



Gross nitrogen fluxes in intact beech-soil-microbe systems under experimentally simulated climate change

Javier Tejedor (1), Silvija Bilela (2), Rainer Gasche Gasche (1), Silvia Gschwendtner (4), Martin Leberecht (5), Carolin Bimüller (3), Ingrid Kögel-Knabner (3), Andrea Polle (5), Michael Schloter (4), Heinz Rennenberg (2), and Michael Dannenmann (1)

(1) Institute for Meteorology and Climate Research, Atmospheric Environmental Research (IMK-IFU), Karlsruhe Institute of Technology (KIT), Garmisch-Partenkirchen, Germany, (2) Institute of Forest Botany and Tree Physiology, Chair of Tree Physiology, University of Freiburg, Freiburg, Germany, (4) Department for Terrestrial Ecogenetics, Helmholtz Zentrum München, Oberschleissheim, Germany, (5) Abteilung Forstbotanik und Baumphysiologie, Büsgen-Institut, Büsgenweg 2, Georg-August Universität Göttingen, 37077 Göttingen, Germany, (3) Lehrstuhl für Bodenkunde, Department für Ökologie und Ökosystemmanagement, Wissenschaftszentrum Weihenstephan, Technische Universität München, Freising-Weihenstephan, Germany

The vulnerability of beech forests of Central Europe to projected climate change conditions is a current matter of debate and concern. In order to investigate the response of N cycling in a typical beech forest to projected climate change conditions, we transplanted small lysimeters with intact beech-soil systems from a slope with N-exposure (representing present day climate conditions) to a slope with S exposure (serving as a warmer and drier model climate for future conditions). Lysimeters transfers within the N exposure served as control. After an equilibration period of 1 year, three isotope labeling/harvest cycles were performed: (1) comparison between N and S slopes under ambient conditions; (2) comparison between N and S slopes after intensified drought at S exposure; (3) rewetting after the drought period. Homogenous triple isotope labeling ($^{15}\text{N}/^{13}\text{C}$ glutamine, $^{15}\text{NH}_4^+$, $^{15}\text{NO}_3^-$) in combination with ^{15}N tracing and -pool dilution approaches as well as molecular analyses of nitrogen cycling genes and mycorrhiza morphotyping allowed to simultaneously quantify all N turnover processes in the intact beech-soil-microbe system.

Nitrate was the major N source of beech seedlings with little importance of ammonium and no importance of glutamine. Experimental simulation of climate change resulted in significantly reduced gene copies of ammonia oxidizing bacteria in soil (AOB), a dramatic attenuation of microbial gross nitrate production from 252 ± 83 mg N m $^{-2}$ day $^{-1}$ for the control treatment to 49 ± 29 mg N m $^{-2}$ day $^{-1}$ for the climate change treatment and associated strong declines in soil nitrate concentrations as well as nitrate uptake by microorganisms and beech, which could not be compensated by uptake of ammonium or glutamine. Therefore, N content of beech seedlings was strongly reduced in the climate change treatment. Hence our data provide a microbial mechanism to explain nutritional limitations of beech under higher temperatures and drought and raise questions about the sustainability of such forests under projected climate change conditions.