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The immense functional attributes of maize rhizosphere microbiome: a shotgun sequencing approach

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Table S1. Mean percentage of major functional hits in rhizosphere soil of maize and its surrounding soils.

Functional Hits Subsystem Level 1	Ls	Rs	Lc	Rc	P-value
Amino Acids and Derivatives	10.38 ± 0.03^{a}	10.64 ± 0.08^{b}	10.41 ± 0.01^{ac}	10.58 ± 0.01^{bc}	0.00
Carbohydrates	14.29 ± 0.05^{a}	14.03 ± 0.27^{a}	14.19 ± 0.09^{a}	13.99 ± 0.23^{a}	0.32
Cell Division and Cell Cycle	0.92 ± 0.01^{a}	0.92 ± 0.01^{a}	0.94 ± 0.03^{a}	0.96 ± 0.01^{a}	0.08
Cell Wall and Capsule	3.64 ± 0.07^{a}	3.55 ± 0.06^{a}	3.68 ± 0.05^{a}	3.57 ± 0.09^{a}	0.23
Clustering-based subsystems	12.76 ± 0.03^{a}	12.92 ± 0.08^{a}	12.84 ± 0.03^{a}	12.93 ± 0.08^{a}	0.05
Cofactors, Vitamins, Prosthetic Groups, Pigments	5.71 ± 0.02^{a}	5.67 ± 0.10^{a}	5.67 ± 0.00^{a}	5.68 ± 0.11^{a}	0.90
DNA Metabolism	4.47 ± 0.05^{a}	4.59 ± 0.03^{ac}	4.56 ± 0.10^{ad}	4.73 ± 0.10^{bcd}	0.03
Dormancy and Sporulation	0.15 ± 0.01^{a}	0.15 ± 0.02^{a}	0.14 ± 0.01^{a}	0.15 ± 0.00^{a}	0.83
Fatty Acids, Lipids, and Isoprenoids	2.69 ± 0.01^{ab}	2.72 ± 0.02^{a}	2.66 ± 0.02^{bc}	2.71 ± 0.02^{ac}	0.04
Iron acquisition and metabolism	0.65 ± 0.04^{a}	0.68 ± 0.04^{a}	0.59 ± 0.02^{a}	0.66 ± 0.00^{a}	0.12
Membrane Transport	3.73 ± 0.03^{a}	3.77 ± 0.13^{a}	3.70 ± 0.09^{a}	3.70 ± 0.10^{a}	0.82
Metabolism of Aromatic Compounds	2.01 ± 0.01^{a}	1.87 ± 0.02^{b}	1.94 ± 0.07^{ab}	1.85 ± 0.06^{b}	0.01
Miscellaneous	5.99 ± 0.11^{ac}	5.83 ± 0.15^{a}	6.40 ± 0.07^{bd}	6.30 ± 0.05^{cd}	0.01
Motility and Chemotaxis	1.03 ± 0.02^{a}	0.93 ± 0.06^{a}	1.00 ± 0.01^{a}	0.95 ± 0.02^{a}	0.07
Nitrogen Metabolism	1.23 ± 0.00^{a}	1.40 ± 0.03^{b}	1.24 ± 0.00^{a}	1.40 ± 0.07^{b}	0.00
Nucleosides and Nucleotides	3.25 ± 0.01^{a}	3.32 ± 0.03^{bc}	3.28 ± 0.02^{ac}	3.36 ± 0.02^{b}	0.01
Phages, Prophages, Transposable elements, Plasmids	0.86 ± 0.02^{a}	0.83 ± 0.01^{a}	0.83 ± 0.00^{a}	0.86 ± 0.05^{a}	0.36
Phosphorus Metabolism	1.27 ± 0.00^{a}	1.30 ± 0.01^{a}	1.30 ± 0.01^{a}	1.31 ± 0.03^{a}	0.07
Photosynthesis	0.09 ± 0.00^{a}	0.10 ± 0.00^{ab}	0.09 ± 0.00^{a}	0.11 ± 0.01^{b}	0.01
Potassium metabolism	0.48 ± 0.02^{a}	0.49 ± 0.02^{a}	0.47 ± 0.01^{a}	0.48 ± 0.02^{a}	0.72
Protein Metabolism	8.13 ± 0.02^{a}	8.34 ± 0.05^{a}	8.45 ± 0.17^{a}	8.44 ± 0.18^{a}	0.05
RNA Metabolism	3.37 ± 0.04^{a}	3.41 ± 0.03^{a}	3.42 ± 0.08^{a}	3.49 ± 0.02^{a}	0.12
Regulation and Cell signaling	1.00 ± 0.03^{a}	0.97 ± 0.01^{a}	0.99 ± 0.01^{a}	0.99 ± 0.01^{a}	0.36
Respiration	4.42 ± 0.02^{a}	4.27 ± 0.06^{ab}	4.50 ± 0.05^{ad}	4.18 ± 0.12^{b}	0.01
Secondary Metabolism	0.29 ± 0.00^{a}	0.31 ± 0.01^{b}	0.29 ± 0.00^{a}	0.30 ± 0.00^{ab}	0.02
Stress Response	3.06 ± 0.23^{a}	3.03 ± 0.24^{a}	2.50 ± 0.06^{b}	2.58 ± 0.06^{b}	0.04
Sulfur Metabolism	1.03 ± 0.01^{a}	1.01 ± 0.02^{a}	0.99 ± 0.04^{a}	0.96 ± 0.05^{a}	0.16
Virulence, Disease and Defense	3.10 ± 0.22^{a}	2.95 ± 0.15^{a}	2.93 ± 0.07^{a}	2.80 ± 0.14^{a}	0.34

Each value is expressed as mean ± standard deviation (n=3). <a-z> indicates difference in values of samples.

Table S2. Mean percentage of major functional hits in rhizosphere soil of maize and its surrounding soils.

Functional Hits Subsystem Level 2	Ls	Rs	Lc	Rc	P-value
Unknown function	20.66 ± 0.11^{a}	20.65 ± 0.12^{a}	20.75 ± 0.03^{ab}	20.90 ± 0.06^{b}	0.03
Protein biosynthesis	4.93 ± 0.02^{a}	5.06 ± 0.02^{ab}	5.14 ± 0.10^{b}	5.19 ± 0.07^{b}	0.00
Central carbohydrate metabolism	4.34 ± 0.01^{a}	4.39 ± 0.04^{ab}	4.41 ± 0.00^{bc}	4.46 ± 0.01^{c}	0.00
DNA repair	2.78 ± 0.03^{a}	2.84 ± 0.02^{ab}	2.84 ± 0.05^{ab}	2.94 ± 0.05^{b}	0.01
Lysine, threonine, methionine, and cysteine	2.75 ± 0.01^{a}	2.78 ± 0.02^{a}	2.82 ± 0.05^{a}	2.81 ± 0.03^{a}	0.09
Resistance to antibiotics and toxic compounds	2.42 ± 0.03^{a}	2.37 ± 0.14^{a}	2.52 ± 0.08^{a}	2.38 ± 0.14^{a}	0.37
RNA processing and modification	2.31 ± 0.03^{a}	2.31 ± 0.01^{a}	2.35 ± 0.06^{a}	2.38 ± 0.01^{a}	0.10
Branched-chain amino acids	2.17 ± 0.01^{a}	2.22 ± 0.03^{a}	2.20 ± 0.02^{a}	2.21 ± 0.02^{a}	0.09
Electron donating reactions	2.06 ± 0.04^{a}	1.98 ± 0.02^{a}	2.15 ± 0.00^{a}	1.94 ± 0.08^{b}	0.00
Monosaccharides	1.99 ± 0.03^{a}	1.96 ± 0.05^{a}	1.90 ± 0.04^{ab}	1.82 ± 0.06^{b}	0.01
Folate and pterines	1.97 ± 0.01^{a}	1.81 ± 0.01^{b}	1.99 ± 0.00^{a}	2.01 ± 0.03^{a}	0.00
Purines	1.77 ± 0.01^{a}	1.81 ± 0.03^{ab}	1.79 ± 0.00^{a}	1.86 ± 0.04^{b}	0.01
Di- and oligosaccharides	1.77 ± 0.03^{a}	1.66 ± 0.07^{a}	1.74 ± 0.03^{a}	1.66 ± 0.08^{a}	0.10
Oxidative stress	1.27 ± 0.02^{a}	1.32 ± 0.04^{a}	1.01 ± 0.02^{b}	1.04 ± 0.05^{b}	<0.0001
Heat shock	0.66 ± 0.02^{a}	0.73 ± 0.04^{b}	0.44 ± 0.00^{c}	0.44 ± 0.00^{c}	<0.0001
Osmotic stress	0.58 ± 0.03^{a}	0.71 ± 0.05^{b}	0.34 ± 0.02^{c}	0.40 ± 0.02^{c}	<0.0001
Cold shock	0.30 ± 0.02^{a}	0.25 ± 0.02^{b}	0.06 ± 0.00^{c}	0.06 ± 0.01^{c}	<0.0001

Each value is expressed as mean ± standard deviation (n=3). <a-z> indicates difference in values of samples.

Table S3. Mean abundance of major pathways and enzymes involved in the metagenome stress response.

Major pathways and enzymes involved in stress response	Ls	Rs	Lc	Rc
Heat_shock_dnaK_gene_cluster_extended	24.52 ± 0.12	24.02 ± 0.21	22.78 ± 0.68	22.45 ± 0.55
Regulation_of_Oxidative_Stress_Response	14.93 ± 0.63	15.01 ± 0.33	11.38 ± 0.50	11.01 ± 0.22
Glutathione:_Biosynthesis_and_gamma-glutamyl_cycle	14.23 ± 0.21	13.03 ± 0.20	10.91 ± 0.00	10.01 ± 0.00
Choline_and_Betaine_Uptake_and_Betaine_Biosynthesis	10.36 ± 0.34	10.25 ± 0.20	9.36 ± 0.72	9.33 ± 0.51
Synthesis_of_osmoregulated_periplasmic_glucans	4.87 ± 0.17	6.82 ± 0.10	6.25 ± 0.05	6.20 ± 0.02
Glutathione:_Non-redox_reactions	5.44 ± 0.28	5.80 ± 0.20	4.78 ± 0.29	4.88 ± 0.30
Protection_from_Reactive_Oxygen_Species	3.84 ± 0.15	3.91 ± 0.10	3.02 ± 0.10	3.05 ± 0.05
Glutathione_analogs:_mycothiol	3.69 ± 0.06	3.50 ± 0.02	3.00 ± 0.36	3.11 ± 0.30
Cold_shock,_CspA_family_of_proteins	2.90 ± 0.09	2.89 ± 0.05	2.50 ± 0.14	2.43 ± 0.20
Rubrerythrin	2.04 ± 0.00	2.01 ± 0.00	2.00 ± 0.03	2.00 ± 0.00
Osmoregulation	1.59 ± 0.02	2.00 ± 0.01	2.00 ± 0.00	2.02 ± 0.01
NADPH: quinone_oxidoreductase_2	0.36 ± 0.02	0.40 ± 0.00	0.30 ± 0.02	0.30 ± 0.01
Glutaredoxins	0.35 ± 0.02	0.30 ± 0.02	0.30 ± 0.00	0.29 ± 0.00
Osmotic_stress_cluster	0.32 ± 0.01	0.33 ± 0.00	0.32 ± 0.00	0.32 ± 0.00
CoA_disulfide_reductase_(EC_1.8.1.14)_containing_cluster	0.26 ± 0.01	0.25 ± 0.02	0.21 ± 0.02	0.22 ± 0.01
Ectoine_biosynthesis_and_regulation	0.21 ± 0.04	0.20 ± 0.02	0.20 ± 0.08	0.21 ± 0.04

Each value is expressed as mean ± standard deviation (n=3).

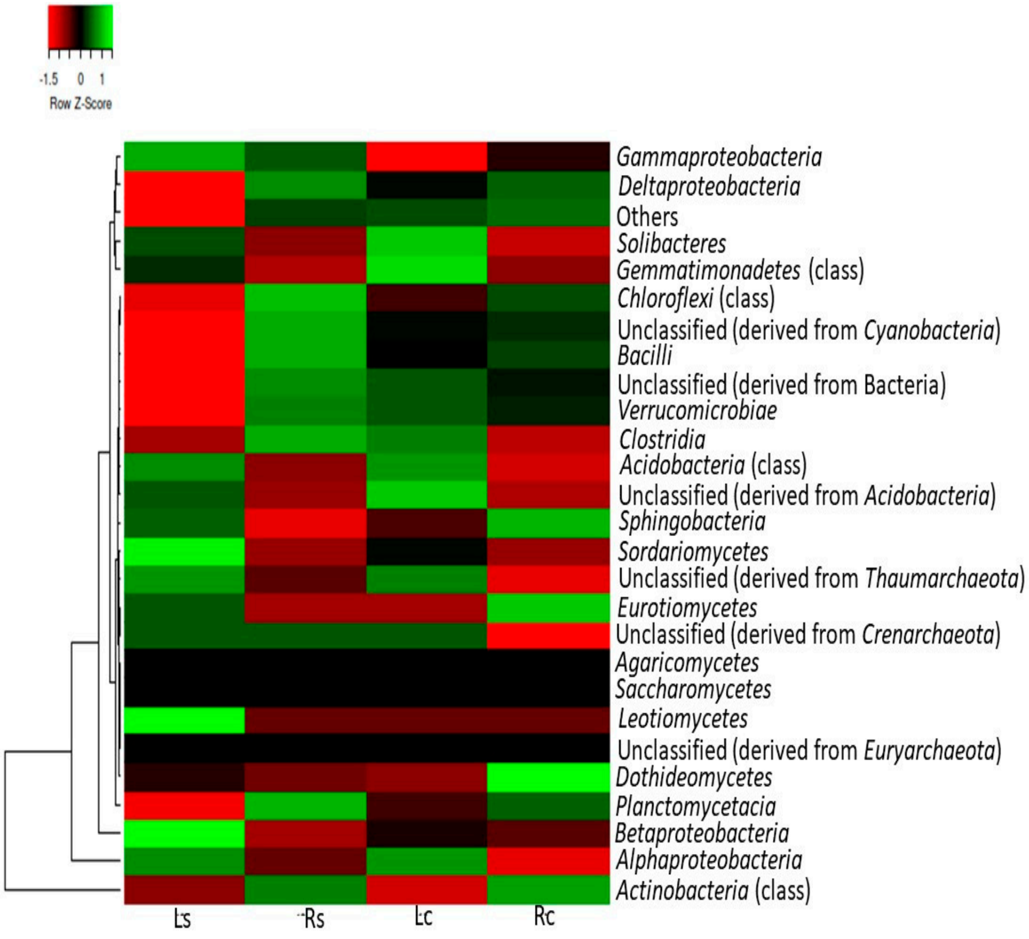

Figure S1. Heatmap of microbial class in maize rhizosphere soils and their surrounding soil samples. The z-score (scale bar) represents the relative abundance of each class.