**MITOGENOME ANNOUNCEMENT**

**The complete mitochondrial genome of *Neoporphyra dentata* (Bangiales, Rhodophyta)**

Sung-Je Choi\*, Yonguk Kim\*, Dong-Wook Kim, Dool-Ri Oh, Yujin Kim and Donghyuck Bae

\*Korea National College of Agriculture and Fisheries, 1515, Kongjwipatjwi-ro, Deokjin-gu, Jeonju-si, Jeollabuk-do, csjchoi@korea.kr
\**Coscience Co. Ltd., Muan-gun, Jeollanam-do, Republic of Korea

**ABSTRACT**

*Neoporphyra dentata* (Kjellman) L.-E. Yang & J. Brodie, 2020 is an economically valuable species in seaweed aquaculture in the southwest coastal regions of Korea. Here, we report the complete mitogenome information of *N. dentata* using Illumina Miseq platform permitted assembly of a circular mitochondrial genome of 26,807 bp from *N. dentata* consisting of 29.9% GC contents, 9 protein coding genes (PCGs), 2 ribosomal RNA genes (12S rRNA and 16S rRNA), 23 transfer RNA (tRNA) genes, and a non-coding region. The overall nucleotide composition was A: 38%, T: 32%, C: 14.7%, and G: 15.2%. The mitochondrial genome of *N. dentata* contributes to revealing the phylogenetic relationships among species of the Bangiaceae family.

Neophyra, a genus of red algae in the Bangiaceae family, is one of the most popular seaweeds for the production of sheet-like dried seafood, commonly referred to as dried laver, mostly in East Asian countries such as South Korea (‘Gim’), China (‘Zicai’), and Japan (‘Nori’) (Choi et al. 2014). The production of Neophyra as a marine crop has been reported that the annual value of laver in 2017 was almost $950 million (Kim 2013; Kim et al. 2017). Neophyra dentata is a native species that is distributed and intensively farmed in the southwest coastal regions of Korea. Although *N. dentata* production represents 10–20% of the domestic laver production in Korea, this species is increasing in economic importance in Korea as an alternative resource due to its plasticity in response to subtropical climate change (Kim et al. 2017; Kim et al. 2019). Therefore, we characterized the complete mitochondrial genome of *N. dentata* based on Illumina’s Miseq platform data.

Young blade samples were collected from Songji-myeon (34°33′00.0″N 126°36′00.0″E), Haenam County, Jeonnam Province, Republic of Korea, and deposited in the Ocean and Fisheries Science Institute Haenam Branch at Haenam, Korea (specimen code JOPF0004562, http://www.jeonnam.go.kr; Sung-Je Choi; csjchoi@korea.kr). Genomic DNA was extracted from young blades using a DNeasy Power Plant Pro Kit (Qiagen, Valencia, CA, USA), in accordance with the manufacturer’s protocol. Whole-genome resequencing was performed at Coscience Co. Ltd. (Mokpo, South Korea) using the Illumina Miseq platform (Illumina, Hayward, CA), yielding 7,731,923 paired raw reads. Assembly was conducted with various k-mers using SPAdes (Bankevich et al. 2012) using *Pyropia yezoensis* (NC_017837) as the reference and a circular contig of the *N. dentata* mitogenome was obtained. Finally, the resulting contig consensus sequence was annotated using MITOS2 (Bernt et al. 2013) and adjusted manually using DOGMA (Wyman et al. 2004). The annotated mitogenome of *N. dentata* was submitted to GenBank under accession number LC650807.

The complete mitogenome of *N. dentata* is a circular molecule that is 26,807 bp in length and contained 9 PCGs, 2 rRNA genes, 23 tRNA genes, one origin of L strand replication, and one control region. The *N. dentata* genome contains nine protein coding genes (rps11, rps12, ymf16, ymf39, atp8, atp9, nad3, nad4L, and cox3). All protein coding genes and ORFs have a conserved, typical ATG codon as a start signal and the common stop (codon is TAA (7 of 9 genes), whereas TAG is used as translation termination codon of nad3 and rps12 genes. To investigate its phylogenetic position, the mitogenome sequences of 11 complete mitogenomes of Bangiaceae and 3 outgroup species were aligned using Mega 7.0 (Kumar et al. 2016) with 1,000 bootstrap replicates (Figure 1). Phylogenetic analysis based on the complete mitogenomes showed that *N. dentata* was most closely related to *N. haitanensis*. The complete mitogenome of *N. dentata* will

**CONTACT** Sung-Je Choi; csjchoi@korea.kr, Korea National College of Agriculture and Fisheries, 1515, Kongjwipatjwi-ro, Deokjin-gu, Jeonju-si, Jeollabuk-do, 54874, Republic of Korea

\*These authors have contributed equally to this work.

© 2022 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-NonCommercial License (http://creativecommons.org/licenses/by-nc/4.0/), which permits unrestricted non-commercial use, distribution, and reproduction in any medium, provided the original work is properly cited.
serve as a valuable tool for understanding the phylogenetic relationship and evolutionary history Bangiaceae.

**Acknowledgment**

No funding was received.

**Author contributions**

S.-J. Choi: conceptualization, methodology. Y. Kim: software, methodology, writing, reviewing and editing. D.-W. Kim: methodology, software, data curation. D.-R. Oh, and Y. Kim: sample collection, data analysis. D. Bae: supervision, reviewing and editing

**Disclosure statement**

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

**Funding**

The author(s) reported there is no funding associated with the work featured in this article.

**ORCID**

Yonguk Kim [http://orcid.org/0000-0003-3026-0893](http://orcid.org/0000-0003-3026-0893)

**Data availability statement**

The data that support the findings of this study are openly available in GenBank of NCBI at [https://www.ncbi.nlm.nih.gov](https://www.ncbi.nlm.nih.gov) (GenBank: LC650807, BioProject: PRJDB12447, BioSample: SAMD00410849, DRA: DRR337305).

**References**

Bankevich A, Nurk S, Antipov D, Gurevich AA, Dvorkin M, Kulikov AS, Lesin VM, Nikolenko SI, Pham S, Prijebelski AD, et al. 2012. SPAdes: a new genome assembly algorithm and its applications to single-cell sequencing. J Comput Biol. 19(5):455–477.

Bernt A, Donath A, Jühling F, Externbrink F, Florentz C, Fritzsch G, Pütz J, Middendorf M, Stadler PF. 2013. MITOS: improved de novo metazoan mitochondrial genome annotation. Mol Phylogenet Evol. 69(2):313–319.

Choi ES, Kim NH, Kim HW, Kim SA, Jo JI, Kim SH, Lee SH, Ha SD, Rhee MS. 2014. Microbiological quality of seasoned roasted laver and potential hazard control in a real processing line. J Food Prot. 77(12):2069–2075.

Kim DH. 2013. The relationship between climatic and oceanographic factors and laver aquaculture production. J Fish Business Admin. 44(3):77–84.

Kim BT, Brown CL, Kim DH. 2019. Assessment on the vulnerability of Korean aquaculture to climate change. Marine Policy. 99:111–122.

Kim JK, Yarish C, Hwang EK, Park M, Kim Y. 2017. Seaweed aquaculture: cultivation technologies, challenges and its ecosystem services. Algae. 32(1):1–13.

Kumar S, Stecher G, Tamura K. 2016. MEGA7: molecular evolutionary genetics analysis version 7.0 for bigger datasets. Mol Biol Evol. 33(7):1870–1874.

Wyman SK, Jansen RK, Boore JL. 2004. Automatic annotation of organelle genomes with DOGMA. Bioinformatics. 20(17):3252–3255.

Figure 1. NJ phylogeny based on 11 complete mitogenomes of Bagiaceae species and one Laminaria and two Saccharina species as an outgroup. All the sequences were downloaded from NCBI’s GenBank.