“Same-same, but different”: an unusual new species of the *Limnonectes kuhlii* Complex from West Sumatra (Anura: Dicroglossidae)

DAVID S. MCLEOD1,3, STEPHANI J. HORNER1, COLIN HUSTED1, ANTHONY BARLEY1 & DJOKO ISKANDAR2

1University of Kansas Biodiversity Institute, 1345 Jayhawk Boulevard, Lawrence, Kansas 66045-7561, USA
2Department of Biology, FMIPA Institut Teknologi Bandung, 10 Jalan Ganesa, Bandung 40132, Indonesia
3Corresponding author. E-mail: dsmcleod@ku.edu

Abstract

A new species in the dicroglossine genus *Limnonectes* from West Sumatra, Indonesia, is described. Analysis of DNA sequence data from the mitochondrial 12S and 16S gene regions places the species within the *Limnonectes kuhlii* Complex and demonstrates it to be the sister taxon of *Limnonectes kuhlii* sensu stricto from Java. Both molecular and morphological data support the recognition of this lineage as a new species. Notably, the presence of a spinule-covered mental plate distinguishes *Limnonectes sisikdagu* sp. nov. from all other members of the *L. kuhlii* Complex. Additionally, pair-wise sequence divergence greater than 10% separate the new species from its sister taxon, *L. kuhlii* from Java.

Key words: dicroglossine, *Limnonectes sisikdagu* sp. nov., mitochondrial DNA, morphology, species complex

Introduction

*Limnonectes* Fitzinger (1843) comprises 55 currently recognized species (AmphibiaWeb, 2010). The genus is characterized by the presence of odontoid processes (hence the colloquial name of “fanged frogs”), male-biased size dimorphism, and male parental care (Emerson et al. 2000). Frogs of the genus *Limnonectes* are distributed throughout east and Southeast Asia, most are tied to forest stream habitats, and it is not uncommon to observe two or more congeners occurring in syntopy. The generotype, *Limnonectes kuhlii* Tschudi (1838), historically considered to be a single, broadly distributed species, was the focus of two recent molecular phylogenetic studies (Matsui et al. 2010; McLeod 2010) that highlighted a considerable amount of diversity hidden within this species complex. McLeod (2010) presented a robust molecular phylogeny of the *L. kuhlii* Complex (hereafter, *kuhlii* Complex) using mtDNA sequences from individuals representing approximately 63 populations across its known distribution. The results corroborated previous phylogenetic treatments of the *kuhlii* Complex (Emerson et al. 2000; Evans et al. 2003; Matsui et al. 2010; J. Zhang et al. 2005). Furthermore, McLeod (2010) demonstrated that *L. kuhlii*, which historically had been recognized as a single species, is a complex of more than 22 well-supported evolutionary lineages (viz., species), 16 of which are currently subsumed under the nominal *L. kuhlii*. Tschudi (1838) designated the island of Java as the type locality for *L. kuhlii*. McLeod (2010) followed this designation and restricted all individuals from Java to retain the name *L. kuhlii*. Additionally, the study also uncovered several cases of sympatric/syntopic lineages, and in no case were co-occurring lineages each other’s closest relatives (McLeod, 2010).

In 2001, a series of anuran specimens was collected from three stream systems in West Sumatra by one of us (D.I.). These specimens were identified as *Limnonectes kuhlii* and deposited in the Field Museum of Natural History. In 2010, these specimens were examined by one of us (D.S.M) as part of a larger study on the *kuhlii* Complex. Tissue samples from these specimens were sequence for mitochondrial DNA data and mensural data were collected from whole specimens. We present these data herein and describe a new species that is part of the *kuhlii* Complex and is demonstrated to be the sister taxon to “true” *Limnonectes kuhlii* from Java.