

The complete plastid genome and phylogenetic analysis of *Gracilaria spinulosa*

Tao Liu^{a,b,c}, Xianming Tang^{a,b}, Xuli Jia^c, Xiangyu Wu^a, Min Huang^{a,b}, Jun Zeng^{a,b} and Weizhou Chen^d

^aHainan Academy of Ocean and Fisheries Sciences, Haikou, People's Republic of China; ^bHainan Provincial Key Laboratory of technology for tropical seawater aquaculture, Haikou, People's Republic of China; ^cLaboratory of Genetics and Breeding of Marine Organism, College of Marine Life Sciences, Ocean University of China, Qingdao, People's Republic of China; ^dMarine Biology Institute, Shantou University, Shantou, People's Republic of China

ABSTRACT

Gracilaria spinulosa is an economical species of marine red algae. The length of its plastid genome sequence is 179,082 bp; a total of 236 genes were determined, including 203 protein-encoding genes, 3 rRNA genes, 29 tRNA genes, 1 ribonuclease gene, and 1 intron inserted into the *trnM* gene. The gene content and structure of Gracilariaceae species were relatively well conserved. Phylogenetic analysis showed that *G. spinulosa* had a closer relationship with *Gracilaria salicornia* in *Gracilaria*. The complete plastid genome sequence provided will help the understanding of *Gracilaria* evolution.

ARTICLE HISTORY

Received 19 June 2019
Accepted 22 June 2019

KEYWORDS

Gracilaria spinulosa; plastid genome; phylogenetic analysis; Gracilariaceae

Gracilaria spinulosa (Okamura) Chang & B.M.Xia is a marine red alga belonging to the family Gracilariaceae. *Rhodymenia spinulosa* (Okamura) is the basionym of *Gracilaria spinulosa*. It is an agar-producing seaweed (Lin 2006). Previous studies focused on the vegetative and reproductive morphology and taxonomic status analyses of *G. spinulosa* (Withell et al. 1994; Lin 2006). It was originally described from Taiwan, with bushy and erect Thalli, irregularly dichotomous branches, flattened blades, a discoid holdfast, and occasionally with a short stipe (1–2.5 mm long; Lin 2006). However, no previous genomic studies on *G. spinulosa* have been reported.

Herein, we report the determination of the *G. spinulosa* plastid genome sequence. The specimen was collected from Yinggehai, Hainan Province (18°30'36" N, 108°42'15" E) was sequenced, and was deposited at the Culture Collection of Seaweed at the Ocean University of China (accession number: 2017060066). Total DNA was extracted via the modified CTAB method (Doyle and Doyle 1990). Paired-end reads were sequenced by using Illumina HiSeq system (Illumina, San Diego, CA, USA). Approximately 27 Gb of paired-end (150 bp) sequence data were randomly extracted from the total sequencing output and used as input for NOVOPlasty (Dierckxsens et al. 2017) to assemble the plastid genome. The complete plastid genome, using *Gracilaria tenuistipitata* var. *liui* (AY673996) as the seed sequence, was annotated with Geneious R10.1.3. The tRNA genes were identified using tRNAscan-SE Search Server (Schattner et al. 2005).

The complete *G. spinulosa* plastid genome is a circular DNA molecule measuring 179,082 bp in length, and the overall A + T content of the complete plastid genome was 71.3%

(GenBank accession number MN053319). The plastid genome contained 236 genes, including 203 protein-coding, 3 rRNA, and 29 tRNA genes, 1 ribonuclease gene (*rnpB*), and 1 intron interrupting the *trnM* gene. The length of the coding region was 145,035 bp, corresponding to 81.0% of the total length. The plastid genome of *G. spinulosa* was compact, with 10 pairs of overlapping genes found with overlap lengths of 3–95 bp (*rpl23–rpl4*, *rpl14–rps17*, *trnT–ilvB*, *ycf40–rps1*, *ycf29–trnH*, *psbD–psbC*, *carA–ycf53*, *chl1–trnR*, *atpF–atpD*, and *rps18–rpl33*). The gene numbers and structures were largely similar among Gracilariaceae species published in the NCBI sequence database; their plastid genomes were relatively well conserved, with no gene rearrangement phenomena.

Phylogenetic analysis was conducted using 82 shared plastid protein sequences from 17 red algal plastid genomes, using *Cyanidioschyzon merolae* as an outgroup. The nucleotide sequences were aligned by using MAFFT (Kato et al. 2002). Concatenated alignments were generated and poorly aligned regions were removed by using the Gblocks server (http://phylogeny.lirmm.fr/phylo.cgi/one_task.cgi?task_type=gblocks) (Castresana 2000). MrBayes 3.1.2 software was used to construct the amino acids phylogenetic tree (Ronquist and Huelsenbeck 2003). The results showed that all red algal taxa were clearly separated according to their original class (Figure 1). The *Gracilaria* species formed a branch, in which *G. spinulosa* showed a closer relationship with *Gracilaria salicornia*. The determination of the complete plastid genome sequence will help the understanding of *Gracilaria* evolution.

CONTACT Tao Liu ✉ liutao@ouc.edu.cn; Xianming Tang ✉ hn.tangxm@aliyun.com  Hainan Academy of Ocean and Fisheries Sciences, No.12, Lingshanzhen Baiju Avenue, Haikou 570206, People's Republic of China; Weizhou Chen ✉ wzchen@stu.edu.cn  Marine Biology Institute, Shantou University, 243, Daxue Road, Shantou 515063, People's Republic of 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.

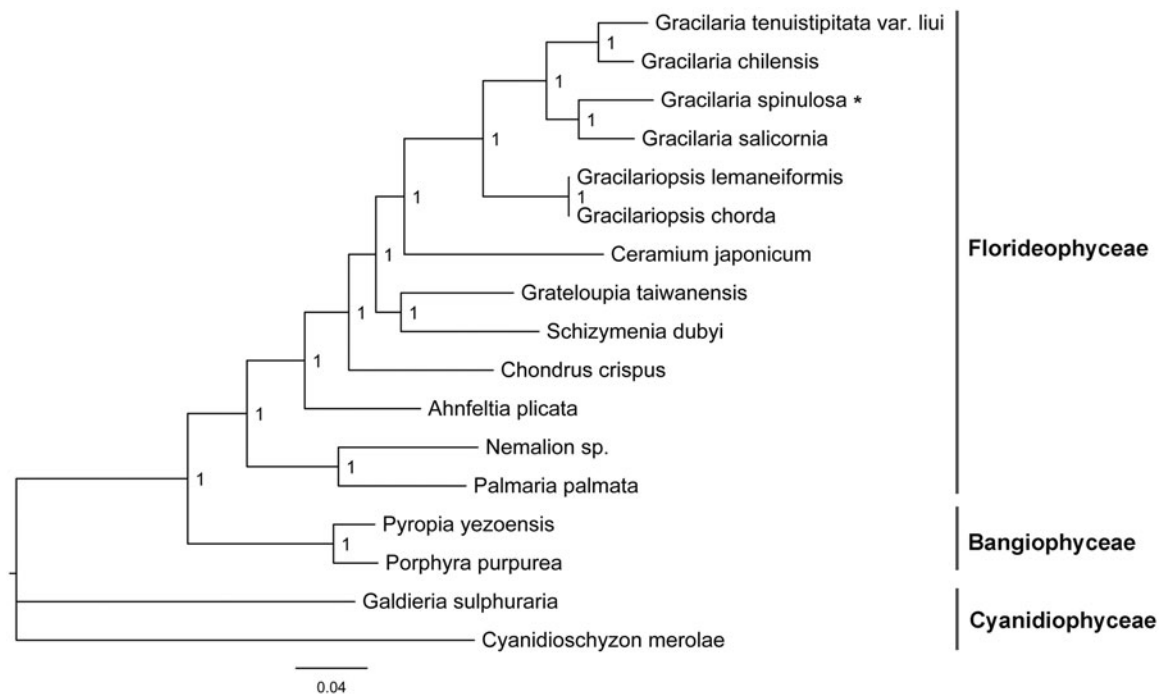


Figure 1. Phylogenetic tree (Bayesian method) based on the complete plastid genome sequence of red algae as shown below: *Gracilaria spinulosa* (MN053319), *Gracilaria salicornia* (NC_023785), *Gracilaria tenuistipitata* var. *liui* (AY673996), *Gracilaria chilensis* (NC_029860), *Gracilariopsis chorda* (NC_031149), *Gracilariopsis lemaneiformis* (KP330491), *Grateloupia taiwanensis* (KC894740), *Schizymenia dubyi* (NC_031169), *Chondrus crispus* (NC_020795), *Ceramium japonicum* (NC_031174), *Nemalion* sp. (LT622871), *Ahnfeltia plicata* (NC_031145), *Palmaria palmata* (NC_031147), *Pyropia yezoensis* (KC517072), *Porphyra purpurea* (U38804), *Galdieria sulphuraria* (KJ700459), and *Cyanidioschyzon merolae* (NC_004799). The asterisks after species names indicate newly determined plastid genomes.

Disclosure statement

No conflict of interest for all the authors including the implementation of research experiments and writing this article was reported.

Funding

This work was supported by Major Science and Technology Programme of Hainan Province [ZDKJ2017002]; Agricultural Environmental Pollution Control Programme of Hainan Province [NWZL2017002]; Technical Research and Development Projects of Research Institutions in Hainan Province [Q60593]; China-ASEAN Maritime Cooperation Fund; Public Science and Technology Research Funds Projects of Ocean [201405020] and China Agriculture Research System-50.

References

- Castresana J. 2000. Selection of conserved blocks from multiple alignments for their use in phylogenetic analysis. *Mol Biol Evol.* 17: 540–552.
- Dierckxens N, Mardulyn P, Smits G. 2017. NOVOPlasty: de novo assembly of organelle genomes from whole genome data. *Nucl Acids Res.* 45: e18.
- Doyle JJ, Doyle JL. 1990. Isolation of plant DNA from fresh tissue. *Focus.* 12:13–15.
- Katoh K, Misawa K, Kuma K-i, Miyata T. 2002. MAFFT: a novel method for rapid multiple sequence alignment based on fast Fourier transform. *Nucl Acids Res.* 30:3059–3066.
- Lin SM. 2006. Observations on flattened species of *Gracilaria* (Gracilariaceae, Rhodophyta) from Taiwan. *J Appl Phycol.* 18: 671–678.
- Ronquist F, Huelsenbeck JP. 2003. MrBayes 3: Bayesian phylogenetic inference under mixed models. *Bioinformatics.* 19: 1572–1574.
- Schattner P, Brooks AN, Lowe TM. 2005. The tRNAscan-SE, snoscan and snoGPS web servers for the detection of tRNAs and snoRNAs. *Nucl Acids Res.* 33:W686–W689.
- Withell AF, Millar AJK, Kraft GT. 1994. Taxonomic studies of the genus *Gracilaria* (Gracilariales, Rhodophyta) from Australia. *Australian System Bot.* 7:281–352.