

One Species into Five: Nucleo-Mito Barcoding Reveals Cryptic Species in 'Frankliniella schultzei Complex': Vector for Tospoviruses

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Abstract : The insect order Thysanoptera includes small insects commonly called thrips. As insect vectors, only thrips are capable of Tospoviruses transmission (genus Tospovirus, family Bunyaviridae) affecting various crops. Currently, fifteen species of subfamily Thripinae (Thripidae) have been reported as vectors for tospoviruses. *Frankliniella schultzei*, which is reported as act as a vector for at least five tospoviruses, have been suspected to be a species complex with more than one species. It is one of the historical unresolved issues where, two species namely, *F. schultzei* Trybom and *F. sulphurea* Schmutz were erected from South Africa and Srilanka respectively. These two species were considered to be valid until 1968 when *sulphurea* was treated as colour morph (pale form) and synonymised under *schultzei* (dark form) However, these two have been considered as valid species by some of the thrips workers. Parallel studies have indicated that brown form of *schultzei* is a vector for tospoviruses while yellow form is a non-vector. However, recent studies have shown that yellow populations have also been documented as vectors. In view of all these facts, it is highly important to have a clear understanding whether these colour forms represent true species or merely different populations with different vector carrying capacities and whether there is some hidden diversity in 'Frankliniella schultzei species complex'. In this study, we aim to study the 'Frankliniella schultzei species complex' with molecular spectacles with DNA data from India and Australia and Africa. A total of fifty-five specimens was collected from diverse locations in India and Australia. We generated molecular data using partial fragments of mitochondrial cytochrome c oxidase I gene (mtCOI) and 28S rRNA gene. For COI dataset, there were seventy-four sequences, out of which data on fifty-five was generated in the current study and others were retrieved from NCBI. All the four different tree construction methods: neighbor-joining, maximum parsimony, maximum likelihood and Bayesian analysis, yielded the same tree topology and produced five cryptic species with high genetic divergence. For, rDNA, there were forty-five sequences, out of which data on thirty-nine was generated in the current study and others were retrieved from NCBI. The four tree building methods yielded four cryptic species with high bootstrap support value/posterior probability. Here we could not retrieve one cryptic species from South Africa as we could not generate data on rDNA from South Africa and sequence for rDNA from African region were not available in the database. The results of multiple species delimitation methods (barcode index numbers, automatic barcode gap discovery, general mixed Yule-coalescent, and Poisson-tree-processes) also supported the phylogenetic data and produced 5 and 4 Molecular Operational Taxonomic Units (MOTUs) for mtCOI and 28S dataset respectively. These results of our study indicate the likelihood that *F. sulphurea* may be a valid species, however, more morphological and molecular data is required on specimens from type localities of these two species and comparison with type specimens.

Keywords : DNA barcoding, species complex, thrips, species delimitation

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