METAGENOMIC ANALYSIS OF THE BACTERIAL COMMUNITIES ASSOCIATED WITH AGRICULTURAL LAND RECLAMATION

By

Mohamed Hassan Mahmoud Mohamed Korkar
B.Sc. Agric. Sc., Biotechnology, Fac. Agric., Cairo University, 2019

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ABSTRACT

Mohamed Hassan Mahmoud Mohamed Korkar: Metagenomic analysis of the bacterial communities associated with agricultural land reclamation. Unpublished M.Sc. Thesis, Department of Genetics, Faculty of Agriculture, Ain Shams University, 2022.

The aims of this work are to identify the bacterial profile of agriculture-related soil samples using metabarcoding technique to compare and explore relevant rhizosphere bacteria associated with plant cultivation in newly reclaimed land and habitual cultivated ones. Total DNA was extracted from 15 samples that represented rhizosphere and non-cultivated areas derived from agricultural, reclaimed and desert land types in Egypt. Then bacterial 16S rDNA gene was amplified using a primer pair (338F and 806R) and PCR products were sequenced of the V3-V4 variable region by NGS technology to profile each sample Among all samples, the most identified phyla were Actinobacteriota (28%), followed by Proteobacteriota (26%), Firmicutes (14%), Acidobacteriota as well as Chloroflexi (7%), Gemmatimonadota (5%), Bacteriodota as well as Crenarchaeota (3%), and Myxococcota (2%), in addition to 37 other phyla with <1% counts. A total of 74 OTU was unique to the plant rhizosphere area and classified as Bacteriodota (5.1%:0.3%), Firmicutes (2.4%:0.1%), and Proteobacteria (3.5%:2%) phyla in agriculture and reclaimed lands, respectively. The bacteria, contained mobile elements, potentially pathogenic or tolerancy to stress, were highly presented in the rhizosphere than the uncultivated area and only high in the reclaimed lands rather than the agricultural or desert lands. Among all samples, the most presented cluster of ortholog genes (COG) was the amino acid transportation and metabolism that counted an average abundance of 30 M genes. Followed by a cluster of genes with unknown function or the genes of general function prediction. The energy production and conversion genes in addition to the transcription genes were among the highly abundant genes clusters. The correlation-based distance matrix revealed positively and negatively several correlation blocks of bacterial genera. The blocks were defined by a descending letter in an accordance with the block size correlation. Major metal elements were detected from the sampling area among all land types including P, Fe, K, Mn, Zn and Cu in addition to the soil organic matter (OM). The species statistical association to soil elements was analyzed, where P was the most influential element value to the number of associated species (14 species). Moreover, the rhizosphere profile included a large portion of uncultured and unidentified bacterial species, which opened a window to further analysis. Our analysis provides a main knowledge about the rhizosphere microbiome and highlights its possible use to create microbial-based biofertilizers targeting plant performance in contrast to traditional fertilizers and their side effect on the agriculture sector.

Keywords: 16S rDNA Metabarcoding, Microbial community, Newly reclaimed lands, Exophyta and Soil microbiota

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