Comparative structural and functional analysis of microbial diversity and physico chemical analysis of the Okhla landfill and compost soil New Delhi India

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Metagenomics provides a culture-independent assessment and gives an insight into complex relationships between microbial composition and functional diversity in soil. Landfill and compost sites provide unique habitat to study microbial interrelationships since they host a great microbial diversity. We report the taxonomic and functional characterization of the microbiome of composite soil sample isolated from typical landfill and compost in Okhla, New Delhi, India. Whole metagenome sequencing was performed to identify the microbial community of the composite soil sample using the Illumina NextSeq500 platform. Prodigal was performed for the gene prediction and resulting genes were considered for downstream analysis. The taxonomical analysis was carried out using Kaiju. The high-quality reads were assembled using CLC genomics workbench. Analysis showed that *Methylocaldum, Thalasobacillus, Acinetobacter* were the most dominant genera where-as Proteobacteria, Acinetobacter, Firmicutes were the most dominant phyla in Landfill. Likewise, Streptomyces, Saccharomonospora, Nocardiopsis the most dominant genera whereas Actinobacteria, Proteobacteria, Firmicutes were the most dominant phyla in compost. This suggests the key role these microbes play in biomass degradation. The structure of microbiota in the landfill was affected by physicochemical properties like pH, EC, organic matter and moisture content and presence of various elements. Physicochemical analysis of various elements was done with ED-XRF. Our results provide applicable analysis and visualization approaches for studying the complexity and heterogeneity of soil microbial communities. For functional analysis COG, KEGG pathways and GO was performed using Cognizer. The COG class 'R' was found to have the highest number of hits for the composite sample. This showed that most of the genes were involved in "Metabolism" of carbohydrates, amino acids, energy, nucleotides and lipids, xenobiotics biodegradation. In our study, a significant decrease in *Candidatus Saccharibacteria* was observed in the presence of *P. Indica*, a plant endomycorrhiza. Further investigations are in process to study the interaction between the prokaryote bacteria and the eukaryote fungus.

Biography

Bindu is pursuing PhD from School of Environmental Sciences, Jawaharlal Nehru University, New Delhi, India under supervision of Dr. Meenakshi Dua. She has enrolled in PhD in Microbial Ecology in 2016. She has completed her graduation in 2014 from Gargi College, University of Delhi, New Delhi, India and post graduation in 2016 from Banasthali University, Rajasthan, India. Recently she attended International Conference on Microbiome Research (ICMR) which was held in Hyatt Regency Pune, India from 19-22 Nov 2018. She participated in The Science Communication & Career Workshop Organized by The Wellcome Trust/DBT India Alliance and Nature India on 17 April 2018 at Jawaharlal Nehru University, New Delhi, India. She has publications in Mycopath and The Scientific Temper in 2016.

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