

MITOGENOME ANNOUNCEMENT



The complete chloroplast genome of *Grateloupia turuturu* Yamada

Hongbin Han^{a,b} and Yan Li^{a,b,c}

^aFirst Institute of Oceanography, Ministry of Natural Resources, Qingdao, China; ^bLaboratory of Marine Ecology and Environmental Science, Pilot National Laboratory for Marine Science and Technology, Qingdao, China; ^cLaboratory of Marine Ecology and Environmental Science, Qingdao National Laboratory for Marine Science and Technology, Qingdao, China

ABSTRACT

In this study, we sequenced and annotated the complete chloroplast genome of *Grateloupia turuturu* Yamada (GenBank accession number: MN853877). The total length of the chloroplast genome is 188,547 bps, including 196 protein-encoding genes, 23 tRNA genes and 3 rRNA. The complete chloroplast genome of *G. turuturu* is 30.68% C + G, which is lower than that of A + T. The phylogenetic tree, which is based on core genes, shows that *G. turuturu* is clustered into the *Grateloupia* clade and has close genetic relationships with algae *Grateloupia filicina* and *Grateloupia taiwanensis*. These data will provide more information to understand the phylogenetic status of *G. turuturu*.

ARTICLE HISTORY

Received 8 January 2020
Accepted 19 January 2020

KEYWORDS

Chloroplast genome;
Grateloupia turuturu
Yamada; phylogenetic
analysis; *Grateloupia filicina*;
Grateloupia taiwanensis

G. turuturu belongs to the phylum Rhodophyta, class Florideophyceae, order Halymeniales, family Halymeniaceae, and the genus *Grateloupia*. It mainly grows on rocks or in tide pools in the low tidal zone and is widely distributed along the coast of China, especially in the Yellow and Bohai Seas (Xia 2004). *G. turuturu* is rich in proteins, carbohydrates, vitamins and other minerals making it a subsidiary food (Fujiwara-Arasaki et al. 1984; Rui et al. 2006). *G. turuturu* has antiviral and anti-tumor activities, which makes it potentially interesting for pharmaceutical and medical developments (Simon-Colin et al. 2002; Hellio et al. 2004). In addition, *G. turuturu* could also be the raw material for agar or carrageenan (Shanmugam and Mody 2000; Fu et al. 2011).

G. turuturu was collected from the Qinhunangdao coastal area (39°49'54.69"N, 119°31'30.50"E) and cultured in the laboratory with VSE medium at 20 °C under a light intensity of 100 µmol⁻² s⁻¹ (Zhou et al. 2016a, 2016b). The specimens were preserved at the Marine Ecology Research Center of the First Institute Oceanography, Ministry of Natural Resources in Qingdao (Accession number: DXWGZ06). Approximately 5 g of fresh algae was harvested for cpDNA isolation using an improved extraction method (Chen et al. 2011). After DNA isolation, 1 µg of purified DNA was fragmented to construct short-insert libraries (insert size of 430 bps) according to the manufacturer's instructions (Illumina), and then sequenced on the Illumina HiSeq 4000 (Borgstrom et al. 2011) at Shanghai BIOZERON Co., Ltd. Prior to assembly, the Illumina raw reads were filtered. The chloroplast

genome of *G. turuturu* was reconstructed using a combination of the Pacbio Sequel data and the Illumina HiSeq data via SPAdes v3.10.1 (Antipov et al. 2016).

The shape of the chloroplast genome of *G. turuturu* is a double-stranded closed loop and has the GenBank accession number of MN853877. The complete chloroplast genome sequence of *G. turuturu* is 188,547 bps long with a C + G composition of 30.68%. The genome contains 196 protein-encoding genes as well as a number of non-coding genes, including 26 tRNA genes and 3 rRNA genes (*rrn23*, *rrn16* and *rrn5*). All of the coding genes begin with ATG except for *chlI*, *dnaB*, *infC*, *psbY*, *rbcS*, *rps8* and *ycf63*, which begin with GTG. The termination codons for *accA*, *acsF*, *apcE*, *atpE*, *bas1*, *carA*, *ccs1*, *dnaK*, *dsbD*, *groEL*, *grx*, *ompR*, *pbsA*, *petA*, *petF*, *petM*, *psaF*, *psaL*, *psaM*, *psbB*, *tsf*, *ycf16*, *ycf20*, *ycf60* and *ycf80* are TAG. On the other hand, *accB*, *cfxQ*, *chlI*, *dnaB*, *infB*, *psbL*, *rne*, *rpoC2*, *rps18*, *rps19*, *secA*, *trpA* and *ycf63* have termination codons of TGA. The rest 158 genes end with TAA.

To determine the phylogenetic position of *G. turuturu*, 24 other complete chloroplast genome sequences were obtained from the Genbank database. A phylogenetic tree was constructed based on core genes. Maximum likelihood (ML) methods were performed for the phylogenetic analysis using PhyML 3.0, and the bootstrap was 1000. The phylogenetic tree (Figure 1) shows that *G. turuturu* clustered into the *Grateloupia* clade and has close genetic relationships with algae *Grateloupia filicina* and *Grateloupia taiwanensis*.

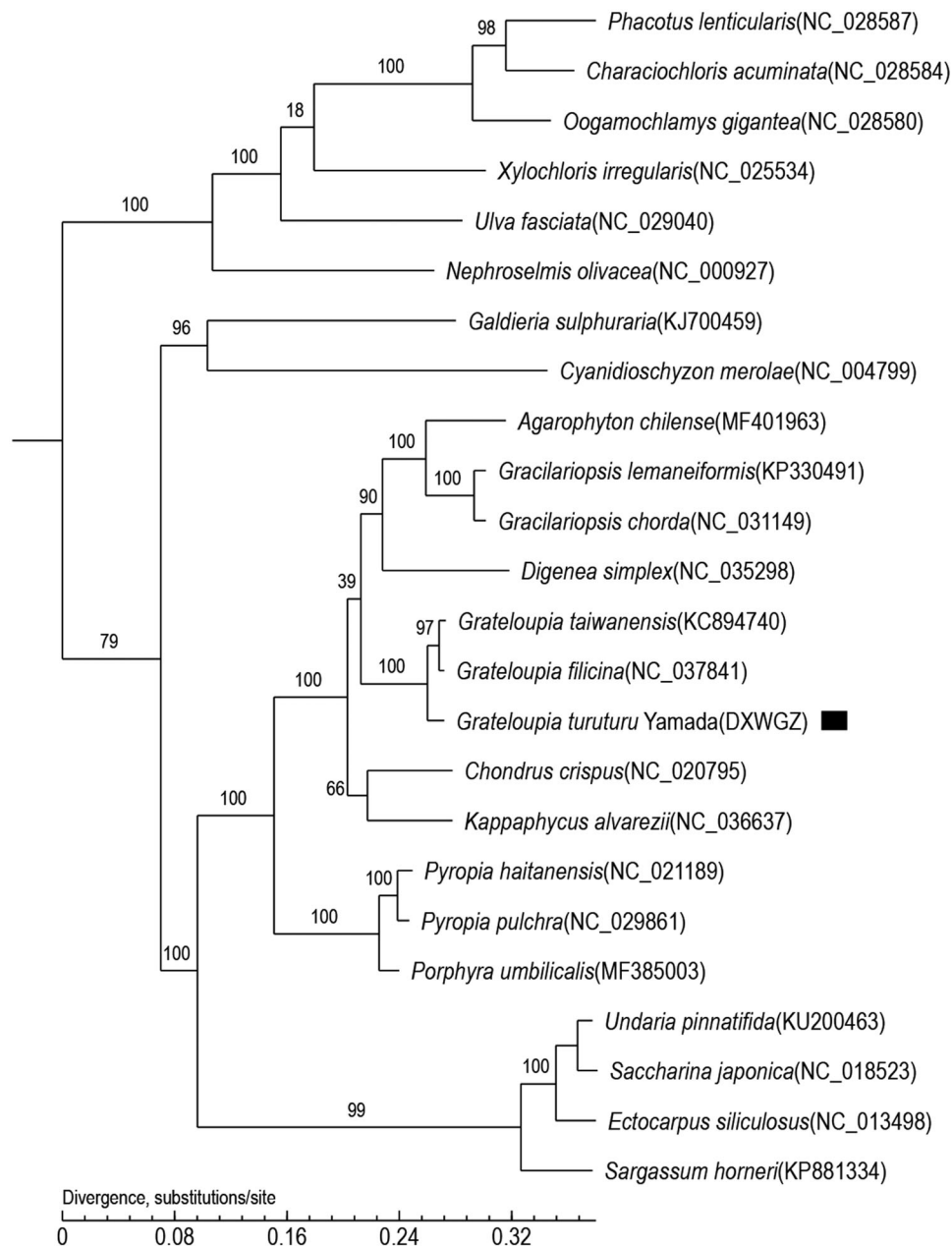


Figure 1. Maximum-likelihood (ML) tree based on the complete chloroplast genome sequences of 25 species. The numbers on the branches are bootstrap values.

Disclosure statement

We declare that we have no conflicts of interest. The authors alone are responsible for the content and writing of the paper.

Funding

This work was financially supported by the National Key R&D Program of China [2019YFC1407902], National Natural Science Foundation of China [41876140/41606190]. The funders did not play a role in the study design, data collection and analysis, decision to publish, or manuscript preparation.

References

Antipov D, Korobeynikov A, McLean JS, Pevzner P. 2016. hybridSPAdes: an algorithm for hybrid assembly of short and long reads. *Bioinformatics*. 32(7):1009–1015.

Borgstrom E, Lundin S, Lundeberg J. 2011. Large scale library generation for high throughput sequencing. *PLoS One*. 6:e19119.

Chen J, Guan R, Chang S, Du T, Zhang H, Xing H. 2011. Substoichiometrically different mitotypes coexist in mitochondrial genomes of *Brassica napus* L. *PLoS One*. 6(3):e17662.

Fu XT, Qin ZH, Xu JC, Gao X, Fang YC. 2011. Analysis and evaluation of nutritional quality of *Grateloupia turuturu*. *Acta Nutrimenta Sinica*. 33(2):199–201.

Fujiwara-Arasaki T, Mino N, Kuroda M. 1984. The protein value in human nutrition of edible marine algae in Japan. *Hydrobiologia*. 116(1): 513–516.

Hellio C, Simon-Colin C, Clare A, Deslandes E. 2004. Isethionic acid and floridoside isolated from the red alga, *Grateloupia turuturu*, inhibit settlement of *Balanus amphitrite* Cyprid Larvae. *Biofouling*. 20(3):139–145.

Rui W, Cen YZ, Li YL, Wu QM, Zhang MY. 2006. Extraction, analysis of sulfated polysaccharides from *Grateloupia turuturu* Yamada and their antiviral activities. *Chin J Marine Drugs*. 25(2):12–16.

Shanmugam M, Mody KH. 2000. Heparinoid-active sulphated polysaccharides from marine algae as potential blood anticoagulant agents. *Cur Sci*. 79(12):1672–1683.

- Simon-Colin C, Kervarec N, Pichon R, Bessieres MA, Deslandes E. 2002. Characterization of N-methyl-L-methionine sulfoxide and isethionic acid from the Red alga *Grateloupia doryphora*. *Phycological Res.* 50(2): 125–128.
- Xia BM, 2004. Flora algarum marinarum sinicarum [A]. In: Tomus II Rhodophyta. Part V. ahnfeltiales gigartinales rhodymeniales. Beijing: Science Press; p. 135–138.
- Zhou LJ, Wang KL, Zhang JH, Cai CE, He PM. 2016a. Complete mitochondrial genome of *Ulva prolifera*, the dominant species of green macroalgal blooms in Yellow Sea, China. *Mitochondr DNA B.* 1(1): 76–78.
- Zhou LJ, Wang LK, Zhang JH, Cai CE, He PM. 2016b. Complete mitochondrial genome of *Ulva linza*, one of the causal species of green macroalgal blooms in Yellow Sea, China. *Mitochondr DNA B.* 1(1):31–33.