



<http://dx.doi.org/10.11646/zootaxa.3962.1.11>

<http://zoobank.org/urn:lsid:zoobank.org:pub:9908D584-DC92-4D28-B53F-A515573A4F1F>

## Genetic identification and structure of *Clarias batrachus* (Linnaeus, 1758) from Southeast Asia using a mitochondrial DNA marker

PAOLIN LEE<sup>1</sup> & ZOHRAH SULAIMAN<sup>1,2</sup>

<sup>1</sup> Environment and Life Science Programme, Faculty of Science, Universiti Brunei Darussalam, Tungku BE1410, Brunei Darussalam; E.mail: paolinlee@yahoo.com; zohrah.sulaiman@ubd.edu.bn.

<sup>2</sup> Institut Teknologi Brunei, Tungku BE 1410, Brunei Darussalam; E.mail: zohrah.sulaiman@itb.edu.bn

### Abstract

A phylogenetic tree and median-joining network based on cytochrome b sequence data revealed clades consistent with morphological differences and geographical distribution of *Clarias batrachus* (Linnaeus, 1758) in Southeast Asia. AMOVA analysis for variation was significant among populations ( $P < 0.05$ ) and was in agreement with morphological differences. Pairwise differences were significant between Java and Brunei/Borneo, Brunei/Borneo and west Malaysia, and Java and west Malaysia samples ( $P < 0.05$ ). Closest relationships were found between samples from Brunei/Borneo and Java, and between west Malaysia and Laos-Sumatra. Nine haplotypes were unique to geographical regions. The Java species had high haplotype ( $1.000 \pm 0.126$ ) but low nucleotide ( $0.017$ ) diversities, suggesting a population bottleneck followed by expansion. However, *SSD* and *Hri* ( $P=0.5$ ) did not support demographic expansion. Instead, purifying selection where mutations occur and accumulate at silent sites is a more acceptable explanation.

**Keywords:** Borneo, Java, Clariidae, cytochrome *b*, phylogenetics

### Introduction

In Southeast Asia, 19 species of the genus *Clarias* are currently recognized (Ng *et al.*, 2011) including 13 species in Borneo (Kottelat, 2013). In spite of the relatively recent colonisation of Southeast Asia from central Asia about 15 MYA (Agnese & Teugels, 2005), *Clarias* shows considerable diversity in morphology and habitat.

*Clarias batrachus* is a common species found in South and Southeast Asia and is widely utilised in aquaculture and the aquarium fish trade, and has been the subject of numerous studies (see Begum, 2004; Hora, 1936; Kottelat, 2001; Ng & Kottelat, 2008; Khedkar *et al.* 2010). The species has been introduced to many parts of the world and has the potential to threaten non-native environments (Lever, 1996).

The identity of *C. batrachus* has recently been studied by Ng & Kottelat (2008). They redescribed *C. batrachus* and designated a neotype from Java. Ng & Kottelat (2008) designated the non-Javanese *C. batrachus* as: *Clarias* aff. *batrachus* ‘Indochina’ from the Mekong River drainage, and *Clarias* aff. *batrachus* ‘Sundaland’ from west Malaysia and Sarawak. They noted morphological differences in these forms in the shape of the supraoccipital process and width of the frontal fontanelles. The morphological difference between *C. aff. batrachus* ‘Sundaland’ and *C. aff. Indochina* was in the shape of the supraoccipital process. The latter was more triangular. The shape of supraoccipital process also is a useful diagnostic character in Asian *Clarias* (Teugels *et al.* 1999). The frontal fontanelle of *C. batrachus* from the Malay Peninsula and Sarawak was wider and referred to as ‘sole shaped’ by Teugels (1986) than that on specimens from Java and mainland Southeast Asia, referred to as ‘knife-shaped’ by Teugels (1986). The morphological differences seemed to correlate with geographical areas of Southeast Asia.

Several molecular genetics studies had been conducted on Asian *Clarias* (Agnese & Teugels, 2005; Pouyaud *et al.* 2009), Asian *C. batrachus* (Islam *et al.* 2007; Khedkar *et al.* 2010) and Southeast Asian *C. batrachus* (Mohindra *et al.* 2007). However, no molecular study has investigated variation in sequence data from the cytochrome *b* gene in *C. batrachus* from Southeast Asia. The objective of the present study is to determine whether genetic data from the cytochrome *b* gene is in agreement with morphological variation in *C. batrachus* from Southeast Asia.