BIODIVERSITY AND FATTY ACID PRODUCTION IN CYANOBACTERIA

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Abstract

In this investigation we examined the genetic diversity of several filamentous clonal cultures of cyanobacteria, from different regions of the Antarctic (*Nostoc*, *Leptolyngbya*, *Plectonema*) and Mediterranean (*Nostoc*).The genetic diversity of different genera obtained by RAPD-PCR technique was correlated to certain physiological features of the cianobacteria such as their fatty acid production.UPGMA analysis revealed two different groups *Oscillatoriales*, *Plectonema* and *Leptolyngbya*, and *Nostocales,* comprising two Antarctic *Nostoc* strains and one *Nostoc* Mediterranean strain. Such a study, which confirms the endemism of *Nostoc* genus in Antarctic and Mediterranean, shows phylogenetic distribution in relation to geographical position. The physiological features of the strains show a high degree of specificity with regard to their content of fatty acids. Differences were noted in production of the two groups. Such information is relevant to many questions, both basic and applied, in monitoring and assessing environmental quality in relation to the production of bioactive metabolites in response to stress.

Keywords : Cyanobacteria, Biodiversity, Physiology.

In this investigation, we examined filamentous clonal cultures of cyanobacteria, from different locations of the Antarctic and Mediterranean. Cyanobacteria (tab.1) were collected in the Antarctic region during the 2004 summer cruise and subsequently grown in axenic laboratory conditions prior to analysis at optimum laboratory conditions (Light intensity 5 μE $m^2 s^{-1}$ PAR Photosynthetic Active Radiation; T=20 °C). Morphological and biomass analysis (Tab.1) were checked before genetic studies. DNA extraction was carried out (MagnaRack, Invitrogen SpA, Italy). Biodiversity was detected by PCR. The amplification products were separated by gel electrophoresis (agarose 1.4%) and photographed under U.V. light after ethidium bromide staining. Eight primers were used: BY11 (5'-ATCCACTGCA-3'); BY12 (5'-GGTCGCAGGC-3'); BY15 (5'-CTCACCGTCC-3'); DN4 (5'-GTCGTGCTAT-3'); DN5 (5'-CCGACGGCAA,-3'); DN6 (5'-TGGACCGGTG-3'); UB24 (5'-GGGTGAACCG-3'); UB28 (5'-GCTGGGCCGA-3'). Cluster analysis (UPGMA) of the similarity index was carried out using NT-SYS software. To analyse fatty acid, the samples were methilated. Fatty Acid Methyl Esters (FAME) were detected by gas chromatography using C19:0 as internal standard.

Tab. 1. Data on the seven populations of cyanobacteria.

Strain	Sampling site	Biomass (cell/mL)
Nostoc (KP1a S01)	Kar Plateau 76°54'S 162°32'E	7,5 x 10^5
Nostoc (EPN 16b S01)	Edmonson point Nord	17,5 x 10^5
Nostoc (Mediterranean)	Mediterranean	5 x 10^6
Leptolyngbya (CK 338b S01)	Cape King 73°53'S 166°40'E	360-490 x 10^5
Leptolyngbya (TN 1b S04)	Teall Nunatak 74°50'S 162°34'E	51-76 x 10^5
Plectonema (KP 1a S04)	Kar Plateau 76°54'S 162°32'E	78-116 x 10^5

Discussion of results

UPGMA phenogram (Fig.1) revealed the pattern of genetic distance, showing two different groups comprising the order of Nostocales and Oscillatoriales. This analysis confirms the endemism of Nostoc genus in the Antarctic and Mediterranean regions, revealing its phylogenetic distribution in relation to geographical position. Data relating to the matrix of similarity [1] revealed an average similarity of 15,37 % between the six populations of cyanobacteria analized; the average value of similarity of 27,04 % appears for *Nostoc* Mediterranean and two *Nostoc* Antarctic. Matrix correlation (r) obtained by Mantel test gave a value of 0.95, revealing a good statistical result. Genomic fingerprinting, revealed by PCR technique, gave several molecular fragments of varying sizes, ranging from 0.1 to 8.0 Kb. The distribution of molecular fragments for each species analysed indicates that the majority of the molecular fragments are in the range of 251-1000 Kb, especially in the *Nostoc* genus. The genetic variability we encountered was correlated to the fatty acid production of the different strains. The physiological features of the strains showed a high degree of specificity regarding their content of fatty acids. We observed that the largest percentage of fatty acid produced by all the strains was the 16:0 (palmitic) and 18: 2 n6 c (linoleic); whilst the 17:0 ante (IUPAC) was produced in large amounts by the Leptolyngbya instead of *Nostoc*. The 18:3 n3 (linolenic) showed an opposite trend with the highest percentage of production by Antarctic *Nostoc* rather than Leptolyngbya genera. Plectonema showed an intermediate concentration in percentage of production regarding this fatty acid. This analysis revealed that the amount of some fatty acids is sometimes correlated to the genus, as seen in linoleic and alpha-linolenic acids that were abundant in *Nostoc* species [2]. The RAPD-PCR amplification revealed that *Nostoc* genera produced the greatest number and weight of molecular fragments. Molecular analysis together with morphological and physiological study, is confirmed to be a valid tool in determining a first screening of the different cyanobacteria, evidencing an ample range of molecular weight between 0.1 to 8.0 Kb. These results evidence the high capacity of these organisms to consolidate their key-role. Cyanobacteria adapt physiologically to different environments, producing secondary biologically active molecules which are useful for human health [3].

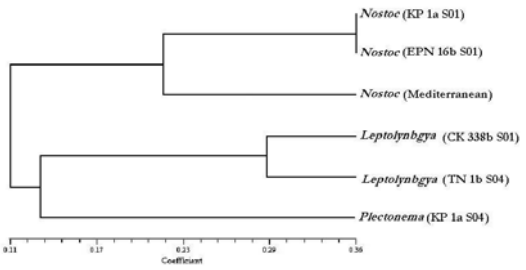

Fig. 1. UPGMA phenogram constructed from matrix of RAPD-based genetic distances of populations.

References

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