

Article

# Metagenomic Study of the Community Structure and Functional Potentials in Maize Rhizosphere Microbiome: Elucidation of Mechanisms behind the Improvement in Plants under Normal and Stress Conditions

Oluwadara Pelumi Omotayo, Ozede Nicholas Igiehon and Olubukola Oluranti Babalola \*

Food Security and Safety Niche, Faculty of Natural and Agricultural Sciences, North-West University, Private Mail Bag X2046, Mmabatho 2735, South Africa

\* Correspondence: olubukola.babalola@nwu.ac.za; Tel.: +27-18-389-2568

**Table S1.** Sequence Information.

Samples	F1	F2	R1	R2
<b>Uploaded Sequence Information</b>				
bp Count	2,623,527,356	2,731,731,774	2,380,333,740	2,250,315,908
Sequence Count	18,942,494	18,442,769	15,666,716	15,045,869
Mean Sequence Length (bp)	150±51	149±50	150±51	149±49
Mean GC content (%)	65±11	64±11	64±10	65±11
<b>Post QC Information</b>				
bp Count	2,483,506,626	2,553,486,961	2,241,569,933	2,121,428,345
Sequence Count	17,309,422	16,779,302	14,404,078	13,867,146
Mean Sequence Length (bp)	154±46	153±47	154±48	153±46
Mean GC content (%)	65±9	65±9	65±9	66±9
<b>Processed Sequences</b>				
Predicted protein features	15,115,042	14,640,757	12,856,164	12,362,029
Predicted rRNA features	32,623	34,297	31,580	30,226
<b>Aligned Sequences</b>				
Identified protein features	5,391,241	5,549,864	4,763,335	4,954,381
Identified rRNA features	7248	7664	6847	7676

**Table S2.** Diversity evaluation of bacteria (at phyla level) in soil samples.

Phylum	F1	F2	R1	R2
<b>Actinobacteria</b>	29.37±1.79	25.17±0.37	23.95±0.31	34.40±0.94
<b>Crenarchaeota</b>	13.21±0.46	9.12±2.65	9.70±0.49	8.99±2.55
<b>Bacteroidetes</b>	3.71±0.56	4.92±0.16	4.86±0.19	4.99±2.25
<b>Euryarchaeota</b>	29.51±2.46	29.77±3.92	22.21±2.70	25.80±8.69
<b>Korarchaeota</b>	0.29±0.02	0.26±0.01	0.26±0.03	0.31±0.12
<b>Chlorobi</b>	0.13±0.00	0.13±0.04	0.16±0.00	0.11±0.01
<b>Chloroflexi</b>	2.67±0.26	2.03±0.20	2.93±0.04	2.19±0.26
<b>Nanoarchaeota</b>	0.01±0.01	0.00±0.01	0.00±0.03	0.01±0.04
<b>Cyanobacteria</b>	1.16±0.09	1.11±0.27	1.51±0.12	1.03±0.17
<b>Thaumarchaeota</b>	23.11±0.85	16.39±6.69	26.51±0.21	22.96±6.59
<b>DeinococcusThermus</b>	0.47±0.04	0.44±0.07	0.47±0.01	0.44±0.01
<b>Ascomycota</b>	32.05±2.06	42.28±12.75	39.98±3.55	40.06±17.50
<b>Basidiomycota</b>	1.72±0.04	2.07±0.49	1.23±0.09	1.71±0.38
<b>Blastocladiomycota</b>	0.01±0.00	0.01±0.00	0.00±0.00	0.01±0.00
<b>Firmicutes</b>	2.72±0.04	2.41±0.55	2.72±0.14	2.72±0.79
<b>Chytridiomycota</b>	0.03±0.01	0.05±0.02	0.05±0.00	0.10±0.08
<b>Gemmatimonadetes</b>	4.53±0.01	6.69±2.28	2.67±0.60	2.32±0.03
<b>Microsporidia</b>	0.06±0.25	0.04±0.02	0.03±0.02	0.03±0.00
<b>Nitrospirae</b>	0.49±0.06	0.46±0.14	0.47±0.04	0.30±0.02
<b>Planctomycetes</b>	1.94±0.09	1.81±0.56	3.49±0.06	2.10±0.34
<b>Proteobacteria</b>	50.59±1.90	52.42±4.32	53.02±0.82	47.17±0.48
<b>Neocallimastigomycota</b>	0.00±0.00	0.00±0.02	0.00±0.00	0.00±0.01
<b>Verrucomicrobia</b>	1.83±0.05	1.99±0.64	3.24±0.20	1.86±0.22

Mean±standard deviation (n=3). F1=maize rhizosphere samples from Lichtenburg (first site), F2= bulk soil samples from Lichtenburg, R1=Rhizosphere soil samples from Randfontein (second site), R2=bulk soil samples from Randfontein.

**Table S3.** Major functional categories in samples at level 1 subsystem.

	<b>F1</b>	<b>F2</b>	<b>R1</b>	<b>R2</b>
<b>Iron acquisition and metabolism</b>	0.60±0.02	0.55±0.01	0.46±0.03	0.51±0.05
<b>Secondary Metabolism</b>	0.36±0.00	0.35±0.02	0.34±0.03	0.32±0.00
<b>Protein Metabolism</b>	6.95±0.00	6.900.02	6.93±0.09	6.96±0.18
<b>RNA Metabolism</b>	15.39±0.01	10.19±7.95	10.12±0.00	4.45±7.91
<b>Cofactors, Vitamins, Prosthetic Groups, Pigments</b>	6.62±0.07	6.66±0.01	6.69±0.00	6.72±0.00
<b>Membrane Transport</b>	2.20±0.04	2.07±0.01	2.10±0.03	2.08±0.05
<b>Virulence, Disease and Defense</b>	2.52±0.01	2.35±0.04	2.47±0.01	2.57±0.07
<b>Potassium metabolism</b>	0.26±0.01	0.25±0.00	0.23±0.01	0.24±0.02
<b>Phosphorus Metabolism</b>	1.02±0.00	0.99±0.01	1.00±0.01	1.01±0.01
<b>Nucleosides and Nucleotides</b>	2.45±0.01	2.46±0.01	2.40±0.01	2.39±0.01
<b>Motility and Chemotaxis</b>	0.78±0.00	0.750.05	0.81±0.02	0.83±0.04
<b>Miscellaneous</b>	7.22±0.00	7.18±0.07	7.23±0.05	7.21±0.03
<b>Cell Wall and Capsule</b>	3.68±0.02	3.55±0.01	3.64±0.02	3.73±0.04
<b>Phages, Prophages, Transposable elements, Plasmids</b>	0.88±0.01	0.91±0.01	0.90±0.00	0.91±0.01
<b>Fatty Acids, Lipids, and Isoprenoids</b>	4.33±0.02	4.40±0.02	4.26±0.03	4.25±0.02
<b>Dormancy and Sporulation</b>	0.15±0.00	0.16±0.01	0.15±0.00	0.15±0.01
<b>Carbohydrates</b>	4.55±0.04	10.04±7.89	10.09±0.04	15.91±7.92
<b>Respiration</b>	2.67±0.03	2.64±0.05	2.86±0.02	2.79±0.01
<b>Regulation and Cell signaling</b>	1.13±0.00	1.09±0.01	1.13±0.02	1.15±0.01
<b>Amino Acids and Derivatives</b>	11.58±0.02	11.65±0.08	11.52±0.08	11.48±0.02
<b>DNA Metabolism</b>	3.75±0.01	3.82±0.11	3.65±0.02	3.75±0.04
<b>Nitrogen Metabolism</b>	0.87±0.01	0.88±0.04	0.78±0.01	0.79±0.00
<b>Photosynthesis</b>	0.09±0.00	0.11±0.00	0.09±0.00	0.09±0.00
<b>Metabolism of Aromatic Compounds</b>	1.95±0.01	1.96±0.02	1.99±0.04	2.03±0.09
<b>Sulfur Metabolism</b>	1.06±0.02	1.04±0.03	1.05±0.01	1.02±0.03
<b>Stress Response</b>	2.19±0.04	2.23±0.03	2.15±0.00	2.12±0.66
<b>Clustering-based subsystems</b>	13.70±0.01	13.74±0.03	13.68±0.01	13.650.04
<b>Cell Division and Cell Cycle</b>	1.03±0.01	1.06±0.02	1.050.01	1.05±0.02

Legend: Mean ± standard deviation (n=3). F1=maize rhizosphere samples from Lichtenburg (first site), F2= bulk soil samples from Lichtenburg, R1=Rhizosphere soil samples from Randfontein (second site), R2=bulk soil samples from Randfontein.