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Polyphasic characterization of the thermotolerant cyanobacterium *Desertifilum* sp. strain IPPAS B-1220

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One sentence summary: Polyphasic characterization of a new thermophilic cyanobacterial strain of *Desertifilum*, IPPAS B-1220, revealed an unusual fatty acid composition and the presence of six genes for the acyl-lipid desaturases.

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ABSTRACT

A cyanobacterial strain from Lake Shar-Nuur, a freshwater lake in Mongolia, was isolated and characterized by a polyphasic approach. According to the 16S ribosomal RNA gene sequence, this strain (IPPAS B-1220) belongs to a newly described genus *Desertifilum*. In general, strains of *Desertifilum* maintain their genetic stability, as seen from the analysis of the 16S rRNA gene and 16S–23S rRNA internal transcribed spacer sequences from strains collected at distant locations. The newly discovered strain is characterized by an unusual fatty acid composition (16:1 Δ^7 and 16:2 $\Delta^{7,10}$). Analysis of its draft genomic sequence reveals the presence of six genes for the acyl-lipid desaturases: two Δ^9 -desaturases, *desC1* and *desC2*; two Δ^{12} -desaturases, *desA1* and *desA2*; one desaturase of unknown specificity, *desX*; and one gene for the bacillary-type desaturase, *desG*, which supposedly encodes an ω^9 -desaturase. A scheme for a fatty acid desaturation pathway that describes the biosynthesis of 16:1 Δ^7 and 16:2 $\Delta^{7,10}$ fatty acids in *Desertifilum* is proposed.

Keywords: *Desertifilum*; molecular phylogeny; polyphasic approach; ultrastructure; fatty acids; fatty acid desaturases

INTRODUCTION

Cyanobacteria are known as producers of many biologically active compounds that may be used for biotechnological or medical purposes. Clearly the search for new bioactive compounds includes both the discovery and thorough analysis of new cyanobacterial strains that can potentially serve as efficient bioproductors. At the present time, unusual extreme environments provide a variety of undescribed microorganisms and are a great source of new strains for cyanobacterial research.

Accurate assessment of a newly isolated cyanobacterial strain is important not only for its individual taxonomic characterization, but contributes to the overall cyanobacterial systematics as well. In this work, we use a polyphasic approach suggested by Komárek and co-authors (Komárek et al. 2014). This approach implies characterization of an organism at morphological, ultrastructural, biochemical and molecular levels and significantly improves the quality of assessment. Current developments in next-generation sequencing allow fast and efficient

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