

## Submitted Abstract

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## Abstract

Biodiversity is a central keyword of the 21st century and has been gaining increasing attention with regards to the stability and vulnerability of soil ecosystems, especially in the light of global change. The diversities of soil microbial communities are major regulators of fundamental ecosystem processes, such as organic matter decomposition, nutrient cycling and gaseous fluxes. Within the soil food web, archaea, bacteria and fungi interact with each other, with organisms of the soil micro- and mesofauna (such as nematodes and collembolans), as well as with soil macrofauna (earthworms, insects, spiders) and plants.

Alpine pastures have been traditionally managed for centuries and harbor specific soil animal and microbial communities; therefore, the concept of an “intact soil” and the definition of “disturbance” is of special concern in these sites. In the inner-Alpine EUREGIO region (Austria/Italy), Alpine pastures provide one of the dominant landscapes and are the basis for mountain agriculture, and a source of agrifood, biodiversity and tourism. Although we know that some soil functions depend on land management (e.g. capacity to sequester carbon), knowledge of the interactions and co-occurrences of microbial communities is critical and virtually non-existent.

The EUREGIO project MICROVALU “Evaluating microbial diversity in alpine pastures” has developed specific protocols to compare the prokaryotic and fungal community composition of different sample types, including bulk soil samples, rhizosphere soil of *Carex* spp. and *Festuca* spp., members of the micro- (nematodes), meso- (collembolans), and macrofauna (earthworms, ground and rove beetles), as well as fecal samples of wild mammals and domestic livestock at replicated sites along an elevational gradient from below to above the treeline (1000-2500 m a.s.l.). The elevational gradient is used as a proxy to determine the influence of climate on the respective sample-specific microbiota and the overlapping microbiota between sample types.

Our results indicate that soil, rhizosphere and faunal samples each have a unique microbial community composition, but also that these microbiota overlap to different degrees, depending on functional traits, trophic relationships and elevation. In addition to a comprehensive soil and meteorological dataset, the study is providing new information on the interactions of microorganisms in the soil-food web and their responses to climate-related environmental properties.