

**Título: N-cycling microbial communities of sugarcane-cultivated soils in Brazil: a metagenomic view**

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**Resumo:** Brazil is the largest world’s producer of sugarcane and this crop has a huge impact on Brazilian agriculture. A better understanding of the microbial composition that is related with nitrogen (N) cycling in soils, especially the role that those microorganisms is of utmost importance for its cultivation productivity and sustainability, once N is a molecule essential to plant development. However, little is known about the relationship between this microbial groups and this crop. Here we targeted three areas used for sugarcane cultivation (named A, F and J), which present a range of different management conditions and soil characteristics. Each area has triplicate sampled, and soil DNA was used to shotgun metagenomics sequencing (SMS) by Illumina HiSeq2500 (average of 3.4 billion of bp per metagenome). The majority of SMS reads were derived from Bacteria (98% hits to M5NR database); but sequences also matched Eukarya (1%) and Archaea (1%). Functions like nitrogen fixation and ammonium oxidation were the most abundant (SEED database) and the bacterial and archaeal groups present in greater amount responsible for carrying them out were *Proteobacteria* and *Thaumarchaeota*, respectively. The next step will be to understand the relationship between these microorganisms and the special characteristics of each area, thus contributing to clarify which type of management and physical/chemical parameters act on the abundance of them.

**Palavras-chaves:** metagenome, microbial ecology, nitrogen, shotgun

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