

Molecular Systematics of Mahseers (Cyprinidae) in Malaysia Inferred from Sequencing of a Mitochondrial Cytochrome C Oxidase I (COI) Gene

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ABSTRACT

This study examined the molecular systematics among three Mahseers (*Tor douronensis*, *Tor tambroides* and *Neolissochilus stracheyi*) using partial sequencing of a Cytochrome C Oxidase I (COI) mitochondrial DNA segment (466bp). The phylogenetic results using the Neighbour-Joining (NJ) method supported the monophyletic status (hence the taxonomic status) among the three putative Mahseer species. The close genetic relationships (0.1-0.4%) found between *T. tambroides* samples from Peninsular Malaysia (kelah fish) and those from Sarawak (empurau fish) also supported their classification as belonging to the same species. The phylogenetic analysis also showed that the *T. douronensis* mtDNA consisted of three highly distinct lineages supported by high bootstrap values, with the Sabah samples forming its own cluster. Thus, this phylogenetic study, although based on a limited number of samples and only a single mtDNA gene managed to provide useful insights into the systematic status of the Mahseers found in Malaysia.

Keywords: Freshwater fish, Mahseers, COI, molecular systematics

INTRODUCTION

Freshwater fishes of the genus *Tor* Gray, commonly known as the Mahseers, belong to the family Cyprinidae (subfamily Cyprininae) (Inger and Chin, 1962; Mohsin and Ambak, 1983; Roberts, 1989; Kottelat *et al.*, 1993). There are currently 17 described species under the genus *Tor* from all across Asia (Ng, 2004) but only three species were reported in Malaysia: *Tor tambroides* Bleeker, *Tor tambra* Valenciennes, and *Tor douronensis* Valenciennes (Kottelat *et al.*, 1993; Kottelat and Whitten, 1996; Ng, 2004). The taxonomic status of *Tor soro* Valenciennes had been revised and it is currently re-classified as *Neolissochilus stracheyi* (Rainboth, 1996). Mahseers are important as food fish as well as ornamental and recreational fishes. However, recently the population sizes of their natural stocks are

decreasing rapidly due to environmental degradation and increased fishing pressure (Ng, 2004).

So far, very little taxonomic work to systematically sort out Malaysian Mahseer has been documented. The most cited work was by Mohsin and Ambak (1983) who described *Tor tambroides* and *Tor soro* as two valid Mahseers found in Peninsular Malaysia while a more recent view by Ng (2004) suggested the occurrence of three species; *T. tambroides*, *T. tambra* and *T. douronensis*. Other taxonomic works recognized *T. douronensis* and *T. tambroides* as two valid species (Roberts, 1989; Kottelat *et al.*, 1993; Rainboth, 1996; Zhou and Chu, 1996), although Roberts (1999) classified them to be a single species, and a junior synonym to *T. tambra*. The presence of the median lobe has been characterized as a

diagnostic morphological character distinguishing the genus *Tor* from the genus *Neolissochilus* (Rainboth, 1996; Ng, 2004), though it cannot be used consistently as a marker to discriminate between fishes of the genus *Tor*. Thus, the application of molecular techniques (such as DNA sequencing) can provide new and better insights into the unresolved taxonomy and phylogenetic relationships of all the putative Mahseers in Malaysia (Nguyen *et al.*, 2006).

Nguyen *et al.* (2006) recently produced the first molecular work on Mahseers in Malaysia by examining the genetic diversity and phylogenetic relationships of broodstocks of *T. douronensis* and *T. tambroides* cultured in Sarawak (Borneo) through sequencing analysis of the mitochondrial DNA (mtDNA) 16S rRNA gene region. Thus,

the present study also aimed to clarify the phylogenetic relationships among Mahseer fishes in Malaysia but with a few different approaches. First, we utilized direct sequencing of the *Cytochrome C Oxidase I* (COI) mtDNA gene region, a gene with a faster evolutionary rate compared to the 16S rRNA (Simon *et al.*, 1994), and thus capable of providing a better resolution at the interspecific level. Secondly, we included additional *Tor* samples from Peninsular Malaysia (kelah fish) and Sabah (pelian fish), to compare with the *T. douronensis* (semah fish) and *T. tambroides* (empurau fish) of Sarawak. Thirdly, *N. stracheyi* representing the genus *Neolissochilus* were included in the phylogenetic study to quantify the genetic differences between the two genera.

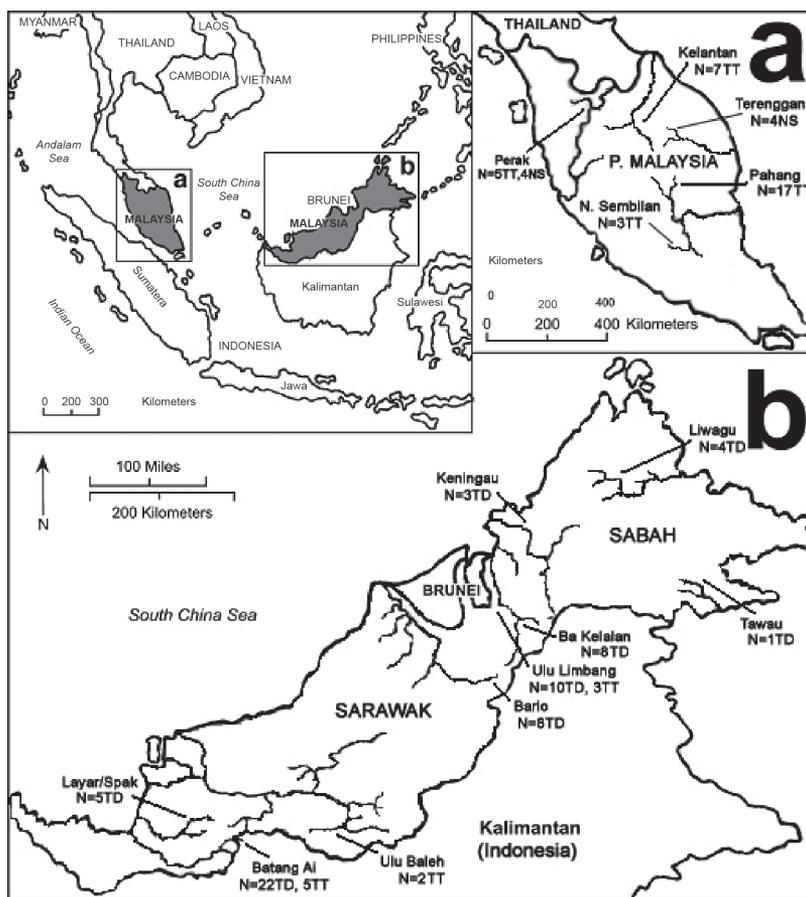


Fig. 1: Map showing sampling locations and sample size (N) in Peninsular Malaysia, Sarawak and Sabah. TD= *T. douronensis*, TT= *T. tambroides*, NS= *N. stracheyi*