

MITOGENOME ANNOUNCEMENT

The complete mitochondrial genome of *Octopus conispadiceus* (Sasaki, 1917) (Cephalopoda: Octopodidae)Yuanyuan Ma¹, Xiaodong Zheng¹, Rubin Cheng², and Qi Li¹¹Laboratory of Shellfish Genetics and Breeding, Fisheries College, Ocean University of China, Qingdao, China and ²College of Pharmaceutical Science, Zhejiang Chinese Medical University, Hangzhou, China

Abstract

In this paper, we determined the complete mitochondrial genome of *Octopus conispadiceus* (Cephalopoda: Octopodidae). The whole mitogenome of *O. conispadiceus* is 16,027 basepairs (bp) in length with a base composition of 41.4% A, 34.8% T, 16.1% C, 7.7% G and contains 13 protein-coding genes, 2 ribosomal RNA genes, 22 transfer RNA genes, and a major non-coding region (MNR). The gene arrangements of *O. conispadiceus* showed remarkable similarity to that of *O. vulgaris*, *Amphioctopus fangsiao*, *Cistopus chinensis* and *C. taiwanicus*.

Keywords

Mitochondrial genome, Octopus, *Octopus conispadiceus*

History

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Octopus conispadiceus (Sasaki, 1917) is a shallow water octopus, belonging to the family Octopodidae. *O. conispadiceus* has a broad distribution, ranging from the Northwestern Pacific off northern Japan and Kuril Islands, and is generally associated with sandy to muddy substrates (Norman et al., 2013). This species reaches maturity quickly, has a short lifespan (<2 years), and a high reproductive output, laying one thousands of eggs at a time and now it has become the second most common species in Hokkaido markets after *Enteroctopus dofleini* (Norman et al., 2013). Unfortunately, numbers of *O. conispadiceus* have been decreasing in recent years which have been attributed to decreasing reproductive output and over exploitation from fisheries. Molecular data is required to help understand the potential source of declining numbers of *O. conispadiceus*. To date, only five entire mitochondrial genomes of Octopodidae, which is by far the most diverse major group of Cephalopoda, have been determined (Akasaki et al., 2006; Cheng et al., 2012, 2013; Yokobori et al., 2004). This report will also provide useful molecular markers for further studies in relation to population genetics and phylogenetics of the marine mussels within the family Octopodidae.

In this study, the complete mitochondrial (mt) genome of a single *Octopus conispadiceus* was sequenced and annotated. The sample was collected from Haishenwai, Amur Bay, Russia. Primers were designed according to the mitogenome sequence of *O. minor* (AB240156), *Cistopus taiwanicus* (NC_023257) and *C. chinensis* (KF017606). The sequence was deposited in the GenBank database under Accession No. KJ789854.

The complete mitochondrial genome of *Octopus conispadiceus* was 16,027 bp in length and encoded 13 protein-coding genes (PCGs), 2 ribosomal RNA genes, 22 transfer RNA genes

and 1 major non-coding region (MNR) which was 971 bp in length (Table 1). The mitogenome was similar in length to already sequenced molluscan mitogenomes. Seven out of thirteen proteins are encoded by the H-strand, while the other six proteins, as well as the two ribosomal RNAs were encoded by L-strand. The overall A + T content in the sense strands of the protein genes (76.2%) was slightly higher than *O. minor* (75.5%) and the coding

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

Gene	Position	Size Nucleotides (bp)	Amino acids	Codon			IGN*
				Start	Stop	Strand	
<i>cox3</i>	1–786	786	262	ATA	TAA	H	971
<i>trnK(ttt)</i>	800–865	66				H	13
<i>trnA(tgc)</i>	866–935	70				H	0
<i>trnR(tcg)</i>	939–1003	65				H	3
<i>trnN(gtt)</i>	1005–1072	68				H	1
<i>trnI(gat)</i>	1073–1141	69				H	0
<i>nad3</i>	1136–1492	357	119	ATA	TAA	H	–6
<i>trnS1(gtc)</i>	1491–1559	69				H	4
<i>nad2</i>	1542–2597	1056	352	ATA	TAA	H	–18
<i>cox1</i>	2569–4101	1533	511	ATG	TAA	H	–29
<i>cox2</i>	4101–4796	696	231	ATA	TAA	H	–1
<i>trnD(gtc)</i>	4798–4864	67				H	1
<i>atp8</i>	4845–5021	177	59	ATA		H	–20
<i>atp6</i>	5011–5715	705	235	ATA	TAG	H	–11
<i>trnF(gaa)</i>	5742–5808	67				L	44
<i>nad5</i>	5780–7501	1722	574	ATG	TAA	L	–29
<i>trnA(gtg)</i>	7502–7566	65				L	0
<i>nad4</i>	7567–8907	1341	447	ATA	TAG	L	9
<i>nad4l</i>	8904–9209	306	102	ATA	TAG	L	–4
<i>trnT(tgt)</i>	9205–9269	65				H	–5
<i>trnS2(tga)</i>	9278–9342	65				L	8
<i>cob</i>	9341–10,486	1146	382	ATA	TAG	L	–2
<i>nad6</i>	10,473–10,985	513	171	ATG	TAG	L	–14
<i>trnP(tgg)</i>	10,987–11,054	68				L	1
<i>nad1</i>	11,056–12,003	948	316	ATA	TAA	L	1
<i>trnL2(taa)</i>	12,001–12,074	74				L	–3

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(continued)

Table 1. Continued

Gene	Position	Size Nucleotides (bp)	Amino acids	Codon		Strand	IGN*
				Start	Stop		
<i>trnL(tag)</i>	12,095–12,160	66				L	20
<i>rrnL</i>	12,137–13,520	1384				L	–24
<i>trnV(tac)</i>	13,537–13,604	68				L	16
<i>rrnS</i>	13,612–14,556	945				L	7
<i>trnM(cat)</i>	14,567–14,634	68				L	10
<i>trnC(gca)</i>	14,649–14,712	64				L	–136
<i>trnY(gta)</i>	14,713–14,777	65				L	0
<i>trnW(tca)</i>	14,778–14,846	69				L	0
<i>trnQ(ttg)</i>	14,847–14,914	68				L	0
<i>trnG(tcc)</i>	14,921–14,986	66				L	6
<i>trnE(ttc)</i>	14,988–15,055	68				L	1

*Intergenic nucleotide: negative number indicates that adjacent genes overlap. For each tRNA genes anticodons are presented in parentheses.

regions were 14,636 bp in length accounting for 91.3% of the whole mt genome. Four protein-coding genes initiated with standard initiation codon ATA (*cox1-3*, *atp6*, *atp8*, *cob* and *nad1-4*), while *nad5* and *nad6* started with ATG. Thirteen genes terminated open reading frames with a complete stop codon, either TAA (*cox1-3*, *nad1-3*, *atp6* and *atp8*) or TAG (*cob*, *nad4*, *nad4l* and *nad6*). All tRNA genes have the typical cloverleaf structure, which lengths range from 64 to 70 bp. The nucleotides content composition of tRNA regions in *O. conispadiceus* was especially A + T rich (65.7% to 85.9%). The size of *12S rRNA* and *16S rRNA* were 945 bp and 1384 bp, a typical DNA structure of the octopus mitochondrial genomes.

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Declaration of interest

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