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A mitochondrial 12S and 16S rRNA phylogeny of critical genera of Phoridae (Diptera) and related families of Aschiza

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Abstract

Phylogenetic analysis of mitochondrial 12S and 16S rRNA gene sequences supports the monophyly of the Phoridae. Within this family the Phorinae clade includes two aberrant termitophilous subfamilies, the Thaumatoxeninae and the Termitoxeniinae, which cluster with *Dohrniphora* and *Diplonevra*. These two genera include termitophiles and parasitoids of termites, so we hypothesize that these termitophilous phorids are a monophyletic group. While the data neither refute nor support the assumed monophyly of the Metopininae, the genera of this subfamily were not monophyletic in our analysis, but fell into two subclades that correspond with the tribes Metopinini and Gymnophorini.

Key words: Diptera, Aschiza, Phoridae, rRNA sequences, phylogeny, maximum likelihood, Bayesian phylogeny, mitochondria, mtDNA, 12S, 16S lsuRNA, ssuRNA

Introduction

The flies, midges, and gnats (Diptera) are a successful and widespread insect order that includes over 120 named families and over 140,000 named species. However, the majority of species still remain undescribed and unnamed. The Diptera exhibit a diverse range of habits, especially as larvae. Indeed, the range of habits is greater than that for any other order of invertebrates. This diversity means that many species are of major medical, veter-inary, forensic or economic importance. Consequently, some families, such as the Culicidae (mosquitoes), have been intensively studied. Furthermore, the family Drosophilidae

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