TITLE: OVERVIEW ON THE *EUCALYPTUS* ROTATION INFLUENCE OVER GREENHOUSE GASES FLUXES AND BACTERIAL COMMUNITIES IN A MIDTERM PERIOD

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ABSTRACT:

Worldwide, fossil fuel burning represents the leading greenhouse gases (GHG) emitter activity but, in Brazil, deforestation, land use change and inappropriate land use are responsible for the majority of the GHG emission. Soil disturbance can cause increases or decreases in emissions through microbial activity since they mediate carbon and nitrogen changes in conformations (including GHG conformations). Brazilian planted forests, which represent 7.84 million hectares of land, supply high demands of cellulose, wood, oils, fuel and industrial biomass. Out of those, *Eucalyptus* plantations covers 5.7 million hectares. Even though, few studies investigate shifts in GHG fluxes and microbial community coming from the planting and rotation of *Eucalyptus*. To address this problem, our group analyzed three adjacent sites: a young *Eucalyptus* (1-month-old trees at the beginning of the experiment), an old *Eucalyptus* (6 years old trees) and a native forest (Atlantic forest) areas. We analyzed two GHG fluxes (CH_4 and N_2O), inorganic nitrogen content and soil microbial community (16S rRNA gene sequencing). Samplings were performed in March and December of 2017, to investigate time fluctuations. Despite there were no statistical difference among areas or time of samplings in GHG fluxes, higher N_2O averages were correlated with bacterial structure in native forest areas. Surprisingly, both bacterial richness and diversity showed higher values in *Eucalyptus* areas compared to native forest. Bacterial community structure was greatly influenced by land use, land management and time, with the first being the most influent. Among bacterial class, Gammaproteobacteria, Acidobacteria Gp3 and Betaproteobacteria were impacted by time. Alphaproteobacteria, Planctomycetia and Spartobacteria were impacted both by time and land use change (native forest x *Eucalyptus*), while Actinobacteria and Acidobacteria Gp1 by time and crop rotation. Ktedonobacteria was impacted only by land use change and Acidobacteria Gp2 was different only under old *Eucalyptus* area. We used the indicator species analysis on the 49 most abundant OTUs. From these, 16 were impacted by time, 23 were impacted by crop rotation and 30 were impacted by land use change. We intend to further our studies by evaluating gene expression of key carbon and nitrogen cycle genes through RT-qPCR in the four seasons of that year, to evaluate possible correlations among microbial gene expression and GHG fluxes.

Keywords: Greenhouse gases, *Eucalyptus*, bacterial community, 16S rRNA gene sequencing