Geophysical Research Abstracts
Vol. 17, EGU2015-8017, 2015
EGU General Assembly 2015

Isotopologue signatures of nitrous oxide produced by nitrate-ammonifying bacteria isolated from soil

Undine Behrendt (1), Reinhard Well (2), Anette Giesemann (2), Andreas Ulrich (1), and Jürgen Augustin (1)

(1) Leibniz-Centre for Agricultural Landscape Research (ZALF), Institute for Landscape Biogeochemistry, Eberswalder Str. 84, D-15374 Müncheberg, Germany, (2) Thünen Institute of Climate-Smart Agriculture, Bundesallee 50, D-38116 Braunschweig, Germany

Agricultural soils are the largest single source of anthropogenic N_2O to the atmosphere, primarily driven by microbiological processes such as denitrification and dissimilatory nitrate reduction to ammonium (DNRA). Both processes occur under similar conditions of low oxygen concentration and therefore, source partitioning of emitted N_2O is difficult. Understanding what controls the dynamics and reaction equilibrium of denitrification and DNRA is important and may allow the development of more effective mitigation strategies. ^{15}N site preference (SP), i.e. the difference between ^{15}N of the central and peripheral N-position of the asymmetric N_2O molecule, differs depending on processes involved in N_2O formation. Hence investigation of the isotopomer ratios of formed N_2O potentially presents a reliable mean to identify its source.

In this study, bacterial isolates obtained from organic soils were screened for their ability to reduce nitrate/nitrite to ammonium and to release N_2O to the atmosphere. Taxonomic characterisation of the strains revealed that N_2O formation was only detected in ammonifying strains affiliated to several genera of the family *Enterobacteriaceae* and strains belonging to the genus *Bacillus* and *Paenibacillus*. Sampling of N_2O was conducted by incubation of strains under oxic and anoxic conditions. Investigation of the ^{15}N site preference showed SP values in the range of 39 to 57 ‰ . Incubation conditions had no influence on the SP. The lowest values were achieved by a strain of the species *Escherichia coli* which was included in this study as a DNRA reference bacterium harbouring the *NrfA* gene that is coding the nitrite reductase, associated with respiratory nitrite ammonification. Soil isolates showed SP-values higher than 40 ‰ . Comparison of these results with SP-values of N_2O produced by denitrifying bacteria in pure cultures (-5 to 0 ‰)[1,2] revealed significant differences. In contrast, N_2O produced by denitrifying fungi displayed SP-values in a range of 21 to 36 ‰ [3] ,which are much closer to the values of N_2O from the investigated DNRA bacteria. However, the N_2O formed under denitrifying conditions by organisms investigated so far can be distinguished with respect to its source (DNRA or denitrification) but a broader database is needed which cover a larger spectrum of taxa.

[1] Sutka *et al*. Distinguishing nitrous oxide production from nitrification and denitrification on the basis of isotopomer abundances. *Appl. Env. Microbiol.* **2006**, 72, 638.

[2] Toyoda *et al.* Fractionation of N_2O isotopomers during production by denitrifier. *Soil Biol. Biochem.* **2005**, 37, 1535.

[3] Rohe *et al.* Dual isotope and isotopomer signatures of nitrous oxide from fungal denitrification – a pure culture study. *Rapid Commun. Mass Spectrom.* **2014**, 28, 1893