XXVI Congresso AIOL

San Michele all‘Adige, 27 giugno - 1 luglio 2022

Esperienze e approcci innovativi per la conoscenza e la salvaguardia degli ecosistemi acquatici

ecosystems with glacier retreat and build a conceptual model of their future evolution. Given the typically high water turbidity and the low biomass associated with these harsh habitats, biological communities will be characterized based on the metabarcoding of the 16S (prokaryotic) and 18S (eukaryotic) rRNA genes from eDNA samples. This approach will allow to obtain a broad overview of the taxonomical groups living in the lakes, while causing as less disturbance as possible.

Does the biodiversity of high-altitude aquatic prokaryotes reflect the expected "Windows of opportunity" in deglaciating Alpine catchments?

Monica Tolotti (1)*, Stefano Brighenti (2), Maria Cristina Bruno (1), Leonardo Cerasino (1), Massimo Pindo (1), Werner Tirler (3), Davide Albanese (1)

(1) Research and Innovation Centre, Fondazione Edmund Mach, Via Mach 1, 38098 S. Michele all'Adige, Italy
(2) Faculty of Science and Technology, Free University of Bolzano/Bozen, Piazza Università 1, 39100 Bolzano, Italy
(3) Eco Research, Via Luigi Negrelli 13, 39100 Bolzano, Italy
* email corresponding author: monica.tolotti@fmach.it

Alpine headwaters are threatened by the global warming that is accelerating the glacier melting and increasing the thermal and hydrological seasonal variability. Changing diversity and seasonal dynamics of aquatic communities reflect this variability and may have great implications for future integrity and functionality of Alpine freshwaters. Prokaryotes in Alpine streams have remained largely unexplored until recently, despite the recognition that microbial communities may have a disproportionate role in driving stream biodiversity, hydrochemistry, and metabolism. Organisms dwelling in glacial streams are expected to preferentially develop during Windows of opportunity (WOs), i.e. short periods of less harsh environmental conditions typically occurring in early summer and, especially, in late summer/autumn. While research demonstrated WOs as favourable periods for biomass accrual, very little is known about parallel changes in biodiversity in both glacial and non-glacial streams. From June to September of 2017 and 2018 we investigated epilithic and sediment prokaryotic communities of streams fed by glaciers, rock glaciers and groundwater in two deglaciating Alpine catchments. We addressed the following questions: i) do WOs drive seasonal changes in microbial diversity? ii) what are the major environmental drivers of prokaryotic diversity in different Alpine water types? iii) are WOs changing under the impact of climate warming?

Microbial pathogen detection in freshwater biomonitoring by amplicon sequencing: range of potential applicability

Sara Vettorazzo (1,2)*, Adriano Boscaini (2), Nico Salmaso (2)

(1) Department of Cellular, Computational and Integrative Biology, University of Trento, Via Sommarive 9, 38123, Povo, Italy
(2) Research and Innovation Centre, Fondazione Edmund Mach, via E. Mach 1, 38098, San Michele all'Adige, Italy
* email corresponding author: sara.vettorazzo@studenti.unitn.it

Pathogen detection is a key aspect to evaluate during freshwater biomonitoring. Studies leveraging high-throughput sequencing (HTS) technologies are providing new and cost-effective insights into the ecology of aquatic microbiomes and pathogen spread. In this work, environmental DNA samples collected from different small Alpine waterbodies and from Lake Garda were analysed by amplicon sequencing of 16S and 18S rRNA hypervariable regions. Bioinformatic analysis was based on the DADA2 pipeline and the amplicon sequence variants (ASVs) approach. Taxonomic assignments of potentially pathogenic bacteria and protists were performed by the naïve bayesian RDP classifier. In addition, a BLAST-based comparison was carried out. The analyses highlighted several limitations of metabarcoding, mainly linked to the limited taxonomic resolution that can be reached at the species level, and showed that amplicon sequencing can be suitable

only as a general first-step screening tool, to monitor particular potentially pathogenic genera (or families), pending a case-by-case evaluation of the experimental objectives. However, when more taxonomic accuracy is required, other HTS methods (e.g., whole genome analysis) can provide more resolution, up to the strain-level microbial detection.