

Metagenomics Analysis on Microbial Communities of Sewage Sludge from Nyeri-Kangemi Wastewater Treatment Plant, Nyeri County-Kenya

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Abstract : The major challenge to proper sewage sludge treatment processes is the poor understanding of sludge microbiome diversities. This study applied the whole-genome, shotgun metagenomics technique to profile the microbial composition of sewage sludge in two active digestion lagoons at the Nyeri-Kangemi Wastewater Treatment Plant in Nyeri County, Kenya. Total microbial community DNA was extracted from samples using the available ZymoBIOMICS™ DNA Miniprep Kit and sequenced using Shotgun metagenomics. Samples were analyzed using MG-RAST software (Project ID: mgp100988), which allowed for comparing taxonomic diversity before β -diversities studies for Bacteria, Archaea and Eukaryotes. The study identified 57 phyla, 145 classes, 301 orders, 506 families, 963 genera, and 1980 species. Bacteria dominated the microbes and comprised 28 species, 51 classes, 110 orders, 243 families, 597 genera, and 1518 species. The Bacteroides(6.77%) were dominant, followed by Acinetobacter(1.44%) belonging to the Gammaproteobacteria and Acidovorax (1.36%), Bacillus (1.24%) and Clostridium (1.02%) belonging to Betaproteobacteria. Archaea recorded 5 phyla, 13 classes, 19 orders, 29 families, 60 genera, and 87 species, with the dominant genera being Methanospirillum (16.01%), methanosarcina (15.70%), and Methanoregula(14.80%) and Methanosaeta (8.74%), Methanospaerula(5.48%) and Methanobrevibacter(5.03%) being the subdominant group. The eukaryotes were the least in abundance and comprised 24 phyla, 81 classes, 301 orders, 506 families, 963 genera, and 980 species. Arabidopsis (4.91%) and Caenorhabditis (4.81%) dominated the eukaryotes, while Dityostelium (3.63%) and Drosophila(2.08%) were the subdominant genera. All these microbes play distinct roles in the anaerobic treatment process of sewage sludge. The local sludge microbial composition and abundance variations may be due to age difference differences between the two digestion lagoons in operation at the plant and the different degradation rates played by the taxa. The information presented in this study can help in the genetic manipulation or formulation of optimal microbial ratios to improve their effectiveness in sewage sludge treatment. This study recommends further research on how the different taxa respond to environmental changes over time and space.

Keywords : shotgun metagenomics, sludge, bacteria, archaea, eukaryotes

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