

Mitochondrial DNA Part A

DNA Mapping, Sequencing, and Analysis

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MITOGENOME ANNOUNCEMENT

Complete mitochondrial DNA sequences of the Victoria tilapia (*Oreochromis variabilis*) and Redbelly Tilapia (*Tilapia zilli*): genome characterization and phylogeny analysis

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Abstract

The Cichlid fishes have played an important role in evolutionary biology, population studies and aquaculture industry with East African species representing a model suited for studying adaptive radiation and speciation for cichlid genome projects in which closely related genomes are fast emerging presenting questions on phenotype–genotype relations. The complete mitochondrial genomes presented here are for two closely related but eco-morphologically distinct Lake Victoria basin cichlids, *Oreochromis variabilis*, an endangered native species and *Tilapia zilli*, an invasive species, both of which are important economic fishes in local areas. The complete mitochondrial genomes determined for *O. variabilis* and *T. zilli* are 16 626 and 16,619 bp, respectively. Both the mitogenomes contain 13 protein-coding genes, 22 tRNAs, 2 rRNAs and a non-coding control region, which are typical of vertebrate mitogenomes. Phylogenetic analyses of the two species revealed that though both lie within family Cichlidae, they are remotely related.

Keywords

Cichlidae, mitochondrial DNA, *Oreochromis variabilis*, *Tilapia zilli*, phylogeny

History

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The Victoria tilapia (*Oreochromis variabilis*) and Redbelly tilapia (*Tilapia zilli*) are Cichlid fish species belonging to a major lineage of African Cichlids, commonly referred to as tilapias (Nagl et al., 2001). *Oreochromis variabilis* (Boulenger, 1906) is endangered (IUCN, 2014) and native to lakes Victoria, Kyoga and their basins, and *T. zilli* (Gervais, 1848) is an exotic species (Twongo, 1995). The two fish species are important and continue to support the growing aquaculture industry, aquarium and ornamental fishery in East Africa (Maithya et al., 2012).

In this study, we sequenced the complete mitochondrial genomes of the two species that are deposited in the GenBank with the accession numbers NC_026109.1 for *O. variabilis* and NC_026110.1 for *T. zilli*. Both fish samples were collected from Borabu dam, Lake Victoria basin, Kenya. The same approach as previously described by Cheng et al. (2011) was adopted to obtain their complete mitochondrial genomes. The complete

mitochondrial genomes of *O. variabilis* and *T. zilli* were 16 626 and 16,619 bp, respectively. Both mitogenome sequences contain 13 protein-coding genes, 2 rRNA subunits, 22 tRNAs and 1 non-coding control region (D-loop), and are typical of vertebrate mitogenomes (Fischer et al., 2013). The overall base composition is highly similar between them: A = 27.70%, C = 30.30%, T = 26.20%, G = 15.50% in *O. variabilis*; A = 27.30%, C = 32.10%, T = 25.60%, G = 15.90% in *T. zilli*. In both species the 13 protein-coding genes contain the start codon ATG except the gene COXI, which is GTG instead. In *O. variabilis* the coding sequence genes are terminated using the following stop codons: TAA for COXI, ATP8, ATP6, ND4L, ND5 and ND6; TAG for ND1; the truncated codons TA+ and T++ appear in ND2 and in COXII, ND3, ND4 and CYTB, respectively. In *T. zilli*, COXI use TAG instead of TAA as stop codon. This is congruent with cichlid mitogenomes (He et al., 2011).

Based on the complete mitochondrial 16S rRNA sequences of other 34 Perciformes species, the evolutionary relationships of *O. variabilis* and *T. zilli* were constructed using Neighbor-Joining (NJ) in MEGA (Hall, 2013) analysis method. Results showed the families Balistidae, Ammodytidae and Cichlidae are composed of a monophyly (Figure 1) in which *O. variabilis* is clustered together with *Oreochromini* sub-tribe while *T. zilli* is clustered together with *Tilapini* sub-tribes, which is consistent with the traditional systematic classification (Nagl et al., 2001; Nwani et al., 2011). Our results enrich the knowledge on mitogenomes of

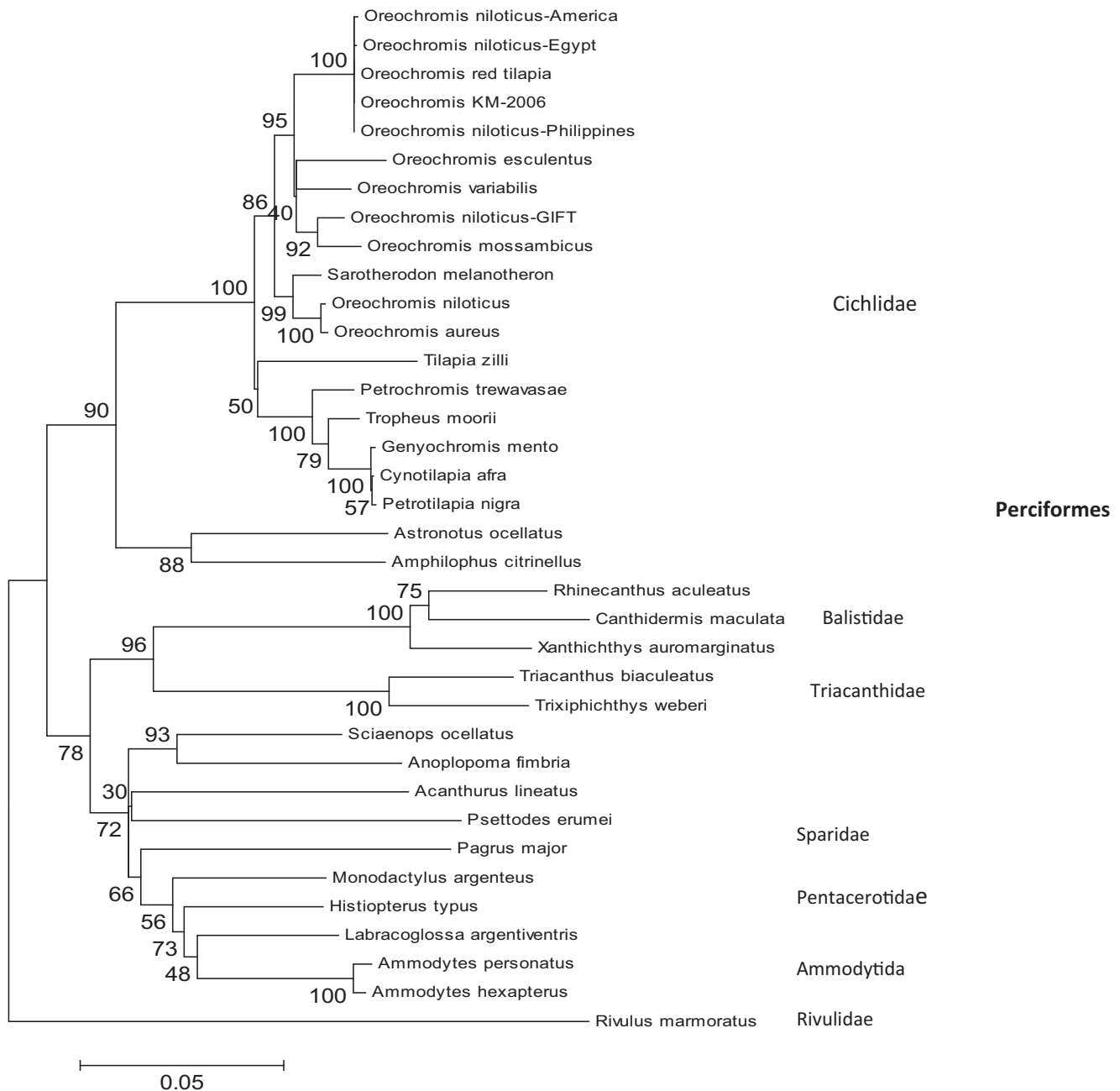


Figure 1. A Neighbor-Joining (NJ) tree reconstructed with MEGA (Hall 2013), showing the evolutionary position and relationship of *Oreochromis variabilis* and *Tilapia zilli* relative to that of 34 other fish species belonging to order perciformes. The tree is based on complete 16S rRNA gene sequences retrieved from GenBank database. The scale bar is show under the tree, whereas the bootstrap value of 1000 replicates is listed on the branches. The analyses included the following species: *Rhinecanthus aculeatus* (NC_011941.1), *Triacanthus biaculeatus* (NC_009863.1), *Psettodes erumei* (NC_020032.1), *Canthidermis maculate* (AP009206.1), *Xanthichthys auromarginatus* (AP009211.1), *Triphichthys weberi* (AP009173.1), *Oreochromis niloticus* (NC_013663.1), *Oreochromis niloticus-America* (GU477628.1), *Oreochromis aureus* (NC_013750.1), *Coptodon (tilapia) zilli* (NC_026110.1), *Sarotherodon melanotheron* (NC_015611.1), *Oreochromis* sp. 'red tilapia' (GU477631.1), *Oreochromis* sp. *KM-2006* (AP009126.1), *Oreochromis niloticus-Philippines* (GU477626.1), *Oreochromis niloticus-Egypt* (GU477625.1), *Oreochromis niloticus-Gift* (GU477624.1), *Oreochromis mossambicus* (NC_007231.1), *Petrochromis trewavasae* (HE961974.1), *Tropheus moorii* (HE961975.1), *Cynotilapia afra* (NC_018564.1), *Oreochromis esculentus* (NC_025555.1), *Genyochromis mento* (NC_018562.1), *Petrotilapia nigra* (NC_018557.1), *Oreochromis variabilis* (NC_026109.1), *Astronotus ocellatus* (AP009127.1), *Amphilophus citrinellus* (KJ562277.1), *Sciaenops ocellatus* (NC_016867.1), *Anoplopoma fimbria* (NC_018119.1), *Acanthurus lineatus* (NC_010108.1), *Pagrus major* (NC_003196.1), *Monodactylus argenteus* (NC_009858.1), *Histioporus typus* (AP006807.1), *Labracoglossa argentiventris* (AP011062.1), *Ammodytes personatus* (KF672362.1), *Ammodytes hexapterus* (NC_020461.1) and *Rivulus marmoratus* (AF283503.1) which was also used as the outgroup taxon.

Cichlidae, and lay ground for further investigations on their life history traits and population genetics.

Declaration of interest

The authors declare no conflict of interest. This article is sponsored by K. C. Wong Magna Fund in Ningbo University.

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