

## Title: DIFFERENTIAL GENE EXPRESSION OF MICROBIAL ACTIVITY ON CORN STOVER DECOMPOSITION INTO TWO TROPICAL SOILS

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### Abstract:

Several studies of soil microorganisms indicate their role in greenhouse gas (GHGs) releasing to atmosphere during crop stover decomposition. However, some studies show the opposite, affirming that soils with crop stover can act as CH<sub>4</sub> or N<sub>2</sub>O sink using gas chromatography analyses. Metatranscriptome sequencing is a reliable approach to obtain gene expressions of microbial activities during metabolic process. The purpose of this study is to evaluate corn stover as CH<sub>4</sub> and N<sub>2</sub>O sink and determine microbial activities by abundance of genes related to C and N cycles through functional and taxonomic characterization of corn stover in decomposition into two tropical soils. For this study, a crop soil (from corn field) in Brazil and Amazonian Dark Earth were disposed into vases in triplicate. Three litterbags with 5 g of dried corn stover each were buried into vases for decomposition during 20, 50 and 80 days of incubation – one litterbag was removed for each sampling time and content were macerated to fine powder in mortar using liquid N<sub>2</sub> for DNA/RNA extractions – initial time samples (T<sub>0</sub>) were collected as control group. During the experiment, soils were maintained at 25 °C and 60% of moisture. Metagenome (T<sub>0G</sub>) and metatranscriptome (T<sub>0T</sub>, T<sub>20</sub>, T<sub>50</sub> and T<sub>80</sub>) were sequenced using Illumina MiSeq System (600-cycles). After, raw sequences were uploaded to COMAN web-server pipeline for automated analysis, including treatment and annotation of sequences with KEGGs Orthologous (KOs) database. Thus, differential gene expression analyses were performed using DESeq2. As results, Amazonian Dark Earth (ADE) at T<sub>0T</sub>= 1208±190 showed a very small expression from total KOs (T<sub>0G</sub> = 5882±43) in comparison to Crop Soil (CS) (T<sub>0T</sub> = 4561±321) that maintained most of gene expressions from metagenome (T<sub>0G</sub> = 5714±103). In ADE, 29% of sequences at T<sub>0T</sub> are from archaeal communities while in CS they represent 10.7%, although this percentage increase to 31% for both soils in T<sub>80</sub>. Differential expression responses (log<sub>2</sub>fold-change > 2) in metatranscriptome were found along decomposition process: (a) most of methane-consuming genes (*pmoABC* and *mmoXYZ*) were mainly expressed between T<sub>0T</sub>-T<sub>20</sub> (for ADE) and T<sub>20</sub>-T<sub>50</sub> (for CS); (b) methane emission genes (*mcrAB*) were not detected from all samples; (c) *nosZ* have 2 times more KOs count than *norBC* for ADE-T<sub>50</sub> and 10.61 of fold-change in comparison to ADE-T<sub>0T</sub>. In conclusion, corn stover can activate microbial communities to reduce of CH<sub>4</sub> and N<sub>2</sub>O emissions.

**Keywords:** mesocosm, methane, carbon cycle, nitrous oxide, nitrogen cycle

**Financial Support:** CNPq, FAPESP