Draft Genome Sequence of the Anoxygenic Filamentous Phototrophic Bacterium Oscillochloris trichoides subsp. DG-6

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Oscillochloris trichoides is a mesophilic, filamentous, photoautotrophic, nonsulfur, diazotrophic bacterium which is capable of carbon dioxide fixation via the reductive pentose phosphate cycle and possesses no assimilative sulfate reduction. Here, we present the draft genome sequence of Oscillochloris trichoides subsp. DG-6, the type strain of the species, which has permitted the prediction of genes for carbon and nitrogen metabolism and for the light-harvesting apparatus.

The anoxicogenic filamentous phototrophic bacteria (AFPB) group belong to the phylum Chloroflexi, which contains two families: Chloroflexaceae and Oscillochloridaceae. Oscillochloridaceae consists of single Oscillochloris genus, to which the investigated bacterium Oscillochloris trichoides subsp. DG-6 belongs. The representatives of the Chloroflexaceae family are in general thermophilic photoorganotrophs (5, 11, 12), while Oscillochloridaceae bacteria are mesophilic photolithoautotrophs (9). The strain O. trichoides subsp. DG-6 was isolated from microbial mats of warm hydrogen sulfide springs in the Caucasus region of southeast Europe (7, 8).

The genomic DNA sequencing was performed using the combined approach which included the Sanger (ABI 3730) sequencing of the genomic DNA library with the insert lengths of 2.5 to 3.0 kbp combined with whole-genome shotgun and paired-end sequencing using a 454 FLX apparatus. The draft assembly of the obtained sequences was carried out using the Phred/Phrap/Consed software (2, 4). The identification and annotation of the found open reading frames (ORFs) were performed using the Glimmer software package (3) and by comparison with the corresponding data from the UniProt, KEGG, and NR-NCBI databases.

The resulting genomic DNA sequence (4,370,273 nucleotides) of O. trichoides subsp. DG-6 included 65 contigs, united into 5 scaffolds separated by ribosomal operons which were placed in 2 separate contigs—16S and 23S-5S. The number of complete (16S-23S-5S) ribosomal operons was four, and one other ribosomal operon was reduced to 23S-5S genes. The mean GC content of the obtained sequence was 59.26%, thus corresponding to the previously published data (9). In the obtained sequence, 3,853 ORFs were found, and between these genes encoding tRNAs were revealed.

In the results of the analysis of the Oscillochloris trichoides subsp. DG-6 genomic DNA sequence, the set of genes corresponding to the photosystem II genes was revealed. Among these genes were those encoding the proteins of light-harvesting antennas together with proteins participating in the synthesis of bacteriochlorophylls and carotenoids. This set was spread between five regions of the genomic DNA.

As it was shown previously (6), the bacteria belonging to the Oscillochloridaceae family are capable in autotrophic assimilation of carbon dioxide via the Calvin-Benson-Bassham cycle. In the results of the analysis of the O. trichoides subsp. DG-6 genomic DNA, the set of genes encoding the enzymes of this metabolic pathway was revealed. The gene order in the set (cbbL-cbbS-cbbX) was specific for the gene clusters encoding RubisCo type I. As for the Calvin cycle gene cluster in the genome of Sulfobacillus acidophilus, Thiobacillus denitrificans, and Thiobacillus neapolitanus (1, 10), whose CbbL amino acid sequence together with that of O. trichoides forms the separate cluster on the phylogenetic tree of these enzymes (13), the regulatory gene cbbR is not present in the corresponding gene cluster but is located in the different genome region.

The capability to fix atmospheric nitrogen is a specific feature of O. trichoides that is not found in all other AFPB. The cluster of genes encoding the molybdenum nitrogenase system was found in the genomic DNA of Oscillochloris trichoides subsp. DG-6, which is responsible for nitrogen fixation (nitrogenase iron protein/nitrogenase molybdenum-iron protein/nitrogenase component I/Fe-S oxidoreductase).

Nucleotide sequence accession number. The obtained sequences were deposited in DDBJ/EMBL/GenBank under accession number ADVR00000000.

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REFERENCES