



## Rapid and persistent change of microbial community and gross N turnover under experimentally simulated climate change conditions in alpine grassland

Changhui Wang (1,2), Zhe Chen (1), Sebastian Untereggelsbacher (1), Silvia Gschwendtner (3), Michael Schloter (3), Klaus Butterbach-Bahl (1), and Michael Dannenmann (1)

(1) Institute for Meteorology and Climate Research, Atmospheric Environmental Research (IMK-IFU), Karlsruhe Institute of Technology (KIT), Garmisch-Partenkirchen 82467, Germany, (2) State Key Laboratory of Vegetation and Environmental Change, Institute of Botany, the Chinese Academy of Sciences (IBCAS), Beijing 100093, ChinaState Key Laboratory of Vegetation and Environmental Change, Institute of Botany, the Chinese Academy of Sciences (IBCAS), Beijing 100093, China, (3) German Research Center for Environmental Health (GmbH) Research Unit Environmental Genomics, 85764 Neuherberg, Germany

Alpine grasslands of Central Europe are exposed to strong warming and to altered precipitation patterns, suggesting that ecosystem nitrogen (N) cycling may be vulnerable to future climatic conditions. In order to investigate the response of soil microbial community and N transformations to predicted climate change conditions, we conducted an ecosystem manipulation experiment following the “space for time” approach in the TERENO (Terrestrial Environmental Observatories) pre-alpine grassland observatory. For this purpose, we dislocated 200 mini-lysimeters containing intact plant-soil systems down an altitudinal gradient from 860m to 550m above sea level, with corresponding control transfers within the high altitude site. After an equilibration period of 2.5 years, a full annual cycle of gross rates of N turnover as well as microbial biomass- and –community dynamics was monitored based on 15 sampling dates in two soil layers. For the monitored year, simulation of climate change via lysimeter transfer had increased mean annual soil temperature in 5 cm depth on average by 2.4 °C, but on the other hand promoted soil frost in winter due to reduced snow cover. Soil moisture was decreased on average by 20%.

Gross N turnover and the abundance of N cycle genes in soil were characterized by pronounced seasonal dynamics, with both summer and winter representing key periods for the annual sum of N turnover. The abundance of ammonia oxidizing archae (AOA) genes exceeded the abundance of ammonia oxidizing bacterial (AOB) genes by approximately three orders of magnitude.

Climate change simulation strongly increased the abundance of both AOB and AOA gene copies in soil, consistent with an increase of annual gross nitrification rates by 41%. Gross N mineralization was even increased by 141% in the climate change treatment. The abundance of AOA genes in soil explained 80% of the variability of gross nitrification rates over the full annual course.

These results provide strong evidence for a rapid but persistent change of the microbial community under expected climate change conditions, leading to strongly increased N mineralization and nitrification with associated high risks for N losses along hydrological and gaseous pathways. Furthermore, our study demonstrates that archaea are key players for nitrification in the investigated ecosystem, and that molecular approaches to determine N cycle gene abundance may have a so far overlooked and unexpectedly high power to predict gross rates of N turnover. Finally, we show that winter is a so far rarely considered key period for understanding seasonal patterns and annual sum of N turnover in alpine grasslands.