Complete mitochondrial genome and phylogenetic analysis of the marine red alga Polyopes affinis (Rhodophyta: Halymeniales)

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Polyopes affinis is a red alga from the phylum Rhodophyta. The entire mitogenome of P. affinis was sequenced and compared to related Halymeniales species. The entire circular-mitogenome is 25,988 bp long, has 27.59% GC content, and comprises 25 protein-coding genes (CDS), 23 transfer RNA (tRNA) genes, and three ribosomal RNA (rRNA) genes. In terms of gene synteny and tRNA composition, the P. affinis mitogenome differs significantly from that of P. lancifolius. Phylogenetic analysis shows P. affinis mitogenome in a branch sister to P. lancifolius, indicating a close relationship with other Halymeniales species.

The complete circular mtDNA (GenBank accession no.: OM960741) of P. affinis was 25,988 bp in length with 27.59% GC content, which is lower than P. lancifolius (MW292567; Kim et al. 2021). The overall base composition was 37.85% for A (9837 bp), 34.55% for T (8979 bp), 14.25% for G (3704 bp), and 13.34% for C (3468 bp). It contains a total of 51 genes, including three rRNA genes, 23 tRNA genes, and 25 CDS genes. The CDS genes include seven for NADH dehydrogenase complex (nad), five for ribosomal proteins (rps), four for ATPase subunits (atp), three for cytochrome oxidase subunits (cox), three for sdh, one for cob, one for tatC, and one for hypothetical protein. The genomic difference between the two Polyopes species is that P. lancifolius (Kim et al. 2021) has fewer rRNA (2), and CDS (24) than P. affinis. While there are differences amongst Halymeniales species, the mtDNA of P. affinis (OM960741) and P. lancifolius (MW292567) lacks an intron in cox1, which is found in Grateloupia taiwanensis (KM999231), G. filicina (KG598532), and G. angusta (KC875853).

A maximum-likelihood phylogenetic tree (Figure 1) was constructed using six mtDNA within the order Halymeniales. Sebdenia flabellata (KJ398164) and Rhodymenia pseudopalmata (KC875852) were used as outgroups. The results are consistent with previous findings, and P. affinis was found on a branch sister to P. lancifolius in the best-scoring tree, revealing a close
relationship with other Halymeniales species. This complete mtDNA analysis of *P. affinis* will improve our understanding of the evolutionary process of Rhodophyta species.

**Ethical statement**

The material involved in the article does not involve ethical conflicts.

**Author contributions**

M.P.P. performed the experiments, analyzed the data, was involved in certain tools for analysis, and drafting of the paper, and approved the final draft. J-O.K. involved in the conception and design of the work, certain tools for analysis and sorting out of the results. Y-R.K. and S.Y. were involved in specimen sample collection, species identification, and prepared figure. K.K. involved in the conception and design of the work, funding acquisition, revising it critically for intellectual content and the final approval of the version to be published.

**Disclosure statement**

The authors report no conflict of interest. The authors are responsible for the content and writing of the article.

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**Data availability statement**

The genome sequence data that support the findings of this study are openly available in GenBank of NCBI ([https://www.ncbi.nlm.nih.gov/](https://www.ncbi.nlm.nih.gov/)) under the accession number OM960741 ([https://www.ncbi.nlm.nih.gov/nuccore/OM960741](https://www.ncbi.nlm.nih.gov/nuccore/OM960741)). The associated BioProject, BioSample, and SRA numbers are PRJNA825647 ([https://www.ncbi.nlm.nih.gov/bioproject/PRJNA825647](https://www.ncbi.nlm.nih.gov/bioproject/PRJNA825647)), SAMN27531872 ([https://www.ncbi.nlm.nih.gov/biosample/SAMN27531872](https://www.ncbi.nlm.nih.gov/biosample/SAMN27531872)), and SRR18728299 ([https://www.ncbi.nlm.nih.gov/sra/SRR18728299](https://www.ncbi.nlm.nih.gov/sra/SRR18728299)), respectively.

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