

Research Article

Genetic Structure and Preliminary Findings of Cryptic Diversity of the Malaysian Mahseer (*Tor tambroides Valenciennes*: Cyprinidae) Inferred from Mitochondrial DNA and Microsatellite Analyses

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This study examines the population genetic structure of *Tor tambroides*, an important freshwater fish species in Malaysia, using fifteen polymorphic microsatellite loci and sequencing of 464 base pairs of the mitochondrial cytochrome c oxidase I (COI) gene. A total of 152 mahseer samples were collected from eight populations throughout the Malaysia river system. Microsatellites results found high levels of intrapopulation variations, but mitochondrial COI results found high levels of interpopulations differentiation. The possible reasons for their discrepancies might be the varying influence of genetic drift on each marker or the small sample sizes used in most of the populations. The Kelantan population showed very low levels of genetic variations using both mitochondrial and microsatellite analyses. Phylogenetic analysis of the COI gene found a unique haplotype (ER8*), possibly representing a cryptic lineage of *T. douronensis*, from the Endau-Rompin population. Nevertheless, the inclusion of nuclear microsatellite analyses could not fully resolve the genetic identity of haplotype ER8* in the present study. Overall, the findings showed a serious need for more comprehensive and larger scale samplings, especially in remote river systems, in combination with molecular analyses using multiple markers, in order to discover more cryptic lineages or undescribed “genetic species” of mahseer.

1. Introduction

Tor tambroides, commonly known as mahseer, Kelah, or Empurau, is a highly priced cyprinid fish in Malaysia due to its delicious flesh and has a great potential for the freshwater aquaculture industry [1, 2]. It is also recognized as an excellent game fish and has a high demand in the ornamental fish industry due to its attractive color [2, 3]. Unfortunately, the natural habitat and effective population size of many freshwater fishes such as *T. tambroides* which require clean running water with gravels and rocks are rapidly being degraded due to anthropogenic disturbances (i.e., river pollution, deforestation, watershed erosion, and others) and uncontrolled fish harvesting [4]. Therefore, considering

the economic importance of *T. tambroides* and given its fragmented distributions and population size, studies on the population structure and level of genetic variations throughout its distribution range are required for the effective management and conservation strategies of this important freshwater resource.

The phylogenetic relationship and taxonomic status between *T. tambroides* and its congeneric species *T. douronensis* have been conducted by several authors such as [5–7] who genetically confirmed their taxonomic status as distinct species. Esa et al. [8] subsequently examined the genetic structure of *T. tambroides* from 5 populations in Malaysia using the mitochondrial COI sequences and found low mitochondrial variations at the intrapopulations level