Mitochondrial DNA diversity of Tor douronensis 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