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Abstract Book



Biomonitoring survey of the hydrographical network in a MAB UNESCO Biosphere Reserve

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The knowledge of microbial biodiversity (bacteria and protists) in aquatic ecosystems is far from complete. This is mainly due to the inadequacy of conventional taxonomic identifications, which are based on the discrimination of diacritical morphological traits. Further, investigations are mainly focused on specific lake and river typologies that are usually also of interest for economic exploitation, often disregarding the small and/or ephemeral water bodies. Nevertheless, due to their physiographical complexity and temporal dynamics, these neglected hydrographical elements can host a vast microbial diversity. In order to fill the gap in the biodiversity estimates in the Alpine region, we carried out a survey using high throughput sequencing (HTS) of 16S and 18S rDNA markers from water and sediments collected in the MAB UNESCO Alpi Ledrensi and Judicaria Biosphere Reserve (Project Acqua Viva). The study sites are located between Lake Garda and the Brenta Dolomites, and include natural environments in a semi- anthropized Alpine context with agricultural and tourist vocation. The survey was carried out during the summer 2019, covering 20 sites of different sizes and characteristics, including lakes, alpine pasture ponds and wetlands. The results allowed disclosing a high number of amplicon sequence variants (ASVs) belonging to a wide variety of bacterial and protists groups, and significant differences linked to lake and sample typologies. Despite a wide presence of potentially toxigenic cyanobacteria, microcystins and anatoxin-a were detected only in a few water bodies, including Lake Ledro, which showed the presence of both *Planktothrix rubescens* and *Tychonema bourrellyi* in the pelagic samples.