

Reduced soil N₂O emission and enhanced denitrifier community size by growing grass versus bare soil

Haitao Wang^a, Lukas Beule^b, Huadong Zang^c, Birgit Pfeiffer^d, Shutan Ma^e, Petr Karlovsky^b, Klaus Dittert^{a,*}

^a Department of Crop Science, Section of Plant Nutrition and Crop Physiology, University of Goettingen, Carl-Neuberg-Weg 1, 37075 Göttingen, Germany

haitao.wang@agr.uni-goettingen.de

^b Molecular Phytopathology and Mycotoxin Research, Faculty of Agricultural Sciences, University of Goettingen, 37077 Göttingen, Germany

^c College of Agronomy and Biotechnology, China Agricultural University, 100193, Peoples Republic of China

^d Institute of Microbiology and Genetics, Department of Genomic and Applied Microbiology, Grisebachstr. 8, 37077 Göttingen, Germany

^e School of environmental science and engineering, Anhui Normal University, Wuhu 241002, China

E-mail: hwang3@gwdg.de

Abstract

Background and objectives In terrestrial ecosystems, nitrogen (N) fertilization is the major source of nitrous oxide (N₂O) emissions. Previous incubation experiments on soil N₂O emission were mostly conducted without plants and, therefore, plant-microbe-soil interactions remain mostly unexplored. This study aimed to investigate the effect of grass presence on soil N₂O emission and denitrification gene abundances.

Methods The experiment consisted of two groups, soil with grass (*Lolium perenne*) and bare soil, each with 4 fertilization levels (0, 5, 10, and 20 g N m⁻²). The closed-chamber approach was used to measure soil N₂O fluxes. Real-time PCR assays were performed to assess the abundance of denitrification genes.

Results The presence of grass decreased soil NO₃⁻ content compared to bare soil, but no effect on dissolved organic carbon (DOC). Cumulative N₂O emissions of soil with grass were lower than in bare soil at a fertilization of 5 and 10 g N m⁻². Although fertilization did not affect gene abundance, soil with grass showed greater gene copies of bacterial 16S rRNA, fungal 18S rRNA, *narG*, *napA*, *nirK*, *nirS*, and *nosZ* clade I.

Conclusion Our results showed that the presence of *Lolium perenne* reduced soil N₂O emission and increased denitrifying gene abundance. Future research should explore how different plants species and communities affect denitrifying communities in soil to further uncover the drivers of denitrification.

Key words: soil N₂O, *Lolium perenne*, fertilization, denitrification genes, real-time PCR