MITOCHONDRIAL DNA PART B: RESOURCES
2024, VOL. 9, NO. 3, 338–341
https://doi.org/10.1080/23802359.2024.2324929

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MITOGENOME REPORT

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The complete mitochondrial genome of *Hyperhalosydna striata* (Kinberg, 1856) (Annelida: Polynoidae) collected from Jejudo Island, Korea

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ABSTRACT

The mitogenome sequence of *Hyperhalosydna striata* was determined for the first time in the present study. The genome is 15,226 bp long and contains 13 protein-coding genes (PCGs), two ribosomal RNA genes (rRNAs), and 22 transfer RNA genes (tRNA). The overall base composition was 28.0% A, 21.9% C, 13.0% G, and 37.1% T. A phylogenetic tree was constructed to infer the phylogenetic position of *H. striata* among polynoid species whose mitochondrial genome sequences are available in GenBank. *Hyperhalosydna striata* was closely related to the species of subfamily Lepidonotinae.

ARTICLE HISTORY
Received 20 July 2023
Accepted 24 February 2024

KEYWORDS
Annelida; Polynoidae; phylogeny; scale worm

Introduction

The scale worm, *Hyperhalosydna striata* (Kinberg 1856), belongs to the family Polynoidae Kinberg, 1856. It is easily distinguished from its congeners by the presence of stripes on the elytra. They are known to be free-living or to live in association with other polychaetes, such as eunicids (Hanley and Bruke 1991; Park et al. 2016). The type locality of *H. striata* is Jackson Port, Sydney, Australia (Kinberg 1856). However, this species is widely distributed throughout the South Pacific and the Indo-West Pacific, including Asian Waters (Grube 1876; McIntosh 1885; Moore 1903; Augener 1922; Fauvel 1932; Knox 1951; Imajima and Hartman 1964; Pillai 1965; Uschakov 1982; Uchida 1988; Imajima 2001; Wehe 2006; Park et al. 2016).

Recently, mitochondrial genomes have been used for phylogenetic and evolutionary studies of the highly diverse Polynoidae (Zhang et al. 2018; Gonzalez et al. 2021). However, studies are still scarce. For this reason, an additional complete mitogenome of the polynoid species *H. striata* was analyzed in this study.

Materials and methods

The specimen was collected by scuba diving in a subtidal rocky zone (depth 18 m) of Jejudo Island (33°13′41.29″N, 126°33′41.29″E, Munseom Islet, Seogwipo-si, South Korea) (Figure 1). Species identification was performed under a stereomicroscope based on the description of Park et al. (2016). The specimen was deposited at the National Institute of Biological Resources (NIBR, http://www.nibr.go.kr/, Eun-Jung Nam, ejnam@korea.kr), Republic of Korea (NIBRIV0000902986). Genomic DNA was extracted from the pygidium of the

Figure 1. Underwater image of the *Hyperhalosydna striata*. The photo was taken by TP, a corresponding author of this paper.

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Supplemental data for this article can be accessed online at https://doi.org/10.1080/23802359.2024.2324929.

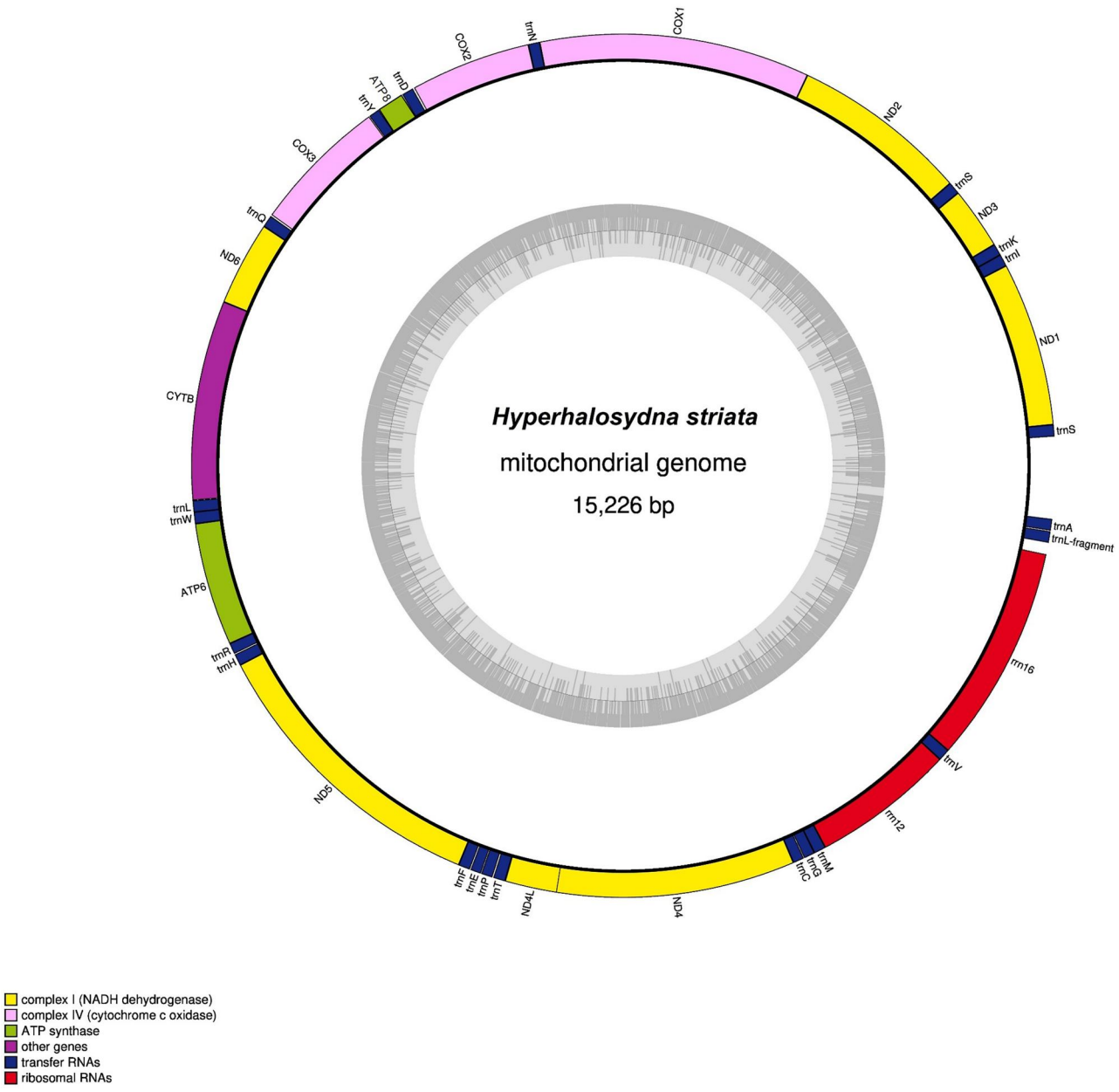

Figure 2. Schematic map of overall features of the *H. striata* mitochondrial genome.

specimen using the DNeasy Blood and Tissue kit (Qiagen, Hilden, Germany). REPLI-g Mitochondrial DNA Kit (Qiagen, Hilden, Germany) was used for mitochondrial DNA amplification, and mitochondrial genome sequencing was performed using the NovaSeq 6000 sequencing system (Illumina, San Diego, CA). Phylogenetic analysis was conducted to examine the phylogenetic position of *H. striata* using MEGA X software (Kumar et al. 2018). The tree was reconstructed using the ML method using the GTR + G + I model with 1000 bootstrap replicates. Illumina sequencing data of *Hyperhalosydna striata* were mapped on *H. striata* mitochondrial genome sequence and depth of mapped reads was calculated respectively using clc_ref_assemble and clc_mapping_info with default parameters in CLC Assembly Cell package ver. 4.2.1 (Qiagen, Aarhus, Denmark). Assembler and annotation tools, NOVOPlasty (Dierckxsens et al. 2017) and Chlorobox (Tillich et al. 2017), were used, respectively.

Results and discussion

The complete mitogenome of *H. striata* (GenBank accession no. MW620990) was 15,226 bp long and consisted of 13 protein-coding genes (PCGs), two ribosomal RNA (rRNA) genes, and 22 transfer RNA (tRNA) genes (Figure 2). The overall nucleotide composition was 28.0% A, 21.9% C, 13.0% G, and 37.1% T, with high G + C content (65.1%). The average mapping depth is ×410,057 (Figure S1). The phylogenetic tree results showed that *H. striata* sister was cluster to the Lepidonotinae species (*Halosydna* sp., *Lepidonotus* sp.) (Figure 3).

Ethical approval

The material of this paper does not involve ethical conflicts. *Hyperhalosydna striata* is neither endangered on the CITES catalogue nor collected from a natural reserve.

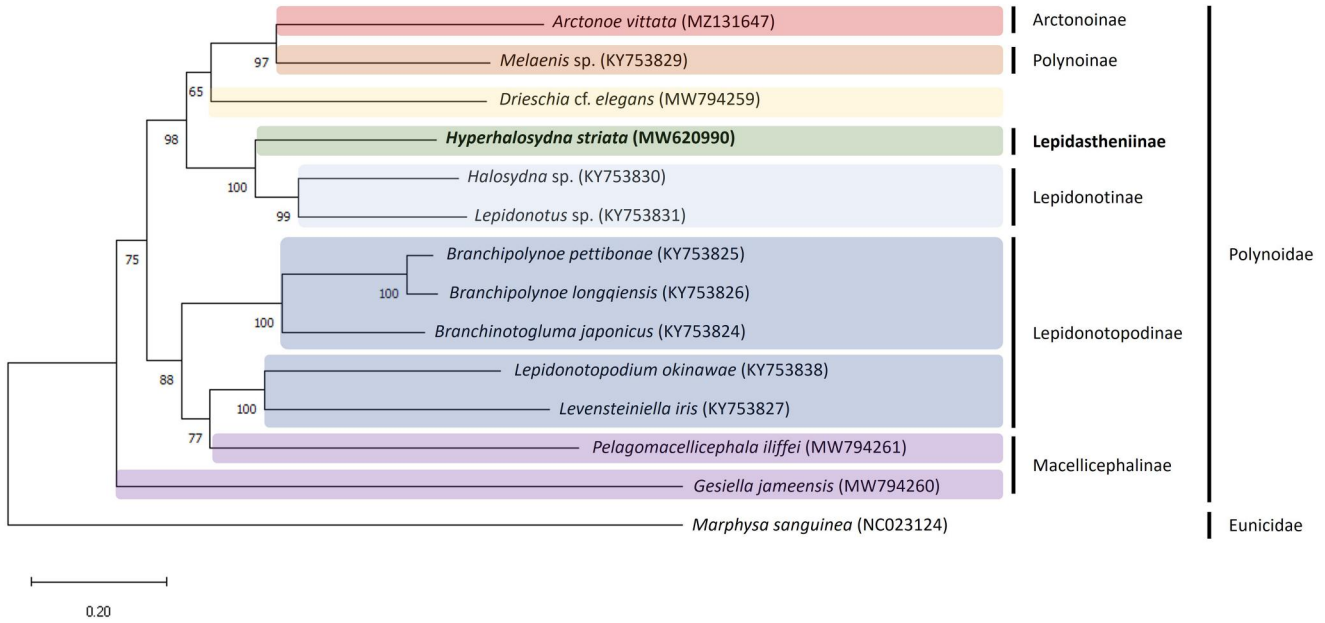

Figure 3. Maximum-likelihood (ML) tree reconstructed using a concatenated data set of 13 protein-coding genes based on 14 mitogenome sequences, including *Hyperhalosydna striata* from the present study. Bootstrap replicates were performed 1000 times. The GenBank accession number of each species is shown in parentheses after the species name. The following sequences were used: *Hyperhalosydna striata* MW620990, *Arctonoe vittata* MZ131647 (Park et al. 2021), *Melaenis* sp. KY753829 (Zhang et al. 2018), *Drieschia* cf. *elegans* MW794259 (Gonzalez et al. 2021), *Halosydna* sp. KY753830 (Zhang et al. 2018), *Lepidonotus* sp. KY753831 (Zhang et al. 2018), *Branchipolynoe pettibonae* KY753825 (Zhang et al. 2018), *B. longqiensis* KY753826 (Zhang et al. 2018), *Branchinotogluma japonicus* KY753824 (Zhang et al. 2018), *Lepidonotopodium okinawae* KY753838 (Zhang et al. 2018), *Levensteiniella iris* KY753827 (Zhang et al. 2018), *Pelagomacellicephala iliffei* MW794261 (Gonzalez et al. 2021), and *Gesiella jameensis* MW794260 (Gonzalez et al. 2021).

Author contributions

Kwang-Soo Kim conducted collecting the specimen, species identification, and wrote draft. Jiseon Park analyzed the mitogenome sequence and wrote draft. Taeseo Park contributed conception, designing this study, and revising manuscript.

Disclosure statement

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

Funding

This work was supported by a Grant [NIBR202313101] from the National Institute of Biological Resources (NIBR), Ministry of Environment of Republic of Korea.

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Data availability statement

The genome sequence data supporting this study's findings are available in the National Center for Biotechnology Information (NCBI) GenBank (https://www.ncbi.nlm.nih.gov) under accession no. MW620990. The associated BioProject, SRA, and BioSample numbers were PRJNA727906, SRR14566003, and SAMN19229862, respectively. The data that support the findings of this study are openly available in Mendeley (https://doi.org/10.17632/9h4gtkx9fn.1).

References

Augener H. 1922. Revision der Australischen Polychaeten-typen von Kinberg. Arkiv Zool. 14(8):1–42.
Dierckxsens N, Mardulyn P, Smits G. 2017. NOVOPlasty: de novo assembly of organelle genomes from whole genome data. Nucleic Acids Res. 45(4):e18. doi:10.1093/nar/gkw955.
Fauvel P. 1932. Annelida Polychaeta of the Indian Museum, Calcutta. Mem Indian Mus. 12(1):1–262.
Gonzalez BC, Martínez A, Worsaae K, Osborn KJ. 2021. Morphological convergence and adaptation in cave and pelagic scale worms (Polynoidae, Annelida). Sci Rep. 11(1):10718. doi:10.1038/s41598-021-89459-y.
Grube AE. 1876. Bemerkungen über die Familie der aphroditeen (Gruppe Polynoina, Acoëta, Polylepidea). Jahresber Schlesische Gesellschaft Vaterländische Cultur Breslau. 53:46–72.
Hanley JR, Bruke M. 1991. Polychaeta Polynoidae: scaleworms of the Chesterfield Island and Fairway Reefs, Coral Sea. Mém Mus Natl d'Hist Nat Paris Sér A. 151:9–82.
Imajima M. 2001. Annelida, Polychaeta II. Tokyo, Japan: Seibutsu Kenkyujo Publishing Co.; p. 1–542.
Imajima M, Hartman O. 1964. The polychaetous annelids of Japan. Los Angeles (CA): University of California Press; p. 1–452.
Kinberg JGH. 1856. Nya slägten och arter af Annelider, Öfversigt af Kongl. Vetenskaps-Akad Förhhandl Stockh. 12(9–10):381–388.
Knox GA. 1951. The polychaetous annelids of Banks Peninsula. Rec Canterb Mus. 5(5):312–329.
Kumar S, Stecher G, Li M, Knyaz C, Tamura K. 2018. MEGA X: molecular evolutionary genetics analysis across computing platforms. Mol Biol Evol. 35(6):1547–1549. doi:10.1093/molbev/msy096.
McIntosh WC. 1885. Report on the Annelida Polychaeta collected by H.M.S. challenger during the years 1873–1876. Report on the scientific results of the voyage of H.M.S. challenger during the years 1873–76. Zoology. Vol. 12; p. 1–554.
Moore JP. 1903. Polychaeta from the coastal slope of Japan and from Kamchatka and Bering Sea. Proc Acad Nat Sci Philadelph. 55:401–490.
Park J, Jung J, Kim K-S, Park T. 2021. Complete mitochondrial genome of the commensal scale worm, Arctonoe vittata (Grube, 1855) (Polychaeta: Polynoidae), collected from benthic habitat of the eastern

coast of Korea. Mitochondrial DNA Part B. 6(8):2455–2457. doi:10.1080/23802359.2021.1955771.

Park T, Lee SK, Kim W. 2016. New record of scale worms, *Arctonoe vittata* (Grube, 1855) and *Hyperhalosydna striata* (Kinberg, 1856) (Polychaeta: Polynoidae) from Korean waters. J Spec Res. 5(3):517–529. doi:10.12651/JSR.2016.5.3.517.

Pillai TG. 1965. Annelida Polychaeta from the Philippines and Indonesia. Ceyl J Sci (Biol Sci). 5(2):110–177.

Tillich M, Lehwark P, Pellizzer T, Ulbricht-Jones ES, Fischer A, Bock R, Greiner S. 2017. GeSeq – versatile and accurate annotation of organelle genomes. Nucleic Acids Res. 45(W1):W6–W11. doi:10.1093/nar/gkx391.

Uchida H. 1988. Polychaeta fauna in Wakayama Prefecture. Nanki Seibutsu. 30(2):75–86.

Uschakov PV. 1982. Polychaetes of the suborder Aphroditiformia of the Arctic Ocean and the Northwestern Part of the pacific, families Aphroditidae and Polynoidae. FAUNA SSSR, Mnogoshchetinkovyye Chervil (fauna of the USSR, Polychaeta). Moscow: Academiya Nauk SSSR; p. 1–272.

Wehe T. 2006. Revision of the scale worms (Polychaeta: Aphroditoidea) occurring in the seas surrounding the Arabian Peninsula. Part I: Polynoidae. Fauna Arabia. 22:23–197.

Zhang Y, Sun J, Rouse GW, Wiklund H, Pleijel F, Watanabe HK, Chen C, Qian PY, Qiu JW. 2018. Phylogeny, evolution and mitochondrial gene order rearrangement in scale worms (Aphroditiformia, Annelida). Mol Phylogenet Evol. 125:220–231. doi:10.1016/j.ympev.2018.04.002.