

THE HIDDEN DIVERSITY OF CYANOBACTERIA UNVEILED BY HIGH THROUGHPUT SEQUENCING APPROACHES

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Abstract

While the use of microscopy can compromise the correct identification of cyanobacteria due to overlap and lack of a suitable number of diacritical features, the use of genetic approaches can limit the taxonomic identification mostly to the isolable and cultivable species. Advances in metagenomics and metabarcoding techniques have opened new rapidly growing fields of research, allowing better identification of the diversity characterizing planktic communities. For example, one of the most exciting discovery was the recent identification of new non-photosynthetic cyanobacteria (NPC) in a variety of environments, including waterbodies and animal guts. At present, owing to the lack of isolates and microscopic descriptions, these new organisms can be identified only using metagenomic analyses of environmental samples. This contribution will evaluate the efficacy of high-throughput sequencing (HTS, Illumina MiSeq) in the study of cyanobacterial diversity in a group of large and deep lakes south of the Alps (lakes Garda, Como, Iseo, Lugano and Idro). The analyses, based on gene marker amplification metagenomics (16S rRNA gene), were carried out on samples collected during the summer months. Bioinformatic pipelines identified several different amplicon sequence variants (ASVs) that coincided with the most abundant taxa previously characterized using traditional microscopic methods and molecular and phylogenetic analyses based on cyanobacterial isolates (e.g. *Tychonema*, *Planktothrix*, *Dolichospermum*, *Microcystis*). In addition, HTS allowed identification of many other abundant small Synechococcales, Chroococcales, rare large Nostocales never identified so far with traditional approaches, as well as several ASVs belonging to the new classes of NPCs, i.e. Melainabacteria and Sericytochromatia (formerly ML635J-21).