GENETIC VARIATION OF THE BORNEAN FANGED FROG,
Limnonectes kuhlii COMPLEX IN WESTERN BORNEO
(AMPHIBIA: ANURA: DICROGLOSSIDAE)

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ABSTRACT

The fanged frog Limnonectes kuhlii is known to be cryptic as seen in the dynamic of species delineation among the complexes. Yet no historical demographic and genetic structure has been fully documented for this species. We investigate historical events, diversification and dispersal of the Bornean Limnonectes kuhlii Complex via Mitochondrial DNA of partial 16S rRNA. Haplotype graphical network, demographic history, neutrality test and population subdivision analysis were used to assess population genetic of the species. Two haplogroups were detected distinct within population and panmictic from East and West of Lupar gap (Batang Ai). The Lupar gap has become the geographical barrier that restricts gene flow from western and eastern populations. Ragged multimodal mismatch distribution, long terminal branches and high mutational site of network showing population in Sarawak and Sabah were rarely migrate and low gene flow. Surprisingly, most of L. kuhlii population showed population constriction and presence of two or more mixed subpopulations. It can be concluded that high levels of sequence divergence suggesting ancient DNA (lineage) and cryptic species hidden within the species. This study should be extended in future with more samples and validate their true species status with morphological data.

Key words: Ancient DNA, cryptic species, genetic variation, mitochondrial (mtDNA), population genetic

INTRODUCTION

Since introduction of Polymerase Chain Reaction (PCR) in 1985 as a molecular technique for species examination and identification, study and research have increase exponentially on discovering and uncovering cryptic species (Bickford et al., 2007). McLeod (2010) stated that identification of these cryptic species is critical to assess accurately genuine biodiversity. This technique opens wide opportunity for detecting and differentiating morphologically similar species. Cryptic species are known as two or more distantly genetically related but possess conspicuously similarly morphological characteristics that were recognized as a single species (Pfenninger & Schwenk, 2007). Several studies suggested that Limnonectes kuhlii represented a cryptic species complex (Emerson et al., 2000; Evans et al., 2003; McLeod, 2010; Matsui et al., 2016). According to Emerson et al. (2000), broad ranging of L. kuhlii is as a matter of fact a number of different species.

McLeod et al. (2011) suggested that the diversity within the L. kuhlii complex was greater than previously suspected. How much greater is the diversity within L. kuhlii complex in Borneo? What are the factors that caused high genetic divergence within the population? To address these and related issues, a comprehensive assessment of the diversity within this species complex is through the population genetic context. Knowledge of genetic structure of populations is very important for one to understand the species evolution. Therefore, we examine the historical events, diversification and dispersal of L. kuhlii to apprehend on its ancient polymorphism and genetic variation among L. kuhlii populations from geographically isolated areas in Borneo.