

Population genetic structure, phylogeography and demographic history of Hilsa shad (*Tenualosa ilisha*) in the Indian Ocean region

Kazi Ahsan Habib¹, Yongshuang Xiao², Jasmin Sathi³, Mohammad Islam¹, Sher Panhwar⁴, A.H.M. Shafiullah Habib³, and Youn-Ho Lee⁵

¹Sher-e-Bangla Agricultural University

²Chinese Academy of Sciences

³Jagannath University

⁴University of Karachi

⁵Korea Institute of Ocean Science and Technology

August 6, 2020

Abstract

Understanding the evolutionary processes that have molded the genetic structure to adapt to environmental changes is an important component of successful and sustainable long-term management for the fisheries resources. In this study, we analyzed mitochondrial control region (D-loop) sequence data to reveal population genetic variation, phylogeography and demographic history of *T. ilisha* collected from six locations of the Indian Ocean regions (Bay of Bengal, Arabian Sea and Persian Gulf). High haplotype diversity was found for all of the populations of *T. ilisha*. The Analysis of Molecular Variance (AMOVA) and conventional population F_{ST} comparisons detected both high population-level genetic variation and high degrees of divergence between groups within the Bay of Bengal (Irrawaddy river, MP; the coast of Cox's Bazar, XP; the delta of Meghna, MP and Hooghly river, IP) and Arabian Sea (the delta of Indus river, PP and the coast of Kuwait, KP). Four cryptic genetic barriers were found for the studied populations of *T. ilisha*, and the highest degree of population divergence was found between the Eastern Indian Ocean (Arabian Sea and Persian Gulf) and Western Indian Ocean (the Bay of Bengal region) regions based on the Voronoï tessellation of BARRIER analysis. The gene flow analysis detected almost no migration between Eastern and Western part of the Indian Ocean regions. Besides, one-way migration was found from IP to MP population in the Bay of Bengal and from PP of Arabian Sea to KP population of Persian Gulf. Mismatch distribution showed that *T. ilisha* underwent long-time stable population size. Distinct cryptic genetic barriers, limited gene flows and complex evolutionary process resulted a significant population genetic and phylogeographic structure, and intricate demographic histories of *T. ilisha* populations. Further, the study provided additional insights for conserving and managing of this fishery resource in its broad geographical distribution coverage.

Hosted file

Main Text-Hilsa D-loop.doc available at <https://authorea.com/users/349157/articles/474254-population-genetic-structure-phylogeography-and-demographic-history-of-hilsa-shad-tenualosa-ilisha-in-the-indian-ocean-region>











