

Complete sequence of mitochondrial DNA of *Gloiopeltis furcata* (Postels and Ruprecht) J. Agardh

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ABSTRACT

Although most red algae produce agar and carrageenan, *Gloiopeltis furcata* produces funoran as polysaccharide component. In this study, the complete *G. furcata* mitochondrial genome was determined. It had a circular mapping molecular with the length of 25,636 bp and contained 49 genes including 24 protein-coding, two rRNA, and 23 tRNA. Phylogenetic analysis showed that *G. furcata* was separated with the other polysaccharide-producing red algae. This is the first report of complete mitochondrial genome from funoran producing red algae.

ARTICLE HISTORY

Received 5 June 2019
Accepted 22 June 2019

KEYWORDS

Mitochondrial genome;
macroalgae; Gigartinales;
red alga

Most red algae produce agar and carrageenan, which were industrially important polysaccharides. *Gloiopeltis* sp. is known as funoran-producing red algae, and the structures differ in species. Funoran from *Gloiopeltis furcata* has a concurrence structure of agaroid and carrageenan chains (Takano et al. 1998). Funoran from *Gloiopeltis complanata* possesses the sulphated agarose structure (Takano et al. 1995). Yang and Kim (2018) reported new species *Gloiopeltis frutex* sp. nov. in Gigartinales, implying a possibility of having a different structural funoran. In addition, Tuvikene et al. (2015) reported that funoran structures differed by the extraction methods. Funoran from *Gloiopeltis tenax* showed the biological activities such as antitumor activity (Ren et al. 1995) and antihypertensive and antihyperlipidemic effect (Ren et al. 1994); however, information about species and funoran structures is limited. To clarify the characteristics of funoran producing red algae, we determined the complete mitochondrial DNA of *G. furcata*.

DNA was extracted from *G. furcata* (Specimen Voucher HUF 20170502001) collected from the intertidal at Nanae beach, Japan (N 41.813175, E 140.703994) using the CTAB method (Cota-Sánchez et al. 2006). The library construction and sequencing were performed by the Ion PGM™ platform. The data were assembled using default *de novo* settings in CLC Genomics Workbench 8.5.1 and annotated following Kumagai et al. (2019). Phylogenetic analyses were performed

using amino acid sequences of *atp6*, *atp8*, *cox1-3*, *nad1-4*, *nad4L*, *nad5*, *rpl16*, *rps11*, and *rps12*. The best-fit model for maximum likelihood was AIC and analysed using RAXML version 8 (Stamatakis 2014). Bootstrap probability values were run with 1000 replicates. *Cyanidioschyzon merolae* was used as outgroup.

The complete mitogenome of *G. furcata* comprised a circular DNA molecule with the length of 25,636 bp (DDBJ accession No. LC484362). The overall GC content of the complete mitogenome was 37.4%. The mitogenome contained 49 genes, including 24 protein-coding, two rRNA, and 23 tRNA genes. Of the 24 protein-coding genes, 22 were terminated with TAA stop codon, except for *sdh2* and *rps12* with TAG. A single intron of 480 bp was detected in the *trnI*. Phylogenetic analysis showed that *G. furcata* was separated from the other carrageenan producing red algae (Figure 1). Yang and Kim (2018) reported that *Gloiopeltis* species were classified in a single tree as the genus of *Gloiopeltis* within Endocladiaaceae, indicating that funoran producing algae would be genetically away from the other polysaccharides producing algae.

Acknowledgments

The computations for phylogenetic analysis were partially performed on the NIG supercomputer at ROIS National Institute of Genetics.

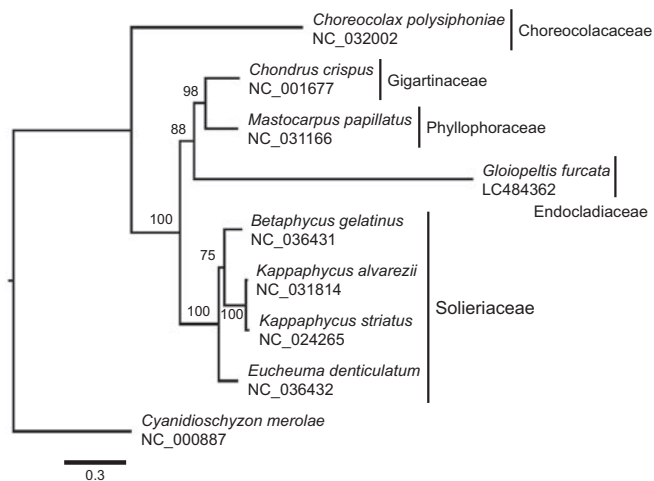


Figure 1. Maximum-likelihood phylogeny of 15 mitochondrial protein coding sequences in Gigartinales. Numbers along branches are RAxML bootstrap supports based on 1000 nreps.

Disclosure statement

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

Funding

This study was supported in part by the “Science and Technology Research Promotion Program for Agriculture, Forestry, Fisheries and Food Industry [27004B]”.

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