



Category: Metagenomics

Metagenomics insights into Cr(VI) effects on structural and functional diversity of bacterial community in chromite mine soils of Sukinda Valley, Odisha

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Abstract

Soil contamination with heavy metal like chromium is a wide-spread environmental problem in mining and its periphery areas causing hazard to the plant, animal and human. Bacterial communities which resist the toxic effect of Cr(VI) can only survive under this hostile condition. In the study assessment of structural diversity of bacterial communities from four different locations of chromite mines area of Sukinda, Odisha (India) were carried out with 16S rRNA amplicon sequencing of V₃ regions using illuminaMiSeq and functional diversity analysis from *in situ* mining site with whole genome metagenomics using illuminaHiSeq. The taxonomic classification was carried out through QIIME program. The samples differed from each other, both in terms of level of contamination and soil characteristics. The variations in pH were small (6.67-7.32) between the mine soils from *in situ* and overburden sites in comparison to forest soil (5.08). The forest soil contains higher amount of available N and K as well as organic carbon as compared to both the mine soils. Heavy metals like Fe, Cr, Ni, and Cd have been detected in higher concentrations in *in situ* sites than both overburden and forest soil samples. Whereas concentration of other heavy metals like Co and Mn is high in overburden than *in situ* and forest soil. In spite of the differences between the samples, they shared many common operational taxonomic units (OTUs) and it was possible to delineate the core microbiome of the soil samples. In general, Actinobacteria were the most dominant phyla with abundance of Deltaproteobacteria, Alphaproteobacteria, and Gammaproteobacteria within the soils. Certain bacterial genera like *Acinetobacter*, *Pseudomonas*, *Lactobacillus*, *Bacillus*, *Clostridium* and *Corynebacterium* were found to be predominant in *in situ* mining sites, whereas genera like *Nitrospira*, DA101, JG37-AG-70 and *Nitrospira* and DA101 were found to be abundant in overburden and forest soil respectively. In *in situ* soil, the bacterial genes are involved in membrane transport, DNA metabolism, Iron acquisition and metabolism, secondary metabolism, motility and chemotaxis. The results of this study add valuable information about the composition as well as structure and function of bacterial communities in chromite mine area soils and shed light on possible bioremediation transformations promoted by bacterial communities.

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