

## First report of mitogenome of Chinese grass shrimp *Palaemonetes sinensis* (Crustacea, Decapoda, Palaemonidae) yielded by next-generation sequencing

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### ABSTRACT

The nearly complete mitochondrial genome of *Palaemonetes sinensis* is 15,504 bp in size, containing 13 protein-coding genes, 22 transfer RNAs, 2 ribosomal RNAs, and a partial control region. The gene content and arrangement were similar to other Palaemonidae species. The mitogenomic information obtained herein will be useful for future studies on population genetic and phylogenetic analyses of this shrimp.

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Chinese grass shrimp *Palaemonetes sinensis* (Decapoda, Palaemonidae) is naturally distributed from the south of China to Siberia in Russia (Holthuis 1950; Liu et al. 1990; Li et al. 2007). *Palaemonetes sinensis* is an important aquarium animal and fisheries resource because of its striking appearance and appealing flavor (Li et al. 2018). However, in recent years, natural resources of this shrimp have sharply declined owing to overfishing and water pollution (Li et al. 2007). To date, biological knowledge of this species is scarce, and studies have mainly focused on their morphological analysis (Imai and Oonuki 2014). Genetic information, which is essential for the sustainable management of the resource, is limited in *P. sinensis*. In this study, the complete mitochondrial genome of *P. sinensis* was sequenced and characterized, which would be useful reference for further studies on resource conservation and management, as well as population genetic and phylogenetic analyses of the species.

The specimen was collected from Yangzhong, Jiangsu Province, China (32°18'24.94"N, 119°47'28.12"E). Genomics DNA was extracted from the whole tail muscle and stored in Freshwater Fisheries Research Center, Chinese Academy of Fishery Sciences (ZHXY1901). Mitochondrial genome was sequenced and reconstructed based on Illumina HiSeq (Borgström et al. 2011) data. The high-throughput sequencing was conducted by Nanjing Genepioneer Biotechnologies Inc. (Nanjing, China). In all, a total of 27.1 million clean reads were retrieved from raw data and were clustered into 10,708

long reads. Reads were used for *de novo* assembly with MEGAHIT v1.1.2 (Li et al. 2016). The assembled mitogenomes were annotated using the MITOS web server (Bernt et al. 2013). tRNA and rRNA genes were predicted using tRNAscan-SE (Lowe and Eddy 1997) and rRNAmmer 1.2 (Lagesen et al. 2007), respectively.

The nearly complete mitochondrial genome of *P. sinensis* was 15,504 bp in length (GenBank accession no. MN296122). It contained 13 protein-coding genes (PCG), 22 tRNA genes, 2 rRNA genes, and a control region. However, the partial control region was not sequenced in this study. The gene content, arrangement, and composition were similar to other Palaemonidae species. Among these genes, 23 are transcribed on the heavy-coding strand (H-strand), whereas the other 14 genes on the light-coding strand (L-strand). All the protein-coding genes start with ATN, and three types of stop codons (TAA, TAG, and T-) were found, and the incomplete stop codons were presumably completed by post-transcriptional polyadenylation (Ojala et al. 1981). The overall nucleotide composition is 35.6% for A, 29.8% for T, 22.1% for C and 12.5% for G, with a AT bias of 65.4% and a strong bias against G.

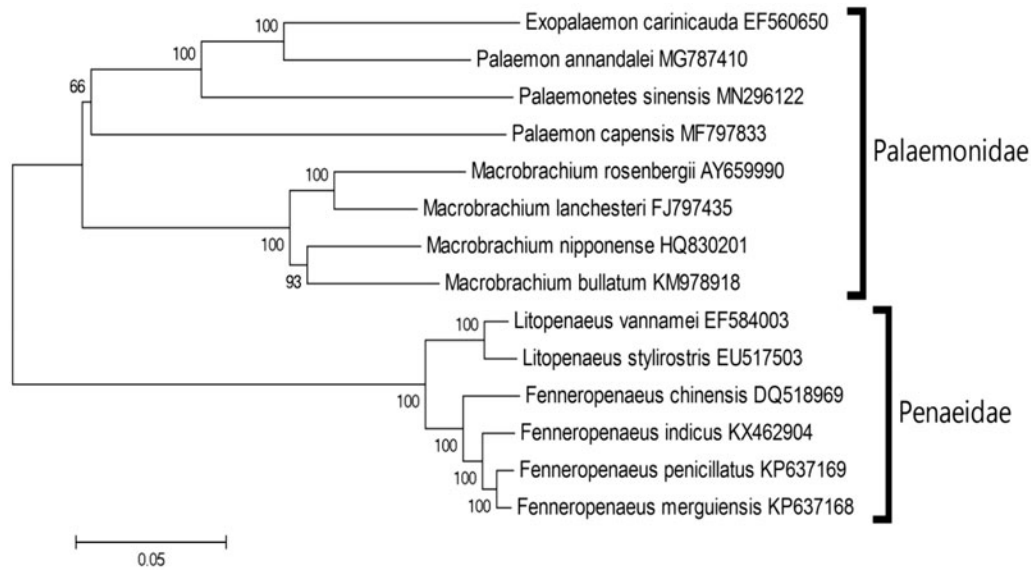
Neighbor-joining (NJ) phylogenetic analysis of *P. sinensis* and other shrimps using the 13 mitochondrial protein-coding genes was conducted by MEGA 6.06 software (Tamura et al. 2013). Different species from the same family clustered together. *Palaemonetes sinensis* clustered together with other shrimps forming the family Palaemonidae (Figure 1).

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**Figure 1.** The phylogenetic relationship of *P. sinensis* with the other species using NJ method with 1000 bootstrap replicates. The bootstrap values for the NJ analysis are shown on the nodes.

## Disclosure statement

No potential conflict of interest was reported by the authors.

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