

MITOGENOME ANNOUNCEMENT

Complete mitochondrial genome of the Antarctic soft-shelled clam, *Laternula elliptica* (Bivalvia; Laternulidae)

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Abstract

The complete mitogenome of the Antarctic soft-shelled clam, *Laternula elliptica* was determined to be 14,622 bp in length, and to contain 13 protein coding genes (PCGs), 22 tRNA genes, and large (rrmL) and small (rrnS) rRNA genes. Its total A + T content is 55.09%. The *L. elliptica* mitogenome is the smallest one among those of bivalvia, due to the existence of relatively small intergenic non-coding sequences. All genes are transcribed from the light-strand as a template like bivalve taxa except Unionoidea.

Keywords

Antarctic, complete mitochondrial genome, *Laternula elliptica*

History

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The Antarctic bivalve *Laternula elliptica* (Bivalvia; Laternulidae) shows widespread geographic distribution in the Antarctic region and represents an important species in coastal water ecosystems, because it is sentinel organisms of slow growing and long-lived (>20 years) cold-water bivalve species (Stilwell & Zinsmeister, 1992). This is the case in the Antarctic soft-shelled clam, *L. elliptica* which is belonged to subclass Anomalodesmata (Runnegar, 1974). The current position of anomalodesmatans is regarded as a basal part of the Heterodonta. Until now, complete mitogenome of 35 species of bivalves are known in NCBI database, there is no report of the complete mitogenome of anomalodesmatans determined yet.

Specimens of *L. elliptica* were collected from intertidal zones in Marian Cove on Barton Peninsula, King George Island, West Antarctica (62°14'S, 58°47'W). We sequenced genomic DNA of *L. elliptica* using next-generation sequencing technologies (GSFLX) and assembled the total sequence information with a software Newbler (Roche, Basel, Switzerland), the assembled mitochondrial genome were completed with design the PCR primer and Long-PCR method. The complete mitogenome sequence of *L. elliptica* (GenBank accession number KF534717) was determined to be 14,622 bp in length containing 13 protein-coding genes (PCGs), 22 tRNA genes and large (*rrnL*) and small (*rrnS*) ribosomal RNA genes, as are found in most bivalves (Table 1).

The *L. elliptica* mitogenome is the smallest known among those of bivalves, due to the small intergenic non-coding sequences. The average mitochondrial genome size of 35 known bivalves is 18,542 bp (largest is *Placopecten magellanicus*: 32,115 nt; and smallest is *Cristaria plicata*: 15,708 nt) (La Roche et al., 1990; Lee et al., 2012). All of 13 PCGs are on the same strand. The nucleotide composition of this strand was 23.03% A (3368 bases), 32.05% T (4687), 19.88% C (2907)

Table 1. Mitogenome organization of *L. elliptica*.

Gene	Location ^a	Size (bp)	Start codon	Stop codon	Anti-codon
<i>nad2</i>	1–1023	1023	ATG	TAA	
<i>tRNA^{Ala}</i>	1033–1097	65			TGC
<i>nad5</i>	1099–2772	1674	ATG	TAA	
<i>atp8</i>	2785–2889	105	ATC	TAA	
<i>cox3</i>	2871–3684	814	ATG	T ^{-a}	
<i>cox2</i>	3685–4380	696	ATG	TAG	
<i>cytb</i>	4386–5523	1138	ATG	T ^{-a}	
<i>tRNA^{Cys}</i>	5524–5594	71			GCA
<i>cox1</i>	5595–7175	1581	GTG	TAG	
<i>tRNA^{Ile}</i>	7176–7242	67			GAT
<i>nad6</i>	7244–7720	477	ATG	TAA	
<i>tRNA^{Leu}</i>	7776–7841	66			TAA
<i>rrnL</i>	7842–8960	1119			
<i>rrnS</i>	8962–9804	843			
<i>nad1</i>	9805–10,716	912	ATT	TAG	
<i>tRNA^{Thr}</i>	10,706–10,770	65			TGT
<i>tRNA^{Trp}</i>	10,771–10,835	65			TCA
<i>tRNA^{Met}</i>	10,838–10,899	62			CAT
<i>tRNA^{Lys}</i>	10,903–10,965	62			TTT
<i>tRNA^{Val}</i>	10,968–11,030	63			TAC
<i>tRNA^{Ser}</i>	11,031–11,097	67			TGA
<i>nad4L</i>	11,098–11,370	273	ATG	TAG	
<i>tRNA^{Asp}</i>	11,373–11,431	59			GTC
<i>tRNA^{Tyr}</i>	11,432–11,493	62			GTA
<i>tRNA^{Arg}</i>	11,497–11,552	56			TCG
<i>tRNA^{Leu}</i>	11,554–11,618	65			TAG
<i>nad4</i>	11,721–13,052	1330	ATG	TAG	
<i>tRNA^{Gln}</i>	13,051–13,116	66			TTG
<i>tRNA^{Asn}</i>	13,117–13,187	71			GTT
<i>tRNA^{His}</i>	13,189–13,252	64			GTG
<i>tRNA^{Ser}</i>	13,255–13,322	68			TCT
<i>tRNA^{Pro}</i>	13,323–13,386	64			TGG
<i>tRNA^{Phe}</i>	13,388–13,455	63			GAA
<i>nad3</i>	13,452–13,790	339	GTG	TAA	
<i>tRNA^{Gly}</i>	13,793–13,857	63			TCC
<i>atp6</i>	13,859–14,554	696	GTG	TAA	
<i>tRNA^{Glu}</i>	14,559–14,621	63			TTC

^aTruncated termination codon.

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and 25.03% G (3660). The A + T base composition (55.09%) was higher than G + C (44.91%). Nine of the 13 PCGs in the *L. elliptica* mitogenome started with the orthodox ATG initiation codon, three with a GTG codon, one with an ATT codon, and one with an ATC codon. Putative translation stop codons for six of 13 genes are TAA and five genes are TAG (the *cox3* and *cytb* genes are truncated T-termination codon).

Declaration of interest

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