

Mitochondrial DNA diversity of *Tor tambroides* Valenciennes (Cyprinidae) from five natural populations in Malaysia

ABSTRACT

In this study, we examined the genetic structure of *Tor tambroides* Valenciennes, an important indigenous freshwater fish species in Malaysia, using sequence analysis of 464 base pairs of the mitochondrial cytochrome c oxidase I (COI) gene. In total, 92 *T. tambroides* samples were analyzed from 4 locations on Peninsular Malaysia (n=87) and a single population from Sarawak (Batang Ai, n=5) on Borneo Island, and 4 sequences of *Tor douronensis* from Sarawak were used for comparisons. In total, 9 haplotypes were found, with 7 haplotypes being unique and 2 haplotypes being shared among the 5 populations. The phylogenetic analysis using Neighbor-joining (NJ) and maximum-parsimony (MP) methods supported the monophyletic status between *T. tambroides* and *T. douronensis*, thus suggesting their status as different species. The clustering of all *T. tambroides* samples into a single clade suggested that their genetic identity belongs to a single species. The sharing of haplotype HKE4 between Batang Ai of Sarawak (n= 4) and Perak of Peninsular Malaysia (n= 3) reflects the historical connection of drainages between the regions possibly during Pleistocene glaciation periods. Limited variations were found among all peninsular *T. tambroides* populations. The low level of mitochondrial (mt)DNA differences currently found among *T. tambroides* populations is probably due to the high proportion of the HKE1 haplotype being found in all the populations (0.736-1.000), or the small number of samples used in the present study. Overall, the present study was able to shed light on the phylogenetic relationships and genetic structure of *T. tambroides* in Malaysia.

Keyword: *Tor tambroides*; Freshwater fish; mtDNA COI; Population structure