Mitochondrial DNA, Early Online: 1–3
© 2015 Informa UK Ltd. DOI: 10.3109/19401736.2015.1007297

MITOGENOME ANNOUNCEMENT

Complete sequence and characterization of mitochondrial and chloroplast genome of Chlorella variabilis NC64A

Massimiliano Orsini1, Cristina Costelli2, Veronica Malavasi2, Roberto Cusano1, Alessandro Concas1, Andrea Angius1,3, and Giacomo Cao1,2,4

1Center for Advanced Studies, Research and Development in Sardinia (CRS4), Pula (CA), Italy, 2Interdepartmental Center of Environmental Science and Engineering (CINSA), University of Cagliari, Cagliari (CA), Italy, 3Institute of Genetic and Biomedical Research (IRGB), National Research Council (CNR), Monserrato (CA), Italy, and 4Department of Mechanical, Chemical and Materials Engineering, Cagliari (CA), Italy

Abstract

The complete nucleotide sequences of the mitochondrial (mtDNA) and chloroplast (cpDNA) genomes of Chlorella variabilis NC64A (Trebuoiophyceae) have been determined in this study (GenBank accession no. KP271968 and KP271969, respectively). The mt genome assembles as a circle of 78,500 bp and contains 62 genes, including 32 protein-coding, 27 tRNA and 3 rRNA genes. The overall GC content is 28.2%, while the coding sequence is 34%. The cp genome forms a circle of 124,793 bp, containing 114 genes, including 79 protein-coding, 32 tRNA and 3 rRNA genes. The overall GC content is 33.9%, while the coding sequence is 50%.

Keywords

Chlorella variabilis, Chlorellaceae, Chloroplast genome, DNA sequencing, Mitochondrial genome

History

Received 20 December 2014
Accepted 30 December 2014
Published online 18 February 2015

Chlorella sp. NC64A, recently renamed Chlorella variabilis by Ryo et al. (2010), is a unicellular photosynthetic green alga which belongs to the true Chlorella genus, i.e. the Trebuoiophyceae (Bock et al., 2011; Huss et al., 1999; Krienitz et al., 2004; Pröschold et al., 2011). Chlorella variabilis is an intracellular photobiont of Paramecium bursaria (Karakashian & Karakashian, 1965). However, similar to other endosymbiotic Chlorella species, it retains the ability to grow autonomously (Kodama & Fujishima, 2009). This symbiotic alga represents a model system to study virus/algal interactions (Blanc et al., 2010). Moreover, for several microalgal strains, there is an increasing interest in using Chlorella variabilis in a variety of biotechnological applications which might involve the production of biofuels (Concas et al., 2014; Schenk et al., 2008), the CO2 capture from flue gases (Chelf et al., 1993; Concas et al., 2012), the production of high added values chemicals and the remediation of wastewaters contaminated by heavy metals (Rajamani et al., 2007). Whole-genome sequencing of the Chlorella variabilis NC64A strain was performed using a Illumina HiSeq2000 platform (Pula (CA), Italy), reads were assembled by a de-novo approach under the Orione framework (Cuccuru et al., 2014), figures were drawn using the OGDraw server (Lohse et al., 2007). The mtDNA sequence of Chlorella variabilis (GenBank accession no. KP271968) assembles as a circular map of 78,500 bp which encodes a total of 62 genes, all present as single copies, including 3 rRNAs, 27 tRNAs and 32 protein coding genes, eighteen of which encode for respiratory proteins of mitochondrial complexes I, IV and V (cf. Figure 1). The overall GC content is 28.2% and the coding sequence is 34% (average length: 835 bp). The cpDNA sequence of Chlorella variabilis (GenBank accession no. KP271969) assembles as a circular map of 124,793 bp which encodes a total of 114 genes (cf. Figure 1). This chloroplast gene repertoire includes 79 protein coding genes (50% of the entire genome with an average length of 790 bp), 3 rRNAs and 32 tRNAs. One tRNA coding gene (tRNA-Leu) and two protein-coding genes (both belonging to the photosystem II) contained introns. Like the others members of the Chlorella genus, the cpDNA of Chlorella variabilis does not display a quadripartite structure. The GC content (33.9%) of the C. variabilis cpDNA is close to the one of Chlorella sp. ArM0029B, which displays a corresponding content of 33.2% (Jeong et al., 2014). On the other hand, it is also very similar to the GC content (34.1%) of C. sorokiniana (Orsini et al., 2014) as well as to the one (31.6%) of C. vulgaris (Wakasugi et al., 1997). The sequences of the symbiotic alga NC64A genomes presented here are relevant both in view of the exploitation of the biotechnological potential of this microalgal strain as well as to further shed light on the evolution of the green lineage.
Figure 1. Gene maps of the chloroplast and mitochondrial genomes of *C. variabilis*. 
Declaration of interest

The authors report no conflicts of interest. The financial support of Department of Mechanical, Chemical and Materials Engineering, University of Cagliari, CRS4 and Sardegna Ricerche is gratefully acknowledged. C. C. and V. M. gratefully acknowledge the Sardinia Regional Government for the financial support of the Scholarship award attended to the International PhD program in Environmental Science and Engineering at the University of Cagliari and the awarded grant INNOVA.RE. WP 2.3-P.O.R.-F.E.S.R. 2007/2013- CUP: F25C10001420008, respectively. We thank Professor James L. Van Etten (University of Nebraska, USA) for providing culture of *Chlorella variabilis* NC64A and Dr James R. Gurnon (University of Nebraska, USA) for the cultivation instructions received.

References


DOI: 10.3109/19401736.2015.1007297

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