

Molecular phylogeny of some genera of Pamphagidae (Acridoidea, Orthoptera) from China based on mitochondrial 16S rDNA sequences

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This paper is in memory of Prof. Shi-Xiang Chen (Sicien H. Chen), who is a Member of the Chinese Academy of Sciences and a famous entomologist, on the centenary anniversary of his birthday.

Abstract

Based on the mitochondrial 16S ribosomal DNA partial sequences (473 bp) of 9 species of Pamphagidae (Acridoidea, Orthoptera) from China and of 4 species of Pamphagidae and 2 species of Pyrgomorphidae and Acrididae (as outgroups) retrieved from GenBank, we constructed the molecular phylogeny using the Neighbor Joining (NJ) and Minimum Evolution (ME) methods based on the nucleotide Kimura 2-parameter model. The results of our study shown that: 1) the ranges of the 16S rDNA nucleotide divergence between two species of a genus were 0.21%, among genera of a subfamily were 0.42–3.38%, and among subfamilies of Pamphagidae were 1.90–8.88%, respectively. The phylogenetic tree shows that: 1) all Pamphagidae taxa form a monophyletic clade, and are well separated from the outgroup; 2) the African taxa Porthetinae (*Lobosceliana brevicornis*) and Akicerinae (*Batrachotetrix* sp.) are distinctly separated from the Chinese taxa Prionotropisinae; 3) *Haplotropis bruneriana* and *Glauia terrea* of Pamphaginae are nested in the middle of the tree, but their phylogenetic status is uncertain in this study; 4) 8 genera of *Asiotmethis*, *Beybienkia*, *Mongolotmethis*, *Sinotmethis*, *Rhinotmethis*, *Filchnerella*, *Eotmethis* and *Pseudotmethis* from China are all grouped into the subfamily Prionotropisinae, but their phylogenetic relationships are not clearly resolved.

Key words: Pamphagidae; Acridoidea; Orthoptera; 16S rDNA; Molecular Phylogeny