Phylogeographic structure of freshwater tor sp. in river basins of Sabah, Malaysia

ABSTRACT

We characterized the genetic diversity, phylogeography, and demography of Tor sp. (Cyprinidae) from Sabah, Malaysian Borneo, by examining nucleotide variation in the D-loop region of the mtDNA. Sequence analysis of 18 populations (N = 173) yielded 35 unique mtDNA haplotypes with mean haplotype and nucleotide diversity of 0.833 and 0.023, respectively. Phylogenetic reconstructions using Bayesian, neighbor-joining, and maximum parsimony methods, as well as haplotype network, revealed four well-defined clades, namely, the eastern, central, northwestern, and southwestern clades, which corresponded to evolutionarily significant units (ESUs). These ESUs were estimated to have become separated since the late Miocene to Pliocene era (between 5 and 1 million years ago), with the central highlands of Sabah Crocker Trusmadi Range (CTR) constituting the main barrier to genetic exchange between clades. Analysis of molecular variance (AMOVA) and pairwise genetic differentiation showed significant population structuring (Φ ct = 0.575–1.000, p < 0.05). We further identified eight major groups of river systems harboring reproductively isolated Tor subpopulations. Neutrality statistics and Bayesian skyline plots (BSP) suggested constant population size over time for most Tor populations. Tor sp. in Sabah is comprised of four ESUs (eastern, central, northwestern, and southwestern ESUs), and that each ESU can be compartmentalized into 1–4 MUs. Due to isolation by distance, the highest number of MU occurs in the low-elevation drainages of Eastern Sabah, which is the largest in terms of land area. The evidence provided by this study supports the hypothesis that the four ESU represent genetically distinct subpopulations of Tor and highlight the urgent need for the in situ conservation of these subpopulations.