## Title: THE MAIZE-MICROBIOTA INTERACTIONS AT RHIZOSPHERE LEVEL

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## Abstract:

At present, many studies on maize have just aimed at the potential production of the plant and their nutrition. On the other hand, many biological processes are in- or directly related to microorganisms, varying in their structure and composition in the ecosystem, governed by physical and chemical characteristics. The purpose of this study is to determine the contribution of different amendment - which are commonly used for maize production - on communities of microorganisms responsible for mitigation/emission of methane (CH<sub>4</sub>) and nitrous oxide (N<sub>2</sub>O) at rhizosphere level. For this study, maize seeds were sowed into soil with N-fertilizer (urea) (F), Azospirillum inoculant (I) and maize straw (S) composing the treatments - varying with one or more of them - in macrocosm greenhouse experiment (3 replicates for each treatment). Soil gases fluxes were measured periodically every 3 days until R1 (early corn kernel stage). At this stage, a set of plants were collected for dry mass and soil samples from rhizosphere were collected for DNA extraction. The mcrA (methanogenics), pmoA (methanotrophics) genes were quantified through PCR quantitative (qPCR) analyses, along with *nifH* (N-fixing) and *nosZ* (N<sub>2</sub>O reduction). CO2 increased significantly at V5 (5<sup>th</sup> mature leaf stage) – reaching higher emissions after 2 weeks from this stage, attributable to elevation of rhizosphere respiration rate due to accelerated plant growth; CH<sub>4</sub> flux presented low emissions with small variation; and N<sub>2</sub>O reached higher emissions after 1 week of N-fertilization at V5 stage. Differences in plant weight indicated that N-fertilizer (F) contributed significantly to plant growth more than other amendment. All treatments presented less mcrA genes copies than pmoA, confirming low CH<sub>4</sub> emissions; furthermore, mcrA communities decreased in response to N-fertilizer addition. On the other hand, the pmoA genes boost due to straw treatments may indicate a possible role of methanotrophics on straw degradation.

Keywords: macrocosm, N-fertilizer, straw, bacterial inoculation, GHG

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