Structural Proteomics of *Microcystis aeruginosa* Species (Cyanobacteria)

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The occurrence of cyanobacteria toxic blooms in freshwaters is commonly favored in eutrophic environments due to nutrients input from seawaters and industrials rejects. In this view, *Microcystis aeruginosa,* normally found in worldwide freshwaters, is able to produce hepatotoxins known as microcystins. Since microcystins are not removed after conventional water treatment, they represent high economical impact and a serious public health problem. For these reasons, report here presented aims to verify what proteins are structurally expressed in *M. aeruginosa* by using a 2DE structural proteomics tool. Cell extracts were obtained from axenic cultures of *Microcystis aeruginosa* PCC7820 in the beginning of the log phase growth (DO_{680}=0.2). Protein concentration was evaluated by Qubit fluorescent assay, showing concentration of 454 µg.mL^{-1}. Initially, SDS-PAGE was carried out in order to evaluate sample protein content showing 20 major protein bands between 70 and 14 kDa. Furthermore, 2-DE was carried out in triplicates in order to obtain protein maps, utilizing non-linear strips of 13 cm with a 3-11 pH range. Gels were analyzed by BioNumerics software showing 152 proteins well resolved. The majority of the detected spots in the gels are between pls 4 to 7. In summary, this report represents a real contribution to understand *Microcystis* cytosolic composition. This knowledge could help in a near future to understand *Microcystis aeruginosa* metabolism and further develop efficient methods to avoid microcystins water contamination.

Key words: *toxic blooms,* Microcystis aeruginosa*, microcystin, structural proteomics, 2-DE.*