The complete mitochondrial genome characterization of Paratrypauchen microcephalus (Gobiiformes: Oxudercidae) and phylogenetic consideration

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ABSTRACT
The complete mitochondrial genome of Paratrypauchen microcephalus (Gobiiformes: Oxudercidae) was completely sequenced by high throughput sequencing method. The complete mitochondrial genome was 16,552 bp in length, consisted of 13 protein-coding genes, 22 tRNA genes, two rRNA genes, a putative control region (CR), and an origin of replication on the light-strand (OL). The base composition values for the mitochondrial genome were 29.1%, 27.6%, 15.7%, and 27.6% for A, C, G, and T, respectively. The gene arrangement is identical to those in typical fishes. Phylogenetic tree based on 13 protein-coding genes shows that P. microcephalus has a close phylogenetic relationship with genus Trypauchen and belongs to Oxudercidae.

The species comb goby, Paratrypauchen microcephalus (Gobiiformes: Oxudercidae), is distributed throughout the Indo-west Pacific, commonly inhabits soft mud bottoms of inshore and estuarine waters, and feeds on benthic invertebrates like crustaceans (Chen and Fang 1999; Murdy 2011). Studies on P. microcephalus were seldom and only research on length–weight relationship was performed (Yoon et al. 2013). Many species of Paratrypauchen have not been well recognized because of the absence of enough molecular information and clear phylogenetic relationship. As well known, mitochondrial DNA was proved effective in species identification and phylogenetic studies, so here we described the complete mitogenome of P. microcephalus for the first time and reconstructed the phylogenetic relationship of the relative species of Oxudercidae, and expecting for better understanding the systematic evolution of genus Paratrypauchen and further phylogenetic study of Gobiiformes.

The specimen was collected from Naozhou Island in Zhanjiang, China (geographic coordinate: N 20°53’20.11”, E 112°28’46.20”). The whole body specimen was preserved in ethanol and registered to the Marine Biodiversity Collection of South China Sea, Chinese Academy of Sciences, under the voucher number SW20181071705.

The complete mitochondrial genome of P. microcephalus was 16,552 bp in length (GenBank accession No. MH678617), containing 13 protein-coding genes, 22 tRNA genes, two rRNA genes, a putative control region (CR) as well as an origin of replication on the light-strand (OL). The gene arrangement is identical to those in typical fishes. Phylogenetic tree based on 13 protein-coding genes shows that P. microcephalus has a close phylogenetic relationship with genus Trypauchen and belongs to Oxudercidae.
Figure 1. Maximum-likelihood phylogenetic tree was constructed based on first and second codon sequences of 13 protein-coding genes of 32 species. The number at each node is the bootstrap probability (only show ≥50%). The number after the species name is the GenBank accession number, and the bold species is studied in this research.

(Agorreta et al. 2013; Thacker et al. 2015; Nelson et al. 2016; Kuang et al. 2018) (Figure 1).

Disclosure statement
No potential conflict of interest was reported by the authors.

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