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Influence of farm management practices on soil bacterial community structure and function

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These microbes in turn are affected by the soil management practices. This study aims at identifying soil bacterial richness evenness and diversity under organic and inorganic soil management practices. The maize rhizosphere soil under organic and inorganic management from past five years was sampled during the vegetative stage. The hyper-variable region (V₃) of bacteria was amplified from organic and inorganic soil DNA and sequenced by Ion torrent personal genome machine. The Q20 reads were phylogenetically classified using M5RNA annotation source of MGRAST. Species richness and diversity estimation was calculated using SPADE and the statistical significance in the species difference was calculated by STAMP. The species richness and diversity were found to be significantly more in organic sample whereas the distribution of species in both the sample is moderately even (0.73). Effective number of species was also found to be slightly more in organic soil. Organic soil is rich in species like *Chloroflexus aurantiacus*, *Sphingomonas wittichii*, *Nocardiopsis kunsanensis* and *Rubrobacter radiotolerans* which are involved in nutrient recycling and degradation of plant litter whereas the inorganic soil is rich in species like *Thermoleophilum album*, *Chitinophaga pinensis*, *Terrimonas lutea* and *Flexibacter elegans* which are known for degradation of plant litter and chemical compounds present in pesticides. The type of bacterial species present in organic and inorganic soil indicates formation of bacterial community structure based on farm management practices.

Biography

Malik Ahmed Pasha is pursuing Ph.D. in Molecular Biology and Biotechnology from University of Agricultural Sciences Dharwad. He is working on metagenomic analysis of soils with organic and inorganic farm management. Couple of papers based on the outcome of his research is under process.

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