



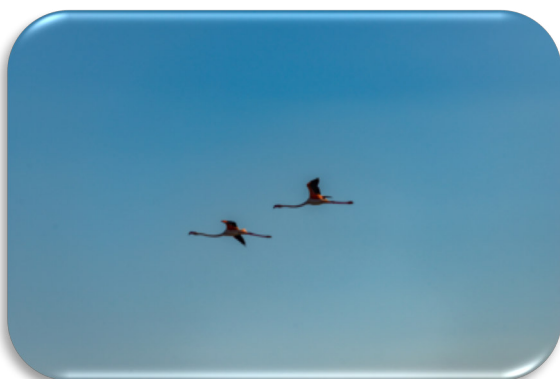
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Comunicazioni

[C001] Disentangling cyanobacterial diversity in a large perialpine lake using high-throughput sequencing and culture dependent approaches

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In phytoplankton, a correct identification of cyanobacteria is of paramount importance, due to the ability of these organisms to produce a great variety of toxic compounds. Traditionally, the study of phytoplankton and cyanobacterial diversity in aquatic ecosystems was typically based on the microscopic examination of specimens and on the adoption of classical culture-dependent approaches and molecular techniques. Nevertheless, owing to the limitations of the traditional approaches, the number of cyanobacterial taxa can be severely underestimated and, in the case of microscopic observations, the correct identification compromised by taxonomic ambiguities and lack of a suitable number of diacritical features. In this contribution, we will evaluate the use of high-throughput sequencing (HTS; Illumina MiSeq) as a tool for the study of cyanobacterial diversity in a large and deep lake south of the Alps (Lake Garda). The analyses, based on gene marker amplification metagenomics (16S rRNA gene) were carried out on monthly samples collected during a two-years sampling campaign. The most abundant operational taxonomic units (OTUs) coincided with the most abundant taxa identified using traditional microscopic and culture dependent approaches based on molecular and phylogenetic analyses (e.g. *Tychonema*, *Planktothrix*, *Dolichospermum*, *Microcystis*). On the other hand, HTS allowed further identification of many abundant small Synechococcales and Chroococcales, and other rare large Nostocales never identified so far with traditional approaches. The concurrent metabolomic analyses confirmed the production of anatoxins and microcystins by the most abundant toxigenic taxa. While HTS approaches enable increasing the knowledge of microbial diversity, their use in the evaluation of target groups is not free of difficulties due, among the others, to the short length of 16S rRNA sequences.

[C002] Influence of the Po River mouths on the microbial community of the prodelta benthic environment

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Within the framework of the CNR flagship project RITMARE, the Po Prodelta Observation Cruise (POPo2014) carried out on the R/V OGS Explora between 2-8 October 2014 was aimed, among other goals, to understand to what extent sedimentary dynamics affect the microbial benthic community. In this work we will report on: 1) identification of prodeltaic areas most influenced by the recent influx of organic and inorganic matter obtained by lithological observation and analyses of short-lived radioisotopes (⁷Be and ¹³⁷Cs); 2) evaluation of the most recent sedimentary supply impact on microbial communities through sedimentological (density, porosity, water content, grain-size and lithology) and geochemical (TOC, $\delta^{13}\text{C}$, C/N) characterization, as well as 3) analysis of microbial community composition (CARD-FISH) in superficial (top 0-2cm) and sub-superficial (the underlying 2 cm) sediment layers. Inshore stations, in front of the main river mouths, showed a sedimentary record characterized by a sequence of 2-5 cm thick fine organic-rich dark graded sediment layers, topped by a thin oxidized surface layer, and maximum accumulation of recent riverine material. Shallower stations located among the main river mouths showed higher concentrations of sand. Offshore stations were characterized by a finer and homogeneous sedimentary record and a thicker oxidized surface layer. Microbial communities showed the highest abundance in front of the main river mouth (Busa Dritta). Differences between superficial and sub-superficial layers, both in term of bacterial abundance and percentage of specific bacterial clusters (e.g. deltaproteobacteria), were observed in sediments close to the river mouths whereas offshore sites did not show significant differences between the two layers. This suggest that deposition of fine organic-rich sediment in proximity of the river mouths could determine an increasing abundance of bacteria in surface sediments, as well as the occurrence of anoxic conditions in sub-surface layers resulting in a predominance of anaerobic metabolisms (e.g. sulfate-reducing deltaproteobacteria).

[C003] The genome of a freshwater planktonic *Synechococcus* strain reveals the potentiality to fix nitrogen

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