

MITOGENOME ANNOUNCEMENT



The complete mitochondrial genome and phylogenetic analysis of *Spondylus violaceus*

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ABSTRACT

Spondylus violaceus is a species of the bivalve family Spondylidae, commonly known as thorny oyster. Here, we report the complete mitochondrial genome of *S. violaceus*. The mitochondrial genome of *S. violaceus* is 30,160 bp in length, which contains 12 protein-coding genes, 2 ribosomal RNA genes and 19 transfer RNA genes. The overall AT content (58.31%) was higher than GC content (41.69%). This is the first record of complete mitochondrial genome in the family Spondylidae, providing the basis for future taxonomic and phylogenetic studies of this bivalve family.

ARTICLE HISTORY

Received 26 July 2019
Accepted 3 August 2019

KEYWORDS

Spondylus violaceus;
mitochondrial genome;
phylogenetic analysis

Spondylus violaceus belongs to the genus *Spondylus* within the bivalve family Spondylidae, which is commonly known as thorny oyster due to its similar appearance to oysters and long spines on the shells (Koyama et al. 2006). Mitochondrial DNAs have been extensively used for studying population structure, phylogeography and phylogenetic relationships at various taxonomic levels (Curole and Kocher 1999; Saccone et al. 1999). To date, the mitochondrial genomes of nearly 200 bivalve species have been sequenced and annotated, none of which came from the family Spondylidae. In this study, we successfully assembled and annotated the mitochondrial genome of *S. violaceus*, representing the first complete mitochondrial genome in the family Spondylidae.

The sample of *S. violaceus* was collected from Tung Ping Chau Bay near Tung Chung village (Guangdong province, China). The DNA sample of *S. violaceus* was extracted by using phenol/chloroform/isoamyl alcohol method (Sambrook et al. 1989). The DNA sample was deposited at the Key Laboratory of Marine Genetics and Breeding (Ministry of Education), Ocean University of China (Specimen code: OUC-MGB-2018-SF-07). Whole genomic sequencing (WGS) of this sample was performed using the Illumina NovaSeq 6000 sequencing platform. We assembled the mitochondrial genome based on the WGS data using the software NOVOPlasty (Dierckxsens et al. 2017). The genome sequence was further analyzed using MITOS software (Bernt et al. 2013) to retrieve gene information.

The complete mitogenome of *S. violaceus* was 30,160 bp in length and encoded 12 protein-coding genes (PCGs), 2 rRNAs and 19 tRNAs, lacking the *atp8* gene as in most bivalves (Wu et al. 2009). The mitogenome sequence was submitted to the GenBank under the accession number of MN019127. The 12 PCGs were cytochrome oxidase subunit (I, II, III), NADH dehydrogenase subunit (1, 2, 3, 4, 5, 6 and 4 L), ATP synthase subunit (6), and cytochrome b apoenzyme. The small subunit ribosomal RNA (12S rRNA) and large subunit ribosomal RNA (16S rRNA) were annotated with sizes of 879 and 1726 bp, respectively. The length of 19 tRNAs ranged from 65 bp to 75 bp. The overall base composition of the mitochondrial genome was 22.46% for A, 35.85% for T, 28.65% for G, and 13.04% for C, demonstrating a bias of higher AT content (58.31%) than GC content (41.69%). All genes of *S. violaceus* were encoded on the same strand, consistent with previous findings for most bivalves (Milbury and Gaffney 2005; Xu et al. 2011).

To assess the phylogenetic relationship of *S. violaceus*, we downloaded the mitochondrial genome sequences of 20 species (representing five orders under the subclass Pteriomorphia) from NCBI database to construct genome-wide sequence alignment. A phylogenetic tree was constructed by the neighbor-joining (NJ) algorithm with 1000 bootstrap trials. Despite the morphological resemblance with oysters, the phylogenetic tree provided strong molecular evidence that *S. violaceus* belongs to the order Pectinoida (Figure 1),

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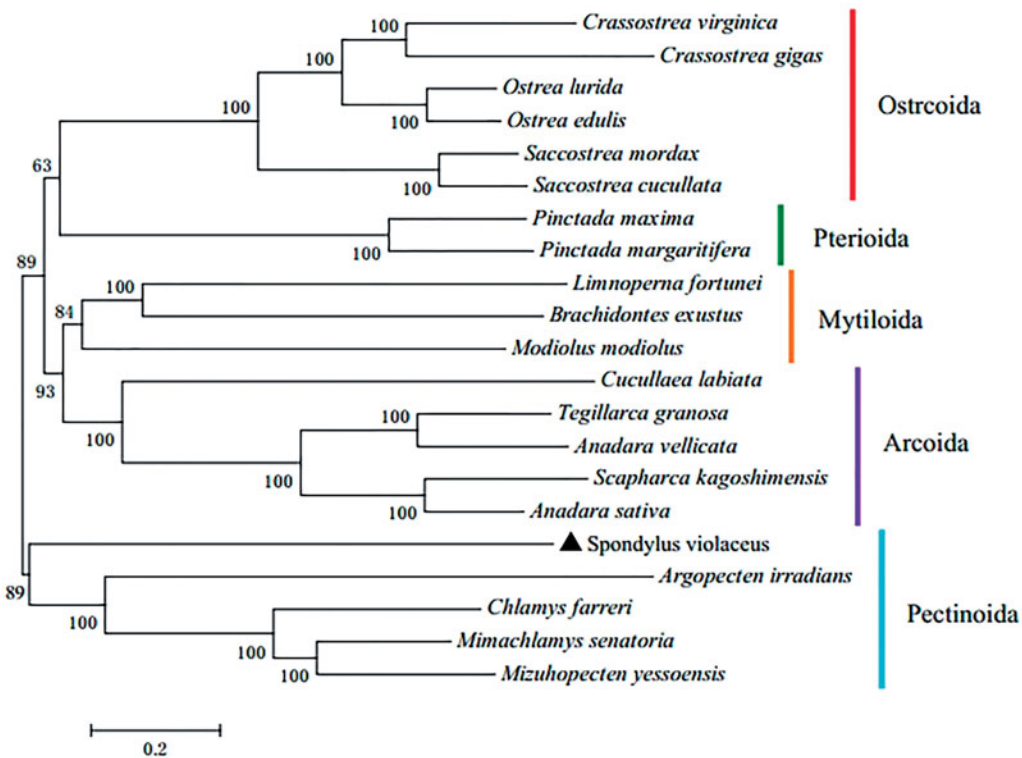


Figure 1. The phylogenetic tree of *S. violaceus* and 20 other bivalves based on complete mitochondrial genomes. The accession numbers of downloaded sequences are as follows: *Crassostrea virginica* (AY905542.2), *Crassostrea gigas* (NC_001276.1), *Ostrea lurida* (NC_022688.1), *Ostrea edulis* (JF274008.1), *Saccostrea mordax* (FJ841968.1), *Saccostrea cucullata* (NC_027724.1), *Pinctada maxima* (NC_018752.1), *Pinctada margaritifera* (NC_021638.1), *Limnoperna fortunei* (NC_028706.1), *Brachidontes exustus* (NC_024882.1), *Modiolus modiolus* (NC_033537.1), *Cucullaea labiata* (NC_029848.1), *Tegillarca granosa* (NC_026081.1), *Anadara vellicata* (KP954700.1), *Scapharca kagoshimensis* (NC_025509.1), *Anadara sativa* (NC_024927.1), *Argopecten irradians* (EU023915.1), *Chlamys farreri* (EF473269.1), *Mimachlamys senatoria* (NC_022416.1), and *Mizuhopecten yessoensis* (FJ595959.1).

consisting with previously inferred phylogenetic relationships of the family Spondylidae based on several nuclear/mitochondria-derived genes (Bieler et al. 2014).

Disclosure statement

The authors report no competing interests declared.

Funding

We acknowledge the grant support from Fundamental Research Funds for the Central Universities [201841001], Marine S&T Fund of Shandong Province for Pilot National Laboratory for Marine Science and Technology [2018SDKJ0302-1], and Key Research and Development Program of Shandong Province [2016ZDJQ0208].

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References

- Bernt M, Donath A, Jühling F, Externbrink F, Florentz C, Fritsch G, Pütz J, Middendorf M, Stadler PF. 2013. MITOS: improved de novo metazoan mitochondrial genome annotation. *Mol Phylogenet Evol.* 69:313–319.
- Bieler R, Mikkelsen PM, Collins TM, Glover EA, González VL, Graf DL, Harper EM, Healy J, Kawauchi GY, Sharma PP, et al. 2014. Investigating the bivalve tree of life an exemplar-based approach combining molecular and novel morphological characters. *Invert Syst.* 28:32–115.
- Curole JP, Kocher TD. 1999. Mitogenomics: digging deeper with complete mitochondrial genomes. *Trends Ecol Evol (Amst).* 14:394–398.
- Dierckxens N, Mardulyn P, Smits G. 2017. NOVOPlasty: de novo assembly of organelle genomes from whole genome data. *Nucleic Acids Res.* 45:e18.
- Koyama T, Chounan R, Uemura D, et al. 2006. Hepatoprotective effect of a hot-water extract from the edible thorny oyster *Spondylus varius* on carbon tetrachloride-induced liver injury in mice. *J Agric Chem Soc Jpn.* 70:729–731.
- Milbury CA, Gaffney PM. 2005. Complete mitochondrial DNA sequence of the Eastern oyster *Crassostrea virginica*. *Mar Biotechnol.* 7:697–712.
- Saccone C, De Giorgi C, Gissi C, Pesole G, Reyes A. 1999. Evolutionary genomics in Metazoa: the mitochondrial DNA as a model system. *Gene.* 238:195–209.
- Sambrook J, Fritsch EF, Maniatis T. 1989. Molecular cloning: a laboratory manual. New York: Cold Spring Harbor Lab Press.
- Wu X, Xu X, Yu Z, Kong X. 2009. Comparative mitogenomic analyses of three scallops (Bivalvia: Pectinidae) reveal high level variation of genomic organization and a diversity of transfer RNA gene sets. *BMC Res Notes.* 2:60–69.
- Xu K, Kanno M, Yu H, Li Q, Kijima A. 2011. Complete mitochondrial DNA sequence and phylogenetic analysis of Zhikong scallop *Chlamys farreri* (Bivalvia: Pectinidae). *Mol Biol Rep.* 38:3067–3074.