

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

Min Yang<sup>a,b,\*</sup>, Wei Shi<sup>a,c,\*</sup> and Hui Yu<sup>c</sup>

<sup>a</sup>CAS Key Laboratory of Tropical Marine Bio-resources and Ecology, South China Sea Institute of Oceanology, Chinese Academy of Sciences, Guangzhou, China; <sup>b</sup>University of Chinese Academy of Sciences, Beijing, China; <sup>c</sup>College of Life Science, Foshan University, Foshan, Guangdong, China

### 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 (O<sub>L</sub>). 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.

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*Paratrypauchen microcephalus*; complete mitochondrial genome; phylogenetic relationship

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 (O<sub>L</sub>). The gene arrangement is identical to those in typical fishes that most of these genes are encoded by the H-stand, except for *ND6* and eight tRNA genes (Boore 1999; Liu et al. 2013; Gong et al. 2017). The 13 protein-coding genes encode 3803 amino acids in total and use the initiation codon ATG except *COI* using GTG and *ATP6* using ATA. Most of them use TAA or TAG as the stop codon, while *ATP6*, *COIII*, and *Cytb* use an incomplete T or TA, *COII* uses an unusual AGA, and *ND4* uses an unusual AGG. Overall base composition values for the mitochondrial genome were 29.1%, 27.6%, 15.7%, and 27.6% for A, C, G, and T, respectively, with slight AT-bias of 56.7%.

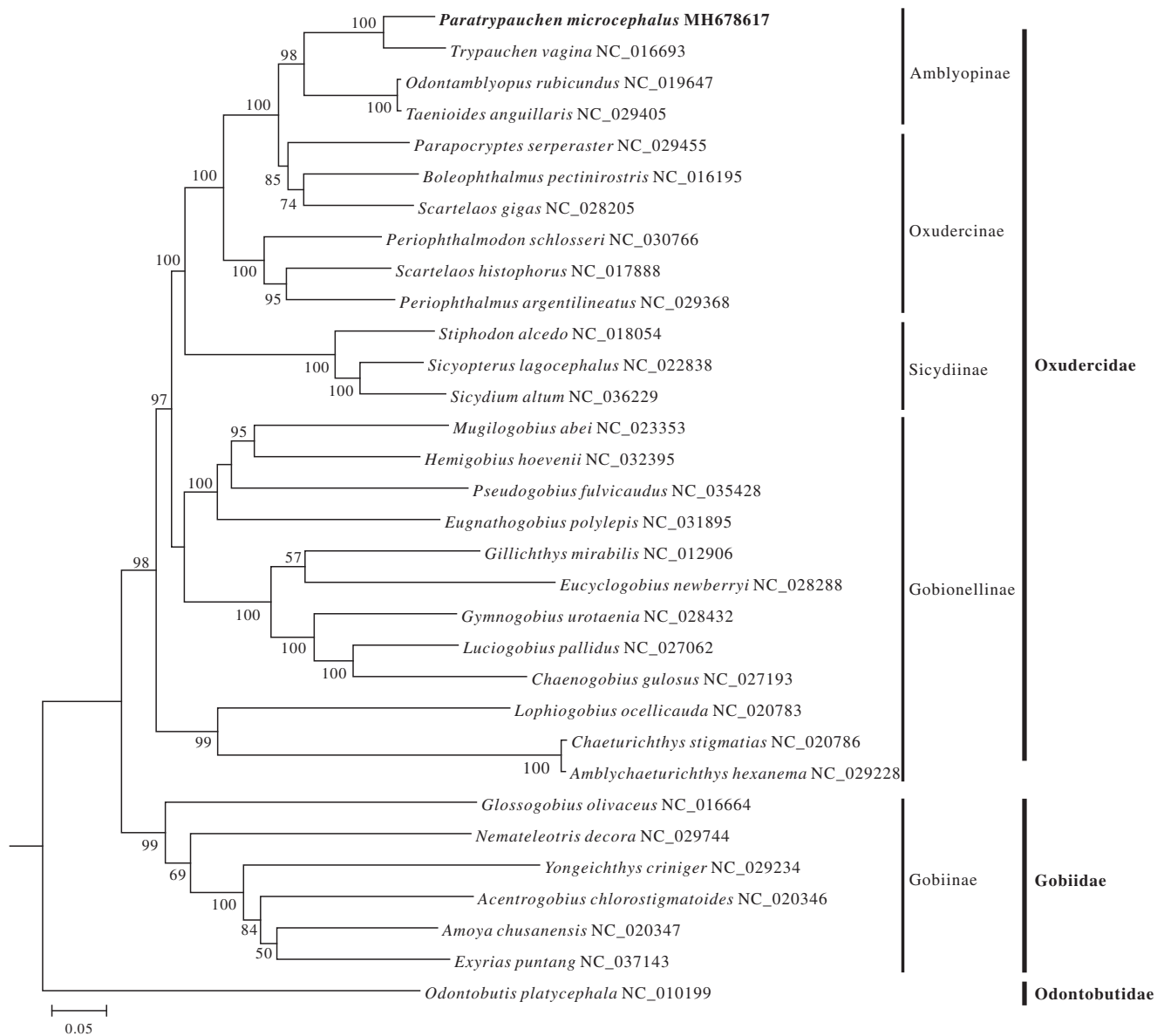
Based on first and second codon sequences of 13 protein-coding genes of each mitogenome from 31 species from Oxudercidae and Gobiidae, with *Odontobutis platycephala* as outgroup species, a maximum likelihood (ML) phylogeny tree was constructed by using MEGA6 (Tamura et al. 2013). In the ML phylogenetic tree, *P. quadrilineatus* and *Trypauchen vagina* first clustered together, and then grouped with *Odontamblyopus rubicundus* and *Taenioides anguillaris* in a strong support. This phylogenetic framework also supported the four subfamilies Amblyopinae, Oxudercinae, Sicydiinae and Gobionellinae together formed the Oxudercidae

**CONTACT** Min Yang ✉ [minyang@scao.ac.cn](mailto:minyang@scao.ac.cn) CAS Key Laboratory of Tropical Marine Bio-resources and Ecology, South China Sea Institute of Oceanology, Chinese Academy of Sciences, 164 West Xingang Road, Guangzhou 510301, China; Wei Shi ✉ [kcool@126.com](mailto:kcool@126.com) CAS Key Laboratory of Tropical Marine Bio-resources and Ecology, South China Sea Institute of Oceanology, 164 West Xingang Road, Guangzhou 510301, China; College of Life Science, Foshan University, Foshan, Guangdong 528000, China; Hui Yu ✉ [yu71hui@126.com](mailto:yu71hui@126.com) College of Life Science, Foshan University, Foshan, Guangdong 528000, China

\*These authors contributed equally to this work.

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**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  $\geq 50\%$ ). 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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