A Draft Mitogenome of *Plectus murrayi*

Xia Xue[1,2,*], Byron J. Adams[2,3] and
Adler R. Dilman[4]

[1]Henan Key Laboratory of Helicobacter
pylori & Microbiota and Gastrointestinal
Cancer, Marshall Medical Research
Center, The Fifth Affiliated Hospital of
Zhengzhou University, Henan, China

[2]Department of Biology and
Evolutionary Ecology Laboratories,
Brigham Young University (BYU),
Provo, UT, USA

[3]BYU Life Science Museum,
Provo, UT, USA

[4]Department of Nematology,
University of California,
Riverside, CA, USA

*E-mail: xue-xiasophia@hotmail.com

This paper was edited by
Erik C. Andersen.

Received for publication
March 24, 2022.

Abstract

Plectus murrayi is a free-living microbivorous nematode endemic to Antarctic soils. Our draft assembly of its mitogenome was 15,656 bp long, containing 12 protein-coding, eight transfer RNA (tRNA), and two ribosomal RNA (rRNA) genes. Mitophylogenomic analyses extend our understanding of mitochondrial evolution in Nematoda

Keywords

Antarctica, genomics, genome decay, mitochondrial genome, MitoZ, phylogeny

Announcement

Plectus murrayi is a free-living, microbivorous, limnoterrestrial nematode endemic to the ice-free Antarctic soils (Andrassy, 1998). The Plectidae are of particular interest for resolving patterns and processes of nematode evolution because they are the sister taxon to the Rhabditida (Blaxter *et al*., 1998; Holterman *et al*., 2006; Blaxter and Koutsovoulos, 2015). Moreover, *P. murrayi's* high tolerance to environmental stresses (desiccation, freezing, high concentration of heavy metals, etc.) makes it a good model for discovering the limits of life and understanding mechanisms of extreme stress survival, including cryptobiosis (Nkem *et al*., 2005; Adhikari *et al*., 2009, 2010; Adhikari and Adams, 2011; Wharton and Raymond, 2015).

The genome of *P. murrayi* was extracted from a population of approximately 5,000 nematodes and sequenced using an Illumina 2000 Genome Analyzer IIx sequencer in a paired-end mode, as described previously (Xue *et al*., 2021). The mitogenome was assembled and annotated using MitoZ (V2.4) based on the genomic raw reads. The pipeline includes filtering, de novo assembly, HMMER (Hidden Markov Models) and protein-coding gene (PCG) annotation, and visualization using Circos (Meng *et al*., 2019). The resulting mitochondrial genome assembly was 15,652 bp in length. Twelve PCGs, two ribosomal RNA (rRNA) genes (r-rRNA and s-rRNA), and eight transfer RNA (tRNA) genes were identified in this mitogenome (Fig. S1 in Supplementary Material). The overall nucleotide composition was 26.80% A, 21.58% C, 21.55% G, and 25.01% T, and the G+C content was 45.30%. Most of the 12 PCGs used ATN as the start codon (ATT for COX1, COX2, COX3, ND1, ATP6, and CYTB; ATA for ND2, ND4, and ND5). ND4L, ND3, and ND5 began with the codon TTG. The stop codon TAA was assigned to most of the PCGs (COX2, ND1, ATP6, ND2, ND4, ND6, COX1, CYTB, ND5, and COX3), but an incomplete stop codon was used by two PCGs (ND3, and ND4L).

Mitochondrial genomes of other nematodes available from GenBank were used to perform mitophylogenomic analysis. A maximum-likelihood analysis using IQ-Tree software (Minh *et al.*, 2020) based on a matrix of aligned PCGs, tRNAs, and rRNAs by Clustal (Sievers *et al.*, 2011) confirms a monophyletic Plectidae as sister clade to the Rhabditida, with *P. murrayi* as sister to *P. acuminatus* and *P. aquatilis*.

This study provides an example of assembling and annotating nematode mitogenomes based on existing genomic data (Meng *et al.*, 2019). It is notable that we recovered fewer tRNA genes than expected, based on existing assemblies of *P. aquatilis* and *P. acuminatus* (Kim *et al.*, 2017). However, we note the absence of ATP8 (Supplementary Fig. S1), which is also missing from other nematode mitogenomes (Kim *et al.*, 2017). Loss of these genes could be an artifact of our analyses, but it is consistent with findings from the *P. murrayi* genome, which suggests that such losses by way of genome decay are an adaptive response to the harsh Antarctic environment (Xue *et al.*, 2021). Our work shows that mining and assembling mitogenomes from whole-genome data can be a powerful tool for understanding the evolution of mitochondria in Nematoda and, in particular, understanding adaptive variations of functional genes related to energy generation and allocation.

Data submission

Nucleotide accession numbers associated with this announcement are PRJNA317772 (BioProject) and SAMN04625768 (SAMN04625768) which are openly available in GenBank.

Acknowledgments

References

Adhikari, B. N., and Adams, B. J. 2011. Molecular analyses of desiccation survival in Antarctic nematodes. Wallingford: CABI, pp. 205–232.

Adhikari, B. N., Wall, D. H., and Adams, B. J. 2009. Desiccation survival in an Antarctic nematode: Molecular analysis using expressed sequenced tags. Bmc Genomics 10:18.

Adhikari, B. N., Wall, D. H., and Adams, B. J. 2010. Effect of slow desiccation and freezing on gene transcription and stress survival of an Antarctic nematode. Journal of Experimental Biology 213:1803–1812.

Andrassy, I. 1998. Nematodes in the Sixth Continent.

Blaxter, M. L., De Ley, P., Garey, J. R., Liu, L. X., Scheldeman, P., Vierstraete, A., Vanfleteren, J. R., Mackey, L. Y., Dorris, M., Frisse, L. M., Vida, J. T., and Thomas, W. K. 1998. A molecular evolutionary framework for the phylum nematoda. Nature 392:71–75.

Blaxter, M., and Koutsovoulos, G. 2015. The evolution of parasitism in Nematoda. Parasitology 142 (S1): S26-S39. doi:10.1017/S0031182014000791

Holterman, M., van der Wurff, A., van den Elsen, S., van Megen, H., Bongers, T., Holovachov, O., Bakker, J., and Helder, J. 2006. Phylum-wide analysis of SSU rDNA reveals deep phylogenetic relationships among nematodes and accelerated evolution toward crown clades. Molecular Biology and Evolution 23:1792–1800.

Kim, J., Kern, E., Kim, T., Sim, M., Kim, J., Kim, Y., Park, C., Nadler, S. A., and Park, J. K. 2017. Phylogenetic analysis of two *Plectus* mitochondrial genomes (Nematoda: Plectida) supports a sister group relationship between Plectida and Rhabditida within Chromadorea. Molecular Phylogenetics and Evolution 107:90–102.

Meng, G., Li, Y., Yang, C., and Liu, S. 2019. MitoZ: A toolkit for animal mitochondrial genome assembly, annotation and visualization. Nucleic Acids Research 47:e63–e63.

Minh, B. Q., Schmidt, H. A., Chernomor, O., Schrempf, D., Woodhams, M. D., von Haeseler, A., and Lanfear, R. 2020. IQ-TREE 2: New models and efficient methods for phylogenetic inference in the genomic era. Molecular Biology and Evolution 37:1530–1534.

Nkem, J. N., Virginia, R. A., Barrett, J. E., Wall, D. H., and Li, G. 2005. Salt tolerance and survival thresholds for two species of Antarctic soil nematodes. Polar Biology 29:643–651.

Sievers, F., Wilm, A., Dineen, D., Gibson, T. J., Karplus, K., Li, W., Lopez, R., McWilliam, H., Remmert, M., Söding, J., Thompson, J. D., and Higgins, D. G.

2011. Fast, scalable generation of high-quality protein multiple sequence alignments using Clustal Omega. Molecular Systems Biology 7:539.

Wharton, D. A., and Raymond, M. R. 2015. Cold tolerance of the Antarctic nematodes *Plectus murrayi* and *Scottnema lindsayae*. Journal of Comparative Physiology. B, Biochemical, Systemic, and Environmental Physiology 185:281–289.

Xue, X., Suvorov, A., Fujimoto, S., Dilman, A. R., and Adams, B. J. 2021. Genome analysis of Plectus murrayi, a nematode from continental Antarctica. G3 Genes|Genomes|Genetics 11:jkaa045.
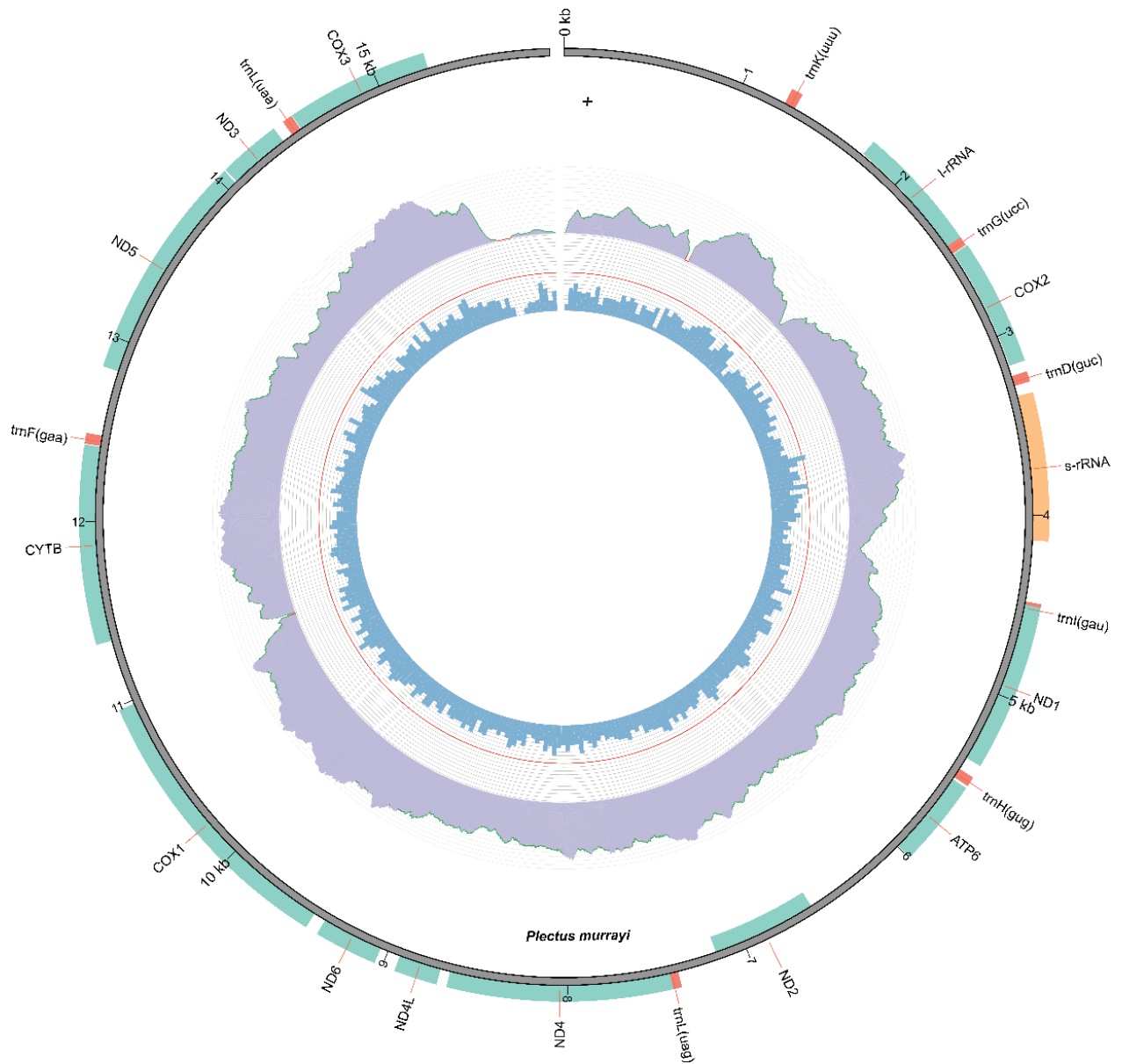
Supplementary Material

Figure S1: The Circos draft mitogenome of *Plectus murrayi* assembled based on MitoZ. The inner and outside of the circos refer to different directions of this draft mitogenome on which all genes were mapped.