

The systematics and evolutionary history of Horseshoe bats (Rhinolophidae)



Cryptic species remain a major challenge for accurate species identification in bats, this is particularly problematic as they represent a substantial portion of undiscovered biodiversity, but also has implications for both species conservation and assaying potential risk of zoonotic spillover. We use integrative taxonomic approaches by combining phenotypic, acoustic, and genetic data to accurately delineate species, evaluate the phenotypic disparities between cryptic species, and identify key traits for their identification. Our results show that around 40% of Asian rhinolophid species are potentially cryptic and have not been formally described. We identified quantitative noseleaf and acoustic traits as the most informative, and each part of the noseleaf plays roles in focusing the acoustic beam. Understanding species evolutionary history is crucial in diagnosing cryptic species, thus, we investigate the species diversification and unravel the conflicting family geographic origin theories. Our results indicate that potential cryptic species may have split recently, in the Plio-Pleistocene, and the Indomalayan region acts as the center of species diversification in Asia. We further unravel the conflicting family and sister family (Hipposideridae and Rhinonycteridae) origin theories using a high-resolution tree covering taxa from each zoogeographic realm across the old-world. The results suggests Rhinolophidae originated from Oriental region, and complex historical events may shape current distribution.



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All are welcome!

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