

# The complete mitochondrial genome of *Dosinia japonica* (Bivalvia: Veneridae)

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**Abstract** *Dosinia japonica* is a marine bivalve mollusk of the family Veneridae, which is distributed in coastal areas of China, Korean peninsula, Japan, and Russia. In this study, the complete mitochondrial genome of the clam *D. japonica* was determined firstly. It is 17,693 bp in length, including 13 protein-coding genes, 2 ribosomal RNAs, 22 transfer RNAs, and a major non-coding control region. Phylogenetic analyses indicated that *D. japonica* was the sister group of Tapetinae clade, which means Dosininae and Tapetinae have a common ancestor. This report provides molecular biology data for the conservation and management of *D. japonica* in future.

**Keywords** *Dosinia japonica* · Veneridae · Mitochondrial genome · Conservation

The bivalve *Dosinia japonica* belongs to the family Veneridae, which inhabits from intertidal zone to muddy sediments of the shallow coastal (Liu et al. 2010). It distributes in coastal areas of China, Korean peninsula, Japan, and the Russian Far East. In recent years, the natural population of *D. japonica* have declined remarkably due to over-exploitation (Zhang et al. 2013). Therefore, it is necessary to create a valid conservation strategy. Now, there is very little molecular information about this species, while the complete mitochondrial DNA sequences could be informative at deep phylogenetic levels (Curole and Kocher 1999). In this study, we sequenced and annotated the complete mitochondrial

genome of *D. japonica* firstly, and examine the phylogenetic position of *D. japonica* within Veneridae to provide the basic data for conservation genetics.

A live individual of *D. japonica* sample was collected from the coastal water of Ganyu, Jiangsu Province, China. The total genomic DNA was extracted from adductor muscle by a modification of the standard phenol–chloroform procedure described by (Li et al. 2002). The complete mitochondrial genome of *D. japonica* was sequenced using long-PCR technique. All sequence data were sequenced and annotated following the methods described by Yuan et al. (2012).

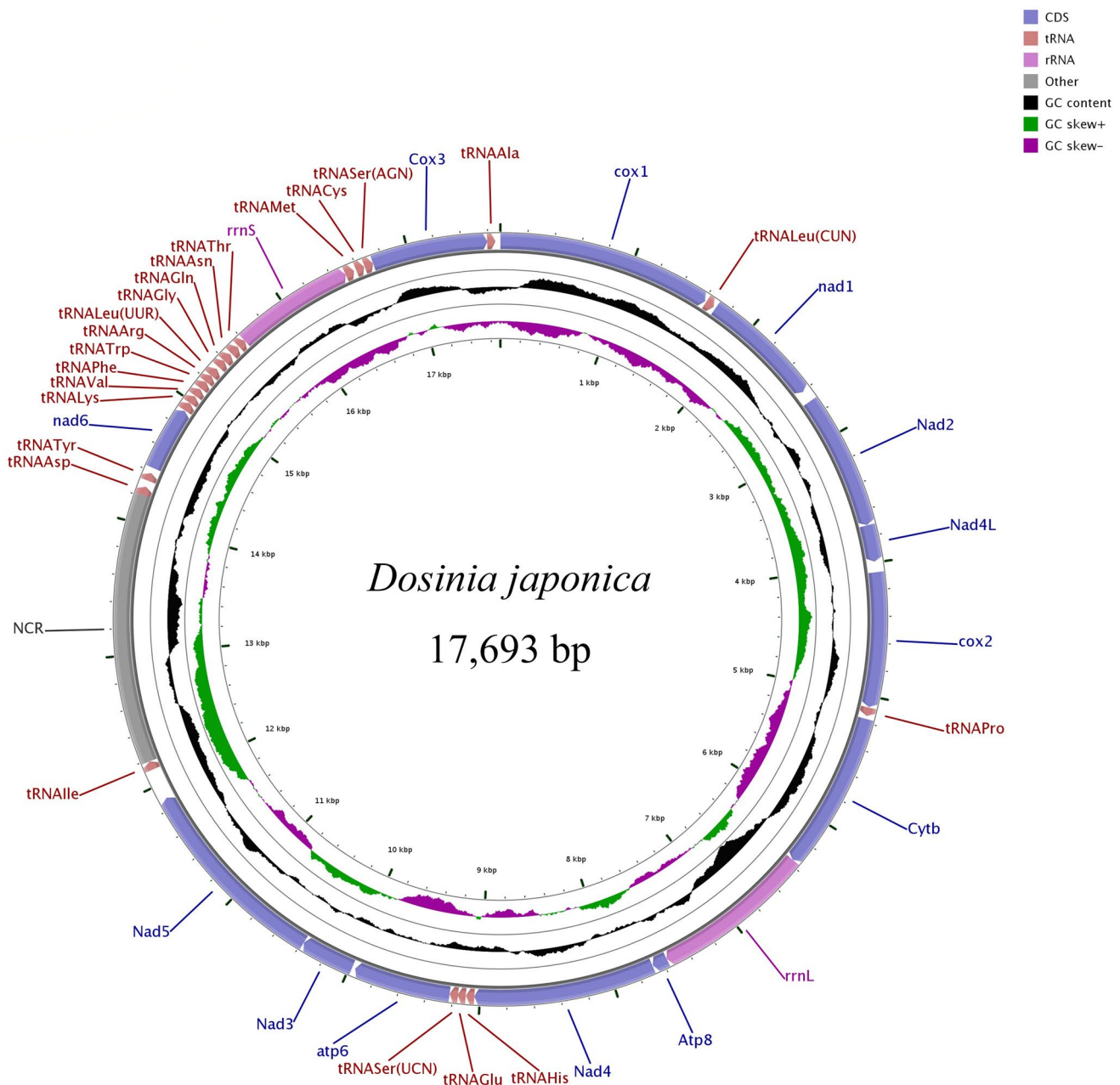
The complete mt genome of *D. japonica* is 17,693 bp in length (GenBank accession no. MF401432) containing 13 protein-coding genes (PCGs), 2 rRNA genes and 22 tRNA genes (Fig. 1). All 37 genes of *D. japonica* were encoded on the (+) strand. The overall base composition for the mt genome sequence of *D. japonica* was as follows: A=28.21%, C=9.12%, G=20.91%, T=41.76%. The A+T content of the PCGs, rRNAs, tRNAs and non-coding regions (NCRs) was 68.2%, 72.02%, 72.23% and 74.56%, giving a total A+T content of 69.97% in the whole mitochondrial genome. The nucleotide compositions of the entire *D. japonica* mtDNA indicate the occurrence of more T and A than G and C (AT skew, -0.1936; GC skew, 0.3926).

Total length of the 13 protein coding genes is 11,478 bp, eight of the 13 protein coding genes start with ATA or ATG, meanwhile, *co2*, *nad2*, *nad3* genes start with the alternative start codon GTG, and the *Cytb* gene starts with a ATT codon. Eight genes are terminated by TAA, but *cox1*, *nad1*, *cox2*, *nad4* and *cox3* by TAG (Table 1).

The *rrnL* and *rrnS* genes are 1203 and 902 bp in length, respectively. There are 22 typical tRNA genes in the mt genome of *D. japonica*, which range from 61 to 68 bp. The mt genome of *D. japonica* contained 25 non-coding regions ranging in size from 1 to 2027 bp. The total length of all

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**Fig. 1** Complete mitochondrial genome of *Dosinia japonica*

non-coding regions was 2708 bp, accounting for 15.31% of the complete mtDNA. The major non-coding region is 2027 bp, which located between *tRNA<sup>Ile</sup>* and *tRNA<sup>Asp</sup>* with an AT content of 54%. The major non-coding region included a 75 bp repeat motif, and one point nine copies were found in it (location: 12,654–12,728, and 12,729–12,792).

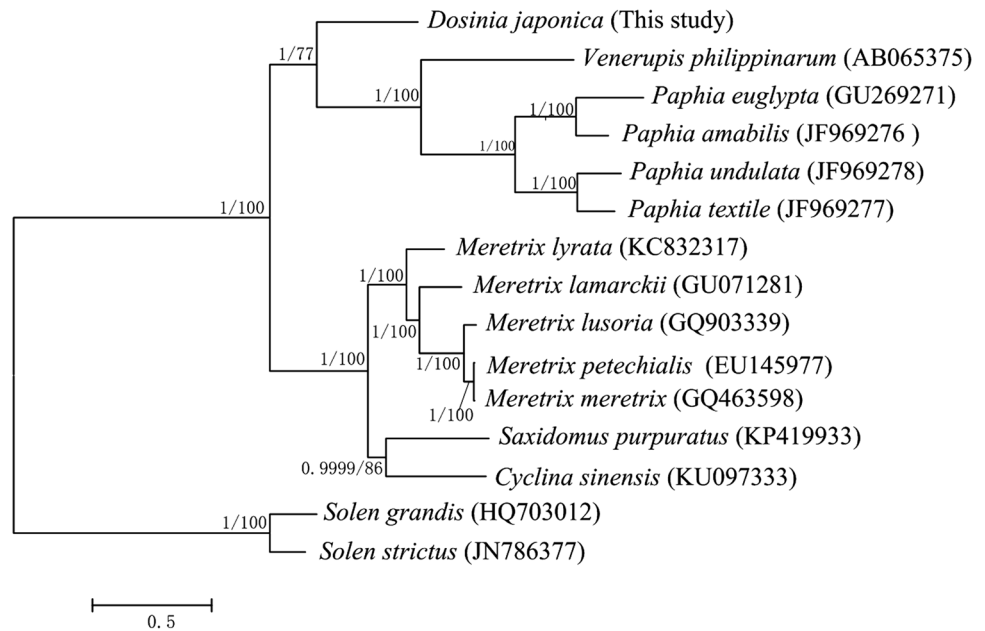
To identify the taxonomic position of *D. japonica* in the family Veneridae, the nucleotide sequences of 12 concatenated protein-coding genes (except *atp8* gene) of another 12 members of the family were downloaded from GenBank to reconstruct the phylogenetic relationships.

Phylogenetic trees were reconstructed using Maximum-likelihood (ML) analysis and Bayesian inference (BI) approaches. The ML analysis was conducted with PhyML 3.0 (Guindon et al. 2010) and 100 bootstraps were used to assess the support of nodes. BI was performed using MrBayes 3.1.2 (Ronquist and Huelsenbeck 2003). The topological structure showed that the results of ML and BI trees were in almost complete agreement (Fig. 2). This indicates that *D. japonica* formed a single branch as the sister group of Tapetinae clade, which is consistent with the findings of Chen et al. (2011).

**Table 1** Organization of the mitochondrial genome of *D. japonica*

Gene	From	To	Size (bp)	Start	Stop	Intergenic nucleotide
<i>cox1</i>	1	1608	1608	GTG	TAG	37
<i>tRNA<sup>Leu(CUN)</sup></i>	1619	1684	66			10
<i>nad1</i>	1702	2607	906	ATG	TAG	17
<i>nad2</i>	2695	3714	1020	GTG	TAA	87
<i>nad4l</i>	3717	3992	276	ATA	TAA	2
<i>cox2</i>	4071	5081	1011	GTG	TAG	78
<i>tRNA<sup>Pro</sup></i>	5086	5150	65			4
<i>cytb</i>	5173	6363	1191	ATT	TAA	22
<i>rrnL</i>	6364	7566	1203			0
<i>atp8</i>	7567	7680	114	ATG	TAA	0
<i>nad4</i>	7684	9042	1359	ATG	TAG	3
<i>tRNA<sup>His</sup></i>	9042	9103	62			-1
<i>tRNA<sup>Glu</sup></i>	9106	9166	61			2
<i>tRNA<sup>Ser(UCN)</sup></i>	9164	9226	63			-3
<i>atp6</i>	9227	9955	729	ATG	TAA	0
<i>nad3</i>	9980	10,384	405	GTG	TAA	24
<i>nad5</i>	10,385	11,887	1503	ATA	TAA	0
<i>tRNA<sup>Ile</sup></i>	12,122	12,186	65			234
<i>tRNA<sup>Asp</sup></i>	14,214	14,279	66			2027
<i>tRNA<sup>Tyr</sup></i>	14,327	14,388	62			47
<i>nad6</i>	14,429	14,914	486	ATG	TAA	40
<i>tRNA<sup>Lys</sup></i>	14,919	14,984	66			4
<i>tRNA<sup>Val</sup></i>	14,986	15,047	62			1
<i>tRNA<sup>Phe</sup></i>	15,053	15,114	62			5
<i>tRNA<sup>Trp</sup></i>	15,121	15,183	63			6
<i>tRNA<sup>Arg</sup></i>	15,184	15,244	61			0
<i>tRNA<sup>Leu(UUR)</sup></i>	15,245	15,309	65			0
<i>tRNA<sup>Gly</sup></i>	15,329	15,390	62			15
<i>tRNA<sup>Gln</sup></i>	15,391	15,457	67			0
<i>tRNA<sup>Asn</sup></i>	15,468	15,534	67			10
<i>tRNA<sup>Thr</sup></i>	15,543	15,604	62			8
<i>rrnS</i>	15,605	16,506	902			0
<i>tRNA<sup>Met</sup></i>	16,507	16,574	68			0
<i>tRNA<sup>Cys</sup></i>	16,592	16,655	64			17
<i>tRNA<sup>Ser(AGN)</sup></i>	16,660	16,726	67			4
<i>cox3</i>	16,727	17,596	870	ATG	TAG	0
<i>tRNA<sup>Ala</sup></i>	17,595	17,656	62			-2

**Fig. 2** Phylogenetic trees of *Dosinia japonica* based on the nucleotide sequences of 12 concatenated protein-coding genes, using *Solen grandis* and *Solen strictus* as the outgroup taxa. The first number at each node is Bayesian posterior probability and the second number is ML bootstrap values



The complete mitochondrial genome sequenced here will be useful for population genomic studies of *D. japonica*, which will play an important role in formulating new conservation and management strategies.

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