A Longitudinal Study of the Microbial Basis of N2O Emissions within a Long-Term Agricultural Experiment

Abstract

Much of the global nitrous oxide emissions are derived from agricultural management driving microbial N transformations. Crop rotation, no-till, and cover cropping are feasible agronomic strategies to prevent N losses to the environment, though their effect on soil microbial N cycling at the field scale remains relatively unknown. Our goal was to determine the effect of crop rotation (continuous corn, CCC; and continuous soybean, SSS), tillage (no-till, NT; and chisel tillage, T), and cover crops (cover crop mixture, CC; and no cover crop, NCC) on the quantification of functional genes related to the N cycle from different times throughout the growing season. The study was conducted during the growing season of the cash crops following a first season of cover crops introduced after 23 years of management. Using quantitative polymerase chain reaction (qPCR) techniques, we quantified *nifH* (N_2 fixation), *amoA* (nitrification) and *nirK*, *nirS*, and *nosZ* (denitrification). Our results show that CCC increased nitrous oxide emissions by 44% compared to SSS and reduced soil pH by nearly 1 unit. The reduction in soil pH, coupled with an increase in fertilizer-derived ammonium, caused ammonia-oxidizing bacteria (AOB) and *nirK* copy numbers to increase. The SSS rotation showed opposite results. Chisel tillage was found to increase all N cycle gene counts compared to no-till. The cover crop mixture of cereal rye (*Secale cereale L.*) and hairy vetch (*Vicia villosa* Roth) significantly reduced soil nitrate levels,

though they did increase nitrous oxide emissions, possibly due to the inclusion of a legume in the cover crop mixture. In corn-dominated systems, more fertilizer N is required to maintain yields, leading to increased nitrous oxide emissions through bacterial nitrification and *nirK* denitrification caused by high ammonium concentrations and acidic soil conditions.

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