

Efficiency of universal barcode gene (Cox1) on morphologically cryptic Mugilidae fishes delineation.

ABSTRACT

An effort was made to assess the utility of 650 bp partial Cytochrome C oxidase subunit I (DNA barcode) gene in delineating the members of taxonomically ambiguous marine fin fishes (Family: Mugilidae). To address the issue we used all the 95 barcode sequences of Mugilidae family available at NCBI (National Centre for Biotechnological Information) along with the barcode data generated from Mugilidae fishes of Parangipettai coastal waters. The average GC content of Mugilidae was found to be 46.46%. *Crenimugil crenilabis* showed less GC content (44.55%) whereas *Liza macrolepis* showed high GC content (48.53%) among the mullet species studied. The phylogenetic and genetic distance data showed that *Mugil platanus* and *M. liza* represent the continuum of same species. Among the members of family Mugilidae, the genus *Mugil* might possibly contains more haplotype diversity as revealed by intra-species genetic distance data. Species within genera of Mugilidae family invariably clustered in single clade with high bootstrap value. We conclude that partial COI sequencing (barcoding) in identifying the members of the family and that way has resolved the taxonomic ambiguity among the members of the family Mugilidae.

Keyword: Molecular phylogene; Mugilidae taxonomy; Intra-speseis variations; DNA barcoding; GC content.