Draft genome sequence of *Cyanobacterium* sp. strain IPPAS B-1200 with unique fatty acid composition

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Abstract

Here, we report the draft genome of *Cyanobacterium* sp. IPPAS strain B-1200 isolated from Lake Balkhash, Kazakhstan, and characterized by the unique fatty acid composition of membrane lipids enriched with myristic and myristoleic acids. The approximate genome size is 3.4 Mb. The predicted number of coding sequences is 3119.

Cyanobacteria are the prolific source of various useful compounds, including fatty acids suitable for biodiesel production (1). The cyanobacterial strain *Cyanobacterium* sp. IPPAS strain B-1200 has been characterized by the unique fatty acid composition of the membrane lipids enriched with myristic (30%), myristoleic (10%), palmitic (40%), palmitoleic (10%) acids (2). The strain was able for growth intensively at temperatures ranging from 24 to 39ºC. Listed advantages make this strain a target candidate for production of high cetane number biodiesel.

Genomic DNA was isolated from cyanobacterial cells by incubation with saturated iodide solution followed by lysozyme treatment and 2% SDS lysis at 70ºC (3). Lysate was treated with phenol/chloroform mixture for DNA purification. DNA libraries for sequencing were prepared using Nextera XT and Ion Xpress kits. Sequencing was performed on MiSeq system with MiSeq reagent kit v3 in 600-cycle paired-end format and Ion PGM with Hi-Q chemistry.

Genome was assembled using SPAdes 3.7.1 (4) and MIRA 4.0.2 software (5). The draft genome assembly quality was analyzed by QUAST (6). For draft genome median coverage was approximately 200x and N50 was 80222. Approximate genome size is 3.4 Mb, the average G+C content was estimated as 37.7%.

Genome was annotated using automated NCBI PGAP. It contained 3119 genes in total with 2934 genes coding for proteins, 137 pseudo genes, 4 rRNA-coding sequences, 40 tRNAs, 4 non-coding RNA. 2 CRISPR arrays have been found in the genome. Genome contained only one gene for the acyl-lipid Δ9- desaturase, *desC*, responsible for Δ^9-dehydrogenation of C14- and C16-fatty acids. This coincides with genomic data of the type-strain of this genus, *Cyanobacterium stanierii* PCC 7202 (7). Therefore, *Cyanobacterium* sp. strain IPPAS B-1200 is an atypical representative of cyanobacteria of Group 1 that containing only monounsaturated fatty acids in both *sn*-1 and *sn*-2 positions of membrane lipids (8).

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