



Two new species of the “*kuhlii*” complex of the genus *Limnonectes* from Thailand (Anura: Dicroglossidae)

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Abstract

Phylogenetic relationships inferred from sequences of the mitochondrial 12S rRNA, tRNA^{val}, and 16S rRNA genes and nuclear POMC and RAG-1 genes revealed that fanged frogs from Thailand usually associated with *Limnonectes kuhlii* are monophyletic and are collectively sister to the clade containing three Chinese and Japanese species. Within the Thai clade, the northern lineage, the southern lineage, and a population originally assigned to *L. megastomias* show unresolved relationships with each other, but are separated by genetic distances that correspond to values found among species of the Chinese-Japanese clade. Hybridization and past gene introgression are not detected among these three lineages of fanged frogs from Thailand. Adult specimens of the northern and southern lineages are phenotypically similar to each other, but can be separated by the combination of several morphometric characters. From the genetic and morphological evidence, they are considered to represent taxonomically different species. We therefore describe the northern lineage as *L. taylori* **sp. nov.** and the southern lineage as *L. jarujini* **sp. nov.** Taxonomic identity of the Loei population of *L. megastomias* requires future morphological investigation. The distribution pattern of fanged frogs within Thailand is discussed and the significance of the Three Pagodas Fault Zone is noted.

Key words: *Limnonectes*; mitochondrial DNA; nuclear DNA; phylogeny; new species; Thailand; biogeography

Introduction

Limnonectes kuhlii Tschudi (1838) originally described from Java, has long been treated as a single, wide-ranging species occurring from Taiwan through eastern and southern continental China, Southeast Asia, to northeastern India (Boulenger 1920; Frost 2010). However, the presence of morphological (e.g. Inger 1966; Matsui 1979; Inger & Tan 1996) and molecular (Emerson *et al.* 2000; Evans *et al.* 2003) variations has also been pointed out. Thus, two Chinese and one Thai species have been described, each distinct from *L. kuhlii* from Java (Ye & Fei 1994; Ye *et al.* 2007; McLeod 2008).

Using mtDNA sequences, Matsui *et al.* (2010b) studied phylogenetic relationships of these Chinese and Thai species and populations of *L. “kuhlii”* surrounding their distribution range. As a result, they ascertained distinct specific status of the three species and clarified their ranges of distribution. In describing *L. megastomias* from eastern Thailand, McLeod (2008) noted that the population of *L. “kuhlii”* from the northern region of the country might not be conspecific with it based on the phylogenetic tree he obtained. McLeod (2010), while further strengthening this idea, also suggested recognizing two taxa within *L. megastomias* and removing the Loei population from it. Matsui *et al.* (2010b) treated the population from Phu Luang, Loei Province, as *L. megastomias* because the population originally comprised the paratypes of the species (McLeod, 2008). However, because McLeod (2010) has changed his view but has not determined the taxonomic status of the Loei population, we tentatively call the population as *L. “megastomias”* from Loei. Taylor (1962) already noted that the Thai populations of *L. “kuhlii”* show morphological variation. However,