

Genomics and Proteomics Pyro-Sequencing Based Metagenomics of Paddy Soils from Uttar Pradesh, India

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Soil biota, the rhizosphere swarms with life in the form of microbes. India is one of the major paddy producers and first predicament to be resolved is to identify the better tool for soil metagenomic analysis and secondly to classify various paddies cultivated soils in assent with its microbial profile. In the present study we try to exploit the untapped genetic and biological pool to connect them to the fertility of the soil from four different sites across Uttar Pradesh (India). DNA was isolated using Epicenter soil DNA isolation kit and was primed for sequencing. The sequencing was carried out using 454-LS (Roche Technologies) according to manufacturer's protocol. The metadata obtained was analyzed using five different tools namely: WebCARMA, MG-RAST, CAMERA, MEGAN, GALAXY and NBC. At Phylum level NBC assigned 99% of all the reads to microbial taxa, whereas WebCARMA at 40-60% followed by MG RAST assigned 18-21%, MEGAN at 3-7% and GALAXY at 2-4% of the total reads. At Phylum level Proteobacteria, Actinobacteria and Acidobacteria were indicated maximum by all the tools among the soils. The percentage of many other phyla has been represented disparately by the tools. Rank correlations have been performed to validate our results which indicated strong correlation between WebCARMA and MG RAST. Taxonomic assignments were enumerated

between four soil types by WebCARMA and identified that two phyla Proteobacteria and Actinobacteria were relatively abundant among all the soils. Proteobacteria are found relatively higher in Inceptisol soil (42.14%) and reasonably less in Red soil (30.71%). Actinobacteria considered next abundant phyla was present more in Red soil (26.21%) and nearly equivalent among other soils. Acidobacteria was discovered higher in Red soil (15.94%). In phylum Proteobacteria, the class Alphaproteobacteria has been found higher, among all the soils with dominance in Red soil (18.26%). Deltaproteobacteria are discovered higher in Terai soil (13.49%) and Betaproteobacteria have been unearthed more from Dhankar soil (9.52%). Chloroflexi has been relatively higher in Terai soil (10.06%). At genus level MG RAST presented distinct data. Red soil has significantly higher percent of *Conexibacter*, *Candidatus Koribacter*, *Candidatus Solibacter* and *Bradyrhizobium* followed by Terai, Dhankar and Inceptisol soil samples. MG RAST was concluded to be one of the best tools for soil metadata analysis due to flexibility of its database and encompassing variations in its analyzing modes both taxonomically and functionally. The soil analysis showed higher fertility in Red soil which could be attributed to high percentage of supportive microorganisms.