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Systematics and molecular phylogenetics of Asian snail-eating snakes (Pareatidae)

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Abstract

The taxonomy of the Asian snail-eating snakes (Pareatidae) is an ongoing controversy, partly because morphological characters do not yield consistent results across studies. We infer phylogenetic relationships within Pareatidae using ~ 2 kilobases of DNA sequences including two mitochondrial (cyt *b* and ND4) and one nuclear gene (c-mos). Results reveal four major lineages: *Aplopeltura*, *Asthenodipsas*, a clade formed by *Pareas carinatus* and *P. nuchalis,* and a clade comprising all other species of *Pareas* sampled in this study. Our data do not have enough signal to either support or reject a monophyletic *Pareas*. However, large molecular divergence (16.5%) is observed between the two major clades of *Pareas*, a level that is comparable to that between *Pareas* and *Aplopeltura*. Scale characters also suggest that *P. carinatus* and *P. nuchalis* are distinct from congeners, and future morphological and/or molecular studies might assess whether a distinct genus should be recognized. The molecular phylogeny further suggests a distant relationship between *P. chinensis* and *P. formosensis* and supports the validity of the former species.

Key words: *Aplopeltura, Asthenodipsas,* genetic divergence, mitochondrial genes, nuclear genes, *Pareas*, scale patterns

Introduction

The Asian snail-eating snakes Pareatidae have long been recognized as a distinct lineage since the early nineteenth century (Boie 1827). They were considered a subfamily (Pareatinae) within Colubridae until recent phylogenetic analyses found strong evidence to support them as a separate family (e.g., Lawson *et al.* 2005; Vidal *et al.* 2007; Wiens *et al.* 2008; Pyron *et al.* 2011). Due to highly conserved morphology, the taxonomy of Asian snail-eating snakes remains contentious and has been frequently revised. Rao and Yang (1992) counted 39 species and subspecies in this family but suggested that most names were synonyms. Grossmann and Tillack (2003) recognized Pareatidae to comprise three genera and 15 species: *Aplopeltura boa* (Boie, 1828); *Asthenodipsas laevis* (Boie, 1827), *Asthenodipsas malaccanus* Peters, 1864, *Asthenodipsas vertebralis* (Boulenger, 1900); *Pareas boulengeri* (Angel, 1920), *P. carinatus* (Boie, 1828), *P. chinensis* (Barbour, 1912), *P. formosensis* (Van Denburgh, 1909), *P. hamptoni* (Boulenger, 1905), *P. iwasakii* (Maki, 1937), *P. macularius* Theobald, 1868, *P. margaritophorus* (Jan, 1866), *P. monticola* (Cantor, 1839), *P. nuchalis* (Boulenger, 1900), *P. stanleyi* (Boulenger, 1914). Jiang (2004) suggested that *P. chinensis and P. formosensis* had no significant difference in coloration and ventral and subcaudal scale pattern so he synonymized the former with the latter. In contrast, Zhao (2006) considered these two species as the *formosensis-chinensis* species complex pending evalution of more morphological data. Huang (2004) synonymized *P. macularius* with *P. margaritophorus* based also on morphological characters. Recently, Guo and Deng (2009) described another new species from southwestern China, *P. nigriceps*.

Molecular data are a frequently used and effective tool to help untangle taxonomic controversies when morphological analyses yield inconsistent results. However, molecular phylogenetic research on Pareatidae is limited and studies that included these snakes mainly aimed at questions at and above the family level (Slowinski and Law-

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