MITOCHONDRIAL DNA PART B: RESOURCES
2024, VOL. 9, NO. 6, 808–811
https://doi.org/10.1080/23802359.2024.2368206

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MITOGENOME REPORT

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The complete mitochondrial genome of bamboo shrimp *Atyopsis moluccensis* (Atyidae, Decapoda)

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ABSTRACT

Atyopsis moluccensis, belonging to the family Atyidae, is one of the popular species in aquarium industry. Here, we sequenced the mitochondrial genome of *A. moluccensis*. The mitogenome of *A. moluccensis* is 15,933 bp in length, consisting 22 transfer RNAs, 13 protein-coding genes (PCGs), and two ribosomal RNAs. The composition of *A. moluccensis* mitogenome is 33.77% for A, 13.81% for G, 28.74% for T, and 23.68% for C. The A + T content of the heavy-strand was 62.51%. Except ND5, most of the PCGs had ATN as the start codon. Only COX2 and ND4 were stopped by incomplete stop codon. The phylogenetic relationship was reconstructed with 16 shrimp from six genera of family Atyidae, which revealed that *A. moluccensis* and *A. gabonensis* clustered together and species of the same genus were grouped together in a clade. The data are beneficial in understanding the evolution and phylogenetic relationships of Atyidae shrimp.

ARTICLE HISTORY
Received 9 April 2024
Accepted 10 June 2024

KEYWORDS
Mitochondrial genome; phylogeny; *Atyopsis moluccensis*; Atyidae

Introduction

The bamboo shrimp *Atyopsis moluccensis* (De Haan, 1849) belongs to the family Atyidae. It is widely found in the Indo-Pacific region, including China, Thailand, Malaya, Indonesia, Sri Lanka, and Philippines (Iwata et al. 2003). The larvae of *A. moluccensis* live in seawater and the adult inhabit freshwater (Bláha et al. 2022). *A. moluccensis* is a popular ornamental crustacean in the aquarium trade (Lipták and Vitázková 2015). The mtDNA genome (mtDNA) is an effective tool for population genetics and reconstruction of phylogeny (Desalle et al. 2017). However, only partial sequence of COX1 and 16S is available in GenBank, which is insufficient for evolution and conservation genetics of *A. moluccensis*. Here, the mitogenome of *A. moluccensis* and phylogenetic relationships with other shrimp were analyzed.

Materials and methods

A live specimen of *A. moluccensis* (voucher no. NH289832; Figure 1) was captured from Beihai (21°24′ N, 109°9′ E), Guangxi Province, China. It was transported and deposited in the South China Sea Fisheries Research Institute (contact person: Sigang Fan, email: fansigang@scsfri.ac.cn). Genomic DNA from muscle was extracted using the TIANamp Marine Animals DNA Kit (Tiangen, Beijing, China). Libraries were generated using the Hieff NGS® MaxUp II DNA Library Prep Kit for Illumina® (Yeasen, Shanghai, China) and sequenced using Illumina HiSeq 2000 (Illumina Inc., San Diego, CA) by Sangon Biotech Co., Ltd. (Shanghai, China). After removing the adapter sequences, low quality bases (base quality $\leq$ 20) and poly-N were deleted using Fastp 0.17.0 from raw data (Chen et al. 2018). The clean reads were obtained and then assembled with SPAdes v3.15.2 and PRICE (Bankevich et al. 2012; Ruby et al. 2013). MITOS (Bernt et al. 2013) was used to annotate transfer RNA (tRNA), protein-coding genes (PCGs), and ribosomal RNA (rRNA). OGDRAW was used to draw the circular mitochondrial genome map (Greiner et al. 2019).

The phylogenetic analyses were conducted based on 13 PCGs of *A. moluccensis* and other 14 species of the family Atyidae. *Saron marmoratus* (Wang et al. 2021) was used as the outgroup. Phylogenetic relationships were constructed using maximum-likelihood (ML) with Jones–Taylor–Thornton (JTT) model in MEGA 7.0.26 (Kumar et al. 2016). The reliability of the tree topology was evaluated using bootstrap support with 1000 replicates.

Results

A total of 23,017,840 raw reads were generated. The Q20 and Q30 of raw reads were 95.91% and 90.43%, respectively.

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Supplemental data for this article can be accessed online at https://doi.org/10.1080/23802359.2024.2368206.

Figure 1. Representative of *Atyopsis moluccensis* collected in the study (photograph by Sigang Fan).

After filtering, 20,749,086 clean reads were obtained, in which 96.54% of bases had a quality score ≥20. The read coverage depth map of *A. moluccensis* is shown in Supplementary Figure S1. The mitogenome of *A. moluccensis* was 15,933 bp in size (GenBank accession number: OP618117.1), with the C + G content of 37.49% (33.77% A, 13.81% G, 28.74% T, and 23.68% C). It consisted of 13 PCGs, 22 tRNA genes, and two rRNA genes (Figure 2; Supplementary Table S1). Of the 37 genes, 23 were encoded by the heavy strand. Remaining 13 genes including four PCGs (ND1, ND4, ND4L, and ND5), eight tRNA genes and two rRNA genes were encoded by the light strand (Figure 2; Table S1). Most of the PCGs had ATN

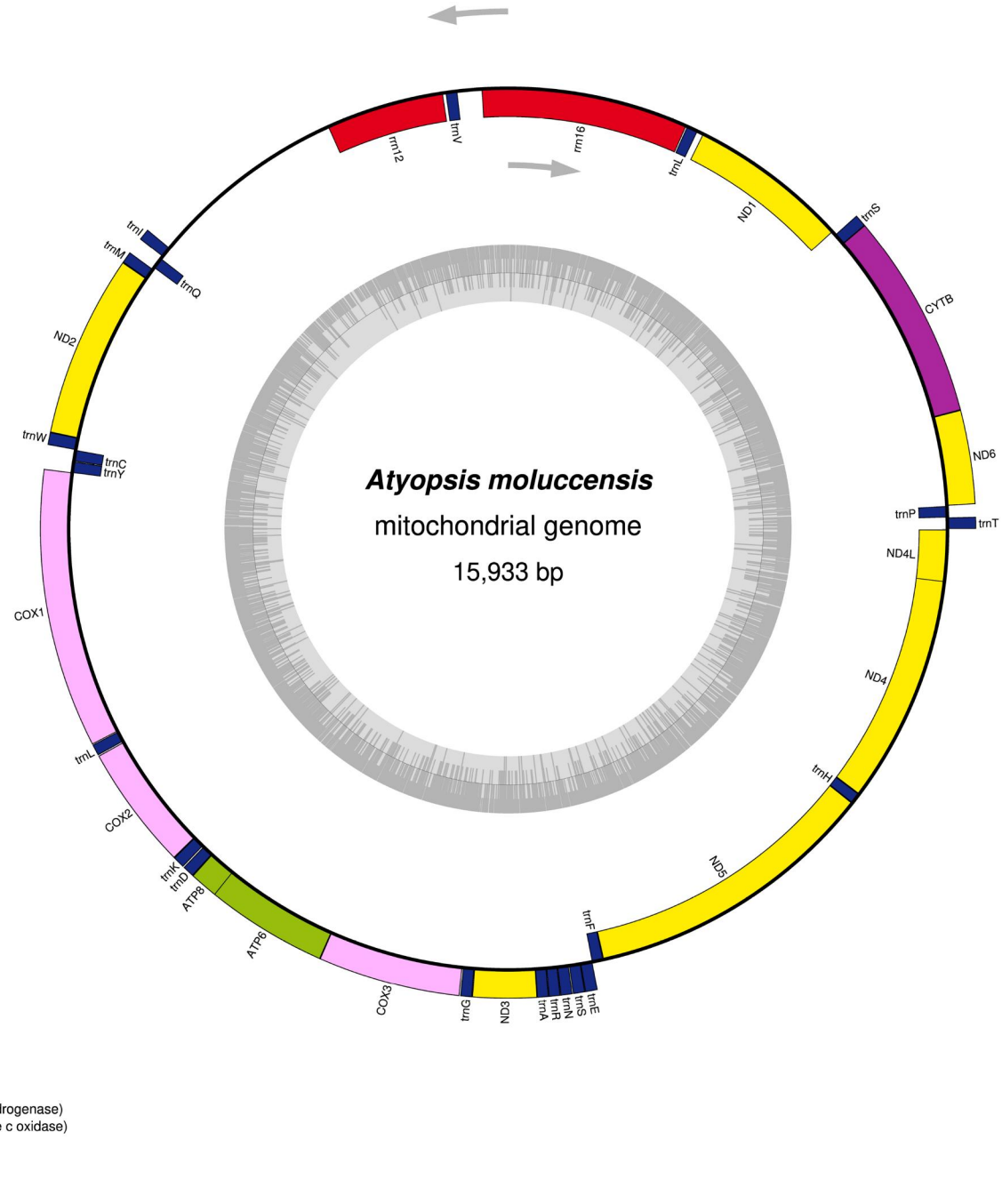

Figure 2. Mitochondrial genome map of *A. moluccensis*. Genes on the outside and inside of the circle are transcribed in the clockwise and counterclockwise directions, respectively. The dark and light gray bars in the inner circle denote G + C and A + T contents, respectively.

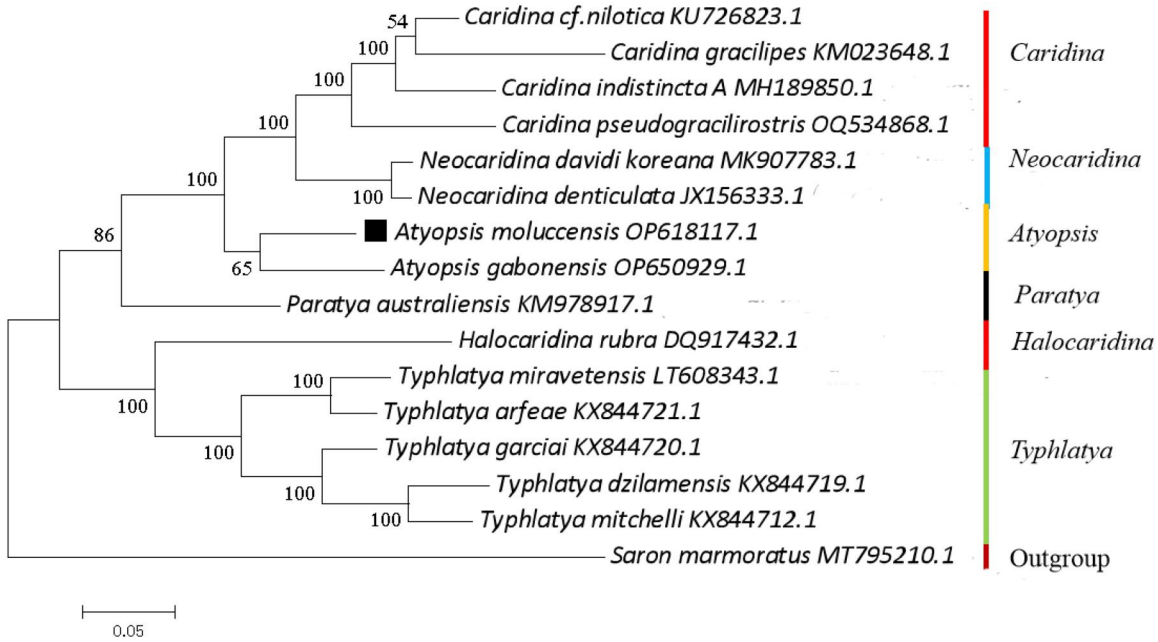

Figure 3. Phylogenetic tree of *A. moluccensis* and related species based on maximum-likelihood (ML) method. Bootstrap support values are indicated at each node. Accession numbers are indicated after the species names. *A. moluccensis* was indicated with a black square. The following sequences were used: *Caridina cf. nilotica* (KU726823.1), *Caridina gracilipes* (KM023648.1), *Caridina indistincta A* (MH189850.1) (Schmidt 2018), *Caridina pseudogracilirostris* (OQ534868.1), *Neocaridina davidi koreana* (MK907783.1) (Park et al. 2019), *Neocaridina denticulate* (JX156333.1) (Yu et al. 2014), *Atyopsis gabonensis* (OP650929.1), *Paratya australiensis* (KM978917.1) (Gan et al. 2016), *Halocaridina rubra* (DQ917432.1) (Ivey and Santos 2007), *Typhlatya miravetensis* (LT608343.1) (Jurado-Rivera et al. 2016), *Typhlatya arfeae* (KX844721.1), *Typhlatya garciai* (KX844720.1), *Typhlatya dzilamensis* (KX844719.1), *Typhlatya mitchelli* (KX844712.1), and *Saron marmoratus* (MT795210) (Wang et al. 2021).

as the start codon except ND5 (initiated with GTG) (Table S1). Eleven PCGs contained TAN as the stop codon except COX2 and ND4 (stopped with incomplete T– stop codon). 16S rRNA and 12S rRNA genes were 1212 bp (66.42% AT content) and 692 bp (64.88% AT content) in length, respectively. All tRNA genes ranged from 64 to 70 bp in size (Table S1). The result of phylogenetic tree showed that *A. moluccensis* and *A. gabonensis* clustered together with lower bootstrap support (65) (Figure 3). Species of the same genus were grouped together in a clade.

Discussion and conclusions

Here, the mitochondrial genome of *A. moluccensis* was first sequenced, analyzed, and reported. The mitogenome of *A. moluccensis* was 15,933 bp in length, which was similar with *A. gabonensis* (15,978 bp). The A + T bias of *A. moluccensis* was 62.51%, which was identical to *A. gabonensis* (61.66%) and lower than *T. miravetensis* (66.28%) and *N. heteropoda koreana* (67.00%) (Jurado-Rivera et al. 2016; Park et al. 2019). The stop codon of COX2 in *A. gabonensis* and *Typhlatya miravetensis* was also incomplete (Jurado-Rivera et al. 2016), which was consistent with this study. The mitochondrial DNA has been widely used for molecular evolution research (Galtier et al. 2009). Here, the phylogenic relationship among species from six genera of Atyidae family was chosen and analyzed. Each species from the same genus was grouped together. *Caridina* and *Neocaridina* were in sister relationship and *Atyopsis* was grouped with them (Figure 3). The phylogenetic relationships among the six genus were consistent with previous studies (Jurado-Rivera et al. 2016; Schmidt 2018; Park et al. 2019). Compared to previous research, these results enriched and supplemented phylogenic relationship of species in Atyidae family (Gan et al. 2016; Jurado-Rivera et al. 2016; Schmidt 2018; Park et al. 2019). In conclusion, this study first presented the complete mitogenome of *A. moluccensis*, which will contribute to investigations on the evolution and conservation of this species.

Author contributions

Chao Peng: analyzed the data and written original draft. Sigang Fan: experiments, formal analysis, and editing.

Disclosure statement

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

Funding

This work was supported by the Earmarked Fund [CARS-48-21], Rural Science and Technology Correspondent Fund of Guangzhou [20212100051], Guangzhou Municipal Science and Technology Project [No. 202206010138], Central Public-Interest Scientific Institution Basal Research Fund [nos. 2023TD44 and 2021SD05].

Data availability statement

The data that support the findings are available in GenBank of NCBI under the accession no. OP618117. The associated BioProject, SRA, and Biosample numbers are PRJNA885166, SRX17742550, and SAMN31078863, respectively. All accession numbers are activated.

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