

MITOGENOME ANNOUNCEMENT

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## Sequencing of complete mitochondrial genome of brown algal *Saccharina* sp. ye-C12

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### ABSTRACT

The complete sequence (37 654 bp) of the mitochondrial DNA (mtDNA) of the *Saccharina* sp. ye-C12 was determined using Illumina sequencing data. The genome contains 38 protein-coding genes (PCG), three ribosomal RNA (rRNA), 25 transfer RNA (tRNA) genes and the phylogenetic analysis based on the mitochondrial genomes of brown algae indicated that *Saccharina* sp. ye-C12 and *Saccharina japonica* are the most closely related species, which strongly supports their close phylogenetic affinity.

### ARTICLE HISTORY

Received 8 December 2015  
Revised 22 December 2015  
Accepted 30 December 2015

### KEYWORDS

Complete mitochondrial genome; illumina sequencing; *saccharina* sp. ye-C12

Recently, the genome of *S. japonica* has been sequenced (Ye et al. 2015), which would powerfully push the genetic improvement of the species. In this study, strains of *Saccharina* collected from different area all over the world

were resequenced, which make us have opportunity to uncover some mitochondrial genomes of these strains to develop more genetic tools due to the enough illumina sequencing data. In this study, the complete mitochondrial

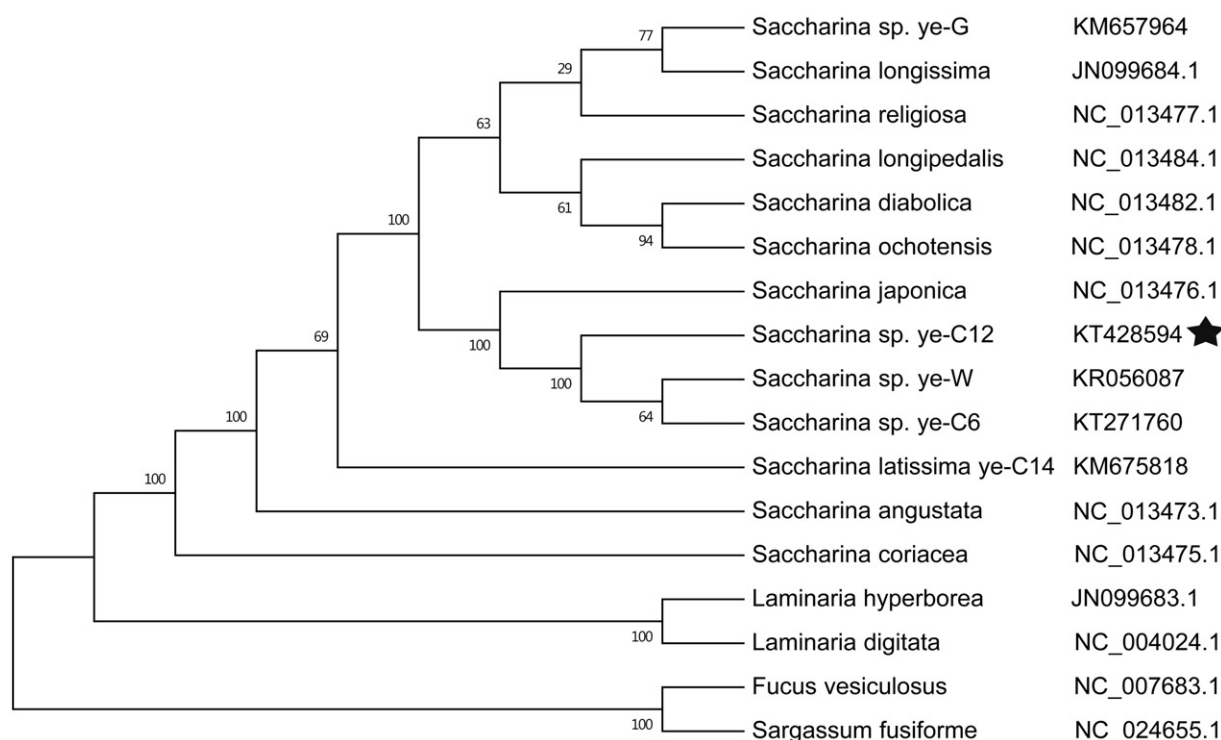


Figure 1. Phylogenetic tree of ML analyses based on complete mitochondrial nucleotide acid sequences of brown algae. Pentagrams stand for the species studied in this work

genome of a wild strain, sampled in Qingdao, China (36°10'N, 120°16'60) and stored in Yellow Sea Fisheries Research Institute Algae Culture Centre (YSFRIACC), Qingdao, China, is uncovered and named as *Saccharina* sp. ye-C12 (YSFRIACC accession number NO. YSFRI-*Saccharina*-sp-ye-C12, NCBI accession number NO. KT428594) based on the phylogenetic analysis with other complete brown algae mitochondrial genomes. Assembly and annotation were performed by the reference of our previous study (Guan et al. 2014).

The length of complete of *Saccharina* sp. ye-C12 is 37, 654 bp and the genome contains 38 protein-coding genes (*rps2-4*, *rps7-8*, *rps10-14*, *rps19*, *atp6*, *atp8*, *atp9*, *cox1-3*, *nad1-7*, *nad9*, *nad11*, *nad4L*, *rpl2*, *rpl5*, *rpl6*, *rpl14*, *rpl16*, *rpl31*, *ORF41*, *ORF130*, *ORF377*, *tatC* and *cob*), 25 transfer RNA (tRNA) genes, three 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 26, 8 and 4, respectively. No incomplete stop codons were found. Nucleotide frequency of the H-strand is as follows: T, 36.29%; A, 28.41%; C, 14.72%; and G, 20.58%. Excluding the stop codons, the mitogenome of *Saccharina* sp. ye-C12 encodes 9637 amino acids. All the 25 typical tRNAs, ranging from 71 to 88. The rRNAs of the 5S rRNA, 16S rRNA and 23S rRNA genes are 133 bp, 1535 bp and 2742 bp in length, respectively.

Phylogenetic analysis shows that *Saccharina* sp. ye-C12 belongs to a *Saccharina* clade and is closely with *S. japonica*. This result is consistent with recent phylogenetic analyses

and certain morphological characters (Zhang et al. 2013; Guan et al. 2014), indicating the related relationship and the proposal common source of the cultured kelp in China. Complete mitochondrial genomes enhanced the resolution and statistical confidence of the phylogenetic analysis (Figure 1).

### Disclosure statement

The authors report no conflicts of interest.

### Funding information

This work was supported by Scientific Research Funds for Central Non-profit Institutes, Yellow Sea Fisheries Research Institutes (20603022015004), National Basic Research Special Foundation of China (2013FY110700), the Science Fund for Distinguished Young Scholars of Shandong Province (JQ201509) the program of leading talents of Qingdao (13-CX-27).

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