Mitochondrial DNA

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MITOGENOME ANNOUNCEMENT

Complete mitochondrial genome of *Ostrea denselamellosa* (Bivalvia, Ostreidae)

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Abstract

The complete mitochondrial (mt) genome of the flat oyster, *Ostrea denselamellosa*, was determined using Long-PCR and genome walking techniques in this study. The total length of the mt genome sequence of *O. denselamellosa* was 16,227 bp, which is the smallest reported Ostreidae mt genome to date. It contained 12 protein-coding genes (lacking of ATP8), 23 transfer RNA genes, and two ribosomal RNA genes. A bias towards a higher representation of nucleotides A and T (60.7%) was detected in the mt genome of *O. denselamellosa*. The rrnL was split into two fragments (3′ half, 711 bp; 5′ half, 509 bp), which seems to be the unique characteristics of Ostreidae mt genomes.

Keywords

Mitochondrial genome, *Ostrea denselamellosa*, Ostreidae

History

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The flat oyster, *Ostrea denselamellosa*, is a potential economically important species, naturally distributed in the subtidal zones along coasts of China, Japan and Korea (Xu & Zhang, 2008). In recent years, the natural populations of this species have decreased dramatically due to over-exploitation and environmental pollution (Chen et al., 2011). By now, attention has been paid to the studies on *O. denselamellosa*, including the culture methods, biological characteristics and so on (Chen et al., 2011; Insua & Thiriot-Quievreux, 1991). However, there is little molecular information about this species. In this study, we report the mitochondrial genome of *O. denselamellosa*. The findings will provide not only useful molecular markers for further studies in relation to population and conservation genetics of *O. denselamellosa*, but also insight into the genetic relationship among different species in the family Ostreidae.

One *O. denselamellosa* individual was collected from Jiaonan, Shandong Province, China. The total genomic DNA was extracted from adductor muscle by a modification of standard phenol-chloroform procedure (Li et al., 2002). The complete mitogenome of *O. denselamellosa* was sequenced using Long-PCR, followed by primer walking. The gene annotation was performed following the methods described by Yu & Li (2012).

The mitochondrial genome of *O. denselamellosa* is 16,227 bp in length (GenBank accession number: HM015199) which is the smallest reported Ostreidae mitogenome to date, containing 12 protein-coding genes (without ATP8), 23 tRNA genes, and 2 rRNA genes (Table 1). The A+T composition of *O. denselamellosa* mtDNA is 60.7%, lower than those of congeneric species *O. edulis* and *O. lurida* (64.9% and 65%; Danic-Tchaleu et al., 2011; Xiao et al., 2013). This pattern of base

Table 1. Organization of the mitochondrial genome of *O. denselamellosa*.

Gene	Sequence location	Size (bp)	Start codon	Stop codon	Intergenic region (bp)
COX1	1–1596	1596	ATG	TAA	8
trnG	1605–1671	67			130
COX3	1802–2681	880	ATG	T	0
trnI	2682–2748	67			8
trnT	2757–2821	65			8
trnE	2830–2896	67			−2
CYTB	2895–4055	1161	ATA	TAA	1
COX2	4057–4752	696	ATG	TAG	6
trnM1	4759–4821	63			6
trnS1	4828–4897	70			144
trmM2	5042–5104	63			0
trnS2	5105–5174	70			0
trnL1	5175–5241	67			1
trnP	5243–5306	64			0
rrnL 5’ half	5307–5896	590			32
ND2	5929–6927	999	ATG	TAA	37
trnC	6965–7026	62			3
trnY	7030–7092	63			0
ATP6	7093–7767	675	GTG	TAG	3
trnN	7771–7839	69			4
trnR	7844–7910	67			8
trnV	7919–7986	68			24
trnH	8011–8073	63			0
ND4	8074–9423	1350	ATG	TAA	0
rrnS	9424–10,441	1018			0
rrnL 3’ half	10,442–11,152	711			49
ND5	11,202–12,872	1671	ATG	TAA	−1
ND6	12,872–13,339	468	ATG	TAA	11
trnQ	13,351–13,416	66			0
ND3	13,417–13,770	354	ATA	TAA	−1
trnK	13,770–13,834	65			2
trnL2	13,837–13,902	66			1
trnF	13,904–13,971	68			12
trnA	13,984–14,048	65			78

(*continued*)

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Table 1. Continued

Gene	Sequence location	Size (bp)	Start codon	Stop codon	Intergenic region (bp)
ND1	14,127–15,059	933	ATG	TAA	1
ND4L	15,061–15,342	282	GTG	TAA	60
trnW	15,403–15,465	63			55
trnD	15,521–15,588	68			689

composition holds for the protein-coding, rRNA, and tRNA genes, as well as the main NC region (MNR). All the protein-coding genes (PCG) are encoded on and transcribed from the same strand. The majority of PCGs (10 of 12 genes) start with ATG/ATA, while ATP6 and ND4L initiate with GTG. Eleven PCGs are terminated by a stop codon (TAA/TAG), while COX3 has an incomplete stop codon (T−−). The most frequently used amino acid is Leu (13.4%) and Arg is the least frequent (1.9%). UUU (Phe) and CGC (Arg) are the most and least frequently used codon in *O. denselamellosa* (6.2 and 0.11%, respectively). In total, 23 tRNA coding genes were identified in the size range of 62 to 70 bp with an additional trnM. The rrnL is split into two fragments (3′ half, 711 bp; 5′ half, 509 bp), which seems to be the unique characteristic of Ostreidae mitogenomes and has not been detected in other animal mitogenomes so far. *Ostrea denselamellosa* mitogenome includes a large number of non-coding nucleotides (1504 bp), with six intergenic regions larger than 50 bp, of which the MNR is 689 bp.

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Declaration of interest

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

References

Chen L, Li Q, Wang QZ, Kong LF, Zheng XD. (2011). Techniques of artificial breeding of the oyster *Ostrea denselamellosa*. Period Ocean Univ China 41:43–6.

Danic-Tchaleu G, Heurtebise S, Morga B, Lapègue S. (2011). Complete mitochondrial DNA sequence of the European flat oyster *Ostrea edulis* confirms Ostreidae classification. BMC Res Notes 4:400.

Insua A, Thiriot-Quievreux C. (1991). The characterization of *Ostrea denselamellosa* (Mollusca, Bivalvia) chromosomes: Karyotype, constitutive heterochromatin and nucleolus organizer regions. Aquaculture 97:317–25.

Li Q, Park C, Kijima A. (2002). Isolation and characterization of microsatellite loci in the Pacific abalone, *Haliotis discus hannai*. J Shellfish Res 21:811–15.

Xiao S, Wu X, Li L, Yu Z. (2013). Complete mitochondrial genome of the Olympia oyster *Ostrea lurida* (Bivalvia, Ostreidae). Mitochondrial DNA. [Epub ahead of print]. doi: 10.3109/19401736.2013.834428.

Xu F, Zhang S. (2008). An illustrated Bivalvia Mollusca fauna of China seas. Beijing: Science Press.

Yu H, Li Q. (2012). Complete mitochondrial DNA sequence of *Crassostrea nippona*: Comparative and phylogenomic studies on seven commercial *Crassostrea* species. Mol Biol Rep 39:999–1009.