

## Systematics of Tephritidae (Insecta: Diptera) Using Mitochondrial 16S Ribosomal DNA

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The family Tephritidae, commonly known as fruit flies, includes more than 4,000 species arranged in about 500 genera throughout the world. This family is the most important group of agricultural pests of all fly families, and studies of tephritids have contributed to development of our understanding of speciation and evolutionary biology. Despite intensive study, the higher classification of the Tephritidae, primarily based on morphological data, is in an unsatisfactory state. Most species of Tephritidae are phytophagous, while its sister-group Pyrgotidae and Tachiniscidae are parasitic, and other families of the superfamily Tephritoidea are primarily saprophagous. Tephritid larvae most commonly develop in fruits, leafmines, or within the flowerheads of Asteraceae. There are also gallmakers, stem or rootborers, and gall commensals. Feeding strategies and host range appear highly correlated with membership in higher taxa. For example, all the leafminers are confined to the subtribe Trypetina and all the flowerhead feeders to the subfamily Tephritinae. Resolving the phylogeny of the Tephritidae would provide a very interesting insight on the origin of phytophagy and how broad patterns of host association evolved. Clarification of monophyly of and relationships among subfamilies and tribes will lead directly to the ability to examine lower taxonomic levels and erect phylogenetically-based classifications for them as well. This process will lead to a tephritid classification with much greater predictive value for other related studies.

The primary aim of this study was to investigate the utility of the 16S rDNA for phylogenetic inferences at different taxonomic levels within Tephritidae. We therefore included a number of relatively well-established tephritid higher taxa and their members (12 suprageneric taxa; 28 genera; and 35 species). These known taxonomic groupings are compared with the phylogeny inferred from our sequence data. We also included some species whose taxonomic memberships are unknown or controversial. This way, within the limits of included taxa, we are able to test the monophyly of each higher taxon and provide some hypotheses of previously unknown relationships.

Sequence data from 925 base pairs within the mitochondrial 16S ribosomal DNA were analyzed. DNA sequences were amplified by the polymerase chain reaction and sequenced by the dideoxy chain-termination method. Pattern of nucleotide composition and substitution were assessed based on the sequence comparison. Phylogenetic relationships among the included taxa were inferred using neighbor joining, maximum parsimony, and UPGMA methods. The neighbor joining tree was found to be most congruent with the morphological classification and suggested the following phylogenetic relationships: (1) monophyly of the tribe Trypetini, s. str., excluding *Parastenopa*; (2) possible sister group relationship between *Platyparea* and the subfamily Tephritinae; (3) sister group relationship between *Hexachaeta* and the tribe Toxotrypanini; (4) monophyly of the Dacinae and possible relationship of *Oedicarena* to this subfamily; and (5) monophyly of the tribe Adramini; (6) non-monophyletic nature of the genus *Rhagoletis*. We propose that the 16S rDNA shows great promise for helping to create a phylogenetically-based higher classification of the Tephritidae.