



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

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Abstract

A new species in the dicroglossine genus *Limnnectes* from West Sumatra, Indonesia, is described. Analysis of DNA sequence data from the mitochondrial 12S and 16S gene regions places the species within the *Limnnectes kuhlii* Complex and demonstrates it to be the sister taxon of *Limnnectes 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 *Limnnectes 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, *Limnnectes sisikdagu* **sp. nov.**, mitochondrial DNA, morphology, species complex

Introduction

Limnnectes 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 *Limnnectes* 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, *Limnnectes 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 *Limnnectes 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 sequenced 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” *Limnnectes kuhlii* from Java.