Profiling soil microbial communities influenced by reduced summer precipitation and farming system history

Dominika Kundel[a,b], J. Truu[c], A. Fliessbach[a], H. Bracht Jørgensen[d], N. Bodenhausen[a] and P. Mäder[a]

[a] *Department of Soil Sciences, Research Institute of Organic Agriculture (FiBL), Switzerland*
[b] *Department of Biology, University of Konstanz, Germany*
[c] *Institute of Molecular and Cell Biology, University of Tartu, Estonia*
[d] *Department of Biology, Lund University, Sweden*

Soil bacteria and fungi are the basis of soil food webs and contribute to a wide range of essential soil functions in arable lands. Intense land use and climate change induced reductions in summer precipitation can have varying influences on abundance, composition, and activity of microbial communities with largely unknown consequences for soil functions and plant growth including crop yields. The impact of altered precipitation patterns on soil biodiversity and associated ecosystem functions is on top of the list of eight major research gaps identified by an expert group for the European Commission still, this relationship is rarely studied under field conditions. To explore the role of soil management and precipitation amounts on microbial communities and soil functions, we manipulated natural precipitation patterns in the long-term farming system comparison trial "DOK" (bio-Dynamic, bio-Organic, and "Konventionell") using fixed location rainout-shelters. Of the organic and conventional farming systems tested side by side in this trial, we chose the two most contrasting ones for the current study: The bio-dynamic (BIODYN) and the conventional (CONMIN) farming system, two systems which profoundly differ in fertilization and plant protection regimes. As model test plant, we grew winter wheat (L. cv. "Wiwa") in the experimental field plots. We assessed plant growth at four time points during the growing season and investigated activity, community structure and dynamics of bacterial and fungal communities with traditional soil ecological methods such as soil respiration, phospholipid fatty acid analysis, and the microbial biomass by chloroform fumigation extraction. We also performed amplicon based, high-throughput sequencing of the 16S rRNA and the ITS gene region for in-depth profiling of microbial communities and assessed abundances of bacteria and fungi with quantitative real-time PCR. We are analysing our data with structural equation modelling to study the direct and indirect effects of reduced summer precipitation and farming system history on characteristics of soil microbial communities and plant performance. Our data obtained so far shows that the two different farming systems harbor distinct microbial communities and that the specific farming system has profound impacts on soil respiration and total microbial biomass carbon.