

SUPPLEMENTARY DATA

Table S1: Analysis of sequenced data and diversity evaluation of the shotgun metagenome from the rhizosphere and bulk soil of the tomato plant

Sample site	HR	DR	BR
		<u>Sequence uploaded</u>	
bp Count	2152004650.3 bp	1409528303.3 bp	1477197003 bp
Sequences Count	13739258.3	19765082	138145859.3
Mean Sequence Length	154 \pm 32 bp	155 \pm 32 bp	155 \pm 32 bp
Mean GC percent	64 \pm 10 %	64 \pm 10 %	65 \pm 9 %
Artificial Duplicate Reads	836435	757641.7	374748
		<u>Post QC sequences</u>	
bp Count	765041235.3	1352124415	1385218693
Sequences Count	12665143.7	11966279.7	5247459
Mean Sequence Length	155 \pm 33 bp	156 \pm 39 bp	156 \pm 34 bp
Mean GC percent	63 \pm 9 %	64 \pm 9 %	64 \pm 9 %
		<u>Processed Sequences</u>	
Predicted Protein Features	7850484.3	4208873.7	11448097.3
Predicted rRNA Features	28853	30027	25322.7
		<u>Alignment Sequences</u>	
Identified Protein Features	3985525.7	4178206.3	2515439.7
Identified rRNA Features	5962.7	7656.7	5439.3

Values presented in the table are the means of the replicates from each cropping site. Healthy rhizosphere (HR), diseased rhizosphere (DR) of the tomato plant, and bulk soil (BR)

Table S2: Evaluation of major phyla in the rhizosphere of the tomato plant, and bulk soil (BR).

Phylum	HR	DR	BR	p-Value
Proteobacteria	54.0±0.42	45.9±2.06	38.8±2.41	0.05
Actinobacteria	35.50±2.3	28.13±0.6	25.36±0.6	0.03
Acidobacteria	5.0±0.2	2.28±0.1	5.18±0.6	0.07
Bacteroidetes	3.0±0.2	3.96±0.2	3.39±0.2	0.08
Planctomycetes	3.40±0.1	2.6±0.1	2.59±0.1	0.08
Chloroflexi	2.84±0.2	2.55±0.2	1.27±0.03	0.05
Firmicutes	2.31±0.2	1.69±0.06	2.43±0.1	0.07
Verrucomicrobia	2.34 ±0.1	2.23 ±0.10	2.15 ±0.1	0.67
Cyanobacteria	1.96 ±0.3	0.92 ±0.05	1.84 ±0.23	0.06
Gemmatimonadetes	1.31 ±0.1	1.6 ±0.07	1.1 ±0.03	0.11
unclassified (derived Bacteria)	0.65 ±0.01	0.89 ±0.02	0.9 ±0.06	0.06
Nitrospirae	0.39 ±0.02	0.37 ±0.03	0.31 ±0.02	0.10
Deinococcus-Thermus	0.43 ±0.02	0.28 ±0.01	0.42 ±0.02	0.05
Euryarchaeota	0.25 ±0.02	0.41 ±0.03	0.43 ±0.03	0.05
Ascomycota	0.79 ±0.11	0.45 ±0.05	0.45 ±0.07	0.07
Thaumarchaeota	0.29 ±0.03	0.18 ±0.04	0.15 ±0.05	0.15
Chlorobi	0.15 ±0.01	0.15 ±0.01	0.12 ±0.01	0.07
Crenarchaeota	0.10 ±0.01	0.06 ±0.01	0.13 ±0.01	0.06
Spirochaetes	0.07 ±0.003	0.08 ±0.001	0.08 ±0.001	0.06
Aquificae	0.04 ±0.002	0.06 ±0.01	0.06 ±0.003	0.07
Synergistetes	0.05 ±0.003	0.05±0.001	0.04 ±0.002	0.06
Thermotogae	0.05 ±0.003	0.05±0.01	0.03 ±0.001	0.07
unclassified (derived from Archaea)	0.04 ±0.002	0.03 ±0.004	0.02 ±0.001	0.06
Basidiomycota	0.03 ±0.004	0.02 ±0.001	0.02 ±0.001	0.19
Korarchaeota (Archaea)	0.03 ±0.000	0.00 ±0.000	0.004 ±0.000	0.04
Nanoarchaeota (Archaea)	0.00 ±0.000	0.00 ±0.000	0.00 ±0.000	0.07
Blastocladiomycota (Fungi)	0.00 ±0.000	0.00 ±0.000	0.00 ±0.000	0.67

Key: Healthy rhizosphere (HR), diseased rhizosphere (DR) of the tomato plant, and bulk soil (BR)

Rarefaction Analysis

The richness and diversity of the endophytic fungi and archaea were assessed using rarefaction analysis through MG-RAST. The rarefaction curve generated revealed that samples from the HR= rhizosphere soil of healthy tomato plant harbored the most rhizospheric microbes, followed by DR= rhizosphere soil of diseased tomato plant; and lowest in BR= bulk soil obtained from the soil without tomato plantation.

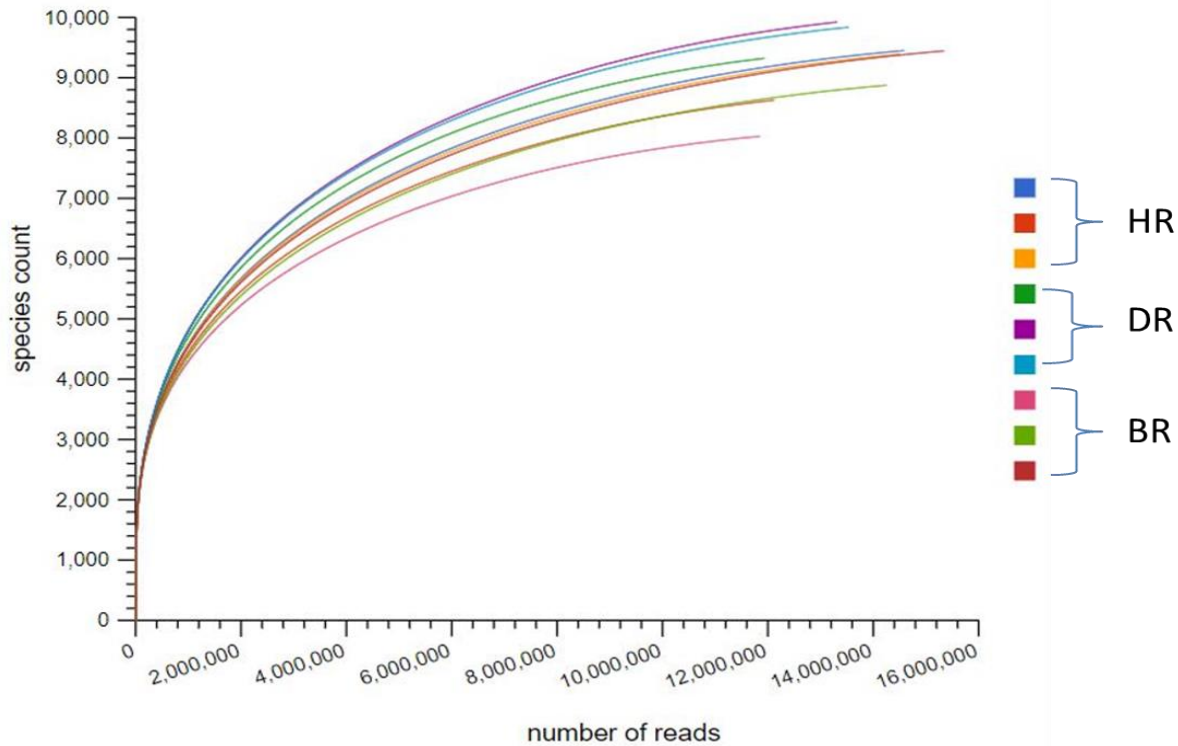


Figure S1: The abundance and Species richness of the microorganisms in the rhizosphere were investigated through rarefaction analysis with MG-RAST.