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Bioinformatics study of Operational Taxonomic Units of fish Anabas testudineus with morphotype Anabas cobojius.

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Abstract:

DNA barcoding using Cytochrome Oxidase 1 Gene is a novel technique in the field of organism identification. Molecular Evolutionary Genetic Analysis is one of the software that aligns DNA and protein sequences. In this study we have dealt with study of the Operational Taxonomic Units of the Indian native fish *Anabas testudineus* with other closely related species on world data base NCBI, *Anabas cobojius*. The sequences were trimmed to get a uniform length of 648 bases and the Operational Taxonomic Units were observed. Many intra-specific differences as well as inter-specific differences were observed in the study in the form of Single Nucleotide Polymorphism although there was no change found in the amino acid content of the translated part.

Keywords: Intra-specific, inter-specific, Operational Taxonomic Units, Single Nucleotide Polymorphisms.

Introduction:

Factors like predation pressure, plant density and macrophyte type affect habitat selection by fishes especially those living in littoral zone (Chick and Mlvor, 2006). Variation in fishes is reduced when they are shifted from natural to cultured environment (Lucian Gorgan, 2008). Fishes at low altitude show greater diversity than those at high altitudes because of different isolating mechanisms acting on those causing spatial isolation; temporal isolation (Lowe-McConnell R H 1969).

COI gene based molecular taxonomy is considered to be a reliable method for species identification of fishes and fish products (Espineira M., et. al. 2008, Ward R. D. et. al. 2005) also for all the life stages (Ahrens D. et. al. 2007). Computers have made it possible to consider large numbers of characteristics in classifying many phenomena, notably living organisms, fossil organisms and even imaginary organisms (Sokal R. R. 1966).

Present study the Operational Taxonomic Units (OTUs) working in one of the native fish *Anabas testudineus* in comparison with its closest related species *Anabas cobojius* on NCBI data base. The fish was first recorded by Bloch in 1795 as *Anthias testudineus*. In taxonomic classification the fish belongs to order Perciformes of family Anabantidae.

Material Methods:

DNA barcoding is one of the novel developing sciences in species identification and can broaden understanding of both phylogenetic signal and population level variation (Hajibabaei, M. et al., 2007). To obtain

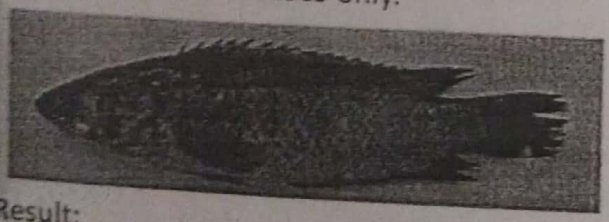
a complete gene of 650 bases is not easy (Hajibabaei, M. et al., 2006).

The COI gene sequences of the fish *Anabas testudineus* and *Anabas cobojius* were downloaded from NCBI and were aligned using the software Molecular Evolutionary Genetic Analysis (MEGA) version 5.05(Tamura et. al. 2011).The sequences were aligned using Clustal W alignment method.

Table 1: The accession numbers of the fishes used for the study are as follows:

No	Fish	Accession number
1	Anabas testudineus	JX260823
2	Anabas testudineus	JX983214
3	Anabas testudineus	JX260824
4	Anabas cobojius	KY124377

Anabas cobojius being close to Anabas testudineus during the blast has been chosen as a part of this study. Although the COI gene measures 652bp present length aligned in the study has been 638 bases only.



Result:

The output of the sequence alignment has been exported in the results showing different point mutations suggesting the sites of coevolution of DNA SNPs with species.

Table 2: Nucleotide composition of the reference sequence and sequences of fishes undertaken.

JX260823.1 Anabas testudineus	T T G G T G C T T G A G C T G G A A
JX983214.1 Anabas testudineus	. . . . . C . . . .
JX260824.1 Anabas testudineus	. . . . . C . . . .
KY124377.1 Anabas cobojius	. . . .
JX260823.1	T G G T G G G C A C C G C T T T A A
JX983214.1	. . . . .
JX260824.1	. . . . .
KY124377.1	. . . . .
JX260823.1	G C C T T C T A A T T C G T G C T G
JX983214.1	. . . . .
JX260824.1	. . . . .
KY124377.1	. . . . .
JX260823.1	A G C T A A G C C A A C C A G G C T
JX983214.1	. . . . .
JX260824.1	. . . . .
KY124377.1	. . . . .
JX260823.1	C C C T T T T A G G T G A C G A C C
JX983214.1	. . . . .
JX260824.1	. . . . .
KY124377.1	. . . . .
JX260823.1	A G A T T T T T A A T G T A A T C G
JX983214.1	. . . . .
JX260824.1	. . . . .
KY124377.1	. . . . .
JX260823.1	T T A C A G C A C A C G C T T T C G
JX983214.1	. . . . .
JX260824.1	. . . . .
KY124377.1	. . . . .
JX260823.1	T A A T A A T T T T C T T T A T A G
JX983214.1	
JX260824.1	
KY124377.1	
JX260823.1	T A A T G C C G A T G A T A A T C G
JX983214.1	
JX260824.1	
KY124377.1	
JX260823.1	G A G G C T T C G G A A A C T G A C
JX983214.1	
JX260824.1	
KY124377.1	
JX260823.1	T T A T T C C C C T A A T A A T T G
JX983214.1	
JX260824.1	
KY124377.1	
JX260823.1	G C G C G C C A G A T A T G G C T T
JX983214.1	
JX260824.1	
KY124377.1	
JX260823.1	T C C C T C G A A T A A A C A A C A
JX983214.1	
JX260824.1	
KY124377.1	
JX260823.1	T A A G C T T C T G A C T C C T T C
JX983214.1	
JX260824.1	
KY124377.1	
JX260823.1	C A C C C T C C T T C C T C C T T C
JX983214.1	
JX260824.1	
KY124377.1	
JX260823.1	T C C T T G C C T C C G C T G C A G
JX983214.1	
JX260824.1	
KY124377.1	
JX260823.1	T A G A A G C C G G T G C G G G A A

JX983214.1	. . . . .
JX260824.1	. . . . .
KY124377.1	. . . . .
JX260823.1	C G G G T T G A A C T G T C T A C C
JX983214.1	. . . . .
JX260824.1	. . . . .
KY124377.1	. . . . .
JX260823.1	C C C C T T T A G C C A G C A A C C
JX983214.1	. . . . .
JX260824.1	. . . . .
KY124377.1	. . . . .
JX260823.1	T A G C C C A C G C A G G A G C A T
JX983214.1	. . . . .
JX260824.1	. . . . .
KY124377.1	. . . . .
JX260823.1	C C G T A G A T T T A A C C A T T T
JX983214.1	. . . . .
JX260824.1	. . . . .
KY124377.1	. . . . .
JX260823.1	T T T C C T T A C A C T T A G C C G
JX983214.1	. . . . .
JX260824.1	. . . . .
KY124377.1	. . . . .
JX260823.1	G G G T T T C T T C T A T C T T G G
JX983214.1	. . . . .
JX260824.1	. . . . .
KY124377.1	. . . . .
JX260823.1	G C G C A A T T A A C T T C A T C A
JX983214.1	. . . . .
JX260824.1	. . . . .
KY124377.1	. . . . .
JX260823.1	C A A C A A T T A T T A A C A T A A
JX983214.1	. . . . .
JX260824.1	. . . . .
KY124377.1	. . . . .
JX260823.1	A A C C C C C T G C C G C C T C T C
JX983214.1	. . . . .
JX260824.1	. . . . .
KY124377.1	. . . . .
JX260823.1	A A T A C C A A A C A C C C T T G T
JX983214.1	. . . . .
JX260824.1	. . . . .
KY124377.1	. . . . .
JX260823.1	T T G T T T G A T C T G T C C T T A
JX983214.1	. . . . .
JX260824.1	. . . . .
KY124377.1	. . . . .
JX260823.1	T T A C C G C T G T A C T T C T C C
JX983214.1	. . . . .
JX260824.1	. . . . .
KY124377.1	. . . . .

JX260823.1	T C C T T T C C C T T C C C G T C C
JX983214.1	. . . . . T . . . . .
JX260824.1	. . . . . T . . . . .
KY124377.1	. . . . . T . . . . .
JX260823.1	T T G C T G C T G G A A T T A C T A
JX983214.1	. . . . .
JX260824.1	. . . . .
KY124377.1	. . . . .
JX260823.1	T A C T T C T C A C A G A T C G A A
JX983214.1	. . . . .
JX260824.1	. . . . .
KY124377.1	. . . . .
JX260823.1	A C C T G A A C A C C T C C T T C T
JX983214.1	. . . . .
JX260824.1	. . . . .
KY124377.1	. . . . .
JX260823.1	T T G A C C C A G C G G G T G G G G
JX983214.1	. . . . .
JX260824.1	. G . . . . .
KY124377.1	. . . . . A .
JX260823.1	G A G A C C C A A T T C T T T A C C
JX983214.1	. . . . .
JX260824.1	. . . . .
KY124377.1	. . . . .
JX260823.1	A A C A C C T A
JX983214.1	. . . . .
JX260824.1	. . . . .
KY124377.1	. . . . .

Observing nucleotide sequences in the data shows that there exists intraspecific variation on 8th, 506th 530th position an exclusive interspecific variation existed on 611th position only.

Conclusion:

It is concluded from the present study that the Single Nucleotide Polymorphism exist in this species at various levels in the gene, suggesting that morphological taxonomy and molecular taxonomy are not acting parallel. Thus there are no significant mutations in both species which vary according to species and speciation mechanism.

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Mixed ligand complexes of zinc metal ion with antibacterial drug Oxytetracycline hydrochloride and amino acids in aqueous media

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Abstract:

The stability constant of the mixed ligand complexes of zinc(II) ion withantibacterial drugOxytetracycline hydrochloride as primary ligand and eightaminoacidsglycine, DL-alanine, L-glutamic acid, DL-isoleucine, DL-methionine, DL-â-phenyl alanine, DL-serine and DL-valine as secondary ligands were determined pH metrically in 20%(v/v) ethanol-water medium at 25°C and at an ionic strength of 0.1 M $NaClO_4$. The formation of complex species has been evaluated bySCOGS computer program and discussed in terms of various relative stability parameters.

Keywords : Stability constant, antibacterial drug, amino acids, mixed ligand complexes.

Introduction :

Metal complexes of drugs are found to