



Provincia di Lecco



Comune di Lecco

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Acqua: elemento vitale, risorsa essenziale
Condividere le conoscenze per affrontare il cambiamento

Abstract Book



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Nico Salmaso obtained a degree in Natural Sciences at the University of Padua and a PhD in Ecology at the University of Parma. He is currently a senior researcher and head of the Hydrobiology Unit at the Fondazione Edmund Mach, Istituto Agrario di S. Michele all'Adige. His research interests encompass microbial ecology, including both prokaryotes and eukaryotic microalgae, as well as the effects of eutrophication, climate change, and other anthropogenic stressors on the biodiversity, abundance, and phenology of aquatic communities. Specific investigations are focused on the biodiversity and ecology of toxigenic cyanobacteria and the identification and impact of cyanotoxins. The detection of toxigenic cyanobacteria is achieved using culture-dependent (isolated strains) and culture-independent (metagenomic) approaches. He is the responsible of the LTER station "Lago di Garda." President of AIOL from 2020 to 2023. He coordinated the project Eco-AlpsWater (2018-2022), funded by the Alpine Space program, which involved 12 European institutions and 6 countries in the study of microbial diversity through the analysis of environmental DNA from over 50 lakes and rivers across the Alps. Currently, his research interests are also implemented within projects funded by the EU Horizon program and PNRR. He has organized three summer schools on the application of "omics" approaches in the study of aquatic ecosystems. The results of the research were disseminated in numerous seminars, courses, and congresses. He is the author of over 100 papers published in refereed journals.

Current status and perspectives in the application of metagenomics to advance knowledge of the taxonomy and functionality of microbial communities

In the limnological and oceanographic disciplines, the last decade has seen one of the most significant changes in approaches to the study of prokaryotic and eukaryotic microorganisms. Traditional methods based on culture-based techniques and morphological analysis have been increasingly complemented by various high-throughput sequencing (HTS) technologies, which are able to directly analyse genetic material extracted from environmental samples and provide a comprehensive snapshot of the microbial community. While metabarcoding is rapidly expanding its application to virtually all aquatic life, its use is limited to the identification of taxonomic repertoires or selected individual genes of functional value. Conversely, metagenomics has been applied to the study of prokaryotic communities and, more rarely, micro-eukaryotic organisms. The characterisation of species at the genomic level allows the functional characterisation of microbial communities, inferring the metabolic pathways and processes that drive ecosystem dynamics. Specific examples include the discovery of new potential metabolic processes relevant to human health (including the biosynthesis of emerging cyanotoxins) or genes involved in antibiotic resistance or the biosynthesis of a wide range of bioactive molecules. In addition to reviewing the present state of HTS approaches, this review will provide concrete examples of the application of HTS to potentially harmful cyanobacteria.