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Genetic Diversity and Geographic Distribution of *Bemisia tabaci* in India: A Brief Overview

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INTRODUCTION

The whitefly, *Bemisia tabaci* (Gennadius) (Hemiptera: Aleyrodidae), holds a notorious reputation as one of the most devastating and highly polyphagous pests among hemipterans worldwide. Its vast host range includes approximately 900 different plant species, encompassing vegetables, ornamental plants, and various field crops (Nauen et al., 2014; Jones, 2003). The damage inflicted by *B. tabaci* is multifaceted. Direct crop damage occurs when whitefly feed in plant phloem, remove plant sap, and reduce plant vigor. Additionally, whitefly excrete a sugary substance called honeydew, which fosters the growth of sooty mold. This black, sticky mold can blanket leaves and interferes with photosynthesis, ultimately diminishing harvest quality. In certain plant hosts, whitefly feeding can lead to specific plant disorders such as the silver leaf of squash (Brown et al., 1992) and irregular ripening of tomato (Schuster et al., 1990). However, the impact of *B. tabaci* extends beyond its direct feeding damage. This pest is a vector for over 40 plant pathogenic viruses (Oliveira et al., 2001), especially transmitting *Begomovirus* to Cucurbitaceae, Leguminosae, Euphorbiaceae, Malvaceae, Solanaceae *etc*. (Bedford et al., 1994).

The year 1994 marked a significant development in the history of *B. tabaci* when biotype B of whitefly was first identified in Australia (Gunning et al., 1995). Subsequently, researchers have identified at least 35 genetically distinct species or groups within *B. tabaci*. These distinctions have been revealed through phylogenetic analysis, primarily relying on the sequencing of the mitochondrial cytochrome oxidase I (mtCOI) gene from numerous haplotypes (De Barro et al., 2011). Molecular markers based on the mitochondrial cytochrome oxidase I (mtCOI) gene are crucial for distinguishing within *B. tabaci* populations.

Therefore, mtCOI gene sequences were employed by any researchers, including Delatte et al. (2005), Bethke et al. (2009), Valle et al. (2011), and Guo et al. (2012) for molecular characterisation of *B. tabaci* around the world with different host range.

In regions like India, where a long, hot, and dry season prevails, high populations of mixed genetic species of *B. tabaci* have been observed in vegetable crops (Singh et al., 2012). These species exhibit a degree of specificity for certain geographic areas and host plants (Boykin et al., 2007). Kanakala and Ghanim (2019) provided comprehensive insights into the global genetic diversity and geographical distribution of *B. tabaci* in different crops. Their findings revealed the presence of multiple genetic groups of *B. tabaci*, including Asia I, Asia I-India, Asia II 1, Asia II 5, Asia II 7, Asia II 8, Asia II 11, Asia II 13, MEAM K, China 3, and MEAM1 throughout India. Additionally, previously published reports by Rekha et al. (2005) and Chowda-Reddy et al. (2012) have identified five distinct species as part of the distribution of cryptic species in India, namely Asia I, Asia II-5, Asia II-7, Asia II-8, and MEAM1.

In addition to the Asia-I, Asia-II-7, Asia-II-8, and MEAM-1 genetic groups, a novel group closely related to MEAM-1, known as Middle East Asia Minor-K, was identified in Karnataka (Roopa et al., 2015). Meanwhile, Ambarish (2020) detected the presence of the Asia I, Asia II-5, and Asia II-8 genetic groups. Furthermore, evidence of Asia II-1 was documented in India, primarily in states bordering Pakistan (Simon et al., 2003), with no evidence of its distribution in other Indian states (Chowda Reddy et al., 2012). Interestingly, Prasanna et al. (2015) also found evidence of Asia II-1, along with Asia I and Asia II-7, in soybean crops across India. The presence of Asia II-1 has also been documented in other countries including China, Syria, Pakistan, and Nepal (Hu et al., 2011; Acharya et al., 2020).

The findings of Ellango et al. (2015) and Singh et al. (2012) revealed a decrease in diversity as one moves towards the northern and northwestern regions of India, where either the Asia II-1 or Asia I genetic groups dominate. Moreover, Devi (2019), Hashmi et al. (2017), and Naveen et al. (2017) independently identified the exclusive presence of the Asia II-1 genetic group in North India, particularly in cotton and soybean crops. Their findings provided information on a distinctive regional pattern of *B. tabaci* distribution in the northern area of India. Tomar et al. (2014), who collected *B. tabaci* samples from various host plants (potato, okra, and brinjal) in Uttar Pradesh, India, and analyzed the mtCOI gene sequence, similarly found the presence of the Asia II-1 genetic group. Therefore, it can be concluded that in northern India, the diversity of *B. tabaci* is comparatively lower, with either Asia II-1 or Asia I predominating.

REFERENCES

Acharya, R., Shrestha, Y. K., Sharma, S. R., & Lee, K. Y. (2020). Genetic diversity and geographic distribution of *Bemisia tabaci* species complex in Nepal. *Journal of Asia-Pacific Entomology*, *23*(2), 509-515.

Ambarish, S. (2020). Molecular characterization of whitefly, *Bemisia tabaci* (genn.) and its transmission efficiency of *Mungbean Yellow Mosaic Virus* in greengram and their management (Ph.D. dissertation). University of Agricultural and Horticultural Sciences, Shivamogga.

Bedford, I. D., Briddon, R. W., Brown, J. K., Rosell, R. C., & Markham, P. G. (1994). Geminivirus transmission and biological characterisation of *Bemisia tabaci* (Gennadius) biotypes from different geographic regions. *Annals of Applied Biology*, *125*(2), 311-325.

Bethke, J.K., Byrne, F.J., Hodges, G.S., Mckenzie, C.L., & Shatters, R.G. (2009). First record of the Q biotype of the sweetpotato whitefly, *Bemisia* *tabaci*, in Guatemala. *Phytoparasitica*, *37*, 61-64.

Boykin, L. M., Shatters Jr, R. G., Rosell, R. C., McKenzie, C. L., Bagnall, R. A., De Barro, P., & 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, J. K., Costa, H. S., & Laemmlen, F. (1992). First report of whitefly-associated squash silverleaf disorder of *Cucurbita* in Arizona and of white streaking disorder of *Brassica* species in Arizona and California. *Plant Disease*, *76*(4), 426.

Chowda-Reddy, R. V., Kirankumar, M., Seal, S. E., Muniyappa, V., Valand, G. B., Govindappa, M. R., & Colvin, J. (2012). *Bemisia tabaci* phylogenetic groups in India and the relative transmission efficacy of *Tomato Leaf Curl Bangalore Virus* by an indigenous and an exotic population. *Journal of Integrative Agriculture*, *11*(2), 235-248.

De Barro, P. J., Liu, S. S., Boykin, L. M., & Dinsdale, A. B. (2011). *Bemisia tabaci*: A statement of species status. *Annual Review of Entomology*, *56*, 1-19.

Delatte, H., Martin, D. P., Naze, F., Goldbach, R., Reynaud, B., Peterschmitt, M., & Lett, J. M. (2005). South West Indian Ocean islands tomato begomovirus populations represent a new major monopartite begomovirus group. *Journal of General Virology*, *86*(5), 1533-1542.

Devi, R. (2019). Studies on molecular variability in whitefly, *Bemisia tabaci* (Gennadius) population in cotton and its management (Ph.D. dissertation). Chaudhary Charan Singh Haryana Agricultural University

Ellango, R., Singh, S. T., Rana, V. S., Gayatri Priya, N., Raina, H., Chaubey, R., & Rajagopal, R. (2015). Distribution of *Bemisia tabaci* genetic groups in India. *Environmental entomology*, *44*(4), 1258-1264.

Gunning, R. V., Byrne, F. J., Condé, B. D., Connelly, M. I., Hergstrom, K., & Devonshire, A. L. (1995). First report of B-biotype *Bemisia tabaci* (Gennadius) (Hemiptera: Aleyrodidae) in Australia. *Australian Journal of Entomology*, *34*(2), 116-116.

Guo, X. J., Qiong, R. A. O., Zhang, F., Chen, L. U. O., Zhang, H. Y., & Gao, X. W. (2012). Diversity and genetic differentiation of the whitefly *Bemisia tabaci* species complex in China based on mtCOI and cDNA-AFLP analysis. *Journal of Integrative Agriculture*, *11*(2), 206-214.

Hashmi, T. R., Dey, D., & Prasad, R. (2017). Endosymbionts and genetic characterisation of whitefly on soyabean. *Bulletin of Environment, Ph armacology and Life Sciences*, *6*, 69-73.

Hu, J., De Barro, P., Zhao, H., Wang, J., Nardi, F., & Liu, S. S. (2011). An extensive field survey combined with a phylogenetic analysis reveals rapid and widespread invasion of two alien whiteflies in China. *PloS one*, *6*(1), e16061.

Jones, D. R. (2003). Plant viruses transmitted by whiteflies. *European journal of plant pathology*, *109*, 195-219.

Kanakala, S., & Ghanim, M. (2019). Global genetic diversity and geographical distribution of *Bemisia tabaci* and its bacterial endosymbionts. *PloS one*, *14*(3), e0213946.

Nauen, R., Ghanim, M., & Ishaaya, I. (2014). Whitefly special issue organized in two parts. *Pest management science*, *10*(70), 1438-1439.

Naveen, N. C., Chaubey, R., Kumar, D., Rebijith, K. B., Rajagopal, R., Subrahmanyam, B., & Subramanian, S. (2017). Insecticide resistance status in the whitefly, *Bemisia tabaci* genetic groups Asia-I, Asia-II-1 and Asia-II-7 on the Indian subcontinent. *Scientific reports*, *7*(1), 40634.

Oliveira, M. R. V., Henneberry, T. E., & Anderson, P. (2001). History, current status, and collaborative research projects for *Bemisia tabaci*. *Crop protection*, *20*(9), 709-723.

Prasanna, H. C., Kanakala, S., Archana, K., Jyothsna, P., Varma, R. K., & Malathi, V. G. (2015). Cryptic species composition and genetic diversity within *Bemisia tabaci* complex in soybean in India revealed by mtCOI DNA sequence. *Journal of Integrative Agriculture*, *14*(9), 1786-1795.

Rekha, A. R., Maruthi, M. N., Muniyappa, V. & Colvin, J. (20050. Occurrence of three genotype clusters of *Bemisia tabaci* and the rapid spread of the B biotype in South India. *Entomologia Experimentalis et Applicata*, *117*, 221-233.

Roopa, H. K., Asokan, R., Rebijith, K. B., Hande, R. H., Mahmood, R., & Kumar, N. K. (2015). Prevalence of a new genetic group, MEAM-K, of the whitefly *Bemisia tabaci* (Hemiptera: Aleyrodidae) in Karnataka, India, as evident from mtCOI sequences. *Florida Entomologist*, *98*(4), 1062-1071.

Schuster, D. J., Mueller, T. F., Kring, J. B., & Price, J. F. (1990). Relationship of the sweet potato whitefly to a new tomato fruit disorder in Florida. *Hort Science*, *25*(12), 1618-1620.

Simon, B., Cenis, J. L., Beitia, F., Khalid, S., Moreno, I. M., Fraile, A., & Garcia-Arenal, F. (2003). Genetic structure of field populations of begomoviruses and of their vector *Bemisia tabaci* in Pakistan. *Phytopathology*, *93*(11), 1422-1429.

Singh, S. T., Priya, N. G., Kumar, J., Rana, V. S., Ellango, R., Joshi, A., & Rajagopal, R. (2012). Diversity and phylogenetic analysis of endosymbiotic bacteria from field caught *Bemisia tabaci* from different locations of North India based on 16S rDNA library screening. *Infection, Genetics and Evolution*, *12*(2), 411-419.

Tomar, S., Malik, K., Ellango, R., & Singh, B. (2014). Analysis of whitefly, *Bemisia tabaci*: sequencing of the mitochondrial cytochrome oxidase I (mtCOI). *International Journal of Genetic Engineering and Biotechnology*, *3073*(2), 185-190.

Valle, G. E., Lourenção, A. L., Zucchi, M. I., Pinheiro, J. B., & Abreu, A. G. (2011). MtDNA variability in whitefly (*Bemisia tabaci*) populations in Brazil. *Genetics and Molecular Research*, *10*(3), 2155-2164.