

Complete mitochondrial genome of *Paralvinella palmiformis* (Polychaeta: Alvinellidae)

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ABSTRACT

We report the complete circular mitochondrial genome of the hydrothermal vent polychaete *Paralvinella palmiformis* (Annelida: Terebellida: Alvinellidae). The mitochondrial genome is 16386 bp in length with a GC content of 38.8%. It contains 36 genes, including 13 protein-coding sequences, 2 rRNA and 21 tRNA genes.

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The family Alvinellidae (Annelida:Terebellida, Desbruyères and Laubier 1986) contains 11 species all endemic to deep-sea hydrothermal vent ecosystems. Nine species are found in eastern Pacific Ocean, two in the western Pacific, and one in the Indian ocean (Desbruyères and Laubier 1989, 1993; Han et al. 2021). Interestingly, the alvinellid family includes several hyper-thermophilic species which live just centimeters away from hydrothermal discharge reaching up to 300 °C. This unique adaptation appears to have evolved multiple times in the group (Fontanillas et al. 2017) and is speculated to reduce resource competition. Indeed, hyperthermophile species are found in sympatry with other less thermo-tolerant species (Desbruyères and Laubier 1982; McHugh 1989; Dilly et al. 2012). The wide biogeographic distribution of these worms, despite the sporadicity of their habitat and their convergent adaptation to extreme thermal and oxygen conditions, raises questions about their evolutive history. Owing to a lack of genetic data, the alvinellid phylogeny is yet to be fully resolved. Furthermore, there are important knowledge gaps about the physiology of the mesophile species.

Here, we report the complete mitochondrial genome of *Paralvinella palmiformis* (Desbruyères & Laubier, 1986), which constitutes with the hyperthermophile *Paralvinella sulfincola* a well-studied model for thermal adaptation. These two species inhabit hydrothermal vents of the northeastern Pacific ocean and have a predator/scavenger lifestyle (Tunnicliffe et al. 1993; Grelon et al. 2006; Lelièvre et al. 2017) but they preferentially occupy different positions on the sulfide chimneys (Sarrazin et al. 1999). *Paralvinella sulfincola* builds mucous houses high on the sulfide accretions whereas *P. palmiformis* typically lives further away from the hydrothermal output.

Experimental evidence shows that *P. palmiformis* thermal preference is between 30 and 40 °C; about 10 °C lower than that of *P. sulfincola*. *P. palmiformis* also has a smaller thermal tolerance (0–45 °C vs. 2–63 °C for *P. sulfincola* (Dilly et al. 2012; Lee 2003; Rinke and Lee 2009)).

One *P. palmiformis* specimen was collected at Endeavor on the Juan de Fuca ridge (47.949993 N 129.096988 W; depth = –2197 m) with the ROV ROPOS during an expedition on board the GSS Tully in June 2016. DNA was extracted from the body wall tissues preserved in 95% ETOH with the phenol-chloroform method followed by ethanol precipitation (Sambrook et al. 1989) and purified with the Genomic DNA Clean & Concentrator-10 kit (ZYMO Research, CA, USA). DNA was then sent for sequencing on the Illumina NovaSeq and Oxford Nanopore platforms ultimately yielding 485973, and 5964 mitochondrial reads, respectively. The Illumina library was trimmed with trimmomatic v0.30 (Bolger et al. 2014) (parameters: leading = 10, trailing = 10, minlen = 50) and two rounds of binning with bbmap (Bushnell 2014) tool bbsplit.sh followed by assembly with SPAdes v3.11.1 (Bankevich et al. 2012) were used to recover a draft assembly of *P. palmiformis* mitogenome. The publicly available mitochondrial genomes of two closely-related species, *P. sulfincola* (FJ976042.1) and *P. hessleri* (MK192098.1), were used to recover mitochondrial reads in the first round.

Nanopore reads corrected with FMLRC v2 (Wang et al. 2018) were then mapped to the draft assembly with mini-map2 v2.17 (Li 2018), extracted with bbmap's filterbyname.sh tool, and assembled into a single circular chromosome (average coverage = 817) with Canu v2.1.1 (Koren et al. 2017). The final assembly was polished with one round of Pilon

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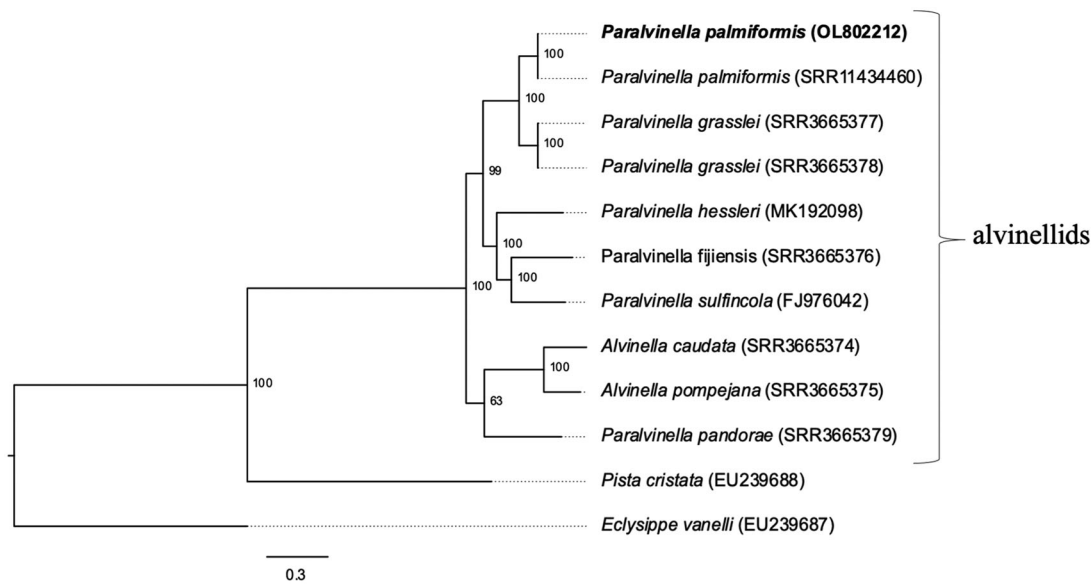


Figure 1. Maximum likelihood phylogeny (GTR nucleotide substitution model) using a 10,665 bp alignment of 12 mitochondrial protein coding genes. The outgroups are species of the polychaete families Terebellidae (*P. cristata*) and Amphraetidae (*E. vanelli*). The mitogenome sequenced in this study is indicated in bold. Numbers below nodes are the bootstrap values.

v1.23 (Walker et al. 2014). *P. palmiformis* mitochondrial genome is 16,386 bp in length with a GC content of 38.8%. Gene and tRNA predictions were performed in GeSeq using ARWEN v1.2.3 (Laslett and Canbäck 2008) for tRNA prediction and MitoS2 webserver (Bernt et al. 2013). The resulting annotations were manually curated in Geneious (Kearse et al. 2012). This mitochondrial genome was deposited in GenBank under the following accessions (BioProject: PRJNA786438, BioSample: SAMN23672631, Accession: OL802212). The *P. palmiformis* specimen and its DNA were deposited in the archives of the Deep-Sea Omics lab, Hong Kong University of Science and Technology under the accession P08H-3¹. Additional mitochondrial gene sequences from another *P. palmiformis* individual and from the species *A. caudata*, *A. pompejana*, *P. fijiensis*, *P. grasslei*, and *P. pandorae*, were recovered from transcriptomic data (Fontanillas et al. 2017; Stiller et al. 2020) by assembling the mitochondrial bins of their respective transcriptomes with Trinity and SPAdes.

The mitogenome of *P. palmiformis* has the same gene order and composition as *P. sulfincola* and *P. hessleri* with the exception of one tRNA which was not annotated in *P. hessleri*. The alvinellid phylogeny based on the concatenated alignment of 12 protein-coding genes (8,643 complete nucleotides, Figure 1) is consistent with all previously reported phylogenies based on genetic, morphologic and transcriptomic data for this group (Zhong et al. 2011; Fontanillas et al. 2017; Stiller et al. 2020) and places *P. palmiformis* as a sister species to *P. grasslei*, which is an alvinellid from the East Pacific Rise occupying a similar ecological niche (Figure 1). It is possible that the two species had speciated due to connectivity barriers created by the fragmentation of the Farallon plate spreading ridge about 30Mya (Tunnicliffe 1988). Concordance analyses with Bucky (Larget et al. 2010) revealed topological variation in two genomic regions, that is, from *cox2* to *cox3* and from *nad5* to *rrn5*. The maximum likelihood topology in these regions places *P. pandorae* as a taxon basal to all alvinellids

whereas *P. pandorae* is basal to the genus *Alvinella* according to the rest of the coding mitochondrial genome.

Ethical approval

No ethical approval was required because the study specimen does not belong to the list of regulated invertebrates.

Disclosure statement

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

Author contributions

MP designed the study, analyzed the data and drafted the manuscript, HW and BA critically revised the manuscript, P-YQ conceived the study and critically revised the manuscript. All authors have approved the final version of the paper and agreed to be accountable for all aspects of the work.

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Data availability statement

This mitochondrial genome was deposited in GenBank of NCBI under the following accessions (BioProject: PRJNA786438, BioSample: SAMN23672631, Accession: OL802212). The *P. palmiformis* specimen and its DNA were deposited in the archives of the Deep-Sea Omics lab, Hong Kong University of Science and Technology under the accession P08H-3 (contact: Eric Lau,

ericlw@ust.hk). Additional data that support the findings of this study (e.g., gene sequence alignments) are openly available at https://github.com/maepz/Ppalmiformis_mitogenome.

Note

1. Collection manager: Eric Lau, ericlw@ust.hk

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