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MITOGENOME REPORT

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The complete mitochondrial genome of *Allogalathea elegans* (Adams & White, 1848) (Decapoda: Galatheidae)

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ABSTRACT

The genus *Allogalathea* belongs to the subfamily Galatheoidea of the family Galatheidae. Here, we report a mitogenome of *Allogalathea elegans* (Adams & White, 1848). In this study, we obtained the complete mitochondrial genome of *Allogalathea elegans* by sequencing, which was 16,263 bp in length. The mitogenome contained 37 genes, including the typical set of 13 protein-coding genes (PCGs), 22 transfer RNA (tRNA) genes, and 2 Ribosomal RNA (rRNA) genes. The nucleotides A, C, G, and T distribution was 36.40%, 19.44%, 9.09%, and 35.07%, respectively. The length of the total protein-coding genes was 11,172 bp, which accounts for 68.69% of the whole mitochondrial genome. The phylogenetic result generated by IQ-Tree based on 13 PGCs showed that the infraorder Anomura is monophyletic, and the infraorder Anomura is a sister group of the infraorder Glypheidea. The discovery of the complete mitochondrial genome of *A. elegans* would help to conduct in-depth research on the infraorder Anomura.

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Mitochondrial genome; *Allogalathea elegans*; phylogenetic analysis

1. Introduction

Allogalathea elegans (Adams & White, 1848) belongs to the genus *Allogalathea* in the family Galatheidae and order Decapoda, which is mainly found in the Indian Ocean and Western Pacific Ocean (Lee et al. 2019). Although morphologically similar to lobsters, *A. elegans* is distinguished from them by having a smaller fifth pereopod, an abdomen that curves behind the thorax (Baba et al. 2009), a thorax that is thoroughly elongate, Flattening dorsal, and carinate in ventral, with between five and nine lateral teeth, and the carapace is covered in setiferous striae (Figure 1). Some scholarly studies have shown that Allogalathea has been discovered to be species complexes with high morphological similarity, but with genetically distinct species (Cabezas et al. 2011). Therefore, to clarify its evolutionary status at the molecular level, we determined the mitochondrial genome sequence of *A. elegans* and analyzed its evolutionary characteristics, which will help us improve the data at the molecular level and clarify the phylogenetic relationship and taxonomic status of *A. elegans* in this study.

2. Materials and methods

2.1. Sample collection and preservation

The specimen of *A. elegans* was obtained from Boundary Island, Lingshui City, Hainan Province, China (E110°11′46.739″N18°35′0.386″) in November 2021. The image of *A. elegans* was taken by Ruan Xinhe on 25 December 2021 (Figure 1). This specimen is deposited in the Laboratory of Aquatic Economic Animal Germplasm Resources and breeding Engineering, South China Agricultural University, China (Xinhe Ruan, rxh.equal@outlook.com), under voucher number CHT2150011.

2.2. DNA extraction and sequencing and phylogenetic analysis method

Total genomic DNA was extracted using a modified cetyltrimethylammonium bromide (CTAB) method (Allen et al. 2006), and NEBNext Ultra DNA Library Prep Kit for Illumina

Figure 1. The image of *Allogalathea elegans*. Its thorax is extremely elongate, dorsally flattened, and ventrally carinate, with between five and nine lateral teeth, and a carapace covered in setiferous striae. The image *A. elegans* was taken by Ruan Xinhe on 25 December 2021.

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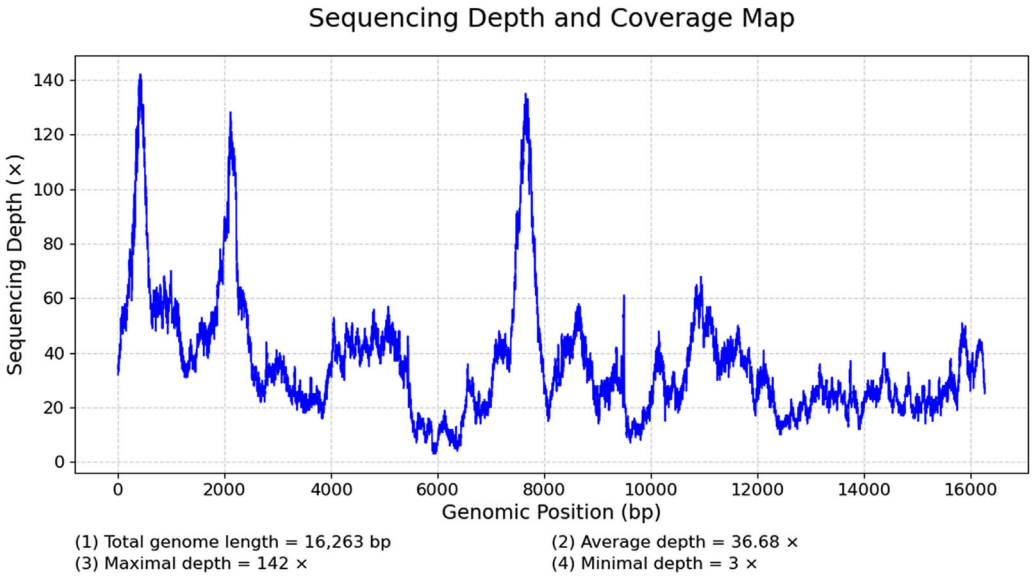

Figure 2. The sequencing depth and coverage map for mitochondrial genomes. The average depth is 36.68×.

sequencing was used to construct a 500-bp paired-end library. The Illumina NovaSeq 6000 platform (BIOZERON Co., Ltd., Shanghai, China) was used for sequencing. The mitogenome was assembled from 8,051.3 Mb of raw reads with a mean depth of 36.68×. The Sequencing Depth and Coverage Map for *A. elegans* mitochondrial Genomes in Figure 2 (Ni et al. 2023). The obtained GC content was 44.01%. Eventually, the assembled sequence was reorganized and oriented based on the reference mitochondrial genome to generate the final assembled mitochondrial genomic sequence (Zhang et al. 2000; Bolger et al. 2014). The CPGView was used to map the mitochondrial genome (http://www.1kmpg.cn/cpgview). The base composition and phylogenetic tree were calculated using IQ-TREE 2.2.0 software (Minh et al. 2020). The phylogenetic tree and optimal model were constructed using IQ-TREE from nucleic acid sequences employing the maximum-likelihood method, 1000 replicates, and GTR + F+R4 model.

3. Results and discussion

3.1. Characteristics of A. elegans mitochondrial genome

The complete mitogenome of *A. elegans* (GenBank accession number: ON968875) was 16,263 bp long and comprised the typical set of 13 protein-coding genes (PCGs), 22 transfer RNA (tRNA) genes, and 2 Ribosomal RNA (rRNA) genes (Table 1). All genes had similar locations and strands as those of other published squat lobsters (Lee et al. 2016; Zhang et al. 2017; Hwang et al. 2019). The CPGView was used to map the mitochondrial genome, as shown in Figure 3. The distribution of A, C, G, and T was 36.40%, 19.44%, 9.09%, and 35.07%, respectively. The total length of the protein-coding genes was 11,172 bp, accounting for 68.69% of the mitochondrial genome, and the base composition was 28.87% A, 15.49% C, 15.47% G, and 40.18% T. Among the protein-coding genes, six genes used the start codon ATG (*COX2*, *ATP8*, *ATP6*, *COX3*, *NAD4L*, and *COB*), four genes used ATT (*COX1*, *NAD2*, *NAD6*, and *NAD3*) as the start codon, two genes used GTG (*NAD5* and *NAD1*), and the *NAD4* gene initiated with ATA codon, respectively.

Table 1. The Organization of the complete mitochondrial genome in *Allogalathea elegan*.

Gene	Strand	Position	Size (bp)	Intergenic spacer	Start coden	Stop coden
COX1	F	1–1539	1539	−16263	ATT	TAA
trnL2-tta	F	1535–1600	66	−5	–	–
COX2	F	1612–2296	685	11	ATG	T
trnK-aaa	F	2297–2362	66	0	–	–
trnI-atc	F	2365–2432	68	2	–	–
trnM-atg	F	2435–2502	68	2	–	–
trnA-gca	F	2512–2576	65	9	–	–
NAD2	F	2592–3608	1017	15	ATT	TAA
trnD-gac	F	3611–3676	66	2	–	–
atp8	F	3677–3835	159	0	ATG	TAA
atp6	F	3829–4503	675	−7	ATG	TAA
COX3	F	4503–5294	792	−1	ATG	TAA
trnS1-aga	F	5326–5391	66	31	–	–
trnE-gaa	F	5394–5460	67	2	–	–
trnF-ttc	R	6498–6563	66	1037	–	–
NAD5	R	6568–8292	1725	4	GTG	TAA
trnH-cac	R	8373–8437	65	80	–	–
NAD4	R	8438–9764	1327	0	ATA	T
NAD4l	R	9770–10072	303	5	ATG	TAA
trnT-aca	F	10075–10140	66	2	–	–
NAD6	F	10154–10672	519	13	ATT	TAA
COB	F	10672–11806	1135	−1	ATG	T
trnS2-tca	F	11807–11874	68	0	–	–
trnP-cca	R	11887–11951	65	12	–	–
NAD1	R	11956–12894	939	4	GTG	TAG
trnL1-cta	R	12919–12986	68	24	–	–
rrnL	R	12947–14323	1377	−40	–	–
trnV-gta	R	14322–14394	73	−2	–	–
rrnS	R	14393–15214	822	−2	–	–
trnW-tga	F	15417–15485	69	202	–	–
trnG-gga	F	15486–15554	69	0	–	–
NAD3	F	15555–15908	354	0	ATT	TAA
trnR-cga	F	15912–15975	64	3	–	–
trnN-aac	F	15983–16050	68	7	–	–
trnQ-caa	R	16062–16129	68	11	–	–
trnC-tgc	R	16133–16198	66	3	–	–
trnY-tac	R	16199–16263	65	0	–	–

In the column intergenic length, the positive number indicates interval base pairs between genes, while the negative number indicates the overlapping base pairs between genes.

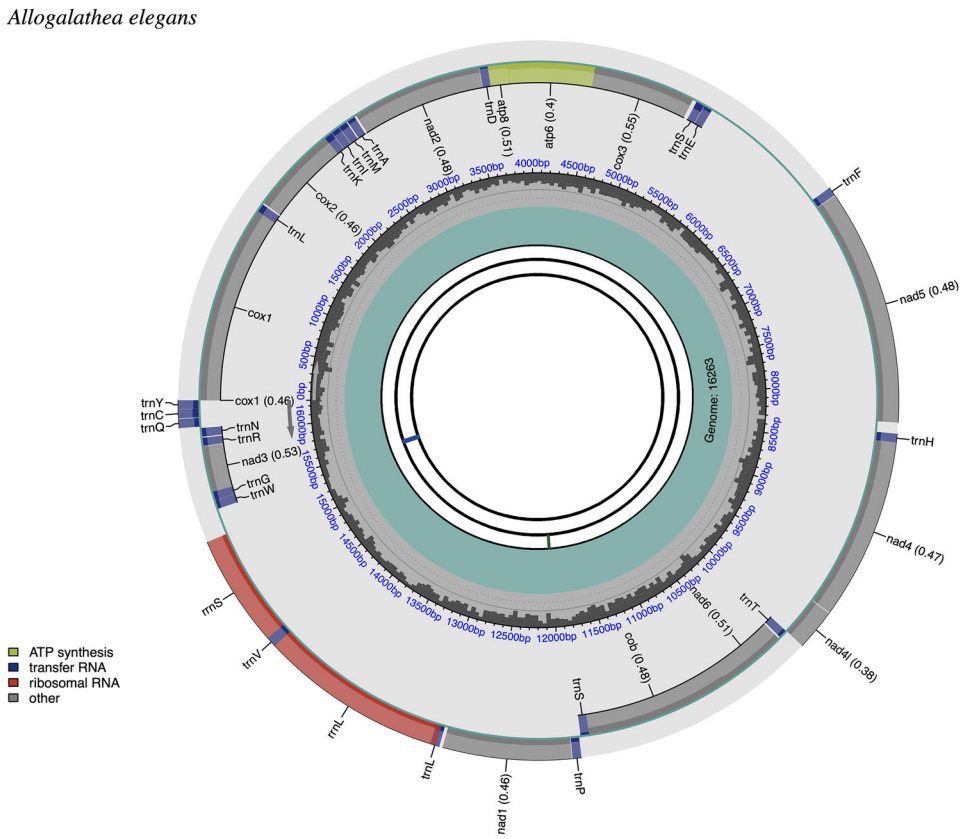

Figure 3. Mitogenome pattern map of *Allogalathea elegans*. The mitochondrial genome is mapped using CPGView. CDS: Coding sequence; tRNA: Transfer RNA; rRNA: Ribosomal RNA.

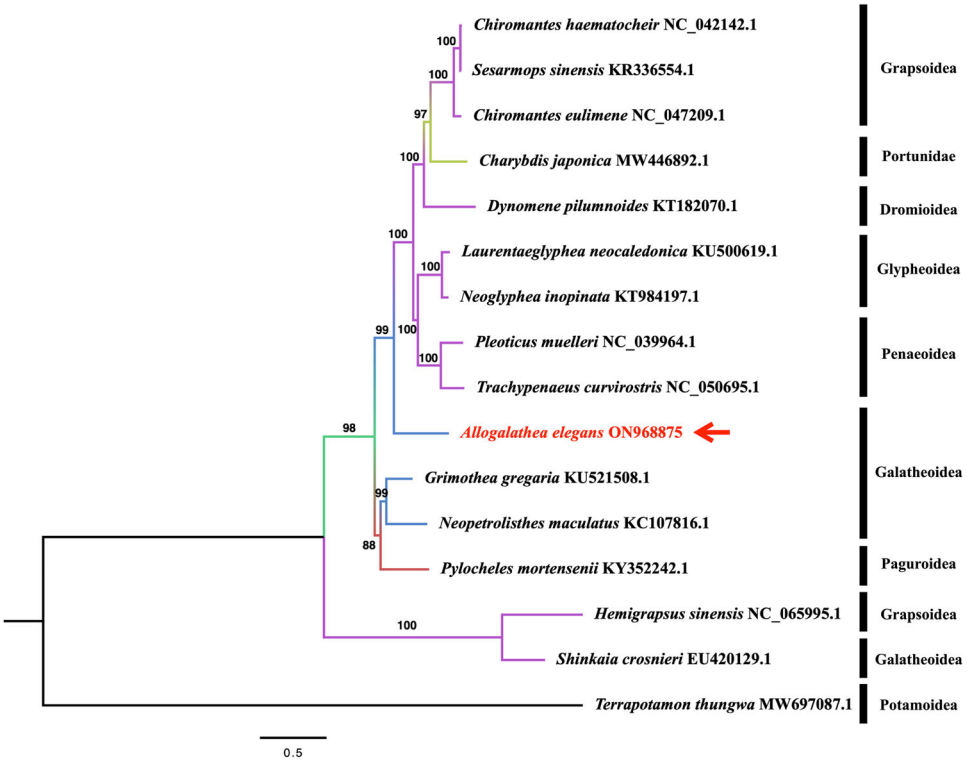

Figure 4. the phylogenetic tree was based on *A. elegans* and other 15 species, which was performed by ML analysis of the 13 protein-coding genes. The base composition and the phylogenetic tree were calculated using IQ-TREE 2.2.0 software with the maximum-likelihood method, 1000 replicates, and GTR + F+R4 model. The phylogenetic position of *A. elegans* was marked with a red arrow. The following sequences were used: *Chiromantes haematochir* NC_042142.1 (Li et al. 2019), *Sesarmops sinensis* KR336554.1 (Xing et al. 2016), *Chiromantes eulimene* NC_047209.1 (Zhang et al. 2020), *Charybdis japonica* MW446892.1 (Liu and Cui 2010), *Dynomene pilumnoides* KT182070.1 (Shi et al. 2016), *Laurentaeglyphea neocaledonica* KU500619.1 (Tan, Gan, Dally, et al. 2018), *Neoglyphea inopinata* KT984197.1 (Tan, Gan, Dally, et al. 2018), *Pleoticus muelleri* NC_039964.1 (Kim et al. 2018), *Trachypenaeus curvirostris* NC_050695.1 (Zhu et al. 2019), *Grimothea gregaria* KU521508.1 (Lee et al. 2016), *Neopetrolisthes maculatus* KC107816.1 (Shen et al. 2013), *Pylocheles mortensenii* KY352242.1 (Tan, Gan, Lee, et al. 2018), *Hemigrapsus sinensis* NC_065995.1 (Jin et al. 2023), *Shinkaia crosnieri* EU420129.1 (Yang and Yang 2008), *Terrapotamon thungwa* MW697087.1 (Yundaeng et al. 2022).

3.2. Phylogenetic analysis

To investigate the evolutionary relationship of *A. elegans*, we constructed a phylogenetic tree using the maximum-likelihood (ML) method based on 13 protein-coding nucleotide sequences from the Decapoda mitogenomes. The topology and nodal support values are shown in Figure 4. The results indicate that *A. elegans* forms a separate branch. Although *A. elegans* belongs to the same Galatheoidea taxonomically as *Grimothea gregaria*, *Neopetrolisthes maculatus*, and *Shinkaia crosnieri*, it does not belong to the same branch in the evolutionary tree, and *A. elegans* has a considerable genetic distance from *Shinkaia crosnieri*. This indicates that many of these taxa have been discovered to be species complexes demonstrating morphological similarities but with genetically distinct species (Demes et al. 2009). This study provides better insights into the phylogeny of this species.

4. Conclusions

We reported the first complete mitochondrial genome assembly and annotation of *A. elegans* using the next-generation sequencing technology. The circular mitogenome was 16,263 bp in length, contained 37 genes encoding 13 PCGs, 22 tRNAs and 2 rRNAs. The phylogenetic tree was inferred by a Maximum-likelihood phylogenetic tree based on the sequences of 18 species, which supported that *A. elegans* forms a separate branch and is inconsistent with the taxonomy. The mitochondrial genomic data of *A. elegans* provided in this study will help provide new insights into the future classification of *A. elegans*.

Ethical approval

This study was conducted with the guidelines of the Council of China and animal welfare requirements. Based on the recommendations of the Regulations for the Administration of Affairs Concerning Experimental Animals of China, the Institutional Animal Care and Use Committee of Guangdong Academy of Animal Science and Veterinary Medicine, South China Agricultural University approved all animal experiments (approval number: ACVM SCAU 2021002).

Author contributions

Conceived and designed the experiments: Huihong Zhao and Jie Yu. Performed the experiments: Huitao Cheng and Zijie Xuan. Analyzed the data and Wrote the paper: Xinhe Ruan and Zongyang Li. Final approval of the version to be published: Jie yu. All authors have read and agreed to the published version of the manuscript.

Disclosure statement

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

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Data availability statement

The genome sequence data supporting this study's findings are openly available in GenBank of NCBI at https://www.ncbi.nlm.nih.gov/ under accession no. ON968875. The associated Bio-Project, SRA, and Bio-Sample numbers are PRJNA904942, SRR22403925, and SAMN31859346 respectively.

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