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Conventional Taxonomy of Four Tilapia Species in South-East Coast of India**Viki R.V., Sathya A.C.R.* and Muthu M.S.***Centre of Advanced Study in Marine Biology, Annamalai University, India*
acrathish@gmail.com*Abstract**

Tilapia belongs to the family Cichlidae. Tilapia is a generic term used to designate a group of commercially important food fishes belonging to the family Cichlidae. Tilapia species have been re-classified into three separate genera viz., *Tilapia*, *Sarotherodon* and *Oreochromis*, based mainly on their reproduction and feeding habits and biogeography. Tilapias are very sturdy in nature. The family Cichlidae is one of the most species-rich families of vertebrates. More than 3,000 species of cichlid fishes are distributed from Central and South America, through Africa and Madagascar to Southern India. Classification of species is fundamental for carrying out researches in biodiversity, ecology, evolutionary biology and conservation biology. With this as the background in the present study, four species of fishes namely *O. mossambicus* and *O. niloticus*, *Tilapia rendalli* and *T. zillii* were sequenced for their 647 bp, 645 bp, 642 and 481 region of cytochrome oxidase sub-unit I (COI) gene to test their efficacy in identifying the species and also to demonstrate their intra-species variations within the barcode region. The sequences were analyzed for their species identification, using the Barcode of Life Database (BOLD's) identification engine. The COI sequences of *O. mossambicus*, *O. niloticus*, *Tilapia rendalli* and *T. zillii* from different geographical regions were extracted from NCBI for analyzing the intra-species variation. While comparing the sequences in the NCBI database with the present sequences, significant alignments with maximum similarity ranging from 99% to 100% were noticed. Four sequences are aligned using ClustalW. A phylogenetic tree was constructed with Bootstrap test. The optimal tree with the sum of branch length showed 0.000976 for *O. mossambicus*, 0.001556 for *O. niloticus* and 0.000000 for *T. rendalli* and *T. zillii*. In *O. mossambicus*, the maximum GC content was 46.9% whereas the GC content in all other closely related species was found to be 46% on an average. In *O. niloticus*, the maximum GC content of 47.9% was noticed and the closely related sequences exhibited 48% average in GC content (*T. zillii* 50.2% and *T. rendalli* 46.6%). The analyses revealed the molar concentration of bar-coded genes.

The evolutionary relationship was inferred with the closely related sequences obtained from the NCBI database. Sequence divergence between individuals of the same species ranged from 0 to 0.057. Both phylogeny and phylogeographic signals were evident from the phylogram constructed with *O. mossambicus* and *O. niloticus* as the same group. Even though the present results confirm that the COI could be a potential barcode gene for species level identification, further research is needed for describing the divergence of sequences in a broader sense. Analysis of data undertaken with conventional tools like PCR amplification and gene sequencing methods clearly revealed the healthy nature of environment along the south-east coast of India.

Keywords: Intra species, Variations, Barcode, Cytochrome oxidase, Phylogenetic