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The complete chloroplast genome of Wakame (*Undaria pinnatifida*), an important economic macroalga of the family Alariaceae

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ABSTRACT

We decoded the complete chloroplast DNA (cpDNA) sequence of the Wakame (*Undaria pinnatifida*), an important economic macroalga of the family Alariaceae, by using next-generation sequencing technology. The genome consists of 130 336 bp containing a pair of inverted repeats (IRs) of 4790 bp, which was separated by a large single-copy region and a small single-copy region of 77 821 and 42 934 bp, respectively. The genic regions account for 77.7% of whole cpDNA, and the GC content of the cpDNA was 30.6%. The *U. pinnatifida* cpDNA encodes 153 unigenes (129 protein-coding genes, 3 rRNA genes and 21 tRNA genes). There are 1 PCG (rpl33) and 1 tRNA genes (trnL) containing an intron. A phylogenetic analysis of the four complete cpDNA from Phaeophyceae showed that *U. pinnatifida* is closely related to *Saccharina japonica* with high bootstrap value supported. The complete cpDNA of *U. pinnatifida* provides essential and important DNA molecular data for further phylogenetic and evolutionary analysis for brown algae.

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Chloroplast genome; next generation sequencing; *Undaria pinnatifida*; Wakame

Introduction

Wakame (*Undaria pinnatifida*) is an important economic macroalga in East Asian countries (Yamanaka & Akiyama 1993). In China, its annual yield has been maintained around 500 000 tons in fresh weight in recent years, ranking second in brown seaweeds. Dalian, which is located in the southernmost of Liaodong peninsula, is the prime farming ground of this macroalga. *Undaria pinnatifida* is regarded as a healthy marine vegetable because it contains high content of nutrition (essential amino acid, vitamins and trace minerals) (Nisizawa et al. 1987; Taboada et al. 2013) and bioactive compounds (fucoidans) (Synytsya et al. 2010; Liu et al. 2012b). *De novo* transcriptome sequencing and assembly of the gametophyte of *U. pinnatifida* has been conducted and putative key genes involved in important biosynthetic pathway of fucoidan, alginate, mannitol, and laminarin were identified (Shan et al. 2015a). A high-density genetic linkage map has very recently been constructed and the sex linked locus was mapped for the first time in this macroalga (Shan et al. 2015b). In this study, we aimed to deduce the complete chloroplast genome to obtain essential sequence information for further research on genetics and evolution.

Sample of *U. pinnatifida* (voucher no. 474) was collected from Dalian, Liaoning province of China. Genomic DNA was extracted following the modified CTAB DNA extraction protocol (Attitalla 2011) and then subjected to build up genomic library and pair-end sequencing (2×300 bp) by MiSeq (Illumina, San Diego, CA). By using commercial software (Geneious V9, Auckland, New Zealand), about 3.9% (408,662 out of 10 472 286) raw reads were *de novo* assembled to produce circular form of complete cpDNA with about an average $974 \times$ coverage.

Annotation of the assembled genome was performed with DOGMA (Wyman et al. 2004), cpGAVAS (Liu et al. 2012a) and manual inspected to predict protein-coding genes (PCGs), transfer RNA (tRNA) and ribosome RNA (rRNA) genes. The complete cpDNA of *U. pinnatifida* has a total length of 130 336 bp (GenBank KU200463) showing 93% identity to *Saccharina japonica*. It has a typical quadripartite structure including a pair of inverted repeats (IRa and IRb 4790 bp), separated by the small single-copy (SSC 42 934 bp) and large single-copy (LSC 77 821 bp) regions. The complete cpDNA of *U. pinnatifida* contains 153 unique genes consisting 21 transfer RNA, 3 ribosomal RNA, and 129 PCGs. Among 153 unique genes, there are two genes (rpl33 and trnL genes) are interrupted by one intron. The chloroplast genome consists 77.7% genic regions, and the overall GC content of the complete cpDNA is 30.6%. The GC content of IR regions is 44.8%, higher than LSC (29.6%) and SSC (29.3%) regions. The relative low GC content of LSC and SSC regions is due to low GC content in the PCGs and non-coding region.

To validate the phylogenetic position of *U. pinnatifida*, we used MEGA6 (Tamura et al. 2013) software to construct a Maximum likelihood tree (with 500 bootstrap replicates) containing complete cpDNA of four algae in Phaeophyceae. *Gracilariopsis lemaneiformis* derived from Florideophyceae was

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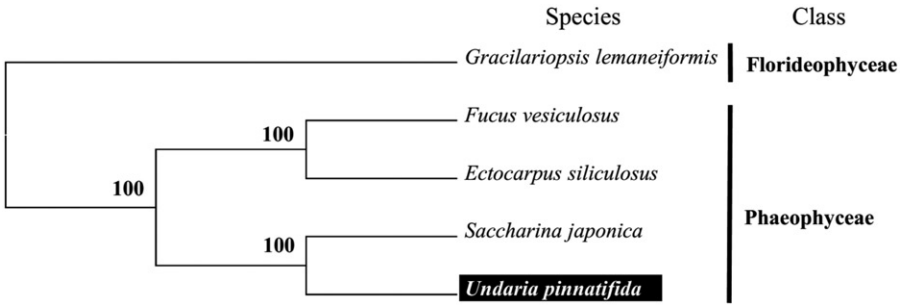

Figure 1. Molecular phylogeny of *Undaria pinnatifida* and other related brown algae based on complete chloroplast genome. The complete chloroplast genome is downloaded from GenBank and the phylogenic tree is constructed by the maximum-likelihood method with 500 bootstrap replicates. The gene's accession number for tree construction is listed as follows: *Gracilariopsis lemaneiformis* (KU179794), *Fucus vesiculosus* (NC_016735), *Ectocarpus siliculosus* (NC_013498), *Saccharina japonica* (NC_018523) and *Undaria pinnatifida* (KU200463).

used as outgroup for tree rooting. Result shows *U. pinnatifida* is closely related to *Saccharina japonica* with high bootstrap value supported (Figure 1). In conclusion, the complete cpDNA of *U. pinnatifida* is decoded for the first time in this study and provides essential and important DNA molecular data for further phylogenetic and evolutionary analysis for Phaeophyceae.

Disclosure statement

None of the authors report any conflict of interest. The authors alone are responsible for the content and writing of the paper.

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