

Title: BACTERIAL BIODIVERSITY IN SOIL CULTIVATED WITH TECA (*Tectona Grandis*) AND BIOCHAR APPLICATION, IN THE CERRADO/AMAZON ECOTONE

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Summary:

Removing of native vegetation for crops introduction, some components necessary to ensure the quality of the soil can be changed, such as organic matter, nutrients and structure of microbial communities. Microorganisms are the base of the food chain and associated with various land ecological processes, thereby bacteria biodiversity has been considered as an important indicator of soil quality. In soils where the management system enables accumulation of organic material, the addition of biochar can contribute to the restoration of soil fertility, like increased organic matter, nutrient cycling and recovery and enrichment of the microbial community, which is fundamental in the balance and sustainability of natural ecosystems. The objective was to study the bacterial biodiversity in soil with biochar application and cultivated with teca (*Tectona grandis*). Soil samples were collected in the experimental field at Embrapa Agrossilvipastoril at a depth of 0-10cm. The experiment was designed in randomized blocks with four repetitions. The treatments were: T1- seedling without biochar + NPK; T2- seedling with biochar + NPK; T3- seedling without biochar + NPK + activated biochar applied to the soil; T4- seedling with biochar + NPK + activated biochar applied to the soil; T5- seedling without biochar + NPK + biochar not activated applied to the soil; T6- seedling with biochar + NPK + biochar not activated applied to the soil. The extraction of total DNA was performed using the Mobio *UltraClean™ Power Soil DNA Kit* following the manufacturer protocol. The bacterial biodiversity was assessed by DGGE technique using universal primers to the region 16 S rDNA of bacteria and diversity index Shannon-Wiener. The software used for making the similarity dendrogram was BioNumerics, version 7.1. The Shannon diversity index of T5 treatment (with not activated biochar) was less than 0.53 compared to T3 (with activated biochar). Regarding the comparison of the bacterial community structure of the coefficient of similarity, it was found that the treatments formed two groups, one of them containing the treatments T1, T2 and T3 and the other group with the treatments T4, T5 and T6. However, it was not possible to correlate the application of biochar, with the diversity of soil bacterial community, probably because it is the first year of assessment. This will be possible, with DGGE analysis of the second year of cultivation, and relate to enzyme activity and microbial biomass.

Keywords: DGGE, soil conditioner, microbial diversity

Promotion: CAPES, FAPEMAT, EMBRAPA