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## Molecular characterization of brackish and marine water fishes of Sundarbans through DNA barcodes

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### Abstract

The present study aims to apply a DNA barcoding tool through amplifying the mitochondrial candidate genes like COI for accurate identification of fish of Sundarbans mangrove wetland, to build a reference library of fish of the unique ecosystems. A total of 83 mitochondrial COI barcode sequences gene were obtained from 26 species of 26 genera, 23 families, 8 orders and one class; among the 26 species, 3 fishes were new records in Sundarbans ecosystem. The collected samples were first identified by examining morphometric characteristics and then assessed by DNA barcoding. The COI sequences of fishes were clearly discriminated among genera in their phylogenies. The average Kimura two-parameter (K2P) distances of COI barcode sequences within all fish species were  $0.37 \pm 0.01\%$ . The base composition analysis for the COI sequence showed that the average percent T content was the highest and the average percent G content was the lowest; the AT content (53.60%) was higher than the GC content (46.40%). The GC contents at the first, second, and third codon positions for all fishes were 46.3%, 47.2%, and 45.7%, respectively. At the first codon position, the usage of C (18.7%) was the lowest, and the usages of the other bases were 23.00%, 27.10%, and 31.30% for T, A, and G, respectively. There were 36 haplotypes comprised this network. Each node of the network represents one unique haplotype and the bar across branches indicates the number of mutations separating two haplotypes. The overall haplotype diversity (Hd) was 0.979. The highest haplotype diversity was found 0.968 in perciformes fishes and the lowest haplotype diversity was found to be 0.000 in beloniformes, Synbranchiformes, Pleuronectiformes, Cichliformes and mugiliformes fishes. The overall nucleotide diversity (Pi) for all groups fishes were 0.37032. The nucleotide diversity was found to be highest (0.3961) in perciformes and lowest (0.000) in beloniformes, synbranchiformes, pleuronectiformes, cichliformes and mugiliformes samples. The present study describes the development of a molecular and morphometric cross-referenced inventory and assess the genetic variability of fishes of the Sundarbans. This inventory will be useful in future biodiversity studies and in forming future conservation plan. High efficiency and fidelity in species identification and discrimination were demonstrated in the present study by DNA barcoding, and we can be added that COI sequencing can be used as an authentic identification marker for Bangladesh brackish and marine fish species.

