

Mitochondrial DNA

The Journal of DNA Mapping, Sequencing, and Analysis

ISSN: 1940-1736 (Print) 1940-1744 (Online) Journal homepage: <http://www.tandfonline.com/loi/imdn20>

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To cite this article: James Theodore Melton III & Juan Manuel Lopez-Bautista (2015): De novo assembly of the mitochondrial genome of *Ulva fasciata* Delile (Ulvophyceae, Chlorophyta), a distromatic blade-forming green macroalga, Mitochondrial DNA

To link to this article: <http://dx.doi.org/10.3109/19401736.2015.1082095>



Published online: 15 Sep 2015.



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MITOGENOME ANNOUNCEMENT

De novo assembly of the mitochondrial genome of *Ulva fasciata* Delile (Ulvophyceae, Chlorophyta), a distromatic blade-forming green macroalga

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Abstract

We present the 61 614 bp circular-mapping mitochondrial genome of *Ulva fasciata*. Fifty-eight genes were identified including 29 protein-coding genes, 27 transfer RNA (tRNA) genes, and two ribosomal RNA (rRNA) genes. Four ORFs from the *Ulva* sp. UNA00071828 mitogenome were conserved compared to the mitogenome of *Ulva fasciata*. The ~10 000 bp size difference was mostly due to fewer introns found in *U. fasciata* mtDNA (4) as compared with the *Ulva* sp. UNA00071828 mtDNA (10). Introns were annotated in *cox1* (3) and *nad3* (1). The AT content was similar to *Ulva* sp. UNA00071828 mtDNA at 67.5%. A phylogenomic analysis of 28 chlorophytes and 17 protein-coding genes (14 115 bp alignment) showed that *U. fasciata* clusters closely with other members of the Ulvophyceae (*Ulva* sp. UNA00071828, *Pseudoclonium akinetum*, and *Oltmannsiellopsis viridis*). This analysis did not recover a monophyletic Ulvophyceae, however, the Trebouxiophyceae and Chlorophyceae were supported as monophyletic groups.

KeywordsGreen algae, marine, mitochondrion, *Ulva*, Ulvaceae, Ulvales**History**

Received 24 June 2015

Accepted 8 August 2015

Published online 11 September 2015

Species of the green algal genus *Ulva* are common members in the rocky intertidal and are morphologically simple thalli composed of monostromatic tubes, distromatic blades, or blades with tubular margins (Norris, 2010). Worldwide, *Ulva* species are notorious for forming economically and ecologically destructive “green tides” in high nutrient conditions (Leliaert et al., 2009; Ye et al., 2011). Approximately 100 *Ulva* species are currently accepted taxonomically (Guiry & Guiry, 2015), and thus far, the mitogenome of only one *Ulva* species has been reported (Melton et al., 2015). The taxonomy for many *Ulva* species remains unclear due to morphological plasticity and cryptic diversity (Hayden et al., 2003; Heesch et al., 2009). Historically, *Ulva fasciata* Delile has been considered to be a distinct species from *U. lactuca* L. However, some reports have suggested that these species are conspecific (Butler, 2007; O’Kelly et al., 2010; Guiry & Guiry, 2015).

Library construction and DNA sequencing on an Illumina MiSeq platform (Illumina Inc., San Diego, CA) was conducted at Cold Spring Harbor Laboratory, Cold Spring Harbor, NY, with the sample of *Ulva fasciata* (Herbarium voucher: UNA00071832), a deeply divided blade collected near Sebastian Inlet, FL. *De novo* assembly and gene annotations were performed following Melton et al. (2015). A total of 291 372 paired end reads formed a

61 614 bp circular-mapping mitogenome of *Ulva fasciata* (GenBank Accession KT364296). The mean coverage was 464.7X, and the pairwise identity was 99.3%. The AT content of the mitogenome was 67.5%. A total of 58 genes were annotated, including 29 protein-coding genes, 27 tRNAs, and two rRNAs. The gene content was similar to the previously published *Ulva* sp. UNA00071828 mitogenome (KP720617) except two additional tRNAs, *trnL*(uag) and *trnM*(cau), were identified in *U. fasciata*. The gene arrangement of shared genes from both mitogenomes was identical. Four conserved ORFs (*orf1*, *orf3*, *orf5*, and *orf14* as per Melton et al., 2015) were found compared to the *Ulva* sp. mitogenome. The mitogenome of *U. fasciata* was composed of 70% coding DNA (including conserved ORFs).

The 11 879 bp difference between the two *Ulva* mitogenomes was in large part due to a higher number of introns in *Ulva* sp. (10 introns) compared with *Ulva fasciata* (four introns). Three introns (1401 bp, 1248 bp, and 1109 bp in length) were present in *cox1*, and one intron (2481 bp) was annotated in *nad3*. Introns that were present in *nad5*, *atp1*, and *rrs* in the mitogenome of *Ulva* sp. (Melton et al., 2015) were absent in *U. fasciata*.

A maximum likelihood analysis with 28 chlorophytes and 17 mitochondrial protein-coding genes placed *U. fasciata* sister to *Ulva* sp. and close to other ulvophyceans (Figure 1). A monophyletic Ulvophyceae was not recovered; however, this analysis supported the monophyly of the Trebouxiophyceae and Chlorophyceae. Increased taxon sampling is needed to further assess the monophyly of the Ulvophyceae and Trebouxiophyceae. This phylogenomic analysis increases our knowledge on mitochondrial evolution of green algae.

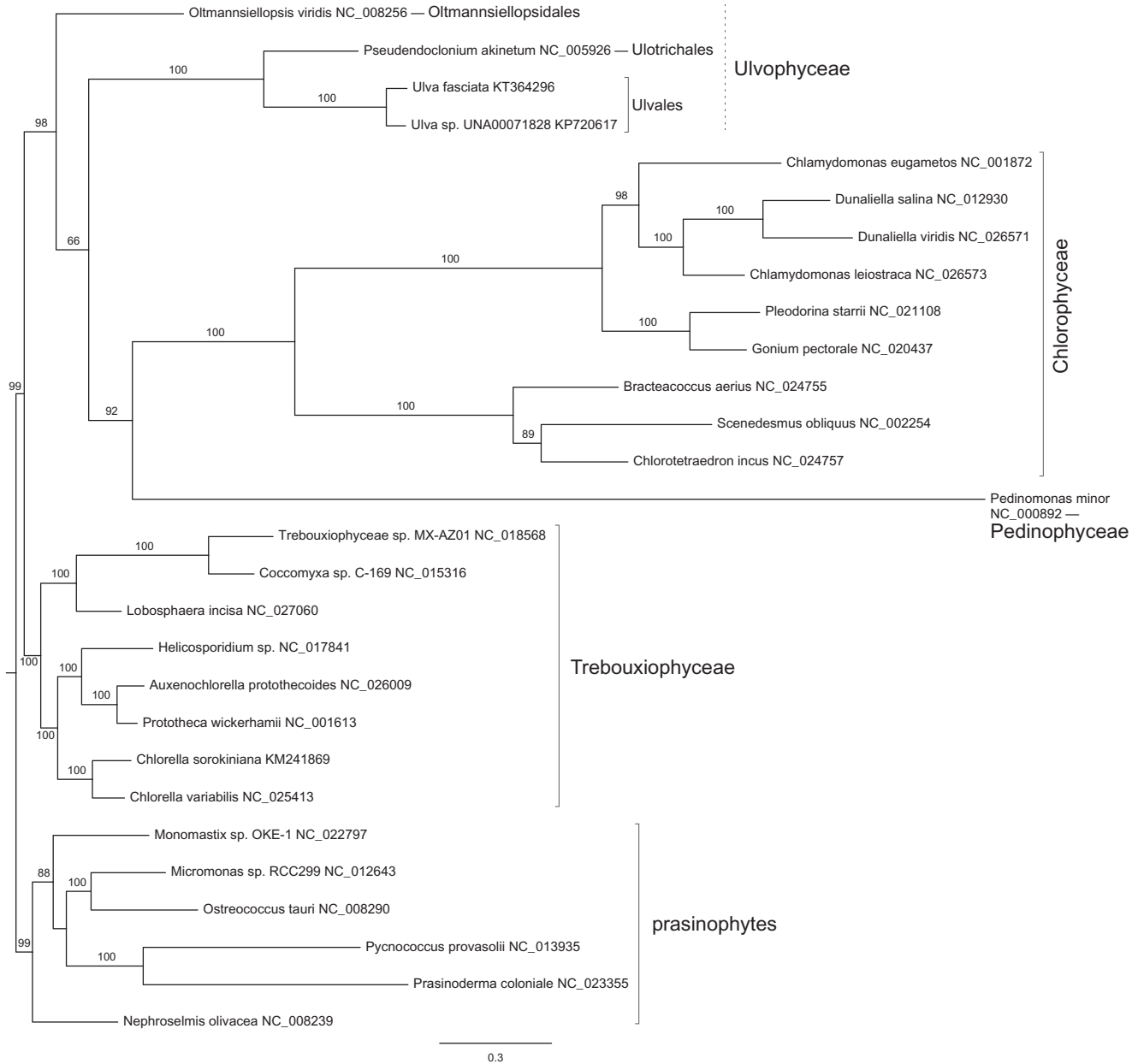


Figure 1. Phylogenomic tree run with 28 taxa and 17 mitochondrial protein-coding genes in RAxML v.7.3.5 (Stamatakis, 2006) with 1000 bootstrap replicates and a GTR + G model of evolution. The alignment was made with the following genes: *atp1*, *atp4*, *atp6*, *atp8*, *atp9*, *cob*, *cox1*, *cox2*, *cox3*, *nad1*, *nad2*, *nad3*, *nad4*, *nad4L*, *nad5*, *nad6*, and *nad7*. An original alignment of 20 316 bp was cut down to 14 115 bp with the Gblocks server (http://molevol.cmima.csic.es/castresana/Gblocks_server.html; Castresana 2000) removing poorly aligned positions. Gblock settings were used following Melton et al. (2015).

Acknowledgements

The authors would like to thank Eric Antoniou for performing the MiSeq run at Cold Spring Harbor, and Frederik Leliaert, Ana Tronholm, and Daryl W. Lam for helping develop a pipeline for assembling and annotating genomes in the PhycoLab (<http://phycolab.ua.edu>). The authors would also like to thank David Ward and Maya Allen for field and technical assistance.

Declaration of interest

The authors report no conflicts of interest and are responsible for the content and writing of this paper. Funds for this investigation were provided by The National Science Foundation through Assembling The Tree of Life for Green Algae GRAToL (DEB 1036495), and the Graduate School and the Department of Biological Sciences at The University of Alabama.

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