

**TITLE:** DYNAMICS OF ACTINOBACTERIA COMMUNITIES IN AN VESSEL COMPOSTING SYSTEM

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**ABSTRACT:** Composting system is an important process, and is a mechanism for decontamination and transforming agricultural waste. Microorganisms in this process play different functions by accelerating the degradation and stabilization of organic materials, besides reducing odors and pathogens. Actinobacteria is a very important Gram-positive bacterial group and have being known to produce antibiotics, enzymes and plant growth regulators; helping plant disease suppression, by hyperparasitism and, or competition; as well as solubilizing phosphate and fixing nitrogen. Therefore, we studied the structure and dynamics of actinobacteria community associated with four stages of a composting system, used to fertilize a commercial banana plantation. The samples were collected on Sitio Barreiras Fruticultura Ltda, Ponto Novo, Bahia, Brazil. Four replications for each one of the four phases of in-vessel composting [0 (I), 25m (II), 50m (III) and 100m (IV)] were collected. This compost was prepared using a mixture of poultry litter, banana stalks, and sugarcane waste. Total DNA samples were extracted using Ultra Clean Soil™ DNA Isolation kit and have sequenced by MiSeq Illumina platform of 16S ribosomal DNA (rDNA). The platforms used for analyses were Brazilian Microbiome Project (BMP) and Quantitative Insights Into Microbial Ecology (Qiime). The class Actinobacteria and the order Actinomycetales were the most abundant in the all stages of the composting. The family Corynebacteriaceae was the most abundant in the first three stages (I: 84%; II: 66.55% and III: 60.73%), but in the stage IV its abundance was only 1.08%, however, in the stages I and II low abundance of other families (less of 1%) was observed. In the stage III, the communities started to diversify and in the stage IV the abundance of families was higher than others stages, presenting: Bogoriellaceae (13.53%), Dermabacteraceae (5.18%), Gordoniaceae (22.95%), Micrococcaceae (21.63%), Pseudonocardiaceae (6.75%), Yaniellaceae (6.9%), and others (23.06%). The decrease of temperature in the stages III, can favored the mesophilic population and at stage IV it reaches the room temperature and the compost was stabilized and ready to use, favoring the higher diversity of actinobacteria. Thus, there is a succession of actinobacterial communities, and the diversity being higher in the end of composting, being influenced by the temperature and nutrient availability.

**Keywords:** Next generation sequencing, bacterial diversity, actinomycetes.

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