Geophysical Research Abstracts
Vol. 19, EGU2017-4805, 2017
EGU General Assembly 2017

Estimating N2O processes during grassland renewal and grassland conversion to maize cropping using N2O isotopocules

Caroline Buchen, Reinhard Well, Heinz Flessa, Roland Fuß, Mirjam Helfrich, and Dominika Lewicka-Szczebak
Thünen Institute, Climate-Smart Agriculture, Braunschweig, Germany (reinhard.well@thuenen.de)

Grassland break-up due to grassland renewal and grassland conversion to cropland can lead to a flush of mineral nitrogen from decomposition of the old grass sward and the decomposition of soil organic matter. Moreover, increased carbon and nitrogen mineralisation can result in enhanced nitrous oxide (N_2O) emissions. As N_2O is known to be an important greenhouse gas and a major precursor for ozone depletion, its emissions need to be mitigated by adjusting agricultural management practices. Therefore, it is necessary to understand the N_2O processes involved, as well as the contribution of N_2O reduction to N_2. Apart from the widely used ^{15}N gas flux method, natural abundance isotopic analysis of the four most abundant isotopocules of N_2O species is a promising alternative to assess N_2O production pathways.

We used stable isotope analyses of soil-emitted N_2O ($\delta^{18}O_{N2O}$, $\delta^{15}N^{bulk}_{N2O}$ and $\delta^{15}N^{SP}_{N2O}$= intramolecular distribution of ^{15}N within the linear N_2O molecule) with an isotopocule mapping approach to simultaneously estimate the magnitude of N_2O reduction to N_2 and the fraction of N_2O originating from the bacterial denitrification pathway or fungal denitrification and/or nitrification. This approach is based on endmember areas of isotopic values for the N_2O produced from different sources reported in the literature. For this purpose, we calculated two main scenarios with different assumptions for N_2O produced: N_2O is reduced to N_2 before residual N_2O is mixed with N_2O of various sources (Scenario a) and vice versa (Scenario b). Based on this, we applied seven different scenario variations, where we evaluated the range of possible values for the potential N_2O production pathways (heterotrophic bacterial denitrification and/or nitrifier denitrification and fungal denitrification and/or nitrification). This was done by using a range of isotopic endmember values and assuming different fractionation factors of N_2O reduction in order to find the most reliable scenario. Investigations were carried out over a study period of one year following grassland renewal and grassland conversion to maize cropping on two different soil sites (Plaggic Anthrosol and Histic Gleysol) near Oldenburg, Lower Saxony Germany.

Our observations indicate heterotrophic bacterial denitrification and/or nitrifier denitrification as the main source of N_2O production, with a significant contribution of N_2O reduction to N_2 rather than nitrification (i.e. hydroxylamine oxidation) and fungal denitrification throughout the entire study period. A tendency to a higher contribution of N_2O reduction to N_2 was observed for the often water-saturated Histic Gleysol, while lower N_2O reduction was found for the Plaggic Anthrosol. For two samples, we attempt to validate our results from the isotopocule mapping approach with a parallel ^{15}N labelling study at the field scale (Buchen et al., 2016), as conditions of soil moisture, nitrate availability and N_2O flux were similar.

References:

Buchen, C., Lewicka-Szczebak, D., Fuß, R., Helfrich, M., Flessa, H., Well, R., 2016. Fluxes of N2 and N2O and contributing processes in summer after grassland renewal and grassland conversion to maize cropping on a Plaggic Anthrosol and a Histic Gleysol. Soil Biology and Biochemistry 101, 6-19.