

METAGENOMIC STUDY OF BACTERIAL CONTAMINATION IN ETHANOL MILLS IN BRAZIL

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Brazil is one of the largest ethanol producers in the world, producing on average about 24 billion liters annually. The plants producing ethanol in Brazil use a non-sterile fermentation process resulting in bacterial contamination during fermentation. To combat them, plants use antimicrobials randomly, a practice that increase the price of the alcohol beyond to generate resistant bacteria and leave combings on the environment.

Therefore, identification of contaminants in different industrial environments, it is necessary, as well as the search for new technologies for the control of contaminants from alcoholic fermentation.

In order to study bacteria contaminations in the process of ethanol production we performed metagenomic analysis of plants in 2013/2014 seasons using 16S sequence. After amplification of V4 variable region according Caporaso *et al.*, 2011, amplicons were submitted to high throughput sequence on a MiSeq Illumina machine. Data were analyzed using CLC Workbench package. About 50.000 hits from each sample were compared with a local database of 16S sequences

Our results confirm the predominance of *Lactobacillus* spp in fermentation, and the presence of other contaminants not previously described as *Rubrobacter xylanophilus*, *Cloacibacterium normanense* and *Diaphorobacter nitroreducens*, which enables the development of personalized treatment.

Metagenomic, bacterial contamination, fermentation, *Lactobacillus* and NGS

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