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Integrative taxonomy places Asian species of *Falsistrellus* (Chiroptera: Vespertilionidae) into *Hypsugo*

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Abstract

The vespertilionid genus *Falsistrellus* currently contains three Asian (*F. affinis*, *F. petersi* and *F. mordax*) and two Australian (*F. tasmaniensis* and *F. mackenziei*) species. The Australian species are characterised with distinct external and craniodental traits, whereas the Asian taxa morphologically more closely resemble *Hypsugo* and the published molecular biological studies also suggested their close phylogenetic affinities. Herewith we provide sequence data of mitochondrial and nuclear genes for both Australian species for the first time, which, together with the combined cranial, dental, and multivariate statistical evidences provide a solid basis to place Asian members of *Falsistrellus* into *Hypsugo* and restrict *Falsistrellus* s. str. to Australia. The phylogenetic reconstructions also revealed the presence of a well-supported ‘Australian clade’ within the Vespertilionini radiation, containing three genera, *Falsistrellus*, *Chalinolobus* and *Vespadelus*, endemic to the Australasian zoogeographical region.

Keywords: Bats, Genus-level revision, Indomalayan Region, Phylogeny, Systematics

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