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The effect of symbiotic association between AMF and maize on GHG emission from agriculture soil and its microbial metabolism study

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Purpose: As a widely distributed fungi in the soil, arbuscular mycorrhizal fungi (AMF) can affect carbon and nitrogen metabolism in the soil through their large network of mycelium. But the research on the relationship between AMF in the soil and the flux of greenhouse gases and related regulatory mechanisms is relatively lacking.

Methods: In this research, we investigated the effect of AMF on GHG especially N_2O and CH_4 from an agricultural soil. Our experimental set-up included a dual microcosm unit with two treatments: Maize inoculated with AMF (AM) and uninoculated (NM). GHG flux was measured using the statistic chamber methods and destructive soil sampling was carried out at different times. Real-time PCR and Illumina sequencing was applied to test the key genes abundance related to N_2O and CH_4 dynamics and soil microbial community changes due to the AMF inoculation.

Results: After 3-month observation, we found that N_2O flux from the soil was affected by the AMF inoculation at 1st month. Furthermore, we also found that the gene abundances of several key genes like nirK and nosZ related to N_2O dynamics in the soil were affected by AMF inoculation. The correlation analysis showed the potential link between AMF inoculation and the N related gene which could explain the GHG emission affected by AMF present in the soil.

Conclusions: This study provided insights into the importance of AMF in controlling the GHG emission from agricultural soils, although AMF are not believed to play direct roles in GHG emission.