


Complete chloroplast genome of *Ulva compressa* (Ulvales: Ulvaceae)

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ABSTRACT

Ulva compressa is one of the causal green macroalgae in many countries. In this study, complete chloroplast genome sequence of *U. compressa* was reported, and the total length of this species was 94,226 bp (GenBank accession number MT916929). The overall base composition of chloroplast genome was A (37.2%), T (37.0%), C (12.7%) and G (13.1%), and the percentage of A + T (74.2%) was higher than C + G (25.8%). *U. compressa* chloroplast genome encoded 90 genes, including 63 protein-coding genes, 23 transfer RNAs genes, and 4 ribosomal RNAs genes. The maximum likelihood phylogenetic analysis showed that *U. compressa* is the closest sister species of *U. linza*. This study will be helpful to understand the genetic diversity of *Ulva* species.

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China has the high-frequency outbreak of the green tides (Smetacek and Zingone 2013; Hu et al. 2014; Zhang et al. 2014; Zhang et al. 2015; Cui et al. 2019; Liu, Zhao et al. 2020; Liu, Zhuang, et al. 2020; Kang et al. 2020; Xiao et al. 2020). The formation of the green tide in the Southern Yellow Sea of China is complicated. Many researches demonstrated that the significant amount of attached *Ulva* species on the *Pyropia* aquaculture rafts were considered as the main source of the blooms in the Yellow Sea (Liu et al. 2009; Hu et al. 2010; Huo et al. 2015; Zhang et al. 2017; Zhang et al. 2019; Shan et al. 2019; Wang et al. 2018; Zhao et al. 2019; Zhao et al. 2020). The attached *Ulva* species consisted of four species which were *Ulva compressa*, *Ulva linza*, *Ulva flexuosa* and *Ulva prolifera*.

Our laboratory had studied the chloroplast genome of *U. flexuosa* (NC035823) (Cai et al. 2017), *U. linza* (KX058323) (Wang et al. 2017) and *U. prolifera* (KX342867) (Jiang et al. 2019) before. In order to study the chloroplast genome of *U. compressa*, we collected *U. compressa* from the estuary of Nantong, China (32°49'42"N, 121°19'05"E). The specimen was stored in the herbarium of Shanghai Ocean University Museum (SHOU2020NT032202). We sent the specimen to Sangon Biotech (Shanghai) Co., Ltd. for high-throughput sequencing.

DNA of the sample was extracted by using the Dzap (Plant) Genomic DNA Isolation Reagent. The genomic shotgun library was prepared by using the TruSeq DNA Sample Prep Kit (Illumina, USA), paired-end sequences were obtained through the Illumina HiSeq 2500 platform later. *U. flexuosa*,

U. linza and *U. prolifera* were taken as models for sequence splicing about the complete chloroplast genome of *U. compressa*. We used GeSeq software and Plastid Genome Annotator (PGA) software for annotation (Qu et al. 2019), and used homology comparison for correction, the chloroplast genome was perfectly assembled. Complete chloroplast genome of *U. compressa* was 94,226 bp in length and was annotated in GenBank with the accession number MT916929. The percentage of A + T (74.2%) was higher than C + G (25.8%). The overall base composition of chloroplast genome was A (37.2%), T (37.0%), C (12.7%), G (13.1%), similar to other *Ulva* macroalgae in chloroplast genome. The *U. compressa* chloroplast genome encoded 90 genes, including 63 protein-coding genes, 23 transfer RNAs genes and 4 ribosomal RNAs genes.

In addition, we downloaded sequences from the NCBI database: *Ulva mutabilis* (MK069584), *Ulva ohnoi* (AP018696) (Suzuki et al. 2018), *Ulva* sp. (KP720616) (Melton et al. 2015), *Ulva fasciata* (KT882614) (Melton and Lopez-Bautista 2016), *Ulva lactuca* (MH730972) (Hughey et al. 2019) and *Ulva pertusa* (MN853875) (Han et al. 2020). A Maximum-likelihood (ML) phylogenetic tree with 10 complete chloroplast genome of *Ulva* and 1 outgroup called *Pseudendoclonium akinetum* (NC008114) (Pombert et al. 2006) was constructed by using the MEGA 7 software based on Kimura-2-parameter model (K2P) (Figure 1) (Kumar et al. 2016). This phylogenetic analysis used 1,000 bootstrap replicates to verify the support rate of each node in the tree, and the result showed *U. compressa* was closely related to *U. linza*.

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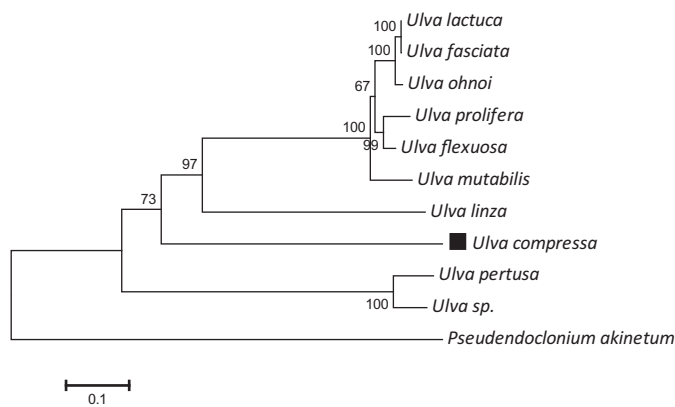


Figure 1. Maximum likelihood phylogenetic tree for *U. compressa* based on the chloroplast genomes. Numbers above each node indicate the bootstrap support value.

In this thesis, we analyzed complete chloroplast genome of *U. compressa* (GenBank accession number MT916929) from the Southern Yellow Sea, which will be useful for studying the genetic diversity of *Ulva* species.

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Disclosure statement

No potential conflict of interest was reported by the author(s).

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Data availability statement

The data that support the findings of this study are openly available in National Center for Biotechnology Information (GenBank accession number MT916929) at <https://www.ncbi.nlm.nih.gov> and ResearchGate at <https://doi.org/10.13140/RG.2.2.30130.43200>.

References

Cai CE, Wang LK, Zhou LJ, He PM, Jiao BH. 2017. Complete chloroplast genome of green tide algae *Ulva flexuosa* (Ulvophyceae, Chlorophyta) with comparative analysis. *PLoS One*. 12(9):e0184196.

Cui JJ, Zhang JH, Monotilla AP, Huo YZ, Shi JT, Zhao XH, Kang XY, He PM. 2019. Assessment of blooming *Ulva* macroalgae production potential in the Yellow Sea. *China. Phycologia*. 58(5):535–541.

Han HB, Yan L, Song W, Wang ZL, Zhang XL. 2020. Complete chloroplast genome of *Ulva pertusa*, one of the causal species of green

macroalgal blooms in the coastal waters of Qinhuangdao, China. *Mitochondrial DNA Part B*. 5(1):1084–1086.

Hu CM, Li DQ, Chen CS, Ge JZ, Muller-Karger FE, Liu JP, Yu F, He MX. 2010. On the recurrent *Ulva prolifera* blooms in the Yellow Sea and East China Sea. *J Geophys Res-Oceans*. 115:C05017.

Hu S, Yang H, Zhang JH, Chen CS, He PM. 2014. Small-scale early aggregation of green tide macroalgae observed on the Subei Bank, Yellow Sea. *Mar Pollut Bull*. 81(1):166–173.

Hughey JR, Maggs CA, Mineur F, Jarvis C, Miller KA, Shabaka SH, Gabrielson PW. 2019. Genetic analysis of the Linnaean *Ulva lactuca* (Ulvales, Chlorophyta) holotype and related type specimens reveals name misapplications, unexpected origins, and new synonymies. *J Phycol*. 55(3):503–508.

Huo YZ, Han HB, Shi HH, Wu HL, Zhang JH, Yu KF, Xu R, Liu CC, Zhang ZL, Liu KF, et al. 2015. Changes to the biomass and species composition of *Ulva* sp on *Porphyra* aquaculture rafts, along the coastal radial sandbank of the Southern Yellow Sea. *Mar Pollut Bull*. 93(1-2): 210–216.

Jiang T, Gu K, Wang LK, Liu Q, Shi JT, Liu MM, Tang CY, Su YZ, Zhong SC, Cai CE, et al. 2019. Complete chloroplast genome of *Ulva prolifera*, the dominant species of green macroalgal blooms in Yellow Sea, China. *Mitochondrial DNA Part B*. 4(1):1930–1931.

Kang XY, Liu JL, Yang XQ, Cui JJ, Zhao LJ, Wen QL, Fu ML, Zhang JH, He PM. 2020. The complete mitochondrial genome of a green macroalgae species: *Ulva meridionalis* (Ulvales: Ulvaceae). *Mitochondrial DNA Part B*. 5(1):760–761.

Kumar S, Stecher G, Tamura K. 2016. MEGA7: Molecular evolutionary genetics analysis version 7.0 for bigger datasets. *Mol Biol Evol*. 33(7): 1870–1874.

Liu DY, Keesing JK, Xing QG, Shi P. 2009. World's largest macroalgal bloom caused by expansion of seaweed aquaculture in China. *Mar Pollut Bull*. 58(6):888–895.

Liu JL, Zhao XH, Kang XY, Zhuang MM, Ding XW, Zhao LJ, Wen QL, Zhu Y, Gu K, Bao QJ, et al. 2020. Good news: we can identify *Ulva* species erupted in the Yellow Sea more easily and cheaply now. *Conservation Genet Resour*. 12(3):447–449.

Liu JL, Zhuang MM, Zhao LJ, Liu YK, Wen QL, Fu ML, Yu KF, Zhang JH, He PM. 2020. Taxonomy and genetic diversity of amphipods living on *Ulva lactuca* L. in Gouqi coast of China. *Pac Sci*. 74(2):137–146.

Melton JT, Leliaert F, Tronholm A, Lopez-Bautista JM. 2015. The complete chloroplast and mitochondrial genomes of the green macroalga *Ulva* sp UNA00071828 (Ulvophyceae, Chlorophyta). *PLoS One*. 10(4): e0121020.

Melton JT, Lopez-Bautista JM. 2016. De novo assembly of the mitochondrial genome of *Ulva fasciata* Delile (Ulvophyceae, Chlorophyta), a distromatic blade-forming green macroalga. *Mitochondrial DNA Part A*. 27(5):3817–3819.

Pombert JF, Lemieux C, Turmel M. 2006. The complete chloroplast DNA sequence of the green alga *Oltmannsiellopsis viridis* reveals a distinctive quadripartite architecture in the chloroplast genome of early diverging ulvophytes. *BMC Biol*. 4:3.

Qu XJ, Moore MJ, Li DZ, Yi TS. 2019. PGA: a software package for rapid, accurate, and flexible batch annotation of plastomes. *Plant Methods*. 15:50.

Shan JZ, Li JM, Xu ZH. 2019. Estimating ecological damage caused by green tides in the Yellow Sea: a choice experiment approach incorporating extended theory of planned behavior. *Ocean Coastal Manage*. 181:104901.

Smetacek V, Zingone A. 2013. Green and golden seaweed tides on the rise. *Nature*. 504(7478):84–88.

Suzuki S, Yamaguchi H, Hiraoka M, Kawachi M. 2018. Mitochondrial and chloroplast genome sequences of *Ulva ohnoi*, a green-tide-forming macroalga in the Southern coastal regions of Japan. *Mitochondrial DNA Part B*. 3(2):765–767.

Wang LK, Cai CE, Zhou LJ, He PM, Jiao BH. 2017. The complete chloroplast genome sequence of *Ulva linza*. *Conservation Genet Resour*. 9(3):463–466.

Wang S, Huo Y, Zhang J, Cui J, Wang Y, Yang L, Zhou Q, Lu Y, Yu K, He P. 2018. Variations of dominant free-floating *Ulva* species in the

- source area for the world's largest macroalgal blooms, China: differences of ecological tolerance. *Harmful Algae*. 74:58–66.
- Xiao J, Wang ZL, Song HJ, Fan SL, Yuan C, Fu MZ, Miao XX, Zhang XL, Su RG, Hu CM. 2020. An anomalous bi-macroalgal bloom caused by *Ulva* and *Sargassum* seaweeds during spring to summer of 2017 in the western Yellow Sea, China. *Harmful Algae*. 93:101760.
- Zhang JH, Huo YZ, Wu HL, Yu KF, Kim JK, Yarish C, Qin YT, Liu CC, Xu R, He PM. 2014. The origin of the *Ulva* macroalgal blooms in the Yellow Sea in 2013. *Mar Pollut Bull*. 89(1-2):276–283.
- Zhang JH, Liu CC, Yang LL, Gao S, Ji X, Huo YZ, Yu KF, Xu R, He PM. 2015. The source of the *Ulva* blooms in the East China Sea by the combination of morphological, molecular and numerical analysis. *Estuar Coast Shelf Sci*. 164:418–424.
- Zhang JH, Shi JT, Gao S, Huo YZ, Cui JJ, Shen H, Liu GY, He PM. 2019. Annual patterns of macroalgal blooms in the Yellow Sea during 2007–2017. *PLOS One*. 14(1):e0210460.
- Zhang JH, Zhao P, Huo YZ, Yu KF, He PM. 2017. The fast expansion of *Pyropia* aquaculture in "Sansha" regions should be mainly responsible for the *Ulva* blooms in Yellow Sea. *Estuar Coast Shelf Sci*. 189:58–65.
- Zhao XH, Cui JJ, Zhang JH, Shi JT, Kang XY, Liu JL, Wen QL, He PM. 2019. Reproductive strategy of the floating alga *Ulva prolifera* in blooms in the Yellow Sea based on a combination of zoid and chromosome analysis. *Mar Pollut Bull*. 146:584–590.
- Zhao XH, Yang XQ, Zhang JH, Wen QL, He PM. 2020. Karyological observations of *Ulva linza* chromosomes. *J Oceanol Limnol*. Early Online, DOI:10.1007/s00343-020-9105-x.