TITLE: PLANT SPECIES AND FERTILIZATION INFLUENCE ON ABUNDANCE OF NITROGEN CYCLE GENES AT PURE AND MIXED *Eucalyptus grandis* AND *Acacia mangium* CULTIVATION

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ABSTRACT:

Nitrogen (N) is a primary macronutrient for plants and is present in macromolecules essentials for life, such as chlorophyll, nitrogenous bases, nucleic acids and others. As an alternative to minimizing the use of N in eucalyptus cultivations, we have opted for the insertion of leguminous trees, such as *Acacia mangium*, in mixed cultivations systems. The objective of this work was to evaluate the influence of pure and mixed cultivation systems of *E. grandis* and *A. mangium* on the abundance of functional genes associated with N cycling in the soil. The study was implemented at the Forest Sciences Station of Itatinga, with four complete blocks and four treatments: *E. grandis* without N fertilization (E) and *E. grandis* with N fertilization (E+N), *A. mangium* (A) and an area with mixed cultivation (E+A). Soil samples (0-20 cm) were collected in two seasons, corresponding to the 2 and 3 years of age of the trees. The E+N treatment received 10 and 90 kg of N ha^{-1} at the base and cover (one year after planting), respectively, in the form of ammonium sulfate. The abundance of the 16S rRNA genes of bacterial and archeae, ITS, *nif*H and *amo*A of bacteria and archaea ammonium oxidant (AOB and AOA) was obtained by real-time PCR (*q*PCR). There were no significant differences in the abundance of the 16S rRNA (bacterial and archeae), ITS and AOA genes among treatments. However, the abundance of the *nif*H gene in treatment A (log_{10} mean= 7.6 copies *nif*H g $soil^{-1}$) and E+A (log_{10} mean= 7.3 copies *nif*Hg $soil^{-1}$) was significantly higher than the others. However, in E+A, there was a greater abundance of *nif*H only in season 1 and the E+N treatment showed a reduction in the abundance of the same gene (mean log_{10}= 5.9 copies *nif*H g $soil^{-1}$). The AOA gene of AOB was significantly higher in treatments E and A (mean log_{10}= 7.2 copies *amo*A g $soil^{-1}$) and it was reduced at time 1 in the treatment that received ammonium sulphate (log_{10} mean= 5,4 copies *amo*A g $soil^{-1}$). We conclude that *A. mangium* increases the abundance of *nif*H genes when in consortium with *E. grandis*. Ammonium sulfate fertilization reduces the abundance of *nif*H and *amo*A genes in *E. grandis* cultivation.

Keywords: soil microbiology, leguminous plant, *q*PCR, functional genes
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