



Category: Metagenomics

Metagenomic analysis of microbial heterogeneity and stress response Mechanisms in Desert

K.K. Sivakala¹, P.A. Jose², T. Thinesh³, R. Anandham⁴, N. Sivakumar^{1*} and S.R.D. Jebakumar^{1#}

¹Department of Molecular Microbiology, Madurai Kamaraj University, Madurai, INDIA

²Marine Biotechnology and Ecology Division, CSIR-CSMCRI, Bhavnagar, Gujarat, INDIA

³Life Science Division, Florida International University, USA

⁴Department of Agricultural Microbiology, Tamil Nadu Agriculture University, Madurai, INDIA

Presenting author: sivakalaarul@gmail.com; *Correspondence; #Deceased

Abstract

Desert environments have high spatial heterogeneity evidenced by the occurrence of relatively low vegetation as small patches. Given the low vegetation cover, soil microorganisms are the main drivers of ecosystem processes in desert environments and thought to have unique stress-response and metabolic adaptation. Therefore, exploring the microbial spatial heterogeneity and metabolic adaptation is crucial for interpreting ecological patterns in the desert environment. In this study, we have evaluated the spatial heterogeneity of physicochemical parameters, soil microbial diversity and metabolic adaptation of microorganisms at meter scale. Soil samples were collected from two quadrates of 4x4 meter size from a desert environment (Bikaner, Thar Desert, India) which face hot arid climate with very little rainfall and extreme temperatures. Analysis of variance of the physicochemical parameters revealed that calcium and sulphate ions were the most important variables between the quadrates. Microbial diversity was studied using Illumina bar coded sequencing by targeting V3-V4 regions of 16S rDNA. As the results, 702504 high-quality sequence reads, assigned to 173 operational taxonomic units at the species level. The most abundant phyla in both quadrates were Actinobacteria, Proteobacteria, and Firmicutes. At the genus level, *Gaiella* was most abundant, followed by *Streptomyces*, *Solirubrobacter*, *Aciditerrimonas*, *Geminicoccus*, *Geodermatophilus*, *Microvirga*, and *Rubrobacter*. Between the quadrates, massive variation was found in the abundance of *Aciditerrimonas* (iron-reducing, moderately thermophilic), *Geminicoccus* (phototrophic), and *Solirubrobacter*. The automated metabolic functional mapping of abundant bacterial community revealed diverse activities, and correlated with physicochemical parameters of quadrates. For instance, relatively large numbers of bacteria were mapped with nitrogen and sulphur mineralizing activities in both quadrates. As the whole, there is a strong correlation between spatial variation of ions, microbial diversity and functional attributes in the studied quadrates, and patchy nature in local scale. Additionally, the relative abundance of Actinobacteria, a phylum with large number of industrially important bacterial species, in both quadrates suggests that the desert environment may be considered for bioprospection of bioactive natural products.

Citation: Sivakala, K.K., Jose, P.A., Thinesh, T., Anandham, R., Sivakumar, N. and Jebakumar, S.R.D. Metagenomic analysis of microbial heterogeneity and stress response Mechanisms in Desert [Abstract]. In: Abstracts of the NGBT conference; Oct 02-04, 2017; Bhubaneswar, Odisha, India: Can J biotech, Volume 1, Special Issue, Page 135. <https://doi.org/10.24870/cjb.2017-a121>