

Genetic Stock Assessment of *Tenualosa ilisha* of Persian Gulf Waters and Western Coast of Malaysia Using MtDNA Genome Sequencing

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Received Date: November 30, 2014

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Accepted Date: November 17, 2015

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Abstract

In this research, genetic stock assessment of Hilsa shad *Tenualosa ilisha* was undertaken from natural distribution of species including rivers and southern coasts of Khuzestan, Bushehr and one sampling area from western coast of Malaysia as an outgroup. For this purpose, analysis of MtDNA genome of D-loop region was carried out for 86 samples of Hilsa shad. Then amplified fragments were automated sequenced and genetic analysis was done using genetic softwares including BioEdit, MEGA and Arlequin. Results showed that there were several subpopulations of *Tenualosa ilisha* at least in Khuzestan waters including rivers, estuaries and marine areas. In addition, the minimum F_{st} ($F_{st}=0$) was in Khuzestan selected sites while maximum F_{st} ($F_{st}=0.64$) was observed in Bushehr and western coast of Malaysia. Phylogenetic analysis showed that Hilsa shad samples originated from western coasts of Malaysia represents higher levels of genetic differentiation compared to subpopulations of this species inhabited in Iranian waters. However, both Malaysian and Iranian *Tenualosa ilisha* occupy the same place on phylogenetic tree.

Keywords: Hilsa shad, *Tenualosa ilisha*, MtDNA, Malaysia, Persian Gulf.
