

Bioinformatics Study of Operational Taxonomic Units of Fish *Rasbora daniconius*

¹ Kharat MM, ² Ade PP, ^{*3} VB Kalyankar

¹ Department of Zoology, Shri. Shivaji College of Arts, Commerce and Science, Akola

^{2,3} Department of Zoology, Toshniwal Arts, Commerce and Science College, Sengaoan

Abstract

Among various genes involved in DNA taxonomy, DNA barcoding is related to COI gene related taxonomy. MEGA is one of the software used to align DNA and protein sequences. Present study deals with study of the operational taxonomic units of the native fish *Rasbora daniconius* with other closely related species *Rasbora wilpita*. Of the evaluated data eleven Operational Taxonomic Units were found out of the present latest data available on NCBI mostly located at the beginning and end part of the sequences. The initial part of the gene was occupied with SNPs and the end part included triplet codons.

Keywords: Operational Taxonomic Units, SNPs, Triplet codons.

1. Introduction

Habitat selection by fishes especially those living in littoral zone is affected by predation pressure, plant density and macrophyte type [1]. The fishes when placed from natural to cultured environment random genetic drift and domestication effects change gene frequency, reducing genetic variation [2]. Among freshwater fishes low altitude fishes show greater diversity than those at high altitudes as various isolating mechanisms act on those causing spatial isolation; temporal isolation [3].

Of the different tools being used for DNA taxonomy COI gene based taxonomy is considered to be a reliable method for species identification of fishes and fish products [4-5] also for all the life stages [6]. Considering large numbers of characteristics in classifying many phenomena, notably living organisms, fossil organisms and even imaginary organisms is possible because of computers [7].

In the present study we have found the Operational Taxonomic Units (OTUs) working in one of the native fish *Rasbora daniconius* in comparison with its closest related species *Rasbora wilpita* on NCBI data base. The black-line Rasbora or *Rasbora daniconius* is a species of ray finned fish inhabiting a variety of habitats like ditches, ponds canals streams, rivers and inundated fields [8]. Rasbora fish is mostly freshwater fish but also found in brackish water and benthopelagic region. Fish reaches its maturity up to maximum length of 15cm. Rasbora having 9 dorsal soft rays and 7 anal soft rays, black stripe running from eye to caudal fin; nearly complete lateral line, with only last few scales lacking pores [9-10]. The fish feeds mainly on aquatic insects and detritus matter as it is a surface feeder [8]. The fish is hardly found in the studies done in the rivers near the study area [11-12] adaptable in the aquarium (National Institute of Malaria Research, 2009) [13].

2. Material Methods

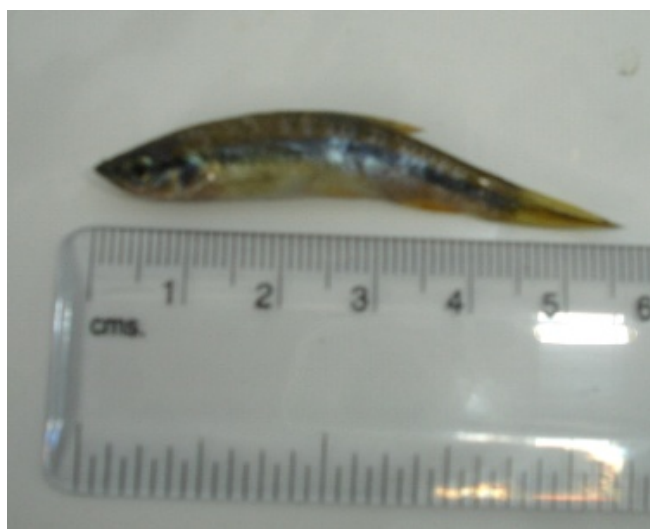
DNA barcoding is one of the emerging sciences in species identification and can broaden understanding of both phylogenetic signal and population level variation [14]. But the region of 650 bases is not easily obtained [15].

The COI gene sequences of the fish *Rasbora daniconius* and *Rasbora wilpita* were downloaded from NCBI and were aligned using the software Molecular Evolutionary Genetic Analysis (MEGA) version 5.05 [16]. The alignment system used for the DNA sequences was Clustal W.

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

No	Fish	Accession number
1	<i>Rasbora daniconius</i>	JX260290
2	<i>Rasbora daniconius</i>	KJ476780
3	<i>Rasbora daniconius</i>	JX983478
4	<i>Rasbora daniconius</i>	JX983476
5	<i>Rasbora daniconius</i>	JX260960
6	<i>Rasbora wilpita</i>	JX260962
7	<i>Rasbora wilpita</i>	JX260962

Fish *Rasbora wilpita* was chosen as it had same length uploaded to NCBI like of *Rasbora daniconius* and is most coinciding morphospecies of the same. Although the COI gene measures 652bp present length aligned in the study has been 513 bases only.



3. 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 1: Nucleotide composition of the reference sequence and sequences of fishes undertaken.

JX260960.1 <i>Rasbora daniconius</i> voucher RDGA03 cytochrome oxidase subunit 1 (COI) gene partial cds mitochondrial	G	A	A	C	T	T	A	G	C	C	A	A	C	C	G	G	G	A	T	C	A	
KJ476780.1 <i>Rasbora daniconius</i> isolate NBFGRD-003 cytochrome c oxidase subunit I (COI) gene partial cds mitochondrial
JX983478.1 <i>Rasbora daniconius</i> voucher NF446 cytochrome oxidase subunit 1 (COI) gene partial cds mitochondrial
JX983476.1 <i>Rasbora daniconius</i> voucher NF780 cytochrome oxidase subunit 1 (COI) gene partial cds mitochondrial
gi 399932588 gb JX260960.1 <i>Rasbora daniconius</i> voucher RDGA03 cytochrome oxidase subunit 1 (COI) gene partial cds mitochondrial
JX260962.1 <i>Rasbora wilpita</i> voucher PMUM01 cytochrome oxidase subunit 1 (COI) gene partial cds mitochondrial	.	.	.	G	T	G
JX260960	C	T	A	C	T	A	G	G	A	G	A	C	G	A	T	C	A	A	A	T	T	
KJ476780
JX983478
JX983476
JX260960
JX260962
JX260960	T	A	T	A	A	T	G	T	C	A	T	T	G	T	A	A	C	T	G	C	T	
KJ476780
JX983478
JX983476
JX260960
JX260962
JX260960	C	A	T	G	C	T	T	T	T	G	T	A	A	T	G	A	T	T	T	T	C	
KJ476780
JX983478
JX983476
JX260960
JX260962
JX260960	T	T	T	A	T	A	G	T	T	A	T	A	C	C	A	A	T	A	C	T	T	
KJ476780
JX983478
JX983476
JX260960
JX260962
JX260960	A	T	C	G	G	A	G	G	A	T	T	T	G	G	G	A	A	C	T	G	A	
KJ476780
JX983478
JX983476
JX260960
JX260962
JX260960	T	T	G	G	T	C	C	C	A	C	T	G	A	T	A	A	T	T	G	G	G	
KJ476780
JX983478
JX983476
JX260960
JX260962
JX260960	G	C	A	C	C	A	G	A	C	A	T	A	G	C	A	T	T	C	C	C	C	
KJ476780
JX983478
JX983476
JX260960
JX260962
JX260960	C	G	A	A	T	A	A	A	C	A	A	T	A	T	A	A	G	C	T	T	T	
KJ476780

JX983478	
JX983476	
JX260960	
JX260962	C	
JX260960	T	G	A	C	T	T	C	T	C	C	C	C	C	A	T	C	A	T	T	C	
KJ476780	
JX983478	
JX983476	
JX260960	
JX260962	
JX260960	C	T	T	C	T	T	T	A	T	T	A	G	C	C	T	C	C	T	C	T	
KJ476780	
JX983478	
JX983476	
JX260960	
JX260962	
JX260960	G	G	T	G	T	T	G	A	A	G	C	A	G	G	T	G	C	C	G	G	G
KJ476780
JX983478
JX983476
JX260960
JX260962
JX260960	A	C	A	G	G	A	T	G	A	A	C	A	G	T	T	T	A	T	C	C	A
KJ476780
JX983478
JX983476
JX260960
JX260962
JX260960	C	C	A	C	T	T	G	C	A	G	G	A	A	A	C	C	T	C	G	C	C
KJ476780
JX983478
JX983476
JX260960
JX260962
JX260960	C	A	C	G	C	A	G	G	A	G	C	A	T	C	A	G	T	A	G	A	C
KJ476780
JX983478
JX983476
JX260960
JX260962
JX260960	C	T	A	A	C	A	A	T	T	T	T	C	T	C	T	C	T	C	C	A	C
KJ476780
JX983478
JX983476
JX260960
JX260962
JX260960	T	T	A	G	C	A	G	G	T	G	T	G	T	C	A	T	C	A	A	T	C
KJ476780
JX983478
JX983476
JX260960
JX260962
JX260960	T	T	A	G	G	G	G	C	T	A	T	T	A	A	T	T	T	C	A	T	T
KJ476780
JX983478
JX983476
JX260960
JX260962
JX260960	A	C	A	A	C	A	A	T	T	A	T	T	A	A	T	A	T	G	A	A	G
KJ476780
JX983478
JX983476
JX260960

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