The East Asian fish-eating bat (Myotis ricketti or M. pilosus), which has large-footed and well-developed claws, is an endemic species in China, although they are also occasionally found in Laos (Ma, Jones, et al. 2003). Previous studies found that Myotis ricketti is a piscivorous bat species through the faecal analysis (Ma, Jones, et al. 2003). This fish-eating species can utilise echolocation to detect water ripples produced by fish on the surface of water (Ma, Zhang, et al. 2003), making it an excellent model for studying the co-evolution between bats and fishes.

The bat was sampled at Yanziyan Mountain (Huizhou, Guangdong Province, China) (g114.394690, 22.951571) on June 30, 2018. Genetic material of this bat (WHU-2018-07236) is stored in the Herbarium of Wuhan University. The genomic DNA was isolated from the liver tissue using the Universal DNA Purification Kit (TIANGEN BIOTECH, Beijing). The complete mitochondrial genome of M. ricketti (GenBank accession number MN245054) was amplified through PCRs using 16 pairs of newly designed primers according to the mitogenome sequences of other deter- mined Myotis species (Nam et al. 2015; Kim et al. 2017). The genome is 17,098 bp in size and contains 13 protein-coding genes (PCGs), two ribosomal RNAs, 22 transfer RNAs, and a non-coding control region (D-loop region). The gene order and organisation of this mitogenome are similar to most of other determined vertebrate mitogenomes, with the nucleotide base composition of A 34.22%, T 30.32%, C 22.80%, and G 12.66%. Besides, the mitogenomic D-loop region contains 29 copies of a tandem repeat sequence of six nucleotides (CATACG). The phylogenetic analysis indicates that M. ricketti is closely related to M. macrodactylus and M. petax. This study will contribute to the investigations of phylogeny and evolution for Myotis and its relevant taxa.

The phylogenetic relationships of 26 Myotis species were reconstructed with neighbour-joining (NJ) and maximum-likelihood (ML) methods based on the alignment of nucleotide sequences of 13 PCGs, with two vespert bat species (Plecotus auritus and P. macrobullaris) as the outgroups (Figure 1). The results showed that both NJ and ML trees contain two strongly supported clades (clade 1 and clade 2) (Figure 1), which were also reported earlier (Chung et al. 2018).
In addition, *M. ricketti* is most closely related to *M. macrodactylus* and *M. petax*.

**Disclosure statement**

The author reports no conflicts of interest. The author alone is responsible for the contents and the writing of the paper.

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