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The phylogenetic position and taxonomic status of the Rainbow Tree Snake *Gonyophis margaritatus* (Peters, 1871) (Squamata: Colubridae)

XIN CHEN^{1,2}, ALEXANDER D. McKELVY^{1,2}, L. LEE GRISMER³, MASAFUMI MATSUI⁴,
KANTO NISHIKAWA⁴ & FRANK T. BURBRINK^{1,2}

¹Department of Biology, The College of Staten Island, The City University of New York, 2800 Victory Blvd., Staten Island, NY 10314, USA. E-mail: xchen1@gc.cuny.edu

²Department of Biology, The Graduate School and University Center, The City University of New York, 365 Fifth Ave., NY, NY 10016, USA

³Department of Biology, La Sierra University, 4500 Riverwalk Pkwy., Riverside, California 92515 USA

⁴Graduate School of Human and Environmental Studies, Kyoto University, Kyoto 606–8501, JAPAN

Abstract

Molecular phylogenies have provided strong evidence for clarifying the taxonomy of groups with ambiguous morphological traits, thus avoiding potentially misleading conclusions based on evolutionary convergence of these traits. For snakes, established molecular databases along with new sequences from rare species allows us to estimate phylogenies, to clarify the phylogenetic relationships and test the monophyly of most taxonomic groups. Using one mitochondrial gene and five nuclear loci, we evaluate the taxonomic status of a rare Southeast Asian serpent, the Rainbow Tree Snake *Gonyophis margaritatus* (Squamata: Colubridae) by inferring a molecular phylogeny of 101 snake species. Both maximum likelihood and time-calibrated Bayesian inference phylogenies demonstrate that *G. margaritatus* is sister to *Rhadinophis prasinus*, previously considered to be part of a radiation of Old World ratsnakes. This group is in turn sister to a group containing *Rhadinophis frenatus* and *Rhynchophis boulengeri* with the entire clade originating in the mid-Miocene (~16 Ma) in Southeast Asia. This group is sister to the genus *Gonyosoma* and together originated in the early Miocene (~20 Ma). We discuss three potential solutions towards eliminating polyphyly of the genus *Rhadinophis*, but recommend using the genus name *Gonyosoma* for all species within this clade, which currently contains all of the species within the genera *Gonyosoma*, *Gonyophis*, *Rhadinophis*, and *Rhynchophis*.

Key words: *Gonyophis*, *Gonyosoma*, molecular phylogeny, polyphyly, *Rhadinophis*, *Rhynchophis*

Introduction

The importance of using phylogenetic trees to uncover genealogical relationships and properly construct a taxonomy of organisms cannot be overstated (de Queiroz & Gauthier 1992). The development of DNA sequencing technology has increased the available genetic data for phylogenetic inference and the development of model-based statistical methods, such as maximum likelihood and Bayesian inference, which has enhanced the reliability of reconstructed phylogenies (Meyer & Zardoya 2003; Yang & Rannala 2012; Danforth *et al.* 2013). Using molecular data to examine phylogenetic relationships provides evidence to clarify systematic ambiguities from morphological characters and helps avoid misleading relationships due to convergence of morphology (Wiens *et al.* 2010). Therefore, an abundance of molecular data with information from independent loci is able to provide strong evidence to assess taxonomic composition and test monophyly (Hillis 1987; Mishler 1994; Townsend *et al.* 2008).

The last decade has seen an incredible rise in the use of molecular phylogenies to examine relationships in snakes, assess biogeographic origins, understand processes of adaptive radiation and ultimately correct taxonomy with regard to paraphyletic and polyphyletic groups at multiple levels (Wüster *et al.* 2008; Zaher *et al.* 2009; Pyron *et al.* 2011; Burbrink *et al.* 2012; Pyron *et al.* 2013). The phylogenetic position of groups at moderately deep levels (e.g., subfamily) appears to have stabilized with regard to content and relationships, however the inclusion of new

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