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Combining different methodological approaches for estimating N_2O processes and N_2O reduction

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Nitrous oxide (N_2O) emissions contribute significantly to greenhouse gas effect and are mainly produced through agricultural practices, particularly following the application of nitrogen-based fertilizers. Identifying the specific microbial processes responsible for N_2O emissions is crucial to better understand the underlying mechanisms and develop targeted climate change mitigation strategies.

In recent decades, the analysis of abundance of the four most abundant isotopocules of N_2O ($^{14}N^{14}N^{16}O$, $^{14}N^{15}N^{16}O$, $^{15}N^{14}N^{16}O$, $^{14}N^{14}N^{18}O$) has represented a promising alternative to evaluate N_2O production pathways (heterotrophic bacterial denitrification, nitrifier-denitrification, fungal denitrification, nitrification) and N_2O reduction to N_2. To obtain a best estimate for N_2O reduction, this approach can be combined with the ^{15}N gas flux method with N_2-depleted atmosphere (^{15}NGF+), which allows direct quantification of N_2. Nevertheless, the N_2O isotopocule approach cannot distinguish between heterotrophic bacterial denitrification and nitrifier denitrification, while the ^{15}NGF+ method cannot differentiate between nitrifier-denitrification and nitrification, but between fungal denitrification/heterotrophic bacterial denitrification and nitrifier denitrification/nitrification. Thus, the combination of both approaches provides values for heterotrophic bacterial denitrification and nitrifier-denitrification and will improve our understanding of the N_2O processes.

We will present the calculation strategies and examples of combined datasets of N_2O isotopocules and ^{15}NGF+ from various laboratory and field studies.