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Esperienze e approcci innovativi per la conoscenza e la salvaguardia degli ecosistemi acquatici
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SESSIONE SPECIALE - Aquatic microbiomes and microbial pathogens across the One Health spectrum – Chair: Grazia Marina Quero, Ester Eckert

**Insights into salinity tolerance from a *Chlamydomonas* strain**

**Emma Bazzani** (1)*, Chiara Lauritano (2), Olga Mangoni (3,4), Francesco Bolinesi (3), Maria Saggiomo (1)

(1) Research Infrastructure for Marine Biological Resources Department, Stazione Zoologica Anton Dohrn, Villa Comunale, 80121 Naples, Italy
(2) Ecosustainable Marine Biotechnology Department, Stazione Zoologica Anton Dohrn, Villa Comunale, 80121 Napoli, Italy
(3) Department of Biology, University of Naples Federico II, 80126 Naples, Italy
(4) Consorzio Nazionale Interuniversitario delle Scienze del Mare (CoNISMa), 00196 Rome, Italy
* email corresponding author: emma.bazzani@szn.it

Salinity is among the main drivers affecting the growth and distribution of photosynthetic organisms in their natural environment, especially in coastal areas, where run-off, rivers and land use have greater impact. As a consequence of climate change, the global salinity patterns are expected to vary, with strong implications on the distribution and composition of microalgal communities, which are the base of the food web.

In our project, we performed a comprehensive experiment exposing a microalga from the genus *Chlamydomonas* (*Chlamydomonas* sp CCMP225) to different concentrations of sea salts. The evaluation of the microalgal responses to this stressor will shed light on the morphological and physiological effects of salinity stress on green algae, allowing us to gain some insights on the possible effects of climate change on this group of organisms. Notably, our strain appeared to be exceptionally resistant to this kind of stress. In fact, even though the growth was considerably reduced under high salinity, the photosynthetic parameters were not substantially affected. These results could help to understand why some organisms are more favored than others under stressful conditions, and which characteristics give them extreme resilience and adaptability.

**EVER-LAKE: Formation, evolution and fate of new proglacial lakes in the deglaciating Alps**

**Maria Vittoria Tenci** (1), Marco Toffolon (1), Walter Bertoldi (1), Stefano Brighenti (2), Francesco Comiti (2), Luca Carturan (3), Maria Cristina Bruno (4), Leonardo Cerasino (4), Massimo Pindo (4), Monica Tolotti (4)

(1) Università di Trento – Dipartimento di Ingegneria Civile, Ambientale e Meccanica, via Mesiano, 77 38123 Trento
(2) Università di Bolzano, piazza Università, 5 39100 Bolzano
(3) Università di Padova - Department of Land, Environment, Agriculture and Forestry, Viale Dell'Università, 16 - Legnaro (PD)
(4) Fondazione Edmund Mach - Centro Ricerca ed Innovazione, Via E. Mach, 1 38098 S. Michele all'Adige (TN)
* email corresponding author: mariavittoria.tenci@unitn.it

The Alpine deglaciation is one of the most evident effects of the ongoing climate change. Under glacier retreat, proglacial lakes are increasing both in number and in volume, thereby becoming important elements of the mountain landscape. An improved knowledge of the ecological characteristics of the newly forming lakes is crucial for the conservation of the Alpine biodiversity and habitats, to identify ecosystem services provided by these environments and to base coherent management strategies in the future iceless Alpine landscape. The “EVER-LAKE” PhD project will focus on a system of recently formed proglacial lakes in the Ortles-Cevedale Mountain group (Italy), with the aim to: (i) characterize the lake ecosystems from a physical, chemical and biological, point of view; (ii) understand the ecological development of proglacial lake...
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 microorganisms 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