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## Molecular Phylogeny of the Superfamily Tephritoidea (Insecta: Diptera) Based on Mitochondrial 12S, 16S, and COII Genes

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The phylogeny of the superfamily Tephritoidea (Diptera: Muscomorpha) was reconstructed from three mitochondrial gene fragments (12S, 16S, and COII) using 49 species representing 19 tephritoid and related families. Patterns of nucleotide composition and substitution were assessed based on sequence comparison. Phylogenetic signal present in different gene fragments was examined. In particular, using the interior branch and bootstrap test values from minimum evolution method, trees based on all possible combinations of gene fragments were compared to see whether or not a particular clade was recognized in different trees. We also compared the resulting molecular trees with the relatively better resolved portions of the current fly higher classification to show robustness of the supported clades. While the monophyly of Tephritoidea is not clear, two monophyletic groups involving tephritoid families are clearly recognized in the ME tree at significantly high P values. These groupings are also recognized in the ML and MP trees. They are compatible with the Hennig's Pallopteroidea and Otitidae respectively. Since this superfamily classification is not currently used, we will call them the Tephritoidea Group-1 and Group-2 for the sake of our discussion. Hennig recognized the Group-1 (as Pallopteroidea) based on a number of morphological characters, but said that the justification of this group was still disputed. Our ME analysis (Fig. 6) clearly support the monophyly of the Group-1 (Pc/Pb = 99/98). Two recent authors, however, did not recognize this group, but at least believed the sister group relationship between Piophilidae and Pallopteridae. They regarded Lonchaeidae as the sister group of all other Tephritoidea. On the contrary, our analyses support the closer relationship between Lonchaeidae and Pallopteridae, and placed Piophilidae in the most basal position within the Group-1. This relationship has never been recognized by the previous morphological studies. Since the statistical supports for the sister relationship between Lonchaeidae and Pallopteridae is not so strong in the ME (Pc/Pb = 89/69), ML (Pb = 83), and MP (Pb = 69) trees, we need to reevaluate this sister group relationship based both on the conventional and molecular evidences. Hennig regarded the Group-2 (as Otitidae) undoubtedly monophyletic based on a number of male and female postabdominal structures. This grouping is recently recognized by Korneyev using a computer-based cladistic analysis based on a number of morphological characters. He hypothesized Richardiidae to be the sister group of the remaining families on the basis of bare taenia in the female ovipositor and the presence of the medial surstylus in the male. Our molecular data strongly support this sister group relationship (Fig. 6, Ps/Pb = 96/91). Within the Group-2, the subclade including Ulidiidae, Platystomatidae, Tephritidae, and Pyrgotidae (Higher Tephritoidea sensu Korneyev) has been consistently recognized by previous authors (Fig. 1). Our molecular data also strongly support the monophyly of this group at high P-values. Among tephritoid families, the monophyly of Platystomatidae is rather weakly supported in the ME trees, and not recognized in ML or MP trees. It is interesting to note that some platystomatids were grouped with Ulidiidae at high P-values (Pc/Pb = 99/73) in the ME tree based on 16S rDNA alone. In the ME tree based on the complete data set (Fig. 7) a close relationship between the Platystomatidae and Ulidiidae is strongly supported (Pc/Pb = 99/77), but the relationship between the two platystomatid subclades is only topologically supported with insignificant P-values. There appears to be a strong possibility that the family Platystomatidae is a paraphyletic group basal to Ulidiidae. The close relationship between the Platystomatidae and Ulidiidae has never been recognized in the previous morphological studies. Unfortunately, relationships among the Pyrgotidae, Tephritidae, and Platystomatidae+Ulidiidae could not be satisfactorily inferred from our results. While our results are highly compatible with the relatively well established phylogenetic hypotheses involving tephritoid higher taxa, there are some new evidences that are useful to improve the tephritoid higher classification: (1) the monophyly of Tephritoidea is neither supported nor rejected; (2) the sister group relationship of Conopidae to any tephritoid taxa is not proven; instead, possibility of Conopidae as a basal group within the section Schizophora is suggested; (3) the monophyly of Platystomatidae is in doubt, and needs further consideration based on additional data; and (4) the most significant findings in our study is the recognition of Hennig's Pallopteroidea and Otitidae (= Group-1 and -2) as well supported monophyletic groups; resurrection of these two superfamilies will be needed as more negative evidences against the monophyly of Tephritoidea accumulate.