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Comparative Analysis of Chloroplast Genome Structure in Four *Sargassum* Species

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[Introduction]

Seaweeds are major edible marine algae, consumed by billions of people around the world and the most seaweeds are cultivated in Asia including Korea, Japan, China and Indonesia. In Korea, the export of seaweeds are continuously increased since 2010 up to 611 million dollars in 2019.

Unfortunately, different seaweed species and/or produced from different country can be mixed during manufacturing process, and consequently it can leads to deterioration in product quality. Therefore, methods for identification of different seaweeds species are needed to avoid contamination of products.

[Materials and Methods]

we sequenced chloroplast DNA of four *Sargassum* species (*S. fulvellum*, *S. horneri*, *S. tortile*, and *S. serratifolium*) for the development of methods for identifying *Sargassum* seaweeds. The lengths of the genomes are 124,215, 124,082, 124,297, and 124,507bp, respectively. Each of the four chloroplast genomes have 145 protein-coding genes, 56 transfer RNA genes, and 13 ribosomal RNA genes, except *S. fulvellum* (15 rRNA genes).

[Results and Discussion]

The phylogenetic analysis showed that *S. tortile* and *S. serratifolium* have close relationship, followed by *S. horneri* and *S. fulvellum*. The complete genome sequence analysis in this study will provide useful information for phylogenetic studies of *Sargassum* and development of identifying markers.

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