

The complete mitochondrial genome of *Panopea abrupta* (Myoida: Hiatellidae)

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ABSTRACT

The geoduck clam *Panopea abrupta* (Myoida: Hiatellidae) is one of the most important freshwater aquaculture species in China. In spite of its economic importance, however, the genomic information of this species remains unavailable. In this study, we report the complete mitochondrial genome sequence of *P. abrupta* along with annotated and fully characterized mitochondrial genes. The genome was found to be 15,381 bp in length with a total of 38 genes (13 protein-coding, 22 transfer RNAs, and 2 ribosomal RNAs). The presence of a gene coding for ATPase subunit 8 was also noted. However, as expected in bivalves, the gene arrangements showed variations with that of the related species. This study adds to the repository of available mitogenomes of various Heterodonta and will greatly aid in future phylogenetic studies and species identification.

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The genus *Panopea* includes large marine bivalves known as geoducks, is one of the largest amongst filter-feeding burrowing bivalves. These clams are renowned for their extreme longevity and are reported to reach a record age of 168 years (Bureau et al. 2002). The geoduck clam, being widely cultivated in Southeast Asia and southeast coastal region in China, has great market demand in China. The species is characterized by the presence of sawtooth in front of the shell, which resembles a hypertrophic meat pipe. In spite of its commercial importance, adequate information about the genetic structure of geoduck clam population is still missing. Here, we report the complete mitochondrial genome sequence of *P. abrupta*, wishing to assist in molecular identification of this species and help improve the phylogenetic classification of the family *Hiatellidae*.

The adult specimen of *P. abrupta* (TA00523) was collected from Guangdong province, China, and stored at -80°C in Third Institute of Oceanography, State Oceanic Administration, Xiamen, China. The total genomic DNA was extracted from the muscle of the specimens using an SQ Tissue DNA Kit (OMEGA, Guangzhou, China) following the manufacturer's protocol. DNA libraries (500bp insert) were constructed with the TruSeq NanoTM kit (Illumina, San Diego) and were sequenced (100bp paired end reads) using HiSeq platform at Gene Denovo Company, China. CLC Genomics Workbench 7.0.3 (CLC bio, Boston, MA) was used for *de novo* assembly. Gene annotation was carried using MITOS (Bernt et al. 2013) and BLAST searches. Boundaries of structural and rRNA genes were resolved using other available bivalve mitochondrial sequences. The tRNA genes were identified by

Table 1. Detailed description of the 38 mitochondrial genes in *P. abrupta*.

Gene	Position	Length(bp)	Start codon	Stop codon
COXI	1–1563	1563	GTG	TAG
COXII	1865–2602	738	ATG	TAA
tRNA-Val	2613–2677	65		
tRNA-Thr	2680–2745	66		
tRNA-Tyr	2815–2876	62		
NAD4L	2887–3177	291	ATG	TAG
ATP8	3230–3343	114	ATG	TAA
NAD4	3507–4694	1188	ATG	TAG
tRNA-His	4713–4758	46		
tRNA-Glu	4759–4822	64		
tRNA-Ser2	4818–4880	63		
NAD3	4884–5249	366	ATG	TAG
tRNA-Ile	5249–5315	67		
tRNA-Asp	5325–5385	61		
tRNA-Lys	5393–5452	60		
tRNA-Leu2	5455–5519	65		
NAD1	5520–6443	924	ATG	TAG
tRNA-Leu	6445–6509	65		
tRNA-Asn	6542–6609	68		
NAD5	6611–8335	1725	ATG	TAA
NAD6	8335–8859	525	ATG	TAG
tRNA-Arg	8865–8925	61		
CYTB	8928–10085	1158	GTG	TAA
tRNA-Trp	10095–10161	67		
16S rRNA	10250–11306	1057		
ATP6	11307–12014	708	ATG	TAA
tRNA-Met	12022–12085	64		
12S rRNA	12087–12946	860		
COXIII	12947–13735	789	ATA	TAG
tRNA-Ser	13741–13805	65		
NAD2	13807–14853	1014	ATG	TAA
tRNA-Gln	14867–14932	66		
tRNA-Phe	14941–15003	63		
tRNA-Cys	15018–15082	65		
tRNA-Pro	15105–15171	67		
tRNA-Gly	15182–15247	66		
tRNA-Ala	15263–15327	65		

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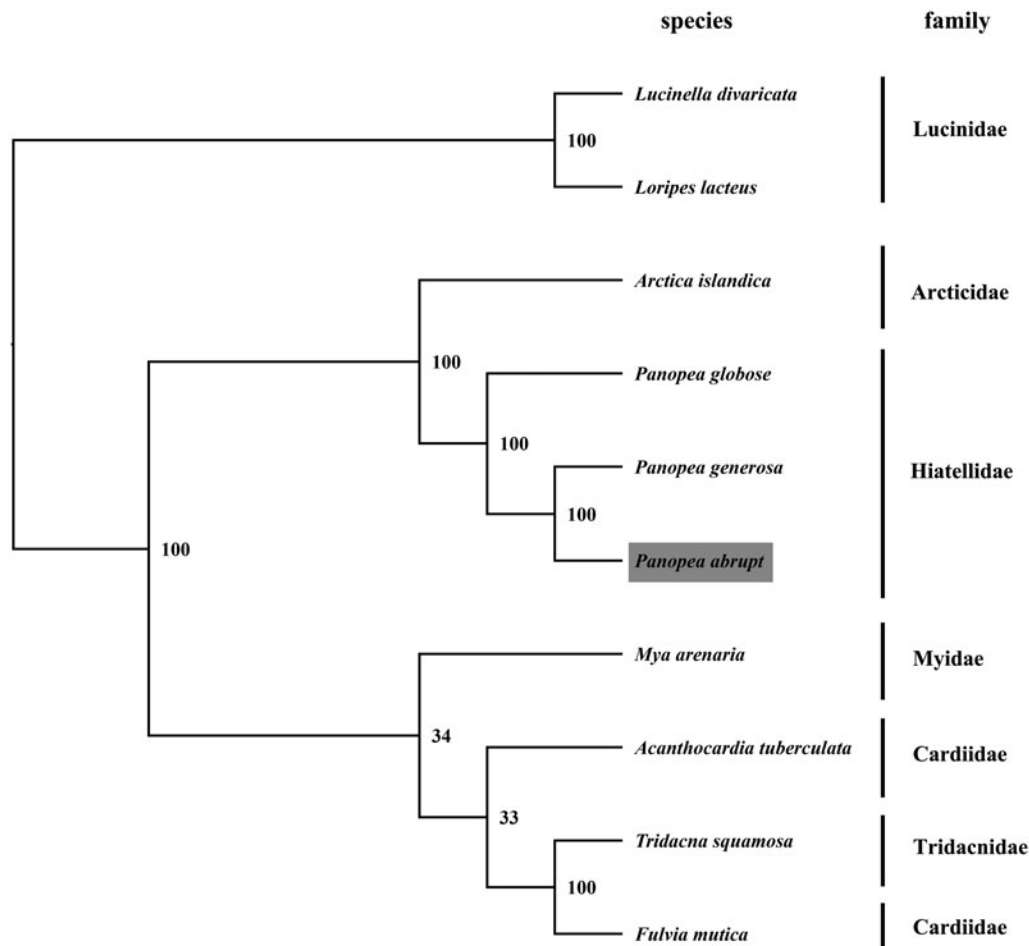


Figure 1. Phylogenetic tree of the complete mitogenomes. The phylogenetic tree is constructed by maximum-likelihood method with 500 bootstrap replicates. The GenBank accession numbers are as follows: *P. globosa* (NC_025636), *P. generosa* (NC_025635), *Mya arenaria* (NC_024738), *Lucinella divaricata* (NC_013275), *Loripes lacteus* (NC_013271), *Arctica islandica* (NC_022709), *Fulvia mutica* (NC_022194), *Tridacna squamosa* (NC_026558), and *Acanthocardia tuberculata* (NC_008452).

DOGMA (Wyman et al. 2004), MITOS, and t-RNA scan-SE Search Server (Lowe & Eddy 1997).

The complete mitogenome of *P. abrupta* was found to be 15,381 bp in length (GenBank accession no. KX494111), consisting of the usual set of 13 protein-coding, 22 tRNA, and 2 rRNA genes. The overall base composition of the mitogenome is: A 25.6%, T 38.78%, C 11.34%, and G 24.27% which is similar, but slightly different from *P. generosa* and *P. globosa* (Bisbal-Pardo et al. 2014a,b). In total, 3688 amino acids were encoded by the 13 identified protein-coding genes in *P. abrupta* mitochondrial genome. Leucine (14.72%) was found to be the most frequent amino acid, while Glutamine (1.18%) was the least prevalent. All protein-coding genes were found to use the initiation codon ATG except for *COXI*, *CYTB*, and *COXIII* genes, where GTG, GTG, and ATA served as the initiation codon, respectively. Twenty-nine intergenic spacers were found, ranging from 1 to 301 bp in length with the highest length recorded between *COXI* and *COXII* genes. The total length of non-coding region was calculated to be 880bp. Intergenic region was lacking between the gene pairs-tRNA-His/tRNA-Glu, tRNA-Leu2/NAD1, 16s rRNA/ATP6, and 12s rRNA/COXIII in addition to the overlapping bases between the structural gene tRNA-Glu/tRNA-Ser2, NAD3/tRNA-Illle, and NAD5/NAD6 (Table 1). The detailed description of 38

mitochondrial gene sequences characterized in *P. abrupta*, has been shown in Table 1, and the phylogenetic tree was constructed using maximum-likelihood method (Figure 1). The complete mitochondrial genome sequence of *P. abrupta* adds to the number of sequenced mitogenomes within the subclass Heterodonta and will aid the detailed phylogenetic studies undertaken henceforth.

Disclosure statement

The authors report no conflicts of interest. The authors alone are responsible for the content and writing of the paper.

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References

- Bernt M, Donath A, Jühling F, Externbrink F, Florentz C, Fritzsche G, Pütz J, Middendorf M, Stadler PF. 2013. MITOS: improved de novo metazoan mitochondrial genome annotation. *Mol Phylogenet Evol.* 69:313–319.

- Bisbal-Pardo CI, Del Río-Portilla MA, Rocha-Olivares A. 2014a. The complete mitochondrial DNA of the Pacific Geoduck clam (*Panopea generosa*). *Mitochondrial DNA*. 27:1955–1956.
- Bisbal-Pardo CI, Del Río-Portilla MA, Rocha-Olivares A. 2014b. Novel gene arrangement in the complete mitochondrial genome of the Cortes Geoduck (*Panopea globosa*). *Mitochondrial DNA Early Online*. 27:1957–1958.
- Bureau D, Hajas W, Surry NW, Hand CM, Dovey G, Campbell A. 2002. Age, size structure, and growth parameters of geoducks (*Panopea abrupta* Conrad, 1849) from 34 locations in British Columbia sampled between 1993 and 2000. *Canadian Technical Report of Fisheries and Aquatic Sciences* 2413. Nanaimo, BC: Fisheries and Oceans Canada; p. 84.
- Lowe TM, Eddy SR. 1997. tRNAscan-SE: a program for improved detection of transfer RNA genes in genomic sequence. *Nucleic Acids Res.* 25:955–964.
- Wyman SK, Jansen RK, Boore JL. 2004. Automatic annotation of organellar genomes with DOGMA. *Bioinformatics*. 20:3252–3255.