

B13G-0705: Antibiotics and Manure Effects on Microbial Communities Responsible for Nitrous Oxide Emissions from Grasslands

ABSTRACT

Monday, 14 December 2015**13:40 - 18:00**📍 *Moscone South - Poster Hall*

Agroecosystems are major contributors of nitrous oxide (N₂O) emissions. Denitrification and nitrification are the primary pathways of N₂O emission in soils. However, there is uncertainty regarding the organisms responsible for N₂O production. Bacteria were previously considered the only microbial N₂O source, however, current studies indicate that fungi also produce N₂O by denitrification. Denitrifying bacteria can be a source or sink of N₂O depending on the presence and expression of nitrous oxide reductase genes (*nosZ*), encoding for the enzyme converting N₂O to N₂. Fungal denitrification may produce only N₂O as an end product due to missing the *nosZ* gene. Animal manures applied to agricultural fields can transfer antibiotics to soils as a result of antibiotic use in the livestock industry. These antibiotics target mostly bacteria and may promote fungal growth. The growth inhibition of denitrifying bacteria may favor fungal denitrifiers potentially enhancing N₂O emissions. Our objective is to examine the effects of antibiotic exposure and manure fertilization on the microbial communities responsible for N₂ and N₂O production in grasslands. Soil slurry incubations were conducted with tetracycline at different concentrations. A mesocosm experiment was also performed with soil cores exposed to tetracycline and cow manure. Production of N₂O and N₂ was measured using gas chromatography with electron capture detector (GC-ECD) and isotope ratio mass spectrometry (IRMS), respectively. Antibiotic inhibition of soil N₂ production was found to be dose dependent, reaching up to 80% inhibition with 1g Kg⁻¹ of tetracycline treatment, while N₂O production was enhanced up to 8 times. These results suggest higher fungal denitrification with a concomitant decrease in bacterial denitrification after antibiotic exposure. We also found higher N₂O fluxes in the soil mesocosms treated with manure plus tetracycline. Quantitative PCR (qPCR) will be conducted to examine the changes in abundance and expression of total bacteria (targeting 16S rRNA), fungi (targeting ITS) and the *nosZ* genes in the soil communities. Thus, this study demonstrates potential impact of antibiotic contaminated manure on microbial communities responsible for agricultural N₂O emissions.

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