
Research Article

Phylogenetic analysis of selected cyprinids inferred from sequencing of a mitochondrial *cytochrome c oxidase I* (COI) gene

Yuzine B. Esa^{1*}, Siti Shapor Siraj¹, Khairul Adha A. Rahim², Siti Khalijah Daud³ and Tan Soon Guan⁴

¹*Department of Aquaculture, Faculty of Agriculture, Universiti Putra Malaysia 43400 Serdang Selangor DE, Malaysia. *email: yuzine@putra.upm.edu.my*

²*Department of Aquatic Science, Faculty of Resource Science and Technology, Universiti Malaysia Sarawak, 94300 Kota Samarahan, Sarawak.*

³*Biology Department, Faculty of Science, Universiti Putra Malaysia 43400 Serdang, Selangor DE, Malaysia.*

⁴*Department of Cell and Molecular Biology, Faculty of Biotechnology and Biomolecular Sciences, Universiti Putra Malaysia 43400 Serdang Selangor DE, Malaysia.*

ABSTRACT. This study examines the phylogenetic relationships of 21 selected freshwater cyprinids using sequence analysis of mitochondrial DNA *cytochrome c oxidase I* (COI) gene (464 base pairs). The phylogenetic study supported the monophyletic status between genus *Tor* and *Neolissochillus*, although their positioning within the mahseer clade (together with mahseers from South Asia) remained unresolved. Thus, the current result supported their taxonomic distinction and further erected the reclassification of *Neolissochillus stracheyi* from the genus *Tor* (previously classified as *Tor soro* into the genus *Neolissochilus* based on morphological characters such as the absence of the median lobe. The phylogenetic results also showed that the genus *Barbus* (represented by *Barbus barbatus*) was the closest taxa to the genus *Tor*, followed by *Cyprinus carpio* and *Barbonymus gonionotus*. Another interesting finding was that *B. gonionotus* was phylogenetically distinct from its morphologically similar species, *Barbonymus schwanenfeldii* (K2P

distance value = 15.1%) and did not group together in a single *Barbonymus* clade. The high genetic divergence observed between *B. schwanenfeldii* and *B. gonionotus* recommends the taxonomic revision of the latter barb from its current position within the genus *Barbonymus*. However, shortcomings of our results are clearly recognized and data should be treated with great caution, since it was based on a limited number of samples and a single maternally inherited gene (COI). Overall, the study managed to provide an insight into the phylogenetic relationships among cyprinids under study.

Keywords: Cyprinidae, freshwater fish, mtDNA, COI, phylogeny.

INTRODUCTION

Freshwater fishes of the Family Cyprinidae form the largest family of freshwater fishes in terms of number of genera and species worldwide, including in Malaysia (Zakaria-