



Phylogenetic analysis of the Prionini (Coleoptera: Cerambycidae: Prioninae) from China based on mitochondrial ribosomal RNA genes and Cytochrome oxidase I gene

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Abstract

This is the first molecular systematic treatment of the Prionini. Here, three mitochondrial genes were partially sequenced from the Chinese Prionini to analyze phylogenetic relationships. Nucleotide compositions of three mitochondrial genes in the Chinese Prionini are biased toward A and T as in other insects. Ratios of transition vs. transversion (Ts/Tv) in 12S rRNA decrease with divergence time. However, ratios in 16S rRNA first increase with divergence time but decrease when divergence time is prolonged. Some nodes have poor bootstrap values or Bayesian posterior probabilities in phylogenetic trees reconstructed from single mitochondrial gene. In addition, some conflicting clades are found among phylogenetic trees based on a different gene. Therefore, a single mitochondrial gene provides limited phylogenetic signal and phylogenetic relationships based on a single gene sequence may be questionable. The Chinese Prionini is a monophyletic group. However, the genus *Dorysthenes* is paraphyletic. *Dorysthenes fossatus* should be transferred from *Dorysthenes* but the true status of *D. fossatus* is currently unknown. Species of *Dorysthenes* (excluding *D. fossatus*) constitute a monophyletic clade and there is close relationship between *Dorysthenes paradoxus* and *Dorysthenes zivetta*.

Key words: Prionini, phylogenetic analysis, 12S rRNA, 16S rRNA, COI

Introduction

The Prionini is one of the oldest tribes in subfamily Prioninae (Coleoptera, Cerambycidae) and was proposed by Thomson (1860). He divided longhorn beetles into three tribes: tribe Prionitae, tribe Cerambycitae and tribe Lamiitae. Studies on species of the Prionini can be traced back to Linné (1758) and Geoffroy (1762). Linné named several species of the Prionini and placed them in the genus *Cerambyx*; Geoffroy defined the genus *Prionus* and distinguished it from others by three spines on lateral margin of pronotum. Evidently, the tribe Prionitae described by Thomson (1860) is the equivalent of our subfamily Prioninae and the tribe Prionini was proposed by Gahan (1906) who distinguished the Prionini from others in the Prioninae by three teeth or spines on each side of the prothorax and more or less strongly curved intercoxal process of the prosternum. Several years later, Lameere (1919) divided the tribe into subtribes Prioni, Acanthophori, Nothophysies and Derobrachi. Several subtribes and genera of the Prionini have been revised, such as subtribe Nothophysies (Quentin & Villiers 1981), subtribe Acanthophori (Quentin & Villiers 1983), genus *Psilotarsus* Motschulsky (Danilevsky 2000) and genus *Pogonarthron* Semenov (Danilevsky 2004). There are currently 204 species belonging to 27 genera in the tribe Prionini (Özdikmen *et al.* 2009), but we believe that several genera separated from the genus *Prionus* are doubtful and we adopt the genus *Prionus* of Lameere (1912) in the paper. There are 46 species belonging to four genera in the tribe Prionini in China (Hua *et al.* 2009; Drumont & Komiya 2008).