

Molecular identification and phylogenetic relationship of Bangladeshi pufferfish based on mitochondrial COI and 16S rRNA genes

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Abstract

Pufferfish is common in marine, brackish and freshwater habitats in Bangladesh. Pufferfish poisoning sporadically occurs due to the consumptions of toxic pufferfish throughout the country. A study was conducted for molecular characterization and phylogenetic analysis of Bangladeshi pufferfish using two markers, mitochondrial cytochrome c oxidase I (COI) and 16S ribosomal RNA (16S rRNA) genes. A total of 34 barcode sequences (19 COI & 15 16S) from 30 collected specimens representing six species and four genera. The mean length of the sequences were 644 bp and 613 bp for COI and 16S, respectively. The average %GC content was 50.06 for COI which was higher compared to the 16S rRNA (46.61). Average Kimura two parameter (K2P) distances within species was found as 0.29 ± 0.01 for COI and 0.70 ± 0.06 for 16S rRNA. The Maximum Likelihood (ML) phylogenetic analysis of COI and 16S rRNA gene sequences revealed that the corresponding species were clustered together in the same clade. Cluster sequence analyses result revealed five Operational Taxonomic Units (OTUs). DNA based identification of the rest puffer species of Bangladesh with multiple sequences and phylogenetic relationship remains to be established.

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