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**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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Approval Sheet

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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 Unpublished M.Sc.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 tolerance 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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CONTENTS

Title	Page
LIST OF TABLES	III
LIST OF FIGURES	IV
1- INTRODUCTION	1
2- REVIEW OF LITERATURE	4
2.1. Plants and Rhizosphere Microorganisms	4
2.2. Microbial Quorum Sensing	9
2.3. Microbial Autoinducers	14
2.4. Metagenomic 16S rDNA	21
3. MATERIAL AND METHODS	23
3.1. Material	23
3.1.1. Sampling locations	23
3.2. Methods	25
3.2.1. Sampling technique and Soil physico-chemical characterization	25
3.2.2. Soil physico-chemical characterization Protocol	26
3.2.3. DNA Extraction	26
3.2.3.1. Power Soil Mobio DNA Isolation Protocol	27
3.2.3.2. Agarose Gel Electrophoresis Protocol	28
3.2.4. 16S rRNA amplicon-based sequencing	30
3.2.5. Metabarcoding data processing and analysis	30
4. RESULTS AND DISCUSSION	32
4.1. DNA extraction & PCR analysis	32
4.2. Species composition analysis	33
4.2.1. Taxonomical representation	33
4.2.2. OTUs inhabiting rhizosphere areas	36
4.3. Prediction analysis	41
4.3.1. Phenotypic prediction	41
4.3.2. Functional prediction	43
4.4. Association analysis	45
4.4.1. Co-occurrence correlation network	45
4.4.2. Association to soil properties	50
5. SUMMARY	53

6. REFERENCES
ARABIC SUMMARY

56

LIST OF TABLES

Table No.		Page
(1)	A list of the soil sample collections describing the land types, plantation, and the area for each sample. Samples were identified by a specific sample code.	24

