Australian National University

16 December 2025
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Dear Editors of Molecular Phylogenetics and Evolution,

We would like to submit the attached manuscript, ***Phylogenomic assessment of microhylid frogs reveals widespread taxonomic confusion in the Asterophryinae and establishes the timing of diversification in Australia*** for consideration as an Article in ***MPE.***

In this study, we present a phylogenomic analysis of the frog family Microhylidae with a particular focus on the hyper-diverse subfamily Asterophryinae. Using anchored hybrid enrichment data, we reconstruct a robust, time-calibrated species tree that includes extensive sampling of New Guinean taxa and, for the first time, complete sampling of mainland Australian Asterophryinae. Our results demonstrate an explosive radiation of the group in New Guinea during the early Miocene, followed by later, independent dispersal events into Australia, and reveal widespread discordance between current generic taxonomy and evolutionary history.

Beyond clarifying relationships and divergence times in a taxonomically unstable group, our study integrates phylogenomics with quantitative morphological analyses to show that commonly used diagnostic traits often fail to reliably delimit genera. We believe this work provides an important phylogenetic framework for future taxonomic revision and contributes broadly to understanding rapid radiations, biogeography, and the limits of morphology-based classification—topics that align closely with the scope and readership of ***Molecular Phylogenetics and Evolution***.

On behalf of myself and coauthors, we thank you for your time and consideration,

Dr. Ian G. Brennan

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