The complete mitochondrial genome of an oleaginous microalga Vischeria stellata strain SAG 33.83 (Eustigmatophyceae)

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ABSTRACT

The complete mitochondrial genome of an oleaginous microalga Vischeria stellata strain SAG 33.83 was sequenced and annotated. The circular genome was 42,608 bp long with 26.7% GC content. The mitochondrial genome of V. stellata strain SAG 33.83 contained 36 protein-coding genes (PCGs), 27 transfer RNA genes (tRNAs), three ribosomal RNA genes (rRNAs). Furthermore, the phylogenetic tree was constructed to validate the evolutionary relationship based on the complete mitogenomes of V. stellata strain SAG 33.83 through combining with seven species of Eustigmatophyceae, two species of Phaeophyceae and one species of Synurophyceae algae. Phylogenetic analysis revealed that Eustigmatophyceae were more closely related to Synurophyceae than Phaeophyceae and V. stellata strain SAG 33.83 had close genetic relationship with Vischeria sp. CAUP Q 202.

Vischeria stellata strain SAG 33.83, an edaphic unicellular microalga, classified into family Eustigmatophyceae, was considered as a promising oleaginous microalga for the production of biofuels and bioproducts (Gao et al. 2016; Wang et al. 2018). It can accumulate large amounts of lipids (66.8% of dry weight (DW)) comprising two important nutritional fatty acids, palmitoleic acid (28% of DW) and eicosapentaenoic acid (1.5% of DW), and other fatty acids. In addition, it could store certain amount of β-carotene (1–2% of DW), which was considered to be a potential nutraceutical. The previous researches about V. stellata focused on cytological character, culture condition and lipid metabolism (Gao et al. 2016). The phylogenetic information of V. stellata, such as 18S rDNA and rbcL gene, is limited.

According to endosymbiosis theory, mitochondrial genome was organelle genetic substance of the eukaryotic cell and directly descendant from endosymbiotic host (heterotrophic eukaryotes) and could provide phylogenetic information of endosymbiotic origins (Lang and Burger 2012). Nevertheless, it was not clear whether the mitochondrial genome of V. stellata plays an important role in lipids metabolism. To reveal the gene content and structure of mitochondria, the whole-genome of V. stellata strain SAG 33.83 was sequenced through Illumina sequencing technology, and the complete mitochondrial genome was obtained.

The origin sample of V. stellata strain SAG 33.83 was collected from Isle Lavsa, Dalmatia, Europe (43.7521° N, 15.3695° W) and deposited in the Culture Collection of Algae at Gottingen University. The total genomic DNA of V. stellata strain SAG 33.83 was extracted by MiniBEST Plant Genomic DNA Extraction Kit (TaKaRa, China) and stored in our laboratory. Then, the purified DNA was used to build fractionated genomic libraries and sequenced with Illumina HiSeq4000 platform by BGI Biotechnology Co. Ltd (Shenzhen, China). After the quality filtration of raw reads, the high-quality reads were assembled by SPAdes 3.9.0 (Bankevich et al. 2012). One contig of the mitochondrial DNA was identified by comparing the sequence similarity to other oleaginous microalgal mitochondrial genomes. Finally, the mitochondrial genome annotation was performed by the UGENE ORFs finder, tRNAscan-SE and RNAmmer 1.2 Server.

The complete mitochondrial genome of V. stellata strain SAG 33.83 was submitted to NCBI (GenBank accession number: MH981596). The length of the mitochondrial genome was 42,608 bp of circular genome, with 26.56% GC content. It contained 3 rRNA genes for 5S, small subunit and large subunits ribosomal RNA (rRNA), 27 tRNA genes and 36 protein-coding genes include four atp genes, three cox genes, 10 mitochondrial ribosomal RNA (rRNA), 27 tRNA genes and 36 protein-coding genes include four atp genes, three cox genes, 10 mitogenomes from seven species of Eustigmatophyceae (Mannochloropsis gaditana strain CCMP526 (GenBank accession number: KJ410686), Mannochloropsis salina strain CCMP537 (KC568458), Nannochloropsis limnetica strain CCMP505 (KC568459), Nannochloropsis oceanica strain IMET1 (KC568456), Monodopsis sp. MarTras21 (KU501222), Trachycoccus minutus strain CCALA 838 (KU501220), Vischeria sp. CAUP Q 202 (KU501221)) (Wei et al. 2013; Sevčíková et al. 2016), two species of Phaeophyceae (Ectocarpus siliculosus (FPB85846), Saccharina japonica (AP011493) (Cock et al. 2010) and one species of Synurophyceae (Synura synuroidea (AF222718)) (Chesnick et al. 2000) and V. stellata strain SAG 33.83 in this study. The concatenated alignments of 11 algal mitochondrial genomes were calculated by HomBlocks (Brewton et al. 2012).
et al. 2017), resulting in alignments of each species with 11,151 bp, including cob, cox1, cox3, nad1, nad4, nad5, nad7, small subunit and large subunits rRNA. The phylogenetic tree was constructed based on neighbour-joining method by MEGA7 (Kumar et al. 2016), relied on Gamma distribution model with 1000 bootstrap replicates. The evolutionary distances were computed using the Kimura 2-parameter method and are in the units of the number of base substitutions per site. The phylogenetic analysis results supported that the mitochondrial genes of Eustigmatophyceae were more closely related to Synurophyceae than Phaeophyceae (Figure 1). Meanwhile, the phylogenetic tree showed that the V. stellata strain SAG 33.83 was clustered in the Eustigmataceae clade and genetically close to Vischeria sp. CAUP Q 202 (KU501221) (Sevčíková et al. 2016).

Declaration statement

No potential conflict of interest was reported by the authors. The authors alone are responsible for the content and writing of the paper.

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Figure 1. Phylogenetic relationships among 11 algae mitochondrial genomes. GenBank accession numbers are shown in parentheses. The scale bar indicates 0.05 substitutions per nucleotide position.

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