



## **Drought legacy affects microbial response to a subsequent extreme drought.**

Alberto Canarini (1), Victoria Martin (1), David Zezula (1), Lucia Fuchslueger (2), Philipp Gündler (1), Marina Jecmenica (1), Michael Bahn (3), and Andreas Richter (1)

(1) University of Vienna, Microbiology and Ecosystem Science, Austria (alberto.canarini@univie.ac.at), (2) Department of Biology, University of Antwerp, Antwerp, Belgium, (3) Institute of Ecology, University of Innsbruck, Innsbruck, Austria

Extreme events, such as drought, can cause substantial alteration of biogeochemical cycles of carbon (C) and nutrients. Soil microorganisms play a key role in C and nutrient cycling by mining resources for growth and maintenance of their metabolism. While considerable progress has been made in understanding the effects of drought on soil microbial community structure and processes, we still lack a thorough understanding on whether recurrent drought events will exhibit legacy effects on microbial responses to a subsequent extreme drought event. The aim of this experiment was to evaluate the microbial responses to extreme drought in an alpine grassland and whether 10 years of previous summer droughts would alter the response. We estimated processes linked to the microbial cycling of C and nitrogen (N), phosphorous (P) and sulphur (S), including potential enzymatic activity of ten different enzymes, microbial community composition based on phospholipid fatty acids (PLFA) pattern, microbial growth and microbial C use efficiency (CUE). Our results showed no changes in the biomass of the main microbial groups (i.e. fungi, gram-positive and gram-negative bacteria) to drought, although the relative distribution of individual PLFA biomarkers was affected by the different drought treatments. Previous drought history had negligible effect on the main microbial groups and was only visible in gram-negative bacteria. Opposite results were found for potential enzymatic activity, where drought treatment decreased the activity in most of the tested enzymes and previous drought history altered many of the responses to drought. Specifically, recurrent droughts increased the resistance of C-related enzymes, had intermediate effects on N-related enzymes and no effects on S and P-related enzymes. Similarly previous drought history significantly increased microbial growth rates and showed a decrease, although not significant, in the CUE.

This study clearly shows that previous drought history has legacy effects on many soil parameters connected to the C, N, P and S cycle, with the potential of decoupling the cycling of such elements. These effects are not clearly reflected in changes at the microbial community level, supporting the idea that physiological acclimation of microbial communities to drought may be more important than changes in community composition. This is further supported by changes in growth rates and CUE, which show legacy effects on microbial physiological processes. By showing how historical contingency can lead to deviation from expected functional responses to climate change, we also highlight the importance of long-term climate change studies for building predictive model of soil responses to climate change.