



Evaluating microbial diversity in Alpine pastures

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Alpine pastures are one of the most common landscapes in the Alps and one of the most threatened by climate change. In this environment the below-ground biomass (such as Bacteria, Fungi, Archaea, etc.) is much greater than above-ground biomass including plant and livestock. Soil microorganisms interact with the other components of the environment such as plants and invertebrates. A great number of Prokaryota and Fungi are predated by soil animals, but they are also symbiotic with them, for example as part of their gut microbiota. Furthermore, the microbiota associated with soil fauna is paramount for the health of soil fauna itself.

Considering that this kind of interactions are almost unknown, the aim of the study is to analyze the relationship between soil microorganism and soil fauna including abiotic factors (temperature, soil moisture, soil organic content, etc.) as well as biotic factors, in order to elucidate the main drivers of soil microbial and soil fauna diversity. Regarding soil fauna, we selected different taxa:

- Nematodes as component of soil microfauna and as important predators of microorganisms.
- Collembola as component of mesofauna, including several fungivores species.
- Earthworms, the soil engineering that affect the soil structure.
- Beetles belonging to two different families: Ground Beetles (Coleoptera: Carabidae) and Rove Beetles (Coleoptera: Staphylinidae) as important predators of invertebrates.

Thanks to Next Generation Sequencing methods such as metataxomics, it is possible to identify entire microorganisms' communities. Sequence of 16S rDNA gene (V4 - V5 regions) for the Prokaryota and sequence of Internal Transcribed Spacer 1 (ITS1) for fungi, will be amplified and cluster in Operational Taxonomic Units in order to clarify the functional role of the microorganisms associated with soil fauna and understand how the interactions between soil fauna and microorganism change along an altitudinal gradient in relation with abiotic factors.