

## **STUDY OF MICROBIAL DIVERSITY OF BRAZILIAN SAVANNA CONSERVED REGION AND EUCALYPTUS CULTURE**

Caldas, V.E<sup>1</sup>, Alessandro, F<sup>1</sup>, Thiemann, O. H.<sup>1</sup>

<sup>1</sup>Departamento de Física e Informática, Instituto de Física de São Carlos, Universidade de São Paulo

The Brazilian savanna-like vegetation of Cerrado is the second largest biome in Brazil, being a very important Brazilian ecosystem not just because of its extension but because of its rich biodiversity. Recently, it was classified as a hotspot for conservation priority since it is one of the most threatened biomes in South America. Part of its total natural cover has already been converted into agricultural, pasture areas and Eucalyptus cultivation, mainly in the interior of São Paulo. To understand the impact caused by the introduction of different cultivations in the native ecosystems is of major importance to evaluate the alterations imposed by this. In view of the little knowledge accumulated concerning the eubacterial community and the importance of these organisms in the maintenance of these ecosystems, this study aimed to characterize and compare the bacterial communities in conserved soil of native area and of Eucalyptus cultivation. A 16S rDNA-based approach was taken to do the data base. Microbial DNA was purified directly from soil samples and subjected to PCR with primers specific for bacterial 16S rDNA gene sequences. 16S rDNA clone libraries were constructed from the two soil samples. These data had been studied using the techniques of community ecology to estimate the similarity, diversity of species, heterogeneities and evenness of the studied communities. Additionally, to validate the identity of species and to better define the observed diversity, we reconstruct the phylogeny of the communities found in each one of environments. It had been analyzed 145 clones from native Brazilian savanna and 132 clones from Eucalyptus cultivation. The great variation in relation to the dominant sorts and its distribution in each biome is notable. Moreover, some sorts had been detected solely in one of ecosystems. Such data will be important to support a future metagenomic study from the constructed libraries.