



Short communication

Improving the phylogenetic resolution of Malaysian and Javan mahseer (Cyprinidae), *Tor tambroides* and *Tor tambra*: Whole mitogenomes sequencing, phylogeny and potential mitogenome markers

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ABSTRACT

The true mahseer (*Tor* spp.) is one of the highest valued fish in the world due to its high nutritional value and great unique taste. Nevertheless, its morphological characterization and single mitochondrial gene phylogeny in the past had yet to resolve the ambiguity in its taxonomical classification. In this study, we sequenced and assembled 11 complete mahseer mitogenomes collected from Java of Indonesia, Pahang and Terengganu of Peninsular Malaysia as well as Sarawak of East Malaysia. The mitogenome evolutionary relationships among closely related *Tor* spp. samples were investigated based on maximum likelihood phylogenetic tree construction. Compared to the commonly used COX1 gene fragment, the complete COX1, Cytb, ND2, ND4 and ND5 genes appear to be better phylogenetic markers for genetic differentiation at the population level. In addition, a total of six population-specific mitolineage haplotypes were identified among the mahseer samples analyzed, which this offers hints towards its taxonomical landscape.

1. Introduction

The *Tor* spp. (true mahseer) is one of the most exorbitant freshwater fish grouped under the Cyprinidae family, valued by their high nutritional value and great food security potential (Day, 1876; Thomas, 1873). These fishes inhabit rapid-flowing waters with rocky bottoms (Shreshtha, 1997). To date, there are a total of 16 *Tor* species identified worldwide and 18.8% (three) of them are found within the freshwaters of Indonesia and Malaysia, namely *Tor tambra*, *Tor tambroides* and *Tor douronensis* (Ng, 2004).

The environmental degradation within the *Tor* habitat is pacing in an unprecedented elevation trend during the recent years with the increasing human activities like dam construction (Ingram et al., 2005). The IUCN (International Union for Conservation of Nature) Red List assessed three Near Threatened, one Vulnerable and one Critically Endangered *Tor* spp. to date while the others remained Data Deficient (Pinder et al., 2019). The three aforementioned Indonesian-Malaysian

Tor fish species are among the 11 Data Deficient *Tor* spp. that lack detailed characterization and conservation evaluation. Some studies have also shown that the different colours (silver-bronze and reddish) exhibited in *T. tambroides* may be associated with environmental influences (Esa et al., 2006; Siraj et al., 2007; Vrijenhoek, 1998). Unfortunately, the ambiguous original descriptions of these three *Tor* species had led to misidentification and confusion among the scientific communities in the past (Walton et al., 2017).

A mitochondrial DNA diversity investigation by Walton et al. (2017) and Esa et al. (2008) using the standard cytochrome oxidase I (COX1) gene fragment, had revealed substantial genetic diversity between the *T. tambra* and *T. tambroides* populations sampled from East Malaysia region of the Borneo Island (Batang Ai, Sarawak, East Malaysia), West Java of Indonesia and Peninsular Malaysia (Pahang, Perak, Negeri Sembilan and Kelantan). The utilization of a single gene fragment for analysis is deemed insufficient in terms of data estimates precision and phylogenetic resolution (Duchêne et al., 2011; Walton et al., 2017).

Abbreviations: COX1, cytochrome oxidase I; DNA, deoxyribonucleic acid; IUCN, International Union for Conservation of Nature.

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