Systematic reassessments of fanged frogs from China and adjacent regions
(Anura: Dicroglossidae)

MASAFUMI MATSUI1,6, NORIHIRO KURAISHI1, JIAN-PING JIANG2, HIDETOSHI OTA1, AMIR HAMIDY1,4, NIKOLAI L. ORLOV5 & KANTO NISHIKAWA1

1Graduate School of Human and Environmental Studies, Kyoto University, Kyoto 606-8501, Japan.
E-mail: fumi@zoo.zool.kyoto-u.ac.jp

2Chengdu Institute of Biology, the Chinese Academy of Sciences, Chengdu 610041, China. E-mail: jiangjp@cib.ac.cn

3Institute of Natural and Environmental Sciences and Museum of Nature and Human Activities, University of Hyogo, Yaoigaoka 6, Sanda, Hyogo 669-1546, Japan. E-mail: ohta@hitohaku.jp

4Museum Zoologicum Bogoriense, Research Center for Biolog, Indonesian Institute of Sciences, Gd. Widyasatwaloka, Jl. Raya Jakarta Bogor km 46, Cibinong West Java, Indonesia. E-mail: amirhamidy@at5.ecs.kyoto-u.ac.jp

5Department of Herpetology and Ornithology, Zoological Institute, Russian Academy of Science, 119034, St. Petersburg, Russia.
E-mail: azemiops@zin.ru

6Corresponding author. E-mail: fumi@zoo.zool.kyoto-u.ac.jp

Abstract

Systematic relationships of fanged frogs usually associated with Limnonectes kuhlii are assessed using 15 samples from Japan, Chinese Mainland and Taiwan, Vietnam, Laos, Thailand, Malaysia (Borneo), and Indonesia. Phylogenetic relationship inferred from the mitochondrial 12S rRNA, tRNA\textsuperscript{val}, and 16S rRNA gene sequences revealed that fanged frogs sampled are not monophyletic with the topotypic L. kuhlii from Java. Samples from Yunnan of southern China (L. bannaensis), northern Laos and central Vietnam, and those from Jiangxi of eastern China (L. fujianensis), Taiwan and Japan (L. namiyei), respectively, form monophyletic groups, and are collectively sister to the Thai sample (L. megastomias). All these samples, L. fragilis from Hainan of southern China, and a group of Bornean samples show unresolved relationships with Javanese L. kuhlii. From the resultant phylogeny and genetic distances found among samples, L. "kuhlii" from Taiwan and L. fujianensis, and L. "kuhlii" from northern Laos and central Vietnam and L. bannaensis, respectively, are surmised to be conspecific. These fanged frogs are morphologically similar to, but phylogenetically distant from, L. kuhlii sensu stricto. Limnonectes namiyei, L. fujianensis, and L. bannaensis are considered to have a common ancestor whose chromosome number was 2n=22, unlike L. fragilis, L. kuhlii and many other frogs with 2n=26 chromosomes.

Key words: Limnonectes; mitochondrial DNA; phylogeny; species identity; Taiwan; Laos; Vietnam; chromosome

Introduction

Recent studies on amphibians in various parts of the world have revealed that there are few single species in the tropics that are really wide-ranging in distribution (e.g. Wynn & Heyer 2001; Fouquet et al. 2007) while most amphibian species have quite small distribution areas. Frogs from the Oriental region are no exception, and presence of cryptic species has been increasingly reported in many lineages (e.g. Polypedates leucomystax [Gravenhorst]: Matsui et al. 1986; Kalophrynus pleurostigma Tschudi: Matsui et al. 1996; Fejervarya limnocharis [Gravenhorst]: Toda et al. 1998; Microhyla ornata [Duméril & Bibron]: Matsui et al. 2005; Euphyctis cyanophlyctis [Schneider]: Alam et al. 2008; Rana chalconota [Schlegel]: Inger et al. 2009). There still remain, however, many species whose taxonomic status should be examined. One example is the fanged frogs that have long been assigned to a single species Limnonectes kuhlii (e.g. Boulenger 1920; Inger 1966).