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MITOCHONDRIAL DNA BASED PHYLOGENETIC ANALYSIS OF INDIAN MAJOR CARPS

ABSTRACT

The present study was conducted on molecular phylogeny of wild and cultured Indian major carps, viz. *Catla catla*, *Cirrhinus mrigala* and *Labeo rohita*. The regions of taxonomic importance, i.e., 16S rRNA and COI genes were sequenced and analysed to obtain genetic diversity among major carps and resolve taxonomic ambiguity to find phylogenetic differentiation based on mtDNA.

The gene sequences, of 16S rRNA gene of wild and cultured species (on the basis of BLAST) of *C. catla*, *C. mrigal* and *L.rohita* showed close similarity to available gene sequence on NCBI, KF641860 (Agra), HM026495 (Lucknow), KC757213(Bhubaneswar), JQ801754 (epithelial cell line, from thymus, Lucknow), JX074115 (USA) of *Catla catla*; AY378176 (Guangdong, China), KF641859 (Agra, India), KC757185(Bhubaneswar, India), DQ464904 (Vietnam), KU559567 (cell line, Lucknow) of *Cirrhinus mrigala*; KC757195 (Bhubaneswar, India), KC757193 (Bhubaneswar, India), KC757191 (Bhubaneswar, India), KC757186 (Bhubaneswar, India), KJ425468 (Dhaka, Bangladesh) of *Labeo rohita* respectively and hence considered as same and proved exact identification based on molecular taxonomy.

The gene sequences, of COI of wild and cultured species(on the basis of BLAST) *C. catla*, *C. mrigal* and *L.rohita* showed close similarity to available gene sequence on NCBI, KX946602 (Northern Ghat, Satara Maharashtra, India), JQ801755 (epithelial cell line from thymus, Lucknow), MG229054 (Muzaffarabad, Pakistan), MG736437 (Tripura, India), MH197228 (Maharashtra, India), of *Catla catla*; MG229059 (Muzaffarabad, Pakistan), MG229057(Muzaffarabad, Pakistan), KY228401 (Gojra, Punjab, Pakistan), KY228396 (Gojra, Punjab, Pakistan), KY228388 (Gojra, Punjab, Pakistan) of *Cirrhinus mrigala*; JX983352(Aurangabad, Maharashtra), KX946693 (Kolhapur, Northern Western, Ghats of Kolhapur, Maharashtra), MG229051(Muzaffarabad, Pakistan), JX260897(Aurangabad, Maharashtra), KX982627(Punjab, Pakistan) *Labeo rohita* repectively and hence considered as same.

In female *Catla catla* (Site 1, cultured samples) the DNA content ranged in 62ng/ µl-68ng/ µl; and at Site 2, 62 ng/ µl-65ng/ µl; at Site 3 (wild samples) 76 ng/ µl -80ng/ µl. In male *Catla catla* (Site 1) the DNA content ranged in 71ng/ µl-78ng/µl, at Site 2, 76 ng/ µl-80ng/ µl and at Site 3 (wild samples) 78 ng/ µl -84 ng/ µl.

In female *Cirrhinus mrigala* (Site 1) the DNA content ranged 62ng/ µl-64ng/ µl; at Site 2, 60 ng/ µl-70ng/ µl and at Site 3 (wild samples) 68ng/ µl -74 ng/ µl. In male *Cirrhinus mrigala* (Site 1) the DNA content ranged 64ng/ µl-78ng/ µl; at Site 2, 70ng/ µl -78ng/ µl and at Site 3 (wild Samples) 67 ng/ µl -74 ng/ µl.

In female *Labeo rohita* (Site 1) the DNA content ranged 60ng/ µl-64ng/ µl; at Site 2 was 59 ng/ µl-68ng/ µl; at Site 3 (wild samples) 60 ng/ µl -62 ng/ µl. In male *Labeo rohita* (Site 1) the DNA content ranged 67ng/ µl-72ng/ µl and at Site 2 ranged between 70 ng/ µl-74ng/ µl and at Site 3 (wild samples) 67 ng/ µl -73 ng/ µl.