



Application of an universal DNA microarray to cyanobacterial diversity assessment

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Our technological goal was to test the new technology of DNA microarrays in the field of biodiversity assessments. The efficiency of DNA microarrays was compared against the "classical" methods for measuring and monitoring the biodiversity. We use cyanobacteria from freshwater lakes as model organisms belonging to a well defined phylum of much ecological relevance. The combination of the information about cyanobacterial biodiversity together with the data describing the water quality of the lakes may reveal useful information to design management actions to control the unwanted mass developments of cyanobacteria. Such blooms prevent the use of water for drinking and for recreation and can be toxic to animals and humans. The possibility to automate the microarray technology in water quality monitoring will be an interesting alternative to time-consuming microscopic enumerations.

KEY WORDS: Cyanobacteria - LDR reaction - Biodiversity assessment.

Cyanobacteria are a group of photosynthetic prokaryotes widely distributed in waters and important in biosphere as primary producers.^{1,2} Recently, with the increased use of surface basins as source of drinkable water, freshwater populations of cyanobacteria have come to the attention of scientists because their blooms are often toxic and constitute high potential risks for human health. The dynamics of a natural cyanobacterial population is not easy to follow, especially if pre-

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cise information on the identity of its members are needed. This is one of the main goals of the EC-sponsored project MIDI-CHIP, addressing the study of the cyanobacterial populations of selected lakes and basins in Northern, Central and Southern Europe. A polyphasic (phenotypic and genotypic) approach has been chosen, which encompasses the morphological description of the cyanobacterial groups retrieved in natural samples, the characterisation of the natural populations with molecular techniques and the use of a DNA microarray able to detect cyanobacterial species as the output of this integrated approach.

Research groups of Finland, Luxembourg/Belgium, Italy and Czech Republic carry out the sampling of biotopes, the isolation and the culture of cyanobacterial strains and the morphological taxonomic analyses. Finnish, Belgian and Italian laboratories are involved in the molecular biodiversity studies, based on classical and new molecular methodologies.

Finally, a computer analysis system will be developed to summarize the collected data and to calculate the microbial biodiversity indexes. A scheme of the MIDI-CHIP project components is shown in Figure 1.