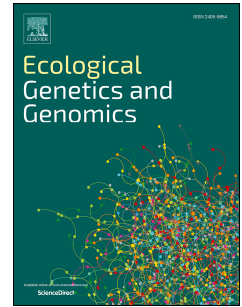


Accepted Manuscript

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

Pushpender Kumar Sharma, Rohit Sharma



PII: S2405-9854(17)30024-1

DOI: [10.1016/j.egg.2017.10.001](https://doi.org/10.1016/j.egg.2017.10.001)

Reference: EGG 18

To appear in: *Ecological Genetics and Genomics*

Received Date: 30 May 2017

Revised Date: 20 September 2017

Accepted Date: 30 October 2017

Please cite this article as: P.K. Sharma, R. Sharma, Metatranscriptome sequencing and analysis of agriculture soil provided significant insights about the microbial community structure and function, *Ecological Genetics and Genomics* (2017), doi: 10.1016/j.egg.2017.10.001.

This is a PDF file of an unedited manuscript that has been accepted for publication. As a service to our customers we are providing this early version of the manuscript. The manuscript will undergo copyediting, typesetting, and review of the resulting proof before it is published in its final form. Please note that during the production process errors may be discovered which could affect the content, and all legal disclaimers that apply to the journal pertain.

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

Authors: Pushpender Kumar Sharma*¹ Rohit Sharma^{1,2}

Affiliations:

¹Department of Biotechnology, Sri Guru Granth Sahib World University, Fatehgarh Sahib, Pb, India

²Present address: Department of Plant Science Crop Technology Center University of Manitoba Winnipeg-R3T2N2, Canada.

1 ***Corresponding author e-mail and address:** Department of Biotechnology, Sri Guru Granth Sahib World University, Fatehgarh Sahib, Pb, India E-mail: pushpg_78@rediffmail.com,psnp7819@gmil.com Phone number: +919872567832

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

Download English Version:

<https://daneshyari.com/en/article/8644131>

Download Persian Version:

<https://daneshyari.com/article/8644131>

[Daneshyari.com](https://daneshyari.com)