

Microbial diversity of inocula and mature compost from thermophilic composting operation at the São Paulo Zoo

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Abstract

Waste composting harbors a high diversity of microorganisms that participate in organic matter degradation. Some of these microorganisms can be promising thermophilic candidates able to degrade plant biomass and produce biorefinery matter. Motivated by high microbial diversity in plant waste composting, our goal is to analyze microbial diversity in inocula and mature compost of the composting process operated by the São Paulo Zoo. These inocula were collected from compost pile in later phases, usually just prior to a turning procedure. These samples are collected because practice has shown that, when added to the waste material at the start of composting, they speed up organic matter degradation. Mature compost refers to the 100-day composting material ready to be used as biofertilizer. This final matter is likely to comprise microorganisms selected by low availability of nutrients and composting thermophilic conditions. In order to investigate the microbial composition and abundance in inocula and mature compost, we collected six inoculum samples from different compost piles and three mature compost samples. Amplified 16S rRNA genes were sequenced on Illumina MiSeq platform. We used USEARCH for OTU clustering, RDP classifier for taxonomy assignment and QIIME (Quantitative Insights in Microbial Ecology) for diversity analysis. After analyzing microbial abundance, we compared our samples with São Paulo Zoo composting time-series samples from a previous study. Taxonomic profile for initial inoculum exhibited reasonable similarity with composting final stage. The most abundant phyla for inoculum and mature composts were Firmicutes, Proteobacteria, and Actinobacteria. For inoculum, Actinomycetales, Clostridiales and Bacillales were the most abundant orders. Actinomycetales and Clostridiales were also the most abundant for mature composts, but Bacillales was present in less abundance. Shared OTUs between inoculum and time-series samples (ZC4) were higher on day 30 and on day 99 compared to other days. The five most abundant OTUs in mature composts were present in inoculum samples. Comparison between inoculum and time-series samples exhibited a trend in microbial dynamic and structure of the composting process with succession of some bacteria over others.

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