Complete mitochondrial genome sequence of *Trachyrhamphus serratus* with phylogenetic implications for the family Syngnathidae

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**ABSTRACT**

In this study, the complete mitochondrial sequence of the crested pipefish, *Trachyrhamphus serratus* (*T. serratus*), has been amplified and sequenced. The mtDNA of *T. serratus* was a circular molecule of 16,597 bp in length with 13 protein-coding genes (PCGs), 2 rRNA genes, 22 tRNA genes, and a control region. The lengths of 12S and 16S rRNA were 936 bp and 1863 bp, respectively. Phylogenetic analysis indicated that *T. serratus* clustered together with *Corythoichthys flavofasciatus*, suggesting a close relationship between the two genera. This was the first record of the complete mitochondrial genome from the genus *Trachyrhamphus*, which will be useful for the elucidation of evolution and conservation strategy in Syngnathidae family.

The crested pipefish *Trachyrhamphus serratus* is a widespread marine pipefish that ranges from southern India and Sri Lanka to Japan and South Korea (Dawson 1985). *Trachyrhamphus serratus* generally inhabits sandy mud substrates and algal beds at depths of 15-100 m, which is used extensively for the treatment of impotence and tumor in China (Kuiter 2000; Wang et al. 2011). Due to the morphological similarities between *T. serratus* and other Syngnathidae species, it was often traded as adulteration of traditional Chinese medicinal pipefish (Gao et al. 2018). Although the appearance between *T. serratus* and other medicinal pipefish is similar, their medicinal efficacy differs considerably (Hu and Li 2002). The complete mitochondrial genome of *T. serratus* would provide basic molecular data for phylogenetic analysis and further development on species identification strategies.

Here, we determined the complete mitochondrial genome of *T. serratus* and constructed the phylogenetic relationship among the family Syngnathidae. The specimen of *T. serratus* was purchased from Bozhou Medicinal Herb Market at Anhui Province of China and identified based on its key morphological characteristics, including extremely short snout, superior trunk, and discontinuous tail ridges (Zhang et al. 1997). The sample of *T. serratus* LM-22 was deposited at the collection center of Zhejiang Chinese Medical University. Total genomic DNA was extracted from the tail muscle and the complete mtDNA of *T. serratus* was determined according to our previous reports (Fang et al. 2018; Zhu et al. 2018; Lai et al. 2019). The mitochondrial genome sequence of *T. serratus* was deposited into GenBank under the accession number MK680823.

The mtDNA of *T. serratus* was a circular molecule of 16,597 bp in length with 13 protein-coding genes (PCGs), 2 rRNA genes, 22 tRNA genes, and a control region. The overall base composition of *T. serratus* was 29.56% for A, 28.35% for C, 16.39% for G, and 25.70% for T, respectively. Similar to the most vertebral mitochondrial genome, nucleotide overlaps and space gaps were very common in *T. serratus* (Cheng et al. 2013; Chen et al. 2018). There are 8 intergenic spacers region and 11 overlap spacer in *T. serratus*. The total length of the 13 PCGs was 11,454 bp, which accounts for 67.55% in the whole mitochondrial genome. The lengths of 12S ribosomal RNA and 16S ribosomal RNA were 936 bp and 1863 bp, respectively. The control region locating between tRNA-Pro and tRNA-Phe gene was 1159 bp in length, ranging from 15,799 to 16,957 bp.

The phylogenetic relationships of *T. serratus* and other Syngnathidae species were inferred utilizing maximum-likelihood (ML) based on the complete mitochondrial sequences (Figure 1). The monophyletic group of Syngnathidae Family was divided into three clades. Clade I includes species from the genus of Hippocampus, Corythoichthys, Trachyrhamphus, and Syngnathus. *Trachyrhamphus serratus* clustered together with *Corythoichthys flavofasciatus* with high-statistical support, suggesting a relatively close relationship between the two genera. The complete mitogenome

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sequence provides basic molecular data of *T. serratus*, which would be helpful for the understanding of phylogenetic relationships in family Syngnathidae.

**Disclosure statement**

No potential conflict of interest was reported by the authors.

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