

MITOGENOME ANNOUNCEMENT

 OPEN ACCESS

Complete mitochondrial genome of *Ulva prolifera*, the dominant species of green macroalgal blooms in Yellow Sea, China

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ABSTRACT

Ulva prolifera (*U. prolifera*), a green macroalgae, is widely known as the dominant species of the world's largest macroalgal blooms in the Yellow Sea, China. In this study, we sequenced and annotated the complete mitochondrial genome of *U. prolifera* (GenBank accession number: KU161104). The genome consists of circular chromosomes of 61 962 bp and encodes a total of 26 protein-coding genes include nine ribosomal protein genes, five *atp* genes, three *cox* genes, eight *nad* genes and *cob* gene. Phylogenetic analysis showed *U. prolifera* clustered into *Ulvo phyceae* clade and had close genetic relationship with algae *Ulva fasciata*.

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Species of green macroalgae genus *Ulva* are ubiquitous throughout the world in marine and estuarine habitats, where they show a great ability to acclimate to adverse circumstances and grow rapidly in nutrient rich waters (Tan et al. 1999). *Ulva prolifera* (*U. prolifera*), a common species in coastal area of China, was identified as the causal species of the world's largest macroalgal blooms in the Yellow Sea based on morphological characteristics and molecular phylogenetic analysis (Wang et al. 2008; Ding et al. 2009; Zhao et al. 2011, 2013). It is also one of the most important seaweeds for producing macroalgal fertilizer, food, biofuel and so on (Hiraoka & Oka 2008; Li et al. 2010; Zhao et al. 2011). Mitogenome of *U. prolifera* has never been reported before, and here, we determined the complete mitochondrial genome of this seaweed to gain insight into blooming mechanism of the *Ulva* green tides and genetic diversity of *U. prolifera*.

The sample of *U. prolifera* was collected from the coast of Rudong. Healthy algal thalli were transported to our laboratory under low-temperature conditions (4–8 °C) within 48 h. Then, the single intact algae chosen were cleaned of debris and epiphytes, rinsed gently using sterile seawater and cultured in von Stosch's enriched (VSE) culture medium for 2 days. The culture condition was maintained at 24 °C, under a 12:12-h light/dark photoperiod, and light intensity 130–160 $\mu\text{mol m}^{-2}\text{s}^{-1}$. The *U. prolifera* mitochondrial genome sequence is circular-mapping molecule (GenBank accession number: KU161104). The overall base composition of *U. prolifera* is T 34.3%, C 17.8%, A 31.8%, G 16.1%, G + C content 33.9%, similar to most of other green algae (30–35%). It contains 26 protein-coding genes, including nine ribosomal protein genes, five *atp* genes, three *cox* genes, eight *nad* genes

and *cob* gene, and 21 tRNA, three rRNA. Majority of genes are encoded on the H-strand except 1 *rrl* and 2 *rrs* genes that are encoded on the L-strand. Comparing the gene content of *U. prolifera* with that of other three *Ulvo phyceae* algae, the *rps4*, *rps14*, *rps10*, *mttB* and *nad9* are missing in *U. prolifera*, which implies the occurrence of the horizontal transfer (HGT). All of the 26 protein-coding genes begin from ATG except *rps11* which begins with TTA. Three typical complete stop codons were detected in open reading frames of *U. prolifera* TAA, TGA and TAG. Among these, eight protein-coding genes (*rps13*, *atp9*, *cob*, *nad4L*, *atp1*, *rps11*, *nad7*, *nad2*) shared the common termination codon TAG, whereas *atp8*, *rpl14*, *nad4*, *nad3*, *rps19*, *rpl16*, *cox1*, *rps2*, *atp4* had the common termination codon TAA. And only the termination codon of *rps3* was TGA.

The phylogenetic analysis based on amino acid sequences of seven mt protein-coding genes (*cob*, *cox1*, *nad1*, *nad2*, *nad4*, *nad5*, *nad6*) from 13 related taxa mitogenome accession number used in this phylogeny analysis: *Polytomella magna*: KC733827 (Smith et al. 2013); *Polytomella capuana*: NC_010357.1 (Smith et al. 2008); *Polytomella piriformis*: GU108480 + GU108481 (Smith et al. 2010); *Polytomella parva*: NC_016916.1 + NC_016917.1 (Smith et al. 2010); *Gonium pectorale*: AP012493 (Hamaji et al. 2013); *Chlamydomonas reinhardtii*: NC_001638.1 (Vahrenholz et al. 1993); *Dunaliella salina*: NC_012930.1 (Smith et al. 2010); *Chlamydomonas Eugametos*: NC_001872.1 (Denovan-Wright et al. 1998); *Scenedesmus obliquus*: AF204057.1 (Kuck et al. 2000); *Pyropia haitanensis*: NC_017751.1 (Mao et al. 2012); *Oltmannsiellopsis viridis*: NC_008256.1 (Pombert et al. 2006); *Pseudoclonium akinetum*: NC_005926.1 (Pombert et al. 2004); *Ulva fasciata*:

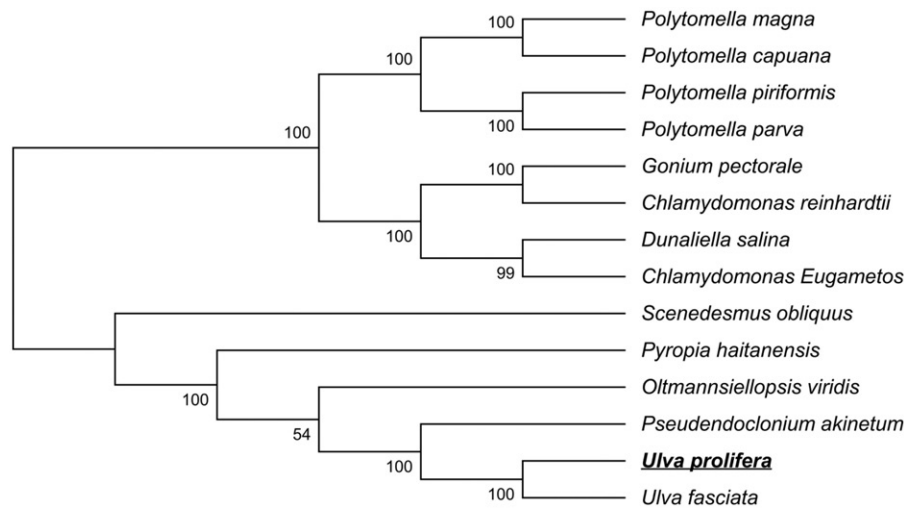


Figure 1. Phylogenetic tree of *U. prolifera* with mitochondrial genome sequence. GenBank accession numbers of species used in the tree: *Polytomella magna*: KC733827; *Polytomella capuana*: NC_010357.1; *Polytomella piriformis*: GU108480 + GU108481; *Polytomella parva*: NC_016916.1 + NC_016917.1; *Gonium pectorale*: AP012493; *Chlamydomonas reinhardtii*: NC_001638.1; *Dunaliella salina*: NC_012930.1; *Chlamydomonas Eugametos*: NC_001872.1; *Scenedesmus obliquus*: AF204057.1; *Pyropia haitanensis*: NC_017751.1; *Oltmannsiellopsis viridis*: NC_008256.1; *Pseudendoconium akinetum*: NC_005926.1; *Ulva fasciata*: KT364296.1.

KT364296.1 (Melton & Lopez-Bautista 2015). Twelve complete mitogenome entries are under green algae and one from red algae. For the construction of tree, MEGA6 software (Tamura et al. 2013) was used with 1000 bootstrap replicates. The phylogenetic tree (Figure 1) showed that the placement of *U. prolifera* within the Ulvo phyceae.

We conclude that the complete mtDNA genome sequence obtained in this study would be useful for studying genetic diversity and phylogenetic history of *U. prolifera* and its related species.

Disclosure statement

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

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