Molecular identification and characterization of some Egyptian marine cyanobacteria

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ABSTRACT

Molecular techniques were applied to study three cyanobacterial isolates (Spirulina, Oscillatoria and Anabaena). Genetic diversity among strains was tested by PCR amplification and DNA sequencing of 16S rDNA gene using universal primers and the obtained sequences wase compared with those available in the GeneBank Database. Phylogenetic tree was inferred by NJ distance method. For more exact distinguishing proof, a set of oligonucleotide primers were developed for the specific amplification of 16S rDNA gene from the three cyanobacterial isolates by PCR. Both universal primer-based sequencing and specific PCR amplification of 16S rDNA gene revealed the same results as the three cyanobacterial species were identified as: Spirulina sp. EEW5, Oscillatoria accuminata PCC 6304 and Anabaena variabilis RPAN54, revealing the usefulness of such PCR fingerprinting profiles for the identification of cyanobacterial isolates. The chemical analysis of cyanobacterial isolates showed that Spirulina had the highest protein percentage and amino acids content in addition to considerable amounts of phytohormones. Oscillatoria recorded higher content of photosynthetic pigments including phycobiliproteins.

Keywords: *Cyanobacteria, PCR, 16S rDNA, Spirulina, Oscillatoria, Anabaena, Chemical analysis.*

INTRODUCTION

Cyanobacteria are a morphologically diverse group of bacteria ranging from unicellular to colonial and filamentous forms. They are significant component of the marine nitrogen cycle and could be found in both freshwater (Dyer, 2003) and hypersaline lakes (Hogan, 2008). Algae also consume extant CO_2 and are able to inhabit nearly all ecosystems of the world, from deserts to popular seas. Cyanobacteria are the most common inhabitants of saline-alkaline lakes in different parts of the world (Grant, 2004). Traditionally, the classification of cyanobacteria has been based on morphological characters such as trichome width, cell size, division planes, shape and arrangement, pigmentation and the presence of structures such as gas vacuoles, sheath, heterocysts and akinetes (Rippka *et al.*, 1979 and Baker, 1992). Beyond the considerable expertise required to identify species by such characters, subjective judgment by operators can lead to errors, resulting in incorrect assignment of isolates. Moreover, some diagnostic features, such as gas vacuoles or akinetes, can show variations with different environmental or growth conditions and even be lost during cultivation (Lyra *et al.*, 2001). Such limitations of phenotypic characters have highlighted the requirement for more reliable