurodicus dispersus* populations in Tamil Nadu, *Indian Journal of Biotechnology* 16: 276–282.
- Boykin L.M., Shatters R.G., Rosell R.C., McKenzie C.L., Bagnall R.A., De Barro P and Frohlich D.R. (2007) Global relationships of *Bemisia tabaci* (Hemiptera: Aleyrodidae) revealed using Bayesian analysis of mitochondrial COI DNA sequences. *Molecular Phylogenetics and Evolution* 44 (3): 1306–1319.
- Brown W. M., George M. and Wilson A.C. (1979) Rapid evolution of animal mitochondrial DNA. The Proceedings of the National Academy of Sciences, USA 76: 1967–1971.
- CABI/EPPO (2006) EPPO A1 List of pests recommended for regulation as quarantine pests. EPPO Reporting Service, Paris, France. <http://archives.eppo.org/EPPOReporting/2006>.
- Callejas C., Beitia F J., Gobbi A., Velasco A and Ochando M.D. (2005) The use of RAPD markers to detect genetic patterns in *Aleurodicus dispersus* (Hemiptera: Aleyrodidae) populations from the Canary Islands. *European Journal of Entomology* 102: 289–291
- Charati S. N., Pokharkar D. S. and Ghorpade S. A. (2003)

- Abundance of spiralling whitefly, a newly introduced pest in Maharashtra State. *Journal of Maharashtra Agricultural Universities* 28: 83–84.
- Chu D., Hu X., Gao C., Zhao H., Nichols R.L. and Li X. (2012) Use of mitochondrial cytochrome oxidase I polymerase chain reaction-restriction fragment length polymorphism for identifying subclades of *Bemisia tabaci* Mediterranean group. *Journal of Economic Entomology* 105(1): 242–251.
- David B.V. and Regu, K. (1995) *Aleurodicus dispersus* Russell (Aleyrodidae: Homoptera), a whitefly pest new to India. *Pestology* 19: 5–7.
- De Barro P.J. (2005) Genetic structure of the whitefly *Bemisia tabaci* in the Asia-Pacific region revealed using microsatellite markers. *Molecular Ecology* 14: 3695–3718.
- De Barro P.J., Scott K.D., Graham G.C., Lange C.L. and Schutze M.K. (2003) Isolation and characterization of microsatellite loci in *Bemisia tabaci*. *Molecular Ecology Notes* 3: 40–43.
- Delatte H., David P., Granier M., Lett J.M., Goldbach R., Peterschmitt M. and Reynaud B. (2006) Microsatellites reveal extensive geographical, ecological, and genetic contacts between invasive and indigenous whitefly biotypes in an insular environment. *Molecular Ecology* 87: 109–124.
- Diaz F., Endersby N.M., and Hoffmann A.A. (2015) Genetic structure of the whitefly *Bemisia tabaci* populations in Colombia following a recent invasion. *Insect Science* 22: 483–494.
- Drisya Pavithran., Jayaprakas C.A. and Sangeetha B.G (2022) Endosymbiotic bacteria associated with the spiralling whitefly, *Aleurodicus dispersus* Russell (Hemiptera: Aleyrodidae). *International Journal of Zoological Investigations* 8(1): 281–290.
- Elfekih S., Etter, P., Tay W. T., Fumagalli M., Gordon K., Johnson E. and De Barro P. (2018) Genome-wide analyses of the *Bemisia tabaci* species complex reveal contrasting patterns of admixture and complex demographic histories. *PLoS One* 13(1): e0190555.
- Folmer R.H.A., Nilges M., Folkers P.J.M., Konings R.N.H. and Hilbers C.W. (1994) A model of the complex between single-stranded DNA and the single-stranded DNA binding protein encoded by gene V of filamentous bacteriophage M13. *Journal of molecular biology* 240(4): 341–357.
- Gauthier N., Dalleau-Clouet C. and Bouvret M.E. (2008) Twelve new polymorphic microsatellite loci and PCR multiplexing in the whitefly, *Bemisia tabaci*. *Molecular Ecology Resources* 8: 1004–1007.
- Gawel N.L. and Jarret R.L. (1991) A modified CTAB DNA extraction procedure of *Musa* and *Ipomoea*. *Plant Molecular Biology Reporter* 9: 262–266.
- Harry M., Solignac M. and Lachaise D. (1998) Molecular evidence for parallel evolution of adaptive syndromes in fig-breeding *Lissocephala* (Drosophilidae). *Molecular Phylogenetics and Evolution* 9(3): 542–551. doi: 10.1006/mpev.1998.0508.
- Hebert P.D.N., Cywinska A., Ball S.L. and de Waard J.R. (2003b) Biological identifications through DNA barcodes. *Proceedings of the Royal Society of London. Series B, Biological Sciences* 270: 313–321.
- Hebert P.D., Ratnasingham S. and de Waard J.R. (2003a) Barcoding animal life: cytochrome c oxidase subunit 1 divergences among closely related species *Proceedings of the Royal Society of London. Series B, Biological Sciences* 270: S96–S99.
- Henri H., Terraz G., Gnankine O., Fleury F. and Mouton L. (2013) Molecular characterization of genetic diversity within the Africa/Middle East/Asia Minor and Sub-Saharan African groups of the *Bemisia tabaci* species complex. *International Journal of Pest Management* 59: 329–338.
- John B., Darryl H. and Greg P. (2007) Spiralling whitefly *Aleurodicus dispersus* exotic threat to Western Australia. Hort Guard TM Initiative AGWEST. Available at (www.agric.wa.gov.au/objectw/imported_assets/.../pw/.../fs01800.pdf)
- Kheirodin A., Simmons A.M., Legaspi J.C., Grabarczyk E.E., Toews M.D., Roberts P.M. and Schmidt J.M. (2020) Can generalist predators control *Bemisia tabaci*? *Insects* 11(11): 823.
- Kress W.J. and Erickson D.L. (2008) DNA barcoding: A windfall for tropical biology? *Biotropica* 40(4): 405–408.
- Kumashiro B.R., Lai P.Y., Funasaki G.Y. and Teramoto K.K. (1983) Efficacy of *Nephaspis amnicola* and *Encarsia haitiensis* in controlling *Aleurodicus dispersus* in Hawaii. *Proceedings of Hawaiian Entomological Society* 24: 261–269. <http://hdl.handle.net/10125/11158>.
- Lundgren J.G., Becerra Lopez Lavallo L.A., Parsa S. and Wyckhuys K.A.G. (2013) Molecular determination

- of the predator community of a cassava whitefly in Colombia: pest-specific primer development and field validation. *Journal of Pest Science* 87: 125–131
- Lunt D.H., Zhang D.X., Szymura J.M. and Hewlitt O.M. (1996) The insect cytochrome oxidase I gene: evolutionary patterns and conserved primers for phylogenetic studies. *Insect molecular biology* 5(3): 153–165.
- Ma D., Gorman K., Devine G., Luo W. and Denholm I. (2007) The biotype and insecticide-resistance status of whiteflies, *Bemisia tabaci* (Hemiptera: Aleyrodidae), invading cropping systems in Xinjiang Uygur Autonomous Region, northwestern China. *Crop Protection* 26(4): 612–617.
- Palaniswami M.S. (2004) Natural enemies of *Bemisia tabaci* G. and their potential as biocontrol components of IPM. USIF - USDA (IN - ARS - 858/ FG - In - 785) project report. ICAR-Central Tuber Crops Research Institute, Thiruvananthapuram, Kerala, India. 504 pp.
- Palaniswami M.S. and Henneberry T.J. (2011) *Bemisia tabaci* (Genn.): Biotypes and Cassava Mosaic Virus in India. Chapter 7. In: *The Whitefly, Bemisia tabaci* (Homoptera: Aleyrodidae) - Interaction with Geminivirus-Infected Host Plants. W.M.O. Thompson (ed.). Springer, Dordrecht Heidelberg, London, New York. doi: 10.1007/978-94-007-1524-0_7.
- Palaniswami M.S., Pillai K.S., Nair P.R. and Mohanadas C. (1995) A new cassava pest in India. *Cassava Newsletter (CGIAR- CIAT)* 19: 6-7.
- Ranjith A.M., Rao D.S. and Thomas J. (1996) New host records of the mealy whitefly, *Aleurodicus dispersus* Russell in Kerala. *Insect Environ* 2(2): 35–38.
- Russel L.M. (1965) A new species of *Aleurodicus douglas* and two close relatives (Homoptera: Aleyrodidae). *Florida Entomologist* 48(1): 47–55.
- Shatters R.G., Powell C.A., Boykin L.M., Liansheng H. and McKenzie C.L. (2009) Improved DNA barcoding method for *Bemisia tabaci* and related Aleyrodidae: development of universal and *Bemisia tabaci* biotype-specific mitochondrial cytochrome oxidase I polymerase chain reaction primers. *Journal of Economic Entomology* 102: 750–758.
- Shoorcheh H.R., Kazemi B., Manzari S., Brown J. and Sarafrazi A. (2008) Genetic variation and mtCOI phylogeny for *Bemisia tabaci* (Hemiptera, Aleyrodidae) indicate that the ‘B’ biotype predominates in Iran. *Journal of Pest Science* 81: 199–206
- Srinivasa M.V. (2000) Host plants of the spiralling whitefly, *Aleurodicus dispersus* (Hemiptera: Aleyrodidae). *Pest Management in Horticultural Ecosystems* 6: 79–105.
- Tamura K., Stecher G., Peterson D., Filipski A. and Kumar S. (2013) MEGA6: molecular evolutionary genetics analysis version 6.0. *Molecular Biology and Evolution* 30(12): 2725–2729. doi: 10.1093/molbev/mst197.
- Thao M.L. and Baumann P. (2004) Evolutionary relationships of primary prokaryotic endosymbionts of whiteflies and their hosts. *Applied and Environmental Microbiology* 70(6): 3401–3406.
- Tsagkarakou A., Tsigenopoulos C.S., Gorman K., Lagnel J. and Bedford I.D. (2007) Biotype status and genetic polymorphism of the whitefly *Bemisia tabaci* (Hemiptera: Aleyrodidae) in Greece: mitochondrial DNA and microsatellites. *Bulletin of Entomological Research* 97: 29–40.
- Waterhouse D.F. and Norris K.R. (1989) *Aleurodicus dispersus* Russell. In: *Biological Control: Pacific Prospects – Supplement 1*, ACIAR Monograph No.12, ACIAR, Canberra, Australia. pp13–22.
- Zindel R., Gottlieb Y. and Aebi A. (2011) Arthropod symbioses: a neglected parameter in pest and disease control programmes. *Journal of Applied Ecology* 48(4): 864–872.

(Received June 15, 2025; revised ms accepted August 26, 2025; published September 30, 2025)