MITOGENOME ANNOUNCEMENT

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

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Abstract

The complete nucleotide sequences of the mitochondrial (mtDNA) and chloroplast (cpDNA) genomes of *Chlorella variabilis* NC64A (Trebouxiophyceae) 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%.

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 Trebouxiophyceae (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 CO_2 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 *C. 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 *C. 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, III, 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 *C. 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 *C. 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.
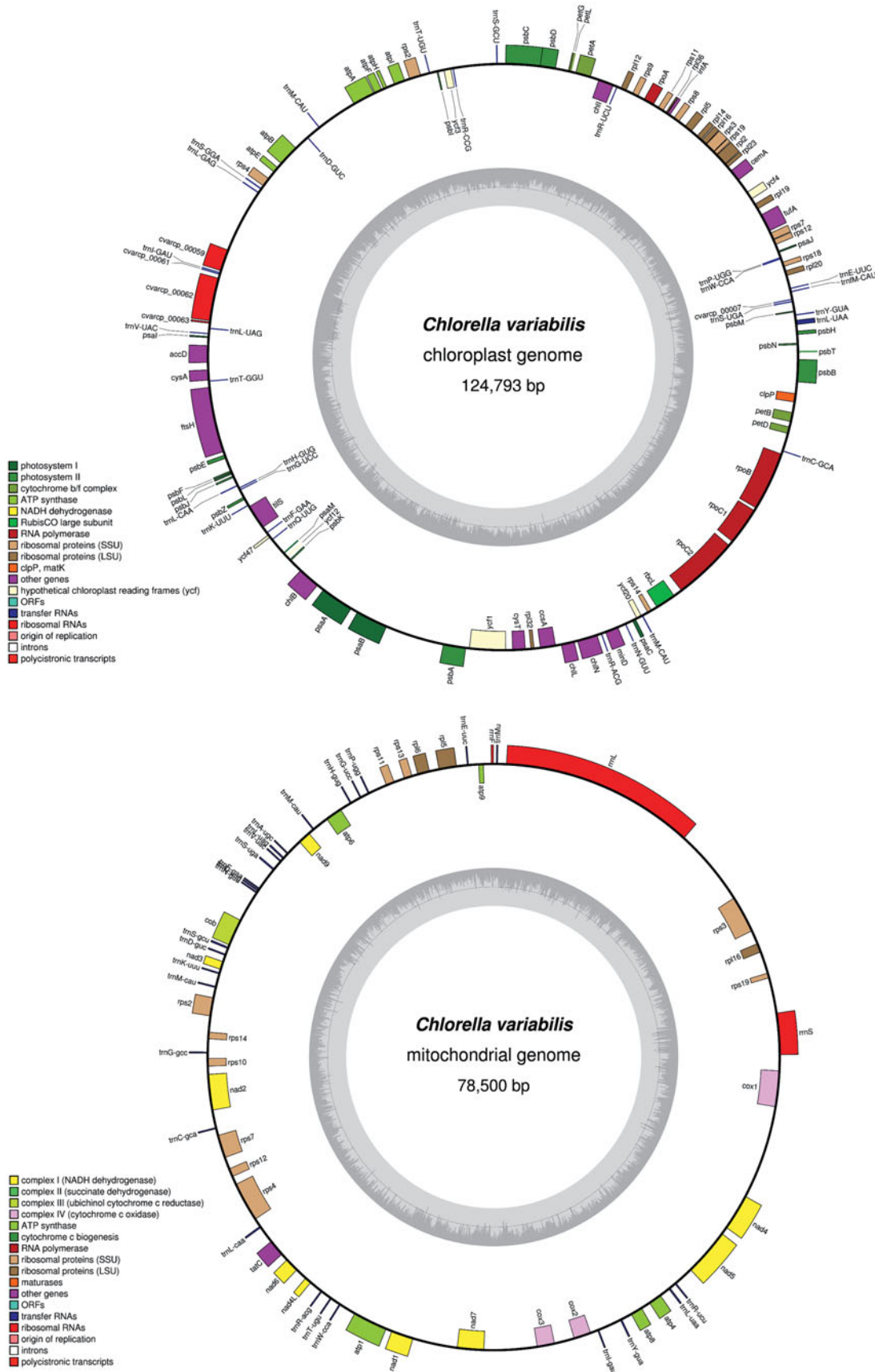
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Figure 1. Gene maps of the chloroplast and mitochondrial genomes of *C. variabilis*.

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