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Bioinformatics Study of Operational Taxonomic Units of Fish Amblypharyngodon Mola

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ABSTRACT

DNA barcoding based on COI gene is the tool used in classifying animal species. The fish mola carplet Amblypharyngodon mola being a native fish has been compared in the present study with different individuals belonging to different states of India. The software for the present alignment is MEGA version 5.05. However there are negligible differences in the individual's gene sequence imply the effectiveness of COI gene in identifying species in the present study.

I. INTRODUCTION

to DNA barcoding is one of the methods of species identification in which short section of DNA from specific gene or genes is used. It is used to obtain the taxonomic information about the new unidentified organisms. It involves sequencing of a short fragment of the mitochondrial cytochrome c oxidase subunit I (1) and remains reliable method (2-3). Random genetic drift and domestication affects change in gene frequency and reduces—genetic variation when fishes are placed from natural to cultured environment(4). Fishes found at low altitude show greater diversity than those at high altitudes (5). For the comparison of the same we have chosen the fish Amblypharyngodon mola (Mola carplet) belonging to low altitude of three different riverine systems in Maharashtra. The fish is found in Afghanistan, Pakistan, India, Bangladesh and Myanmar. It belongs to carp family cyprinidae which is also known as carp family or minnow family.

II. MATERIAL METHOD

DNA barcoding is an emerging science of species identification and can elaborate understanding of both phylogenetic signal and population level variation (6). However it is not easy to obtain 652 bases of the region (7). The COI gene sequences of fishes from Maharashtra, West Bengal and Gujarat state were obtained from

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NCBI and were aligned using the software Molecular Evolutionary Genetic Analysis (MEGA) version 5.05 (8) using the Clustal W alignment method.

The accession numbers of the fishes used for the study are as follows:

No.	Name of fish	Site	Accession number
1	Amblypharyngodon mola	Maharashtra state	JX260818.1
2	Amblypharyngodon mola	Maharashtra state	KX946586.1
3	Amblypharyngodon mola	Maharashtra state	KX946584.1
4	Amblypharyngodon mola	West Bengal state	MG954367.1
5	Amblypharyngodon mola	Gujarat State	JX983212.1
6	Amblypharyngodon mola	Gujarat State	JX983211.1

III. RESULTS

The output of the sequence alignment has been exported in the results showing different point mutations. The point to be noted in the results is the presence of single point mutation in the first gene sequence at 606th base of 654 bases compared. The length of nucleotide has increased from 652 nucleotides to 654 because of frame shifting done to get rid of stop codons appearing in the table.

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Table 1: Nucleotide comparison COI gene sequence of individuals belonging to Amblypharyngodon mola.

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Image 1: Cladogram of individuals belonging to Amblypharyngodon mola.

IV. CONCLUSION

Through the present study it can be concluded that COI gene is one of the most successful tools that does not vary within single species at all and can be used as a tool for molecular taxonomy for further studies effectively. The reason behind the individual of Godavari river to stand apart is the single nucleotide change and shorter length of the COI gene.

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