

Microbial Communities in Different Components of an Alpine Grassland Ecosystem

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Aim:

Biodiversity is a central keyword of the 21st century and is gaining even increasing attention in the light of global change. Whereas traditional concepts of studying microbial diversity consider individual components or taxa in a given habitat (e.g. bulk soil, plants, earthworms), these concepts neglect that complex interactions and co-occurrences of microbial communities may exist between these components.

Methods:

The prokaryotic and fungal community composition of different sample types (components), including bulk soil, rhizosphere soil of *Carex* spp. and *Festuca* spp., members of the micro- (nematodes), meso- (collembolans), and macro- (earthworms, ground and rove beetles) fauna, as well as fecal samples of wild mammals (hare, deer) and domestic livestock (cattle, equids) are investigated by amplicon sequencing along an elevational gradient from 1000 to 2500 m a.s.l. A meta-dataset of soil properties, soil microbial and meteorological data contributes to the interpretation of the community data of the almost 2000 samples within the alpine grassland ecosystem.

Results:

Soil, rhizosphere and faunal samples each have unique microbial communities, but these microbiota overlap to different degrees, depending on functional traits, trophic relationships and elevation. Our data indicate connections between microbial communities of different ecosystem components and that certain animals can serve as vectors for various microorganisms. Generally, results reveal key drivers for the microbial biodiversity within the different components of alpine grasslands.

Conclusions:

Our data prove – even across the elevation gradient – connected microbial communities in alpine pastures and allow conclusions about the sensitivity of the complex interactions especially in light of climate change.