

## **Diversity and abundance of nitrifying and denitrifying communities associated with crop residue removal in a biofuel cropping system**

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Recently, the Canadian government has released a biofuel strategy as a way to combat the country's dependence on fossil fuels. A major environmental issue associated with biofuel cropping systems is the long-term sustainability of soil health, because of the large volumes of agricultural residues that are removed from fields. These crop residues are vital resources for sustaining soil productivity and an important source of nutrients. The taxonomic diversity of soil microbial communities is intrinsically linked to the quality of crop residue that is returned to soils. The soil microbial community drives important biogeochemical processes, such as crop decomposition, nutrient mineralization and denitrification, therefore alterations in quality and quantity of residue in biofuel agro-ecosystems may be of functional significance. The objective of this research was to provide new knowledge linking soil microbial processes with a field scale emissions of a key agricultural greenhouse gas, nitrous oxide (N<sub>2</sub>O). In a long term field study a corn-soybean-wheat rotation has been grown under contrasting agricultural management practices on four 1.5 ha fields. Two fields had conventional tillage management (CT), and two fields had no-tillage management (NT). Starting in November 2008, a differential crop residue management was applied to the fields with two continuing to have residue returned (+R), and two having residue removed or no residue returned (-R). N<sub>2</sub>O fluxes were measured from the soil half hourly as atmospheric gas samples using a tunable diode laser trace gas analyzer. Soil samples were collected over the growing season at spring tillage, crop physiological maturity, crop senescence, post biomass harvest and fall tillage treatment, non-growing (frozen soil), spring thaw, and pre-seeding. From the soil samples, DNA was extracted and quantitative PCR was used to enumerate abundance, followed by next-generation sequencing to determine functional gene diversity and composition of nitrifying and denitrifying communities. Daily N<sub>2</sub>O fluxes varied between treatments within the year. A major emission of N<sub>2</sub>O occurred in association with spring thaw, and significant differences were observed between fields with the highest emissions from the CT field with residues removed (-R). All nitrifying and denitrifying genes (amoA, nirS, and nosZ) were successfully quantified and sequenced in both fields throughout the study. Copies of the amoA gene were higher in the +R compared to the -R fields. Gene quantities of nirS indicated that a population of denitrifiers containing the nitrite reductase gene was present at similar levels in both fields. Significant differences in the population of denitrifiers containing nosZ were evident, with nosZ gene copies being more abundant in CT+R field. The results identify changes in the soil microbial populations, and provide ecologically meaningful associations between changes in abundance and N<sub>2</sub>O emissions in situ. These results contribute to the development of a scientific basis for choosing sustainable cropping systems that are productive and provide biomass for biofuel systems while minimizing their environmental impact through decreasing their contribution to GHG emissions and maximizing C sequestration.