



The effects of climate change on microbial community composition of a montane grassland

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Soil microbial communities have a prominent role in regulating carbon (C) dynamics in terrestrial ecosystems. Climate change factors that alter the composition of the soil microbial community therefore can influence ecosystem processes. While effects of elevated atmospheric CO₂ (eCO₂) and temperature (eT) on soil microbial community composition have been extensively studied, their combined effect in concomitance with extreme stress events (such as drought) are not well understood.

The aim of this study was to examine the impact of different climate change factors, either individually or in combination, on soil microbial community composition of a montane grassland in Styria, Austria. At the experimental site, field plots were subjected to either ambient conditions or simulated future climate, with combinations of eT (+1.5 or +3 °C) and eCO₂ (+150 or +300 ppm), for 3 years in a response surface design. A summer drought treatment was superimposed on ambient climate plots and future climate plots (combined +3 °C and +300 ppm CO₂), in a full factorial design in 2017. Samples were collected in 3 different seasons: May, July (peak drought) and October (drought recovery). To estimate soil microbial biomass and microbial community composition, phospholipid fatty acids (PLFA) were extracted and quantified. Neutral lipid fatty acids (NLFA) in soils and roots were used to estimate the abundance of arbuscular mycorrhizal fungi (AMF; based on the neutral lipid biomarker 16:1 ω 5).

Multivariate analysis demonstrated distinct differences in microbial community composition of control soils between the three sampling dates, indicating a strong seasonal change in microbial community composition. In addition, individual PLFA biomarkers showed a clear separation of drought versus non-drought treatments as well as of ambient and future climate treatments, indicating shifts in microbial community composition caused by these climate change factors. During drought, in both the future climate and the ambient climate plots, we detected a decrease in all bacterial groups, but not in saprotrophic fungi. However, the strongest negative effect of drought was found in the NLFA biomarker of AMF in roots. Using a response surface model (RSM) approach we examined the individual and combined effects of eT and eCO₂ on the biomass of different microbial groups. Significant effects of elevated CO₂ and temperature on microbial biomass and community composition were only detected during the first sampling (May) but not during the other sampling dates.

Our study demonstrates that climate change strongly affects soil microbial community composition in montane grasslands. Extreme stress events, such as prolonged droughts, induced the strongest shifts in both, microbial community composition and in the biomass of various microbial groups, including bacteria and AMF, but not saprotrophic fungi. Elevated temperature and CO₂ did not modulate these drought effects. Moreover, eT and eCO₂ showed weaker effects on soil microbial community composition and these effects were dependent on season, highlighting the importance of seasonality when analysing climate change effects on soil microbial community composition and function.