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Stable isotope techniques for N_2O source partitioning: Recent advances and future challenges

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Nitrous oxide (N_2O) is produced in terrestrial systems during several microbial processes which may occur simultaneously in different microsites of the same soil. As a consequence, there is often uncertainty as to which process is predominantly contributing to measured emissions. Stable isotopes are fundamental in resolving this. Here we will introduce the techniques we have developed, presenting selected results, and will critically assess their potential, alone and in combination with new nano and molecular techniques, to help address key research questions for terrestrial biogeosciences.

We have developed ^{15}N- ^{18}O-enrichment techniques to distinguish between, and to quantify, N_2O production during ammonia oxidation, nitrifier denitrification and denitrification. This provides a great advantage over natural abundance approaches as it enables quantification of N_2O from each microbial source, which can be coupled with quantification of N_2 production, and used to examine interactions between different processes and cycles. For example, we have shown increased denitrifier N_2:N_2O production in response to greater belowground C allocation under elevated pCO_2. Positive relationships have been discovered between denitrifier-N_2O production and ^{13}C-CH_4oxidation suggesting either methanotroph-dependent denitrification or anaerobic CH_4 oxidation, and nitrification has been shown to be the predominant N_2O source in soils of 35-65% water-filled pore space and at high pH. Our approach has also highlighted the significance of denitrification by ammonia oxidising bacteria (nitrifier

denitrification) as a N_2O source even under aerobic conditions. Recently, isotopomers have been proposed as an alternative for source partitioning N_2O at natural abundance levels, and offers the potential to investigate N_2O production from nitrate ammonification, although will only provide an estimated, not a quantified, contribution. Despite some limitations, these techniques become even more powerful when linked with other recent developments, such as nanoSIMS, gene expression and stable isotope probing of microbial RNA, and when linked to other disciplines.