

Molecular Phylogenetics among Three Families of Bats (Chiroptera: Rhinolophidae, Hipposideridae, and Vespertilionidae) Based on Partial Sequences of the Mitochondrial 12S and 16S rRNA Genes

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Xiao-Ming Gu, Shu-Yan He, and Lei Ao (2008) Molecular phylogenetics among three families of bats (Chiroptera: Rhinolophidae, Hipposideridae, and Vespertilionidae) based on partial sequences of the mitochondrial 12S and 16S rRNA genes. *Zoological Studies* 47(3): 368-378. Extensive morphologic and molecular analyses of the phylogenetics of bats have been carried out, but controversies still exist. In order to further deduce the phylogenetic relationships among the families Vespertilionidae, Hipposideridae, and Rhinolophidae of microbats (Chiroptera), partial mitochondrial 12S and 16S rRNA gene sequences (2400 bp) for 32 species of the 3 families were obtained, among which the sequences of 19 species were amplified in this study and the other 13 were retrieved from GenBank. Meanwhile, those of 3 species in the family Pteropodidae and 1 species in the family Molossidae were also obtained from GenBank. The phylogenetics of all 5 families were assessed using a maximum-parsimony (MP) analysis. Second, the intrafamily relationships of the Vespertilionidae as well as the intra- and interfamily relationships of the Rhinolophidae and Hipposideridae were addressed using Bayesian, minimum-evolution (ME), and Neighbor-joining (NJ) methods. The following results were clearly demonstrated. (1) The paraphyly of microbats was revealed. (2) The subfamily Miniopterinae could not be elevated to family status, and it was the 1st clade separated from the Vespertilionidae. (3) *Myotis* should be elevated to the subfamily Myotinae, which was sister to a clade containing the Kerivoulineae and Murinae. (4) In the genus *Myotis*, all assayed New World and Old World species were respectively placed together in clades, and the 3 subgenera were not closely phylogenetically related. (5) As for *Pipistrellus*-like bats, 3 genera (*Ia*, *Scotomanes*, and *Eptesicus*) were successively placed together in clades, and were sister to the clade containing *Pipistrellus*, indicating a higher probability that the genus *Ia* belongs to Eptesicini than to *Pipistrellus*. (6) The Rhinolophidae and Hipposideridae should be treated as separate families. (7) In the genus *Hipposideros*, *Hipposideros armiger* was first placed together with *H. larvatus* in a clade, then with *H. pratti*, and *H. bicolor* was the 1st branch separated from other species of *Hipposideros*. (8) Finally, *R. ferrumequinum* and *Rhinolophus* sp. were the 1st branch separated from other Rhinolophids.
<http://zoolstud.sinica.edu.tw/Journals/47.3/368.pdf>

Key words: Phylogeny, Bats, Mitochondrial rRNA.

The order Chiroptera contains about 1100 species, making up more than 20% of extant mammals (Simmons 2005). Among them, there are about 120 species in China (Wang et al. 2003). Phylogenetic relationships of bats have been extensively analyzed, but many controversies still exist. Traditionally, the microchiroptera was

considered a monophyly with complex laryngeal echolocation systems (Simmons and Geisler 1998). Porter et al. (1996) and Hutcheon et al. (1998) proposed the paraphyly of microchiroptera, and the hypothesis was supported by Teeling et al. (2000 2002 2005), whose research indicated that the superfamily Rhinolophoidea was sister to the

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