

## Sequencing of complete mitochondrial genome of brown algal *Saccharina* sp. ye-C

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### ABSTRACT

The complete sequence (37,609 bp) of the mitochondrial DNA (mtDNA) of the *Saccharina* sp. ye-C was determined using Illumina sequencing data. The genome contains 38 protein-coding genes (PCG), 3 ribosomal RNA (rRNA), 25 transfer RNA (tRNA) genes that are typical of *Saccharina* mtDNA. The phylogenetic analysis based on the mitochondrial genomes of brown algae showed that *Saccharina* sp. ye-C formed a robust clade with *Saccharina coriacea*, which strongly supports their close phylogenetic relationship.

### ARTICLE HISTORY

Received 9 February 2017  
Accepted 19 February 2017

### KEYWORDS

*Saccharina* sp. ye-C;  
complete mitochondrial  
genome; Illumina  
sequencing

The kelp *Saccharina* are large seaweeds with two distinctive generations of microscopic gametophytes and large elaborate sporophytes (Kawai et al. 2016). They belong to the brown algae (Phaeophyceae) in the order *Laminariales*. *Saccharina japonica* is an important economic alga which has been widely cultivated in China, Japan and Korea (Wang et al. 2013). However, in China *S. japonica* suffered close breeding for generations which have caused significant issues such as loss of genetic varieties, decreasing growth rate and massive mortality (Guan et al. 2016). Recently, the genome of *S. japonica* has been sequenced (Ye et al. 2015), which could strongly promote the genetic improvement of the species. In the study, genomes of several strains of *Saccharina* collected from different locations all over the world were re-sequenced. Under this background, we have enough Illumina sequencing data to recover some mitochondrial genomes of the re-sequenced strains to develop more reliable genetic tools. In this study, the complete mitochondrial genome of a wild strain (NO. KT315643), sampled in Sakhalin in Russia is recovered and named *Saccharina* sp. ye-C based on the phylogenetic analysis with 16 complete brown algae mitochondrial genomes.

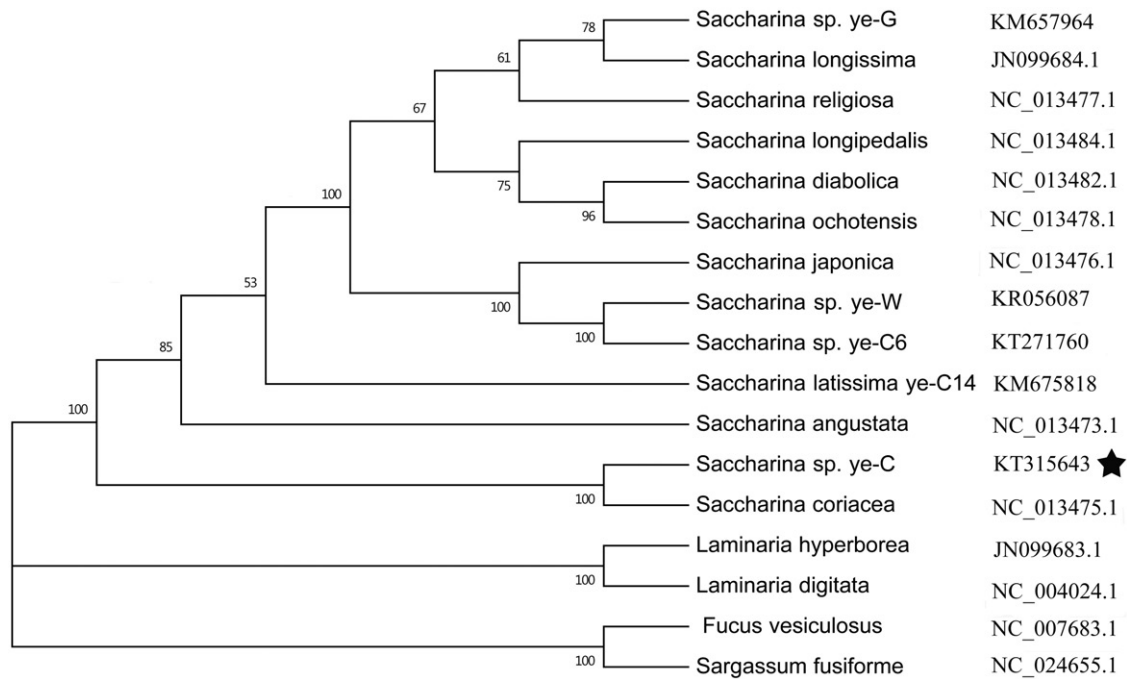
Modified phenol-chloroform procedure was used to extract the total genomic DNA (Greco et al. 2014). 4G PE100 reads in total was produced by the second-generation Illumina sequencing.

42,452 reads were mapped to the *S. japonica* mitochondrial genome (37,609 in length) using Genious (<http://www.genious.com>) and no gap region was found in the mapping result. BLAST (Altschul et al. 1997), DNASTAR (Burland 2000), and DOGMA (<http://dogma.cccb.utexas.edu>) were employed

to annotate the mitochondrial genome and the annotated file was submitted to NCBI using Sequin (<http://www.ncbi.nlm.nih.gov/projects/Sequin/>).

The length of complete *Saccharina* sp. ye-C is 37,609 bp and the genome contains 38 protein-coding genes (*rps2-4*, *rps7-8*, *rps10-14*, *atp6*, *atp8*, *atp9*, *cox1-3*, *nad1-7*, *nad9*, *nad11*, *nad4L*, *rpl2*, *rpl5*, *rpl6*, *rpl14*, *rpl16*, *rpl19*, *rpl31*, *ORF41*, *ORF130*, *ORF377*, *tatC* and *cob*), 25 transfer RNA (tRNA) genes, 3 ribosomal RNA (rRNA) genes (5S rRNA, 16S rRNA and 23S rRNA). All 38 protein-coding genes (PCGs) have typical initiation codons (ATG). The numbers of PCGs that have complete termination codons TAA, TAG, TGA are 27, 7 and 4, respectively. No incomplete stop codons were found. The overall GC content is 35.35%, which is well within the normal range of brown mitochondrial DNAs. Nucleotide frequency of the H-strand is as follows: T, 36.29%; A, 28.36%; C, 14.74%; and G, 20.61%. The mitogenome of *Saccharina* sp. ye-C encodes 9644 amino acids, excluding the stop codons. All the 25 typical tRNAs, ranging from 71 to 88, possess a complete clover leaf secondary structure. The rRNAs of the 5S rRNA, 16S rRNA and 23S rRNA genes are 133 bp, 1535 bp and 2736 bp in length, respectively.

Phylogenetic analysis based on other 16 brown algae complete mitochondrial sequence data show that *Saccharina* sp. ye-C belongs to a *Saccharina* clade and is closely related to *S. coriacea*. The result was consistent with recent phylogenetic analyses and certain morphological characters (Zhang et al. 2013; Xu et al. 2016). Complete mitochondrial genomes have enhanced the resolution and statistical confidence of inferred phylogenetic trees (Figure 1).



**Figure 1.** Phylogenetic tree of ML analyses based on complete mitochondrial nucleotide acid sequences of 17 brown algae. Pentagrams stand for the species studied in this work.

## Disclosure statement

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

## Funding

This work was supported by AoShan Talents Program Supported by Qingdao National Laboratory for Marine Science and Technology (No. 2015ASTPES03), the Science Fund for Distinguished Young Scholars of Shandong Province (JQ201509), the program of leading talents of Qingdao (13-CX-27), Talent Projects of Distinguished Scientific Scholars in Agriculture, National Natural Science Foundation of China (41676145), Shandong Province key R&D projects (2015GSF115008), the National Science & Technology Pillar Program (2013BAD23B01), National Basic Research Special Foundation of China (2013FY110700), Scientific Research Funds for Central Nonprofit Institutes, Yellow Sea Fisheries Research Institutes (20603022015004).

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