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[단보, Short communication]

Full-length mitochondrial genome of the boring polychaete species, *Polydora hoplura* (Annelida) isolated from abalone, *Haliotis discus hannai* shells

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ABSTRACT

The mitochondrial genome (mitogenome) of the invasive and harmful polychaete species, *Polydora hoplura* (Annelida), was analyzed by next generation sequencing (NGS). Its mitogenome was found to be 17,597 bp in length, comprising 13 protein-coding genes, two ribosomal RNA genes, and 23 transfer RNA genes, with one additional *trnM* gene. The gene composition and order of *P. hoplura* were distinct from those of polychaetes and even differed from those of *Marenzelleria neglecta* belonging to the same family, Spionidae.

Key words: Invasive species, harmful species, mitochondrial genome, polychaete, *Polydora hoplura*

The polychaete *Polydora hoplura* (Annelida) is an invasive and harmful species that has been distributed in new regions by the anthropogenic transportation of live imported shellfish worldwide (Radashevsky and Migotto 2017). It is one of the most notorious pests that bores into mollusk shells (Lleonart *et al*. 2003; Boonzaaier *et al*. 2014), and has caused serious damage to abalone and oysters on shellfish farms along the southern coast of South Korea since first reported in 2004 as *P. uncinata* (Radashevsky *et al*. 2017; Sato-Okoshi *et al*. 2012).

A voucher specimen of *P. hoplura* I-13 (NIFS Lot No. Ab-WB-2019-004) was collected from an abalone farm on the southwestern coast of South Korea (34°16'24"N, 126°62'89"E) and deposited in the invertebrate collection of the National Institute of Fisheries Science (NIFS, Busan, South Korea). Its genomic DNA (gDNA) was extracted from a piece of excised tissue according to Asahida *et al*. (1996). For next generation sequencing (NGS), a library was constructed with the gDNA according to the manufacturer's instruction of MGIEasy Universal DNA Library Prep Set (MGI Tech Co. Ltd., Shenzhen, China). A library with an average insert size of ca. 420 bp was generated and subjected to a NGS analysis using Genetic Sequence MEISEQ-2000 (MGI Tech Co. Ltd.). Approximately 11 gigabyte (Gb) of raw data were obtained by 150 bp paired-end sequencing. The raw data were trimmed with cutadapt v1.9.1 (Martin 2015) and subjected to de novo assembly and annotation using Geneious Prime v2020.2 (Biomatters Ltd, Auckland, New Zealand). The gene composition and order of *P. poplura* were further confirmed through online MITOS WebServer (http://mitos.bioinf.uni-leipzig.de/index.py). The full-length mitogenomic sequence analyzed in this study was deposited in the GenBank under the accession number MW248165.

In this study, the mitogenome of *P. hoplura* was a circular molecule of 17,597 bp in total length. It

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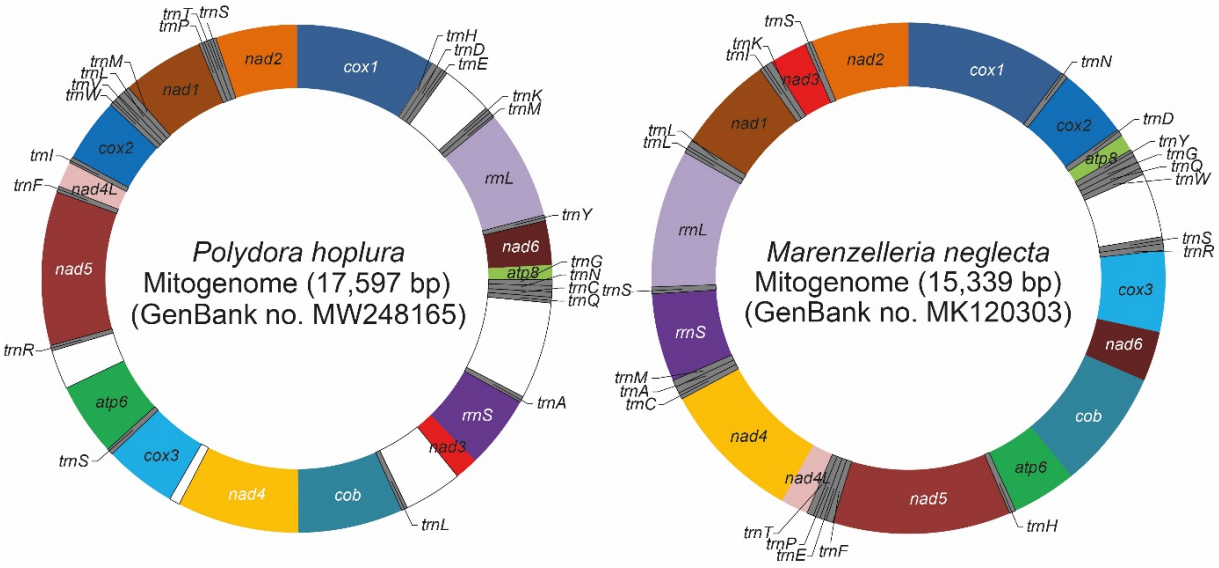

Fig. 1. Comparison of mitogenomic maps of an invasive and harmful polychaete species, *Polydora hoplura* analyzed in this study and *Marenzelleria neglecta* belonging to the same family, Spionidae.

encoded 13 protein-coding genes, two ribosomal RNA genes, and 23 transfer RNA genes. The gene composition of *P. hoplura* was different from that of typical metazoan mitogenomes by having one additional *trnM* gene, while its gene order was distinct from that of annelids (Weigert *et al*. 2016) and *Marenzelleria neglecta*, which belong to the same family, Spionidae (Fig. 1). BLAST reach in the National Center for Biotechnology Information (NCBI; https://blast.ncbi.nlm.nih.gov/) was performed on the *rrnL* and *cox1* genes, the gold standard for DNA barcoding, and showed 97.47 %-100.00% and 98.37 %-99.39% genetic similarities, respectively, to the conspecific specimens in the GenBank database. The mitogenomic information in this study will provide baseline data for research on the population structure and development of effective plans for monitoring invasive and harmful polychaete species, *P. hoplura*. In addition, these data will be used for comparative molecular phylogenetic studies of shell-boring polychaetes infecting commercially valuable shellfish fisheries resources, abalone, oysters, mussels, and others.

요 약

전복 패각에 침입하여 피해를 입히는 천공성 다모류 (*Polydora hoplura*; Annelida) 의 mitochondrial genome (mitogenome) 을 next generation sequencing (NGS) 로 분석하였다. 이 mitogenome은 13개의 protein-coding genes, 2개의 ribosomal RNA genes, 23개의 transfer RNA genes 및 1개의 *trnM* gene으로 구성된 17,597 bp 크기로 확인되었다. *P. hoprula*의 유전자 구성과 순서는 다른 다모류와 구분되며, 같은 Spionidae에 속하는 *Marenzelleria neglecta*와도 달랐다.

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