

MITOGENOME ANNOUNCEMENT

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## Complete mitochondrial genome of *Ulva linza*, one of the causal species of green macroalgal blooms in Yellow Sea, China

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### ABSTRACT

*Ulva linza*, a green macroalgae, is one of the causal 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. linza* (GenBank accession no. KU189740). The genome consists of circular chromosomes of 70 858 bp and encodes a total of 28 protein-coding genes including eight *rps* genes, three *rpl* genes, five *atp* genes, three *cox* genes, eight *nad* genes and *cob* gene. Phylogenetic analysis showed *U. linza* clustered into Ulvophyceae clade and had close genetic relationship with algae *Ulva prolifera*.

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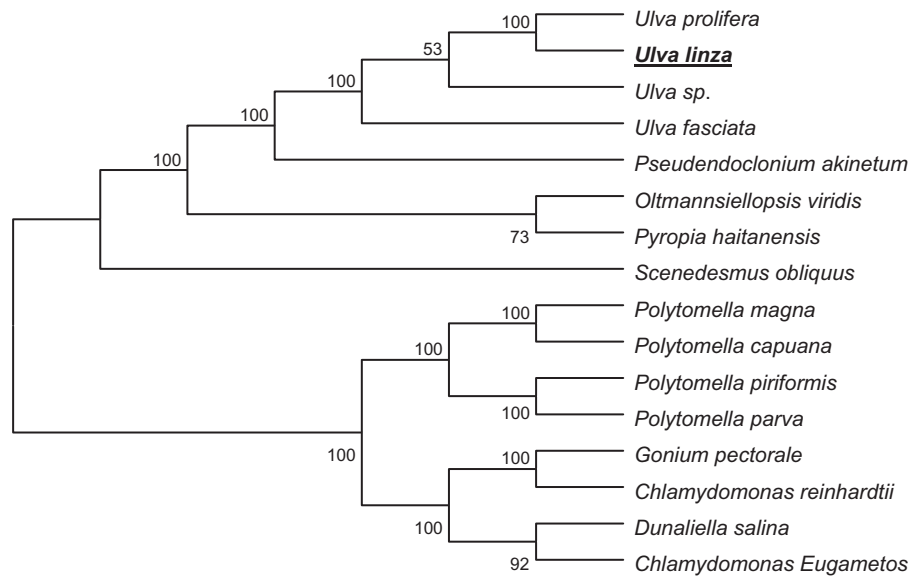
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Species of green macroalgae genus *Ulva* are ubiquitous throughout the world in marine and estuarine habitats, where they show a great ability to acclimate to adverse circumstances, and grow rapidly in nutrient rich waters (Tan et al. 1999). Although *Ulva* species are ecologically important green macroalgae, so far, only three complete mitochondrial genome sequences from *Ulva* have been reported (Liu & Pang 2015; Melton & Lopez-Bautista 2015; Melton et al. 2015). The macroalgal blooms in the Yellow Sea have broken out for nine consecutive years since 2007, resulting in great damage of marine environment and ecosystem service functions (Nelson & Lee 2001; Franz & Friedman 2002). *Ulva linza*, a common species in coastal area of China, was identified as one of the causal species of the macroalgal blooms at the early stage (Han et al. 2013). MtDNA has been widely used as a genetic marker for genetic structures, species identification, systematic and phylogeography (Avice et al. 1987), so in this study, we determined the complete mitogenome sequence of *U. linza*.

The sample of *U. linza* was collected from the coast of Rudong. Healthy algal thalli were transported to our lab 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 VSE culture medium for 2 d. The culture condition was maintained at 24 °C, under a 12:12 h LD photoperiod and light intensity 130–160  $\mu\text{mol m}^{-2} \text{s}^{-1}$ . The *U. linza* mitochondrial genome sequence is circular-mapping molecule (GenBank accession no. KU189740). The overall base composition of *U. linza* is T 31.1%, C 16.4%, A 34.3%, G 18.2% and G + C content 34.6%, similar to most of other green algae (30–35%).

It contains 28 protein-coding genes, including eight *rps* genes, three *rpl* genes, five *atp* genes, three *cox* genes, eight *nad* genes and *cob* gene, and 22 tRNA and two rRNA. Majority of genes are encoded on the H-strand except four ORFs which are encoded on the L-strand. Comparing the gene content of *U. linza* with that of other five Ulvophyceae algae, the *rps3*, *mttB* and *nad9* are missing in *U. linza*, which implies the occurrence of the horizontal transfer (HGT). All the 28 protein-coding genes begin with ATG except *atp8* and *cox3* which begin with TTG and CTG respectively. Two typical complete stop codons were detected in open reading frames of *U. linza*, TAA and TAG. Among these, 17 protein-coding genes (*cox1*, *cox2*, *atp4*, *atp6*, *atp8*, *nad1*, *nad3*, *nad4*, *nad6*, *rps2*, *rps4*, *rps10*, *rps12*, *rps14*, *rps19*, *rpl14* and *rpl16*) shared the common termination codon TAA, whereas *cob*, *cox3*, *atp1*, *atp9*, *nad2*, *nad4L*, *nad5*, *nad7*, *rps11*, *rps13* and *rpl5* had the common termination codon TAG.

The phylogenetic analysis based on the amino acid sequences of seven mt protein-coding genes (*cob*, *cox1*, *nad1*, *nad2*, *nad4*, *nad5* and *nad6*) from 15 related taxa Mitogenome accession number used in this phylogeny analysis: *Polytomella magna*: KC733827 (Smith et al. 2013); *Polytomella capuana*: NC\_010357.1 (Smith & Lee 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*



**Figure 1.** Phylogenetic tree of *U. linza* 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; *Ulva sp.*: UNA00071828: KP720617; *Ulva proliferata*: KT428794.

*haitanensis*: NC\_017751.1 (Mao et al. 2012); *Oltmannsiellopsis viridis*: NC\_008256.1 (Pombert et al. 2006); *Pseudendoconium akinetum*: NC\_005926.1 (Pombert et al. 2004); *Ulva fasciata*: KT364296.1 (Melton et al. 2015); *Ulva sp.*: UNA00071828: KP720617 (Melton et al. 2015); *Ulva proliferata*: KT428794 (Liu & Pang 2015). Fourteen 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 *U. linza* clustered into Ulvophyceae clade and had close genetic relationship with algae *Ulva proliferata*.

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

## Declaration of interest

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