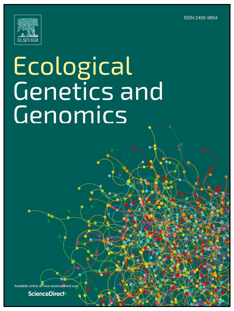

Metatranscriptome sequencing and analysis of agriculture soil provided significant insights about the microbial community structure and function

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"Metatranscriptome Sequencing and Analysis of Agriculture Soil provided significant insights about the Microbial Community Structure and Function"

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Abstract

In the present study, we report sequencing and analysis of metatranscriptome from agriculture soil having long history of usage of chemical fertilizers and pesticides. To meet our objectives, we estimated the presence of pesticides and heavy metals in this agriculture soil, followed by extraction of total RNA from soil in replicates. Enrichment of prokaryotic mRNA, and preparation of cDNA libraries from soil yielded ~11.49 and ~8.43 Gb data, after Hiseq 2000 Illumina sequencing. Sequences recovered showed ~55% GC contents and a Phred score >30. Taxonomic annotation of affiliated sequences and their subsequent analysis revealed presence of organisms from diverse origin, in the following order: Bacteria >Archeae >Eukaryotes >Viruses. Among several bacterial genera, Achromobacter, Pseudomonas, Bacillus, Sphingobium, Micrococcus, Serratia and Streptomyces involved in pesticide degradation showed high