



Molecular phylogenetic analysis of Acridoidea (Orthoptera: Caelifera) based on mitochondrial cytochrome oxidase subunit sequences

LIJUN DONG¹, JIANPING SHI², XIAOHONG ZHANG¹, YULONG ZHANG¹, XINJIANG LI^{1,2} & HONG YIN^{1,3}

¹The Key Laboratory of Zoological Systematics and Application, College of Life Sciences, Hebei University, 071002 Baoding, P. R. China

²Northwest Plateau Institute of Biology, Chinese Academy of Sciences, Xining, 810001, P. R. China

³Corresponding author. E-mail: yinhong@hbu.edu.cn



Prof. Kailing Xia (1916–2013)

This paper is in memory of Prof. Kailing Xia (1916–2013), who is our career mentor and an eminent insect taxonomist, on his centenary birth anniversary.

Abstract

Phylogenetic relationships of Acridoidea were examined using mitochondrial cytochrome oxidase subunit sequences (*COI*, *COII* and *COIII*, total 2970bp). Fourteen grasshopper species of thirteen genera from seven families were sequenced to obtain mitochondrial genes data, along with twenty-two grasshopper species were obtained from the GenBank nucleotide database. The purpose of this study is to infer the phylogenetic relationships among families within Acridoidea and testing the monophyly of Acridoidea and each families of it. Phylogenic trees were reconstructed using Maximum Likelihood (ML) and Maximum Parsimony (MP) methods with Tettigonioidea and Gryllotalpoidea as outgroups. The putative initiation codon for *COI* is CCG in thirteen studied species and ATC in *Bryodema luctuosum luctuosum*. The 2970 bp concatenated sequences included 1431 conserved sites, 1539 variable sites, and 1216 parsimony-informative sites, the nucleotide compositions were significantly biased toward A and T (68.8%). The resulted phylogenetic trees supported the

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