TITLE: SOIL GREENHOUSE GASES FLUXES AND THE EXPRESSION OF ASSOCIATED GENES IN RESPONSE TO RAIN ON PASTURES

AUTHORS: SANTAREN, K.C.F.[1]; ARMACOLO, N.M.[2]; BALIEIRO, F.C.[3]; RODRIGUES, R.A.R.[3]; ALVES, B.J.R.[4]; FONTANA, A.[3]; RACHID, C.T.C.C.[1]

INSTITUTIONS: 1. UNIVERSIDADE FEDERAL DO RIO DE JANEIRO (AVENIDA CARLOS CHAGAS FILHO, 373, ILHA DO FUNDÃO, CEP 21941-902, RIO DE JANEIRO - RJ, BRAZIL); 2. UNIVERSIDADE ESTADUAL DE LONDRINA (RODOVIA CELSO GARCIA CID, PR-445, KM 380, CEP 86057-970, LONDRINA - PR, BRAZIL); 3. EMBRAPA SOLOS (RUA JARDIM BOTÂNICO, 1024, CEP 22460-000, RIO DE JANEIRO – RJ, BRAZIL); 4. EMBRAPA AGROBIOLOGIA (RODOVIA BR-465, KM 7, CEP 23897-970, SEROPÉDICA – RJ, BRAZIL)

ABSTRACT

The increase of greenhouse gases (GHGs) - such as CH_4 and N_2O - concentration in the atmosphere contributes to the phenomenon of climate change, which is aggravated through human practices including land-use change for livestock. Soil microorganisms can produce GHG from their metabolism and different environmental conditions, especially soil moisture content, are related to this process. However, the dynamics between GHG flows and soil microorganisms are poorly understood. This work sought to understand the connection between GHG fluxes, soil moisture content and soil bacteriome in two pasture areas. It was also aimed to comprehend how these parameters are related to the transcription of some methane and nitrogen cycle genes. For this, a degraded and a non-degraded pasture area were monitored for 16 days, facing a simulated rain event. Soil bacteriome was analyzed by next-generation sequencing, and RT-qPCR reactions were performed to evaluate gene transcriptions. Different physicochemical soil attributes, such as fertility parameters, were also determined. The two pastures differed mainly by the levels of C, N, nutrients and plant biomass, which were lower in degraded area. These differences may have contributed to the distinct responses in GHG flux dynamics after the rain simulation. It was found a higher CH_4 emission in the non-degraded area, and an increase in degraded and a decrease in the non-degraded area for N_2O flux. Analyzing the soil bacterial communities, it was observed similar values in alpha diversity between the different pasture areas and between the first and last day of monitoring. In contrast, the bacterial community structure was highly altered by pasture degradation. The transcripts evaluation was performed only for non-degraded area, due to higher RNA concentration. For *nifH*, *nirS*, *mcrA* and *pmoA* genes, an increase in the number of transcripts was observed three days after the rain simulation, which may indicate a delayed response to this stimulus. For *nosZ* expression it was observed a direct relation with soil moisture. These results show that soil moisture alter GHG flux differently in degraded and non-degraded areas. For the majority of the genes, it was needed a longer period of time to note a peak of transcription after the rain simulation. Since significant changes were found with pasture degradation, it is also important to reinforce the need to adopt practices that maintain the soil integrity and contribute to GHG mitigation.

Keywords: Climate change, Pasture degradation, RT-qPCR, 16S rRNA