Microbial and functional diversity of a full-scale UASB reactor applied to poultry slaughterhouse wastewater treatment: integration metabarcoding (16S rRNA gene amplicon) and metagenomic sequencing

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Abstract:

Metabarcoding and metagenomics analysis were used to understand the taxonomic and metabolic potential from full-scale UASB reactor applied to poultry slaughterhouse wastewater treatment. The information gained by integration both approaches revealed the microdiversity and major genes of the core energy and carbohydrate metabolism. For in-depth microbiome evaluation two strategies were adopted: (i) the sequencing of 16S rRNA gene for phylogenetic characterization (metabarcoding sequence; 16S_PS sample) and (ii) metagenomic sequencing for functional and diversity characterization (metagenomics sequence; MET_PS sample). The samples were sequencing using the MiSeq 2x250 bp and HiSeq 2x150bp Illumina platform respectively. The microbial structure was evaluated using the 16S rRNA gene sequence (all sequence of 16S_PS sample and only the 16S rRNA sequence extracted from the MET_PS dataset) against the M5RNA database. The functional diversity was assessed from the taxonomies found (metabarcoding sequence) using the PICRUSt software against the KEGG database and from metagenomic sequences against the SEED and KEGG database using the MG-RAST. In the total were obtained 52.826.969 and 293.825 sequences. After the trimming process, 66.4 % and 34.0 % of sequences were removed, and the average lengths reduced to 336±156 bp and 213±91 bp, MET_PS e 16S_PS, respectively. By analyzing of coverage from 16S rRNA gene sequence, it was determined that 99.93 – 99.88 % of all the microbial communities were accessed. The values of Shannon_H and Chao-1 ranged from 3.32 to 3.67 and 1.124 to 1.204, respectively. The distinct microbial composition was observed from metabarcoding and metagenomics sequence. In the 16S_PS sample were found *Clostridium* (10.5 %), *Methanosaeta* (9.5 %), *Ornithobacterium* (7.8 %), while it was observed high percentage of *Pseudomonas* (55.8 %), *Sporosarcina* (3.2 %), *Clostridium* (1.8 %) and *Bacillus* (1.3 %) from MET_PS samples. Qualitatively, the functional diversity by Picrust software and MG-RAST were similar. In the MET_PS sample, the iron, sulfur, nitrogen, phosphorus and potassium metabolism showed around 2 % (relative abundance) each. The carbohydrates and protein cycles showed 12 and 6 %, respectively. It is noteworthy the presence of methanogenesis, hydrogenases, butanol biosynthesis, and aromatic compounds degradation genes. Thus, the biomass represented the source of important genes related to bioenergy produce and aromatic compounds degradation.

Palavras-chaves: PICRUSt, MG-RAST, ANAEROBIC REACTOR

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