

MITOGENOME ANNOUNCEMENT



The complete mitochondrial genome of *Sargassum kjellmanianum* (Sargassaceae) and phylogenetic analysis of *Sargassum kjellmanianum* (Sargassaceae)

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ABSTRACT

Sargassum kjellmanianum plays an important role in marine ecosystem and biological resource utilization. Here, we analyzed the characteristics and evolution of mitochondrial genome of *S. kjellmanianum* by paired-end sequencing. The complete mitogenome comprises a circular DNA molecule measuring 34,723 bp in length with 35 coding genes. The circular genome consisted of seven protein-coding genes, 25 *tRNA* genes, and three *rRNA* genes, with a total length of 26,553 bp. The overall A + T content was 63.43%, higher than the G + C content (36.57%). Phylogenetic analysis confirmed *S. kjellmanianum* was closely clustered with *S. muticum*.

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Sargassum kjellmanianum Yendo (1907) is a common intertidal macroalgae, belonging to Phaeophyta, Fucales, and Sargassaceae (Cao et al. 2008). In addition to being one of the most economically valuable brown algae in the world's cultivated seaweed, it is also an ideal material for algal genetics, molecular physiology research of anti-stress and genomics (Ogawa 1976). With the discovery of more bioactive substances in brown algae, its research has collected many attentions from lots of investigators over recent years.

S. kjellmanianum used in this experiment was collected from the Lidao Bay (37°26' N, 122°56' E) of Shandong Province, and approved by the Rongcheng Oceanographic Bureau. A specimen was deposited at the First Institute of Oceanography, Ministry of Natural Resources (<https://www.fio.org.cn/>, Jinlai Miao, miaojinlai@fio.org.cn) under the voucher number FIO2020059703. The genomic DNA was

extracted using the E.Z.N.A.[®] soil DNA Kit (Omega Bio-tek, Norcross, GA) according to manufacturer's protocol. Mitochondrial genome was subjected to paired-end sequencing on the Illumina NovaSeq 6000 platform (Shanghai BIOZERON Co., Ltd, Shanghai, China). The raw data was filtered to make the consequent results more accurate. Then NOVOPlasty version 4.2 and GeSeq software are used for high quality data assembly and function prediction, respectively (Dierckxsens et al. 2017; Tillich et al. 2017). The complete mitochondrial genome had been submitted to GenBank with accession number OK235333. The results showed that the mitogenome had a circular DNA molecule measuring 34,723 bp in length with 36.57% overall G + C content. This genome contains 35 coding genes with a total length of 26,553 bp, accounting for 76.5% of genomic full-length.

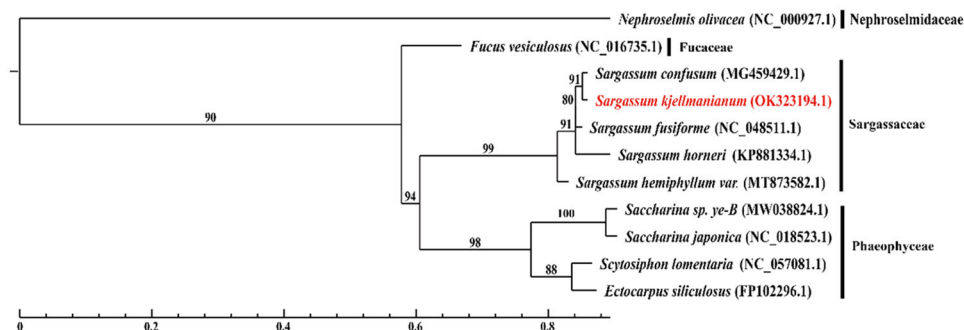


Figure 1. Phylogenetic tree of *S. kjellmanianum* and 10 species constructed using the ML method based on mitochondrial genome sequences. Numbers on the nodes were bootstrap values from 1000 replicates. *Nephroselmis olivacea* was selected as an outgroup.

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Among the coding genes, there were seven protein-coding genes, 25 *tRNA* genes and three *rRNA* genes.

MEGA X was used to construct the maximum-likelihood (ML) phylogenetic tree to clarify the phylogenetic relationship between *S. kjellmanianum* and other species (Kumar et al. 2018). Ten mitochondrial genome sequences used to elucidate phylogenetic relationships were downloaded from the GenBank database. Here, the nucleotide substitution model is General Time Reversible (GTR, $nst = 6$) (Rodríguez et al. 1990). Phylogenetic analysis proved that *S. kjellmanianum* was most associated with *Sargassum confusum* (Figure 1). All genes show the typical gene arrangement conforming to the Sargassaceae family consensus.

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Ethical approval

Ethical approval for the study was obtained from the Ethical Committee of Qingdao University of Science and Technology.

Author contributions

Conceptualization, methodology, software, validation, writing – original draft and investigation, Hui Xu and Xixi Wang; formal analysis, resources and data curation, Liping Zhang; software, validation, writing – original draft and investigation, Yingying He and Yuanyuan Zhang; Modifying the manuscript, sample collection, methodology, conceiving, and designing the project, Changfeng Qu and Jinlai Miao. All the listed authors have approved the manuscript, and agree to be accountable for all aspects of the work.

Disclosure statement

No potential competing interest was reported by the author(s).

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Data availability statement

The genome sequence data that support the findings of this study are openly available in GenBank of NCBI at (<https://www.ncbi.nlm.nih.gov/>) under the accession no. OK235333. The associated BioProject, SRA, and Bio-Sample numbers are PRJNA789766, SRR17110432, and SAMN24149239, respectively. The SRA number is the same as that of chloroplast.

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