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 cyclo-16:1 desaturase.

Abstract

A cyanobacterial strain from Lake Shan-Nuur, a freshwater lake in Mongolia, was isolated and characterized by a polyphasic approach. According to the 16S ribosomal RNA gene sequence, this strain (IPNAS 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 (16:1A7 and 16:2Δ9). Analysis of its draft genomic sequence reveals the presence of six genes for the cyclo-16:1 desaturase: two Δ9-desaturases, desA and desC; two Δ12-desaturases, desA1 and desA2; one desaturase of unknown specificity, desX; and one gene for the bicyclic type desaturase, desG, which supposedly encodes an α9 desaturase. A scheme for a fatty acid desaturation pathway that describes the biosynthesis of 16:1A7 and 16:2Δ9 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 bioproducers. 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 Komnik and co-authors (Komnik et al. 2004). 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