

Unusually high genetic diversity in the Bornean *Limnonectes kuhlii*-like fanged frogs (Anura: Dicoglossidae)

ABSTRACT

A fanged frog *Limnonectes kuhlii* was once thought to be wide-ranging in Southeast Asia, but is now confined to its type locality Java through recent phylogenetic studies, which clarified heterospecific status of non-Javanese populations, and monophyly of Bornean populations. However, large genetic differences among Bornean populations suggest occurrence of cryptic species, which we test using dense geographic sampling. We estimated the phylogenetic relationships among samples of Bornean populations together with their putative relatives from the continental Southeast Asia, using 2517 bp sequences of the 12S rRNA, tRNA^{Val}, and 16S rRNA of mitochondrial DNA, and 2367 bp sequences of the NCX1, POMC, and RAG1 of nuclear genes. In the mtDNA trees, Bornean *L. kuhlii*-like frogs formed a monophyletic group split into 18 species lineages including *L. hikidai*, with the deepest phylogenetic split separating *L. cintalubang* from the remaining species. Almost all of these lineages co-occur geographically, and two to three lineages were found syntopically in each locality. Co-occurrence of more than one lineage may be maintained by differential morphology and microhabitat selection. These syntopic lineages should be regarded as distinct species. Our results clearly indicate that taxonomic revision is urgent to clarify many evolutionary problems of Bornean *L. kuhlii*-like frogs.