

Genetic Structure of *Hylarana erythraea* (Amphibia: Anura: Ranidae) from Malaysia

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Ramlah Zainudin, Shukor Mohd Nor, Norhayati Ahmad, Badrul Munir Md-Zain, and Mustafa Abdul Rahman (2010) Genetic structure of *Hylarana erythraea* (Amphibia: Anura: Ranidae) from Malaysia. *Zoological Studies* 49(5): 688-702. We studied the genetic structure and evolutionary relationships among populations of *Hylarana erythraea* in Sarawak, Malaysian Borneo (Borneo Heights of Padawan, Sadong Jaya, and Bario) and central Peninsular Malaysia (Tasik Chini of Pahang) using the partial cytochrome oxidase subunit 1 (CO1) gene of mitochondrial (mt)DNA. Two distinct geographical clades were observed, i) the 1st clade, haplogroup 2 included 7 divergent haplotypes in Bario, whereas ii) the 2nd clade (haplogroup 1) contained 16 haplotypes of the remaining populations. Gene flow estimators indicated high numbers of migrants per generation and panmictic populations of this species, except for a low number of migrants per generation and genetic isolation of the Bario population. The species was estimated to have undergone population expansion either for the whole population or for each population as shown by small and nonsignificant values of the sum of the standard deviation of the observed and expected mismatch distributions and Harpending raggedness index. However, multimodal distributions were seen in the scatterplot of mismatch distributions for the entire populations of Sadong and Bario. Geographical subdivision might explain the anomalies in the mismatch distribution for these populations. Furthermore, a large negative value and significant test of F_u and F_s in the Bario population suggested recent expansion and are indicative of dispersal from ancient Sunda Shelf populations (Pahang, Sadong, and Borneo Heights) to East Sarawak (Bario). The results suggested that populations of *H. erythraea* were subdivided where populations in central Peninsular Malaysia and western Borneo were more closely related than those in western Borneo were to those of eastern Borneo. The study implied that a feature in the landscape of Borneo (the Lupar line) created a greater barrier than repeated intervening ocean between glacial periods. Our study also supports the notion that a widely distributed frog species includes different evolutionary lineages that are possibly cryptic species. <http://zoolstud.sinica.edu.tw/Journals/49.5/688.pdf>

Key words: *Hylarana erythraea*, mtDNA CO1, Population expansion, Population subdivision.

The green paddy frog *Hylarana erythraea* Schlegel is a small to medium sized frog with bright to dark green color dorsally and laterally (Inger and Stuebing 2005). Although the species occurs in natural grasslands and open areas, the frog is an important indicator of habitat disturbance in

Malaysia, as it is mostly found in disturbed habitats created by man, such as flooded paddy fields, plantations, and irrigation ditches. The species is widely distributed in Southeast Asia (Borneo, Peninsular Malaysia, Singapore, Indonesia, Thailand, the Philippines, Vietnam, Laos,

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