The complete mitochondrial genome of Scyra compressipes Stimpson, 1857 (Decapoda: Epialtidae)

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ABSTRACT

The family Epialtidae is the most diversified family within superfamily Majoidea but there is no report for complete mitogenome of any species in this family. This study was performed to sequence a complete mitogenome of Scyra compressipes Stimpson, 1857, as the first mitochondrial genome report from the Epialtidae. The complete mitogenome sequence of S. compressipes was 16,415 bp and it consisted of 36 genes, including 13 protein-coding genes (PCGs), two rRNA genes, and 21 tRNA genes excluding tRNA-Leu (UAG). The phylogenetic position of S. compressipes in the superfamily Majoidea was examined based on 13 PCGs. The phylogenetic analysis showed that S. compressipes was most closely related to Maguimithrax spinosissimus, a representative of the family Mithracidae.

The family Epialtidae comprising approximately 100 genera and 500 species is the most diversified family within the superfamily Majoidea (Tavares et al. 2017). In spite of species diversity of the family, there is no report of mitochondrial genome from the representative species of the family until now. As a member of the Epialtidae, Scyra compressipes Stimpson, 1857, was recorded from Korea and Japan (Oh and Ko 2010). In this study, we provided a complete mitogenome sequence of S. compressipes and examined the phylogenetic position of the species in the molecular phylogeny of the superfamily Majoidea based on amino acid sequences of 13 protein-coding genes (PCGs).

An adult specimen of S. compressipes used in this study was collected from the offshore area of Namhae-gun, Gyeongsangnam-do, Korea (34°44′29.4″N, 128°02′54.0″E) in 9 October 2020. The specimen of S. compressipes was preserved in absolute ethanol and deposited in the Department of Biotechnology, Sangmyung University, with voucher number SMU00222. The genomic DNA of the specimen was prepared from gills using Qiagen DNeasy Blood & Tissue Kit (Qiagen, Germany) according to the manufacturer’s protocol. The complete mitogenome sequence of S. compressipes (GenBank accession number: MW451225) was 16,415 bp in length and contained 34.7% A, 15.3% C, 10.2% G, and 39.8% T nucleotide distribution. It consisted of 36 genes, including 13 PCGs, two rRNA genes, and 21 tRNA genes. Of 13 PCGs, nine of PCGs, including cox1, cox2, cox3, cyt b, nad2, nad3, nad4, nad5, and nad6 were encoded on H-strand while four PCGs, including, nad1, nad4a, nad4l, and nad5 were encoded on L-strand. All PCGs had start codon as ATN (nine of ATG, two of ATA, one of ATT and ATT) and most of PCGs had stop codon as TAA except cox1, cox3 (incomplete stop codon as T), and nad2 (stop codon as TAG). rRNA genes were 1376 bp and 810 bp in length for 16S rRNA and 12S rRNA, respectively. Twenty-one tRNA genes ranged from 63 bp (tRNA-Ala) to 72 bp (tRNA-Val) in length. Although we searched secondary structures for the whole mitogenome sequences using ARWEN (Laslett and Canback 2008) and tRNAscan-SE (Chan and Lowe 2019), tRNA-Leu (UAG) was not found. For confirmation of the absence of the tRNA, new primer sets were designed for PCR and resequencing was executed by Sanger sequencing method. The experiments reconfirmed the absence of tRNA-Leu (UAG) gene in the mitogenome.

The phylogenetic analysis was performed based on the amino acid sequences of 13 PCGs in mitogenomes of six representative species from superfamily Majoidea: S. compressipes (GenBank accession number: MW451225), Maguimithrax spinosissimus (=Damithrax spinosissimus) (KM405516),
Chionoecetes japonicus (MT750295), Chionoecetes opilio (MT335860), Maja crispata (KY650651), Maja squinado (KY650652), and two species from the superfamily Bythograeoidea: Austinograea alayseae (JQ035660) and Gandalfus puia (KR002727) and two species from the superfamily Portunoidea: Scylla paramamosain (FJ827761) and Portunus trituberculatus (AB093006) as outgroups. The molecular phylogeny suggested that Scyra compressipes clustered with Maguimithrax spinosissimus, a representative of the Mithracidae (Figure 1). The molecular phylogenetic relationship between families in the superfamity Majoidea presented in this study was consistent to previous studies (Hultgren and Stachowicz 2008; Jeong et al. 2020; Kim et al. 2020).

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

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Data availability statement
The genome sequence data that support the findings of this study is openly available in GenBank of NCBI at https://www.ncbi.nlm.nih.gov/ under the accession no. MW451225. The associated BioProject, SRA, and Bio-Sample numbers are PRJNA694515, SRR13555153, and SAMN17526022, respectively.

References
Bernt M, Donath A, Jühling F, Externbrink F, Florentz C, Fritzsch G, Pütz J, Middendorf M, Stadler PF. 2013. MITOS: improved de novo metazoan mitochondrial genome annotation. Mol Phylogenet Evol. 69(2): 313–319.
Chan PP, Lowe TM. 2019. tRNAscan-SE: searching for tRNA genes in genomic sequences. Gene prediction. Methods Mol Biol. 1962:1–14.
Hahn C, Bachmann L, Chevreux B. 2013. Reconstructing mitochondrial genomes directly from genomic next-generation sequencing reads—a baiting and iterative mapping approach. Nucleic Acids Res. 41(13): e129.
Huelsenbeck JP, Ronquist F. 2001. MRBAYES: Bayesian inference of phylogenetic trees. Bioinformatics. 17(8):754–755.
Hultgren KM, Stachowicz JJ. 2008. Molecular phylogeny of the brachyuran crab superfamily Majoidea indicates close congruence with trees based on larval morphology. Mol Phylogenet Evol. 48(3): 986–996.
Jeong J, Ryu S, Kim W. 2020. The complete mitogenome of the Chionoecetes opilio (Crustacea: Decapoda: Oropneustidae) and its unique characteristics. Mitochondrial DNA Part B. 5(3):2550–2552.
Kim YH, Kim KR, Park JY, Sung MS, Yun BH, Jeon AH, Kim MS, Bang IC. 2020. The complete mitochondrial genome of Chionoecetes japonicus (Crustacea: Decapoda: Majoidea). Mitochondrial DNA Part B. 5(3): 3524–3544.
Laslett D, Canback B. 2008. ARWEN: a program to detect tRNA genes in metazoan mitochondrial nucleotide sequences. Bioinformatics. 24(2): 172–175.
Oh SM, Ko HS. 2010. Larval development of Scyra acutifrons (Crustacea: Decapoda: Euphausiidae) with a key from the northern pacific. Anim Cells Syst. 14(4):333–341.
Stamatakis A. 2014. RAxML version 8: a tool for phylogenetic analysis and post-analysis of large phylogenies. Bioinformatics. 30(9): 1312–1313.
Tavares AI, Cabezas MP, Xavier R, Branco M, Lima FP, Seabra R, Ribeiro PA, Lopes EP, Santos AM. 2017. Phylogeography and phylogeny of the genus Acanthonyx (Decapoda, Epialtidae) in the North-East Atlantic and Mediterranean. Zool Scripta. 46(S):571–583.