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HIGH-THROUGHPUT SEQUENCING REVEALS HIGH CYANOBACTERIAL DIVERSITY IN A LARGE PERIALPINE LAKE

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The study of phytoplankton and cyanobacterial diversity in aquatic environments has been traditionally limited mostly to the microscopic examination of samples and to the use of molecular techniques based on culture-dependent approaches. In the case of cyanobacteria, a correct identification of individuals is of paramount importance, due to the ability of these organisms to produce a wide variety of toxic compounds. Nevertheless, owing to the limitations of the traditional approaches, the number of cyanobacterial taxa can be severely underestimated and identifications affected by taxonomic ambiguities. This is especially true in the detection of rarest and/or smaller individuals. In this study, we evaluated the use of high-throughput sequencing (HTS; Illumina MiSeq) as a tool for the study of cyanobacterial diversity in a large lake south of the Alps (Lake Garda). Results obtained from two years of monthly samplings allowed discovering a wide diversity. The most abundant operational taxonomic units recovered coincided with the most abundant taxa identified using traditional microscopic and molecular approaches (e.g. *Tychonema*, *Planktothrix*, *Dolichospermum*, *Microcystis*). Conversely, HTS allowed identifying many other small abundant *Synechococcales* and *Chroococcales*, as well as other rare large *Nostocales* never identified so far. The concurrent metabolomic profiling provided results consistent with the production of anatoxins and microcystins by the most abundant taxa. Though HTS enables increasing the knowledge of microbial complexity in response to environmental changes, its use in the evaluation of the specific diversity of target groups is not free of complications, e.g. due to the short length of 16S rRNA sequences.