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ISSN: (Print) (Online) Journal homepage: <https://www.tandfonline.com/loi/tmdn20>

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To cite this article: Chen Li , Lu Qi & Lingfeng Kong (2020) The complete mitochondrial genome of *Nassarius graniferus* (Gastropoda: Nassariinae), Mitochondrial DNA Part B, 5:3, 2964-2965, DOI: [10.1080/23802359.2020.1791000](https://doi.org/10.1080/23802359.2020.1791000)

To link to this article: <https://doi.org/10.1080/23802359.2020.1791000>



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Published online: 23 Jul 2020.



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The complete mitochondrial genome of *Nassarius graniferus* (Gastropoda: Nassariinae)

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ABSTRACT

Nassarius graniferus is a marine gastropod species in family Nassariidae. In the present study, we firstly determined the complete mitochondrial genome of *N. graniferus* by next-generation sequencing. The mitochondrial sequence is a circular molecule of 16,417bp in length, with the typical structure of 13 protein-coding genes (PCGs), 22 transfer RNA genes (tRNAs) and 2 ribosomal RNA genes. The GC% across the genome is 30.7%.

ARTICLE HISTORY

Received 9 June 2020
Accepted 27 June 2020

KEYWORDS

Nassarius graniferus;
mitochondrial genome;
phylogeny

The gastropod family Nassariidae, a speciose group containing more than 600 extant species within the order Neogastropoda, is distributed worldwide from intertidal zone to a depth of about 1000 m (Cernohorsky 1972; Galindo et al. 2016). Taxonomy of nassariids is mainly based on morphological characters, often fail to get more credible results (Cernohorsky 1984). The nassariids are delicious and popular seafood in Asia, but some of species could accumulate algal toxins that cause paralytic shellfish poisoning (Lin et al. 1999; Choi et al. 2006). Therefore, accurate species identification is of great significance to solve the food safety problem of nassariids. Here, we present annotated mitochondrial genome of *Nassarius graniferus*, a small intertidal nassariid species which inhabits in coral and weedy sand of tropical Indo-Pacific, to provide an additional genetic resource for further study of species identification.

The individual of *N. graniferus* was collected from the Yongle Atoll in the Xisha Islands, Hainan Province, China (16°27'51"N, 111°44'17"E) and stored in 95% ethanol at the Specimen library of Shellfish Genetics and Breeding Laboratory, Ocean University of China (accession number: OUC-SGB-N-YL13). The total genomic DNA was extracted from the foot muscle, using the TIANamp Marine Animals DNA Kit (Tiangen Biotech, Beijing, China) according to manufacturer's recommended protocol, then stored at -4 °C for short-term use. The DNA was sequenced on an Illumina HiSeq X sequencer using a PE150 protocol. Short-read DNA sequences were assembled using NOVOPlasty 3.7.2 (Dierckxsens et al. 2017). The mitogenome data were annotated using MITOS web servers (Bernt et al. 2013) (<http://mitos.bioinf.uni-leipzig.de/index.py>) and ORF Finder (<https://www.ncbi.nlm.nih.gov/orffinder/>), gene boundaries were

compared manually with published Nassariidae mitochondrial genome to identify protein-coding (PCGs), ribosomal RNA (rRNAs) and transfer RNA (tRNAs) genes. Additionally, the ribosomal (*rrnS* and *rrnL*) genes were also identified by their similarity to gene sequence of *Nassarius foveolatus* (MH346209.1). The nucleotide compositions were computed using MEGA 6 (Tamura et al. 2013).

The mitochondrial genome of *N. graniferus* is 16,417 bp in length and was deposited in the Genbank (Accession number: MT374078). It encodes 35 metazoan mitochondrial genes, including 13 protein-coding genes (PCGs), 22 tRNA genes, and 2 rRNA genes, consistent with other nassariid mitochondrial genomes. The *rrnS* and *rrnL* genes are 966 bp and 1392 bp in length, respectively. The overall nucleotide composition is as follows: 30.7% for A, 14.6% for C, 16.1% for G, and 38.6% for T, with a total A + T content of 69.3%. The GC skew value is 4.78%. Twelve of the 13 PCGs start with ATG, while ND4 start with ATA. Nine genes are terminated by TAA, four of which are terminated by TAG. All of the PCGs were encoded on the (+) strand.

Phylogenetic relationships were inferred from available mitogenomes of 9 species of genus *Nassarius* using the maximum-likelihood (ML) method with 13 PCGs, and *Tritia reticulatus* was used as the outgroup. Maximum-Likelihood analysis was conducted using RAXML (Stamatakis 2014) and 1000 bootstraps were used to assess the support of nodes. The results of phylogenetic analysis showed that *N. graniferus* belongs to genus *Nassarius* (Figure 1). This mitogenome sequence of *N. graniferus* would help in evolutionary biology, population genetics, and species diagnosis studies of Nassariinae.

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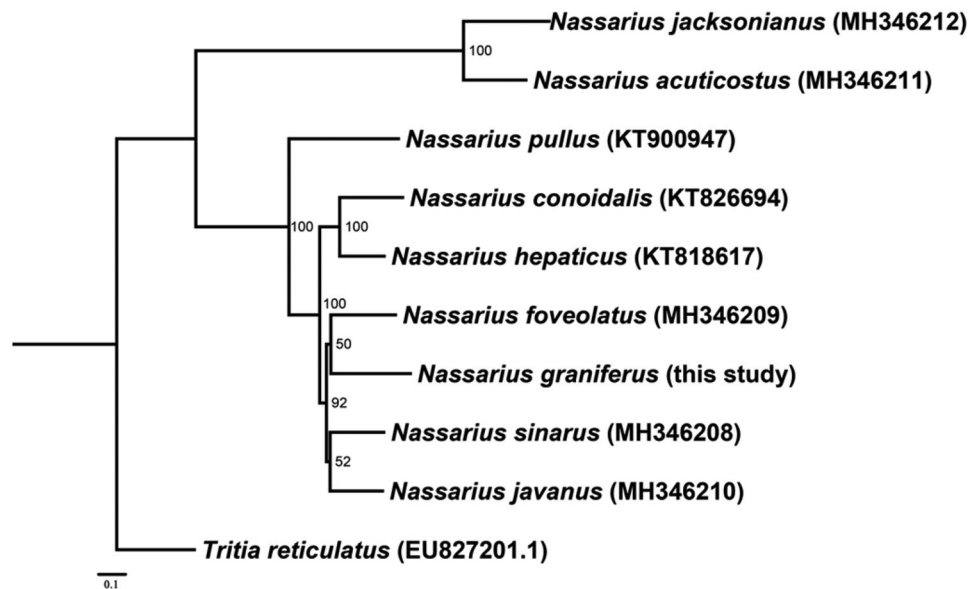


Figure 1. Maximum likelihood tree was constructed based on the concatenated nucleotide sequences of the 13 protein-coding genes, using 1000 bootstraps to assess the support of nodes.

Disclosure statement

No potential conflict of interest was reported by the author(s).

Funding

This research was supported in part by the National Natural Science Foundation of China [31772414], the Fundamental Research Funds for the Central Universities [201964001] and the National Infrastructure of Fishery Germplasm Resources [2019DKA30470].

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Data availability statement

The data that support the findings of this study are openly available in National Center for Biotechnology Information at GenBank reference number MT374078 (<https://www.ncbi.nlm.nih.gov/nucleotide/MT374078>).

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