



Remarkably low genetic variation but high population differentiation in the climbing perch, *Anabas testudineus* (Anabantidae), based on the mtDNA control region

A.F.J. Jamsari¹, Z.A. Muchlisin^{1,3}, M. Musri⁴ and M.N. Siti Azizah^{1,2}

¹School of Biological Sciences, Universiti Sains Malaysia, Minden, Penang, Malaysia

²Centre for Marine and Coastal Studies, Universiti Sains Malaysia, Minden, Penang, Malaysia

³Department of Aquaculture, Coordinator of Fishery and Marine Sciences, Syiah Kuala University, Banda Aceh, Indonesia

⁴Department of Marine Sciences, Coordinator of Fishery and Marine Sciences, Syiah Kuala University, Banda Aceh, Indonesia

Corresponding author: M.N. Siti Azizah

E-mail: sazizah@usm.my

Genet. Mol. Res. 9 (3): 1836-1843 (2010)

Received June 24, 2010

Accepted July 18, 2010

Published September 14, 2010

DOI 10.4238/vol9-3gmr933

ABSTRACT. *Anabas testudineus* (Anabantidae) is an important food fish in Southeast Asia. We analyzed the mitochondrial DNA control region sequence data to evaluate the genetic variability and population structure of this species. Sixty specimens were collected from four populations in Sumatra and two populations in Peninsular Malaysia. We found a very low level of genetic variability, with five of the six populations exhibiting total absence of genetic variation. Based on analysis of molecular variance, 84.72% of the total variation was among populations and 15.28% within populations. A geographical division based on F_{ST} values indicated highly significant genetic differentiation

among populations from the four drainage systems: Aceh, Sumatra Utara, Pulau Pinang, and Terengganu (F_{ST} ranging from 0.633 to 1.000). No phylogeographic relationships among populations were detected, despite the generation of four distinct clades in a neighbor-joining phylogenetic tree.

Key words: *Anabas testudineus*; Climbing perch; Sundaland; Population genetics; Control region