Complete sequence of mitochondrial DNA of Gracilaria edulis (Rhodophyta)

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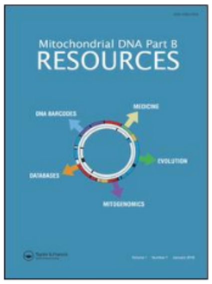

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MITOGENOME ANNOUNCEMENT

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Complete sequence of mitochondrial DNA of *Gracilaria edulis* (Rhodophyta)

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ABSTRACT

Herein, the complete *Gracilaria edulis* mitogenome was determined and analysed. The complete *G. edulis* mitogenome length was 25,708 bp. The mitogenome contains 50 genes, including 24 protein-coding, two rRNA, and 23 tRNA genes and one unidentified open reading frame (ORF). Of the 24 protein-coding genes, 23 (95.83%) ended with the TAA stop codon, and one (4.17%) with TAG (*rpl*20). All protein-coding genes in *G. edulis* were concluded to use the start codon ATG. Mitogenome phylogenetic analysis revealed that *G. edulis* clustered together with *G. changii* and *G. salicornia*. The complete mitogenome sequence provided herein would help understand *Gracilaria* evolution.

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Gracilaria edulis (Rhodophyta) is a marine red alga belonging to the family Gracilariaceae. *Gracilaria edulis* is a rich source of sulphated polysaccharides, carbohydrates, proteins, vitamins, minerals, and dietary fibres (Sakthivel and Pandima Devi 2015). The polyunsaturated esters in *G. edulis* showed antibacterial activity against several human pathogens. *G. edulis* extracts can inhibit carcinoma cell activity (Sakthivel et al. 2016). To date, studies have mainly focused on the identification of antitumor active compounds in *G. edulis* (Patra and Muthuraman 2013). However, information on its genetics and systematics is limited.

Herein, we determined the complete *G. edulis* mitogenome sequence. Genomic DNA from one *G. edulis* individual collected from a population in eastern China (Yingge Sea, Hainan Province, 18°30′36″N, 108°42′15″E) was used for genome sequencing. The specimen (GenBank accession number: 2017060064) was deposited at the Culture Collection of Seaweed at the Ocean University of China. Paired-end reads were sequenced using Illumina HiSeq × Ten system (Illumina, San Diego, CA). Approximately, 9 Gb of paired-end (150 bp) sequence data was randomly extracted from the total sequencing output, as input to NOVOPlasty for assembling the mitogenome (Dierckxsens et al. 2017). *Gracilaria salicornia* (GenBank accession number: NC_023784) was used as the seed sequence. tRNA genes were identified using tRNAscan-SE Search Server (Schattner et al. 2005). Other mitogenomic regions were annotated from *G. salicornia* mitogenome using Geneious R10 (Biomatters Ltd., Auckland, New Zealand). Phylogenetic mitogenome analysis was conducted. Bayesian inference (BI) was performed using MrBayes v. 3. 1.2 (Huelsenbeck and Ronquist 2001). The phylogenetic analysis was done using two independent runs with four Monte-Carlo Markov Chains running for 1,000,000 generations. Output trees were sampled every 100 generations. The phylogenetic analysis was run until the average standard deviation of split frequencies was below 0.01 and the first 25% of samples was removed as burn-in. *Rhodymenia pseudopalmata* (KC875852) served as the out-group.

The complete *G. edulis* (MG592725) mitogenome comprises a circular DNA molecule measuring 25,708 bp in length. The overall A + T content of the complete mitogenome is 75.6%. The mitogenome contains 50 genes, including 24 protein-coding, two rRNA, and 23 tRNA genes and one unidentified open reading frame (ORF). Of the 24 (95.83%) protein-coding genes, 23 ended with the TAA stop codon, and one (4.17%) with TAG (*rpl*20). All protein-coding genes in *G. edulis* were concluded to use the start codon ATG. The lengths of two rRNA genes are 2642 bp (*rnl* rRNA) and 1401 bp (*rns* rRNA). Bayesian inference showed that *G. edulis* clustered together with *G. changii* and *G. salicornia* (Figure 1). The complete mitogenome sequence provided herein would help understand *Gracilaria* evolution.

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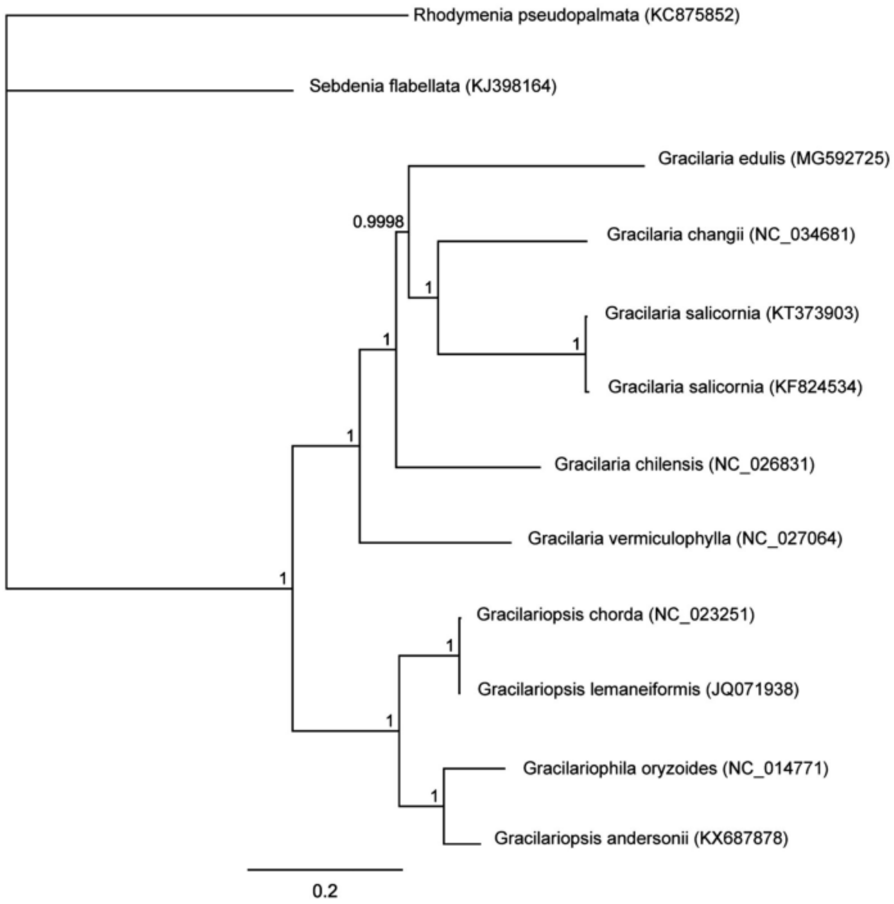

Figure 1. Phylogenetic tree (Bayesian inference) based on complete mitogenomes of species within Gracilariaceae. Support values for each node were calculated from Bayesian posterior probability (BPP).

Disclosure statement

The authors report no conflicts of interest.

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