

The complete mitochondrial genome of *Salmacis sphaeroides variegata* (Mortensen, 1942)

Wenfei Zhao, Zhe Li, Xiaofang Huang, Yang Zhang, Jun Ding and Yaqing Chang

Key Laboratory of Mariculture & Stock Enhancement in North China's Sea, Ministry of Agriculture and Rural Affairs, Dalian Ocean University, Dalian, Liaoning, P. R. China

ABSTRACT

In this study, the complete mitochondrial genome of *Salmacis sphaeroides variegata* was determined on Illumina HiSeq platform. The genome was 15,770 bp in size and contains 22 tRNA genes, 13 protein-coding genes, 2 rRNA genes, and 1 control region (180 bp). The composition of A + T in *S. sphaeroides* mtDNA was 61.90%. Except *ND6* and 6 tRNAs, the others are on the H-strand. The phylogenetic relationships of 11 species of sea urchins were analyzed using the neighbor-joining method using software MEGA 7.0. *S. sphaeroides* was most closely related to *Temnopleurus hardwickii*.

ARTICLE HISTORY

Received 14 May 2019
Accepted 16 August 2019

KEYWORDS

Mitochondrial genome; sea urchins; *Salmacis sphaeroides variegata*

Salmacis sphaeroides variegata is a kind of sea urchin in the family Temnopleuridae. It lives in warm temperate regions and shallow waters (0–90 m). Although its nutritional value is very high (Chen et al. 2010), *S. sphaeroides* is not cultivated on a large scale in China. At present, the research on *S. sphaeroides* mainly focuses on biological development (Rahman et al. 2012, 2016). By comparing with the mitochondrial genome of other sea urchins, it provides basic data and important scientific data for the phylogenetic evolution and diversity of sea urchins. Therefore, the research on the mitochondrial whole genome of *S. sphaeroides* becomes very important.

Our sample was collected from Sanya, Hainan province, China (20°06'08.3"N, 110°16'15.0"E). The complete mitochondrial genome of *S. sphaeroides* was determined using on Illumina HiSeq platform. Using SOAP denovo V2.04 software (<http://soap.genomics.org.cn/>), the sequence was assembled (Luo et al. 2012). DOGMA software (<http://dogma.cccb.utexas.edu/>) was used to predict gene, rRNA, and tRNA contained in the genome. MEG A7.0 (Kumar et al. 2016) was used for multiple alignments. The mtDNA map of *S. sphaeroides* mitochondrial genome was drawn with the online tool OGDRAW (<https://chlorobox.mpimp-golm.mpg.de/OGDraw.html>) (Lohse et al. 2013). The specimen is stored in the Key Laboratory of

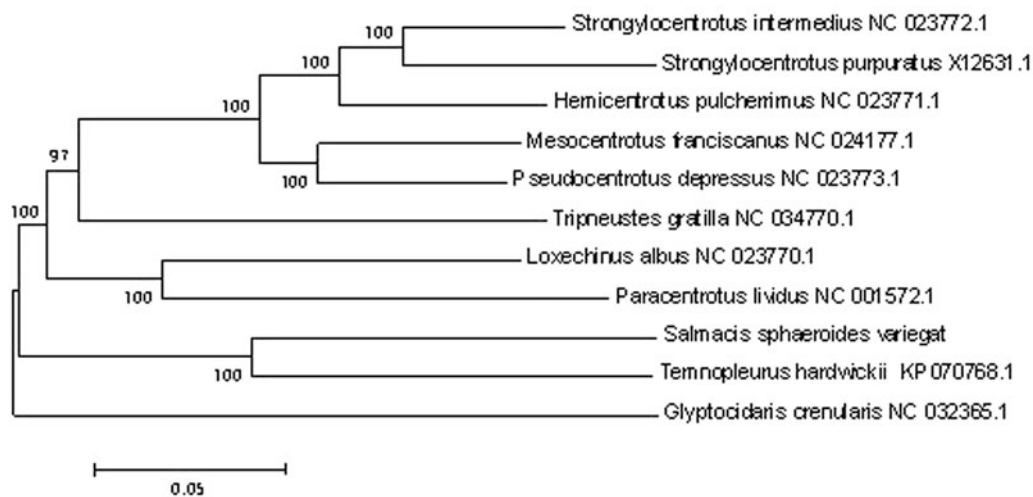


Figure 1. Consensus neighbor-joining tree based on the complete mitochondrial sequence of *S. sphaeroides* and other 10 species of sea urchins. The phylogenetic tree was constructed using MEGA 5.0 software by the neighbor-joining method. The numbers at the tree nodes indicate the percentage of bootstrapping after 1000 replicates.

CONTACT Jun Ding  dingjun19731119@hotmail.com; Yaqing Chang  yaqingchang@hotmail.com  Key Laboratory of Mariculture & Stock Enhancement in North China's Sea, Ministry of Agriculture and Rural Affairs, Dalian Ocean University, Dalian 116023, Liaoning, P. R. China

© 2019 The Author(s). Published by Informa UK Limited, trading as Taylor & Francis Group.

This is an Open Access article distributed under the terms of the Creative Commons Attribution License (<http://creativecommons.org/licenses/by/4.0/>), which permits unrestricted use, distribution, and reproduction in any medium, provided the original work is properly cited.

Mariculture & Stock Enhancement in North China's Sea, Ministry of Agriculture and Rural Affairs, Dalian Ocean University (voucher number: DLOU-KLM-SU05).

The mitochondrial genome of *S. sphaeroides* has a total length of 15,770 bp (GenBank registration number: MK692949), including 13 protein-coding genes, 22 tRNA genes, 2 rRNA genes, and a non-coding region with a length of 180 bp, which is consistent with the mitochondrial genome structure of the echinacea reported (Cantatore et al. 1989; Giorgi et al. 1996). The composition of A+T in *S. sphaeroides* mtDNA was 61.90%. Except *ND6* and 6 tRNAs, the others are on the H-strand. Most protein-coding genes (10 of 13 genes) started with ATG, *ATP8* with GTG, and *ND4* with ATC. The termination codon of most protein-coding genes was TAG (8 of 13 genes) or TAA (3 of 13 genes). The termination codon of *ND4* was TAT and the termination codon of *ND1* was TTA. The size of 22 tRNA coding genes ranged from 68 to 74 bp. The largest intergenic region of the mitochondrial genome was 36 bp.

The phylogenetic relationship of 11 species of sea urchins was analyzed using the neighbor-joining method by MEGA 7.0. The results showed that the *S. sphaeroides* were most closely related to the *Temnopleurus hardwickii*. The distance between *Strongylocentrotus* sea urchin and *S. sphaeroides* was the farthest (Figure 1).

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

Disclosure statement

No potential conflict of interest was reported by the authors.

Funding

This work was supported by the National Key Research and Development Program of China [2018YFD0901601], Liaoning Innovation Talents in University [LR2017064].

References

- Cantatore P, Roberti M, Rainaldi G, Gadaleta MN, Saccone C. 1989. The complete nucleotide sequence, gene organization, and genetic code of the mitochondrial genome of *Paracentrotus lividus*. *J Biol Chem.* 264(19):10965–10975.
- Chen G, Xiang W-Z, Lau C-C, Peng J, Qiu J-W, Chen F, Jiang Y. 2010. A comparative analysis of lipid and carotenoid composition of the gonads of *anthocardis crassispina*, *diadema setosum* and *salmacis sphaeroides*. *Food Chem.* 120(4):973–977.
- Giorgi CD, Martiradonna A, Lanave C, Saccone C. 1996. Complete sequence of the mitochondrial dna in the sea urchin *Paracentrotus lividus*: conserved features of the echinoid mitochondrial genome. *Mol Phylogenet Evol.* 5(2):323–332.
- Kumar S, Stecher G, Tamura K. 2016. Mega7: molecular evolutionary genetics analysis version 7.0 for bigger datasets. *Mol Biol Evol.* (7):1870–1874.
- Lohse M, Drechsel O, Kahlau S, Bock R. 2013. Organellargenomedraw—a suite of tools for generating physical maps of plastid and mitochondrial genomes and visualizing expression data sets. *Nucl Acids Res.* 41(W1):W575–W581.
- Luo R, Liu B, Xie Y, Li Z, Huang W, Yuan J, He G, Chen Y, Pan Q, Liu Y, et al. 2012. Soapdenovo2: an empirically improved memory-efficient short-read de novo assembler. *GigaSci.* 1(1):18.
- Rahman MA, Yusoff FM, Arshad A, Ara R. 2016. Growth and survival of the tropical sea urchin, *salmacis sphaeroides* fed with different macroalgae in captive rearing condition. *J Env Biol.* 37(4 Spec No):855.
- Rahman MA, Yusoff FM, Arshad A, Shamsudin MN, Amin SM. 2012. Embryonic, larval, and early juvenile development of the tropical sea urchin, *salmacis sphaeroides* (echinodermata: echinoidea). *Sci World J.* 2012(4):938482.