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Intercomparison of three isotopic methods for source differentiation of gaseous N emissions from soils

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The application of stable isotopes has become a promising tool for revealing and quantifying the direct sources of N_2O. Up to now, three reliable methods have evolved, which use natural abundance and artificial enrichment of ^{15}N and ^{18}O.

The first one comprises numerical ^{15}N tracing models, which quantify simultaneous N transformations via non-linear parameter optimization routines in combination with the application of triple ^{15}N-labelling (i.e. NH_4^+, NO_3^- or both are labelled) and the consideration of process-specific NO_2^- dynamics. These models estimate simultaneous emission pathways associated with nitrification, denitrification, coupled heterotrophic nitrification with denitrification (or other pathways leading to N_2O produced from NO_2^- and organic N oxidation) and co-denitrification (Müller et al., 2007; Müller et al., 2014). However, they do not enable the estimation of the contribution from nitrifier denitrification.

The second one – the dual isotope method – combines ^{15}N and ^{18}O tracers with either ^{15}N-labelled NH_4^+ or NO_3^- or ^{18}O-labelled water (H_2O) or NO_3^- (Kool et al., 2011). Besides the differentiation between nitrification-coupled denitrification and fertilizer denitrification, especially the consideration of O exchange between NO_3^- or NO_2^- and H_2O during nitrification and denitrification enables the evaluation of nitrifier denitrification. However, a further method development could gain estimations that are more precise.

The third method uses the intramolecular distribution of ^{15}N in the linear but asymmetric N_2O molecule ("site preference") at natural abundance to distinguish between fungal denitrification or nitrification on the one hand and all other known pathways associated with denitrification (with exception of codenitrification) on the other hand (Decock and Six, 2013). However, this method is able to distinguish neither between nitrifier denitrification and bacterial denitrification nor between nitrification and fungal denitrification, because each pair produces an indiscernible SP.

It is obvious that each method mentioned above has its unique advantages but concurrently specific drawbacks to distinguish particular pathways. Although each single one provided improvements of our knowledge, no single method seems to enable a comprehensive tracking of the different N_2O forming pathways of N turnover in soils. However, up to now, these isotopic approaches has never been cross-validated. We present the results of an inter-comparison to check the strengths and weaknesses of each single one on the one hand and to give rise for possible supplementary outcomes on the other.

References

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