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## The complete mitochondrial genome of a marine polychaete, *Prionospio* cf. *japonica* (Annelida: Spionidae)

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### ABSTRACT

*Prionospio* Malmgren 1867 is one of the abundant genera of the family Spionidae Grube, 1850. Despite its rich diversity, information on their complete mitochondrial genome has remained unknown. In this study, we determined the complete mitochondrial genome of a spionid polychaete, *Prionospio* cf. *japonica* Okuda 1935. The specimen was collected from the fine sand in the intertidal zone of South Korea. The mitogenome consists of 15,267 base pairs, harboring 13 protein-coding genes (PCGs), 22 transfer RNAs, and two ribosomal RNAs. The maximum-likelihood phylogenetic tree based on the 11 PCGs showed that *Prionospio* cf. *japonica* grouped with other spionid polychaetes and formed a monophyletic group. Also, the mtDNA of *P.* cf. *japonica* was more closely related to that of non-polydorin spionid, *Marenzelleria neglecta*, than polydorin spionids. The molecular data will be valuable for studying evolutionary relationships among annelids.

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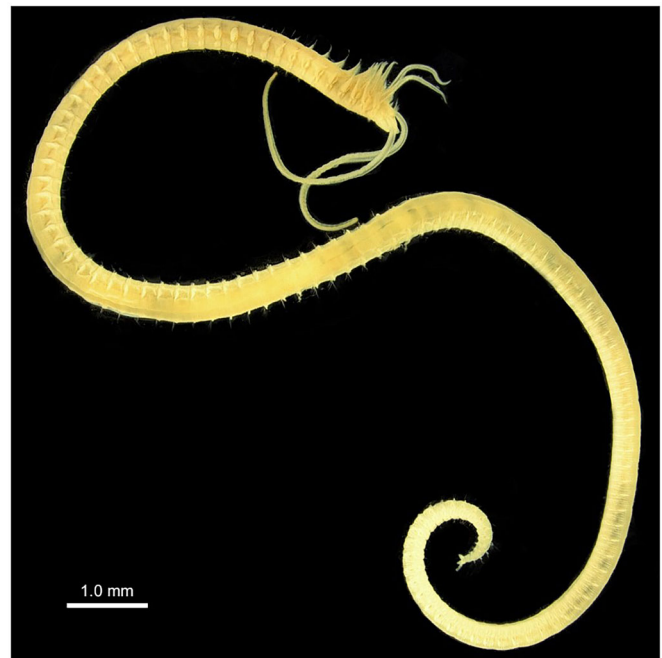
*Prionospio* cf. *japonica*;  
illumina sequencing;  
mitogenome; mtDNA;  
phylogeny; Korea

## 1. Introduction


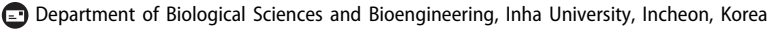
*Prionospio* Malmgren 1867 is one of the most diverse polychaetous annelid groups belonging to the family Spionidae Grube, 1850. More than 100 species are currently known worldwide (Read and Fauchald 2022). Among them, *P. japonica* Okuda 1935 was originally described in the brackish water of lakes on the southern coast of Japan. This species has been reported by several authors in Northeast Asia, including China, Japan, and Korea (Imajima and Hartman 1964; Paik 1975, 1982; Zhou and Li 2009; Lee et al. 2020). It is morphologically characterized by having four pairs of apinate branchiae (first branchiae distinctly long), prostomium truncates anteriorly with a small median peak, and hooded hooks with four to five pairs of small teeth above the main fang (Okuda 1935). Recently, Lee et al. (2020) determined the mitochondrial and nuclear gene fragments of *P. japonica* based on the specimens collected from the Yellow Sea, Korea. Later, Abe and Sato-Okoshi (2021) provided the molecular information of *P. japonica* collected from Sendai Bay, Japan.


Complete mitogenome sequences provide valuable evolutionary information (Chen et al. 2016). To date, the complete mitogenome sequences of five spionid species, *Boccardiella hamata* (Webster 1879) (Lee et al. 2021), *Marenzelleria neglecta* (Sikorski and Bick 2004; Gastineau et al. 2019), *Polydora brevipalpa* Zachs, 1933, *Polydora websteri* Hartman in

Loosanoff & Engle, 1943 (Ye et al. 2021), and *Polydora hoplura* (Claparède 1868; Lee and Lee 2022) have been reported. In this study, we determined the complete



**Figure 1.** Image of *Prionospio* cf. *japonica* Okuda 1935 (sample collected from the Yellow Sea of Korea in January 2021; photo by Geon Hyeok Lee).

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showed 8.1% difference in 16S rDNA. The levels of inter-specific differentiation in 16S rRNA are comparable to those observed among other polychaete species, which usually exceed 5% (Wiklund et al. 2009; Álvarez-Campos et al. 2017; Meißner et al. 2017). This result indicated that these are different species. Nevertheless, no morphological differences were observed between the Korean and Japanese specimens (Okuda 1935). Therefore, the authors referred to the Korean samples as *P. cf. japonica* in this study.

### 3.2. Genomic analysis results

The newly determined complete mitogenome of *P. cf. japonica* was 15,267 bp in length and contained 13 PCGs, 22 transfer RNAs (tRNAs), two ribosomal RNAs (rRNAs), and one control region (AT-rich region) (Figure 2). In the segment between *nad6* and *nad5*, there is a total of 500 bp inter-genic spacer that may correspond to the control region. The overall base composition of Korean *P. cf. japonica* is 32.4% A, 16.2% C, 16.2% G, and 35.3% T, revealing a G + C content of 32.4%.

### 3.3. Phylogenetic analysis

To infer the molecular phylogenetic relationships, a maximum-likelihood tree was constructed based on the concatenated nucleotide sequences of 11 protein-coding genes (*cox1*, *cox2*, *cox3*, *cytb*, *atp6*, *nad1*, *nad2*, *nad3*, *nad4*, *nad4l*, and *nad5*) from 16 annelids, including the mtDNA sequence obtained in the present study. The concatenated mtDNA sequences of *P. cf. japonica* were grouped with those of the other five species of the family Spionidae (*Boccardiella hamata*, *Marenzelleria neglecta*, *Polydora brevipalpa*, *Polydora hoplura*, and *Polydora websteri*) (Figure 3). *Prionospio cf. japonica* was more closely related to *Marenzelleria neglecta*, one of the non-polydorin spionids (worms without modified spines in the fifth chaetiger), than to the other four polydorin spionids in the analysis (worms with modified spines in the fifth chaetiger).

## 4. Conclusion

The assembled mitogenome of *P. cf. japonica* was 15,267 bp in length and contained 13 PCGs, 22 transfer RNAs, two ribosomal RNAs, and one control region. The phylogenetic analysis of 11 protein-coding genes showed that the sequences of the Korean *P. cf. japonica* were grouped with those of the other species belonging to the family Spionidae. The newly determined complete mitogenome provides valuable data for further taxonomic and phylogenetic studies.

### Ethical approval

This study did not involve endangered or protected species. All the experiments involving animal samples were approved by the animal care and use committee of Inha University (Incheon, South Korea).

### Author's contributions

GH Lee contributed to the sampling in the field, identified worms, performed DNA experiments, analyzed the data, and wrote the manuscript. G-S Min contributed to the design and draft of the manuscript and revising the final version of the manuscript.

All authors agreed to be accountable for all aspects of the work.

### Disclosure statement

The authors declare no conflicts of interest and are responsible for this study.

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### Data availability statement

The data supporting the findings of this study are openly available in the NCBI GenBank database (<https://www.ncbi.nlm.nih.gov/nucleotide/ON470577>) under accession no. ON470577. The associated BioProject, SRA, and Bio-Sample numbers were PRJNA823822, SRR18651217, and SAMN27361394, respectively.

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