

## Complete mitogenome and phylogenetic analysis of *Oryzias celebensis* (Teleostei: Beloniformes)

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### ABSTRACT

The complete *Oryzias celebensis* mitogenome was determined using next-generation sequencing (NGS) method and the resulting data analyzed in this article. The mitochondrial genome was 16,493 base pair (bp) length, and its content and structure were highly homologous to that of other teleostean fishes, including 13 protein-coding genes (PCGs), 2 rRNAs, 22 tRNA, and 1 control region. Among the PCGs, ATG was used as the initiation codon, except for GTG in the COI gene. There were 6 overlapping genes with overlap lengths ranging from 1 to 10 nucleotides (nt), while 10 intergenic regions with a total of 59 nt and a maximum interval of 38 nt between tRNA-Asn and tRNA-Cys were detected during the annotation of this complete mitochondrial DNA.

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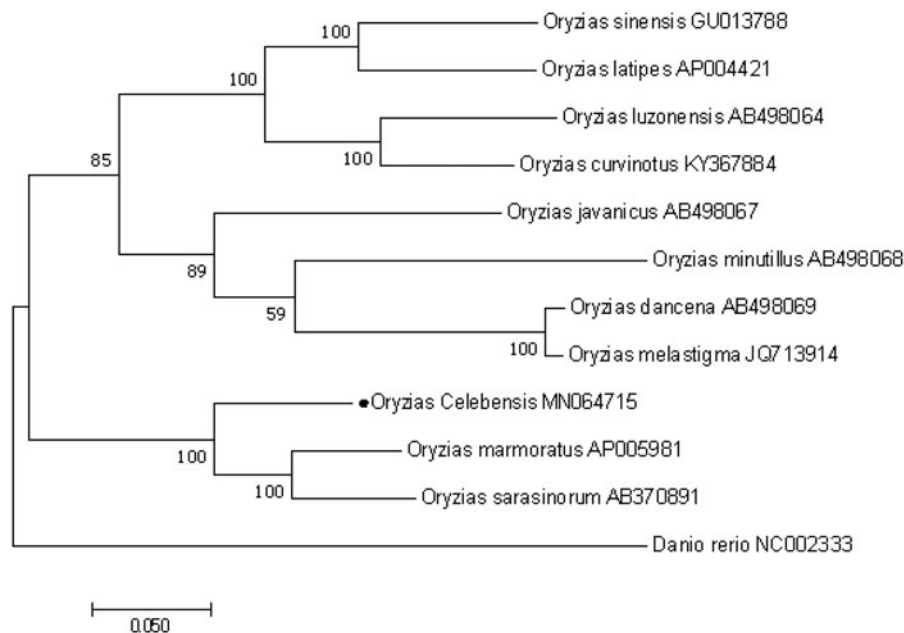
### KEYWORDS

*Oryzias celebensis*;  
mitogenome; phylogenetic analysis



Celebes medaka, *Oryzias celebensis*, (Teleostei: Beloniformes) is a small fish that can grow up to 4.5 centimeters in length, mainly distributed in rivers and lakes in the Indonesian island of Sulawesi (formerly known as Celebes) and East Timor (Weber 1894). It is a potential fish akin to the freshwater Japanese medaka (*Oryzias latipes*). However, the complete

mitogenome genome of *O. celebensis* was still not determined until now.

The mature Celebes medaka were collected from the river in near the national university of Singapore (N1°17'46.81" E103°45'33.75"). The typical specimen were deposited in the Guangdong Ocean University aquatic museum (O.cele-001).



**Figure 1.** Maximum-Likelihood (ML) consensus tree based on complete mitochondrial DNA (mtDNA) gene sequence of *Oryzias* species with *Danio rerio* as an outgroup.

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We extracted total RNA using Celebes medaka F1 larvae for sequencing (Wang et al. 2009). According to the sequencing result combined with the information on GenBank database, the complete mitochondrial sequence of the Celebes medaka was obtained, submitted to GenBank and was assigned the accession MN064715. The complete *Oryzias celebensis* mitogenome is 16,493 bp, and its content and structure are highly homologous to those of other teleostean fishes, including 13 protein-coding genes (PCGs), 2 rRNAs, 22 tRNA and 1 control region (Kim and Lee 2004; Liu and Cui 2009). Among the PCGs, except for GTG in the COI gene all genes were initiated with the ATG start codon. There were 6 overlapping genes with overlap lengths ranging from 1 to 10 nucleotides (nt), while ten intergenic regions with a total of 59 nt and a maximum interval of 38 nt between tRNA-Asn and tRNA-Cys.

We constructed the Maximum-Likelihood (ML) consensus tree based on the complete mtDNA gene sequences of *Oryzias* species (Figure 1). Phylogenetic analysis showed that *O. celebensis* clustered together with *O. sarasinorum* and *O. marmoratus* which is consistent with the previous reports using the nuclear tyrosinase and mitochondrial 12S and 16S rRNA genes (Naruse 1996; Takehana et al. 2005). This indicated the phylogenesis classification of *O. celebensis* is true. The determination of the complete mitogenome sequences provided new molecular data to illuminate the *Oryzias* evolution.

## Disclosure statement

The authors report no competing of interest.

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