T.R. Elsayed, N.A.M. El-Said, F.A. Safhi, N.El-Houda A. Reyad (2024). ***Bacillus velezensis*** **B63 and chitosan control root rot, improve growth and alter the rhizosphere microbiome of geranium.** ***Phytopathologia Mediterranea*** **63(1): 137–154. doi: 10.36253/phyto-15093**

Table S1. Primers used in this study.

Target gene	Primers used	Sequence	Temp	Size (bp)
16S rRNA	Eub338 Eub518	ACTCCTACGGGAGGCAGCAG ATTACCGCGGCTGCTGG	55°C	123
nifH	DVV IGK3	ATIGCRAAICCICCRCAIACIACRTC GCIWTHTAYGGIAARGGIGGIATHGGIAA	53°C	454
bacC	Bacc1f Bacc1r	GAAGGACACGGAGAGAGTC CGCTGATGACTGTTCATGCT	55°C	875
ituD		GATGCGATCTCCTTGGATGT ATCGTCATGTGCTGCTTGAG	55°C	647
16S Amplicon PCR Forward Primer		TCGTCGGCAGCGTCAGATGTGTATAAGAGACAGC CTACGGGNGGCWGCAG		
16S Amplicon PCR revers Primer		GTCTCGTGGGCTCGGAGATGTGTATAAGAGACAG GACTACHVGGGTATCTAATCC		

Table S2. Relative abundance of dominant genera in the rhizosphere of geranium under the effect of chitosan, B63 compared to untreated control plants.

Genera	Control	Chitosan	B63
Kaistobacter	3.5	6.1	6.7
Agrobacterium	6.51	0.64	3.64
Acidobacteria iii1-15_unclassified	2.67	6.22	3.86
*Comamonadaceae*_unclassified	1.73	1.05	4.94
*Rhizobiales*_unclassified	4.15	2.72	3.64
Gemmata	1.58	3.47	1.76
*Bacillales*_unclassified	2.25	3.44	0.91
*Nocardioidaceae*_unclassified	3	1.49	2.44
*Gaiellaceae*_unclassified	1.6	2.74	2.33
Bacteria_unclassified	2.29	1.69	2.73
*Enterobacteriaceae*_unclassified	0.81	2.22	0.63
*Actinomycetales*_unclassified	2.01	0.88	1.25
*Micrococcaceae*_unclassified	2.01	0.68	0.4
*Sphingomonadaceae*_unclassified	1.31	1.31	1.93
*Micrococcales*_unclassified	1.12	1.78	1.48
*Xanthomonadaceae*_unclassified	0.85	0.63	1.7
*Rhodospirillaceae*_unclassified	1.09	1.63	1.53
WD2101_unclassified	0.89	1.47	1.59
*Rhizobiaceae*_unclassified	1.56	0.5	1.42
Paracoccus	1.25	1.53	0.51
*Gemmataceae*_unclassified	0.93	1.46	0.68
Balneimonas	1.23	1.44	1.02
Streptomyces	1.07	0.47	1.42
*Micromonosporaceae*_unclassified	0.71	0.63	1.42
Planctomyces	1.36	1.06	0.97
Rhodoplanes	0.76	1.36	0.57
*Rhodospirillales*_unclassified	1.34	1.21	0.97
*Pirellulaceae*_unclassified	1.26	1.26	1.19
*Alphaproteobacteria*_unclassified	1.07	0.6	1.25
*Kineosporiaceae*_unclassified	1.25	0.22	0.11
Sinorhizobium	0.73	0.89	1.19
Devosia	1.19	0.31	1.02
*Solirubrobacterales*_unclassified	1.15	1.09	0.85
Sphingomonas	0.89	0.49	1.14
mb2424_unclassified	0.3	1.14	0.51
*Promicromonosporaceae*_unclassified	1.03	0.41	0.28
*Acidimicrobiales*_unclassified	0.96	1.01	0.97
*Chthoniobacteraceae*_unclassified	0.53	0.97	0.74
*Myxococcales*_unclassified	0.49	0.75	0.97
Steroidobacter	0.86	0.92	0.68
Bacillus	0.92	0.88	0.23
*Chitinophagaceae*_unclassified	0.4	0.59	0.91
Acinetobacter	0.23	0.91	0.63
*Sinobacteraceae*_unclassified	0.64	0.88	0.8
*Erythrobacteraceae*_unclassified	0.84	0.28	0.85
Pirellula	0.43	0.82	0.63

(Continued)

Table S2. (Continued).

Genera	Control	Chitosan	B63
RB41_unclassified	0.19	0.82	0.68
Rubellimicrobium	0.8	0.55	0.63
Mycobacterium	0.77	0.15	0.45
*Solirubrobacteraceae*_unclassified	0.75	0.44	0.23
*Gemmatimonadetes*_unclassified	0.25	0.65	0.68
Erwinia	0.18	0.68	0.17
Agromyces	0.67	0.59	0.4
JG30-KF-CM45_unclassified	0.65	0.43	0.4
Aeromicrobium	0.49	0.25	0.57

Genera	Control	Chitosan	B63
Actinoplanes	0.26	0.08	0.57
*Bradyrhizobiaceae*_unclassified	0.52	0.56	0.45
*Microbacteriaceae*_unclassified	0.55	0.11	0.23
*Cytophagaceae*_unclassified	0.48	0.53	0.34
*Solibacterales*_unclassified	0.21	0.53	0.45
*Betaproteobacteria*_unclassified	0.37	0.51	0.51
*Verrucomicrobiaceae*_unclassified	0.42	0.39	0.51
Rhizobium	0.26	0.1	0.51

Table S3. Relative abundance of dominant phyla and classes in the rhizosphere of geranium under the effect of chitosan, B63 compared to untreated control plants.

Phylum	Class	Control	Chitosan	B63
Proteobacteria		43.98	39.25	47.78
	Alphaproteobacteria	33.62	25.91	33.18
	Betaproteobacteria	2.9	2.75	6.48
	Deltaproteobacteria	1.66	2.44	1.88
	Gammaproteobacteria	5.54	7.97	5.85
	*Proteobacteria*_unclassified	0.24	0.15	0.4
Actinobacteria		27.83	19.93	21.59
	Acidimicrobiia	2.42	2.92	2.1
	Actinobacteria	20.31	10.28	14.6
	*Actinobacteria*_unclassified	0.94	1.8	0.85
	Nitriliruptoria	0.07	0.09	0.23
	Rubrobacteria	0.31	0.32	0.23
	Thermoleophilia	3.78	4.53	3.58
Planctomycetes		6.92	10.06	7.56
	Phycisphaerae	0.91	1.54	1.65
	Planctomycetia	5.94	8.41	5.85
	*Planctomycetes*_unclassified	0.02	0.06	0
Acidobacteria		5.06	12.57	8.41
	Chloracidobacteria	1.33	3.36	3.07
	*Acidobacteria*_unclassified	0.02	0.03	0.06
	Acidobacteria	3.32	8.32	4.72
	Solibacteres	0.22	0.56	0.4
Firmicutes		4.7	5.18	1.53
	Bacilli	4.6	5.03	1.48
	Clostridia	0.09	0.14	0.06
Chloroflexi		3.61	3.92	2.78
	Anaerolineae	0.4	0.33	0.34
	Chloroflexi	0.84	0.66	0.8
	*Chloroflexi*_unclassified	0.11	0.11	0
	Thermomicrobia	0.77	0.48	0.45
Bacteria_unclassified	Bacteria_unclassified	2.29	1.69	2.73
Bacteroidetes		1.9	1.81	2.44
	Rhodothermi	0.06	0.06	0

(Continued)

Table S2. (Continued).

Phylum	Class	Control	Chitosan	B63
	Saprospirae	0.67	0.9	1.14
	*Bacteroidetes*_unclassified	0.03	0.04	0.23
	Cytophagia	0.64	0.63	0.74
	Flavobacteriia	0.2	0.09	0.11
	Sphingobacteriia	0.3	0.1	0.23
Verrucomicrobia		1.61	2.34	2.05
	Pedosphaerae	0.22	0.34	0.17
	Spartobacteria	0.72	1.43	1.25
	Opitutae	0.14	0.15	0.17
	Verrucomicrobiae	0.51	0.41	0.45
Gemmatimonadetes		0.82	1.63	1.59
	Gemmatimonadetes	0.35	0.76	0.85
	*Gemmatimonadetes*_unclassified	0.45	0.795	0.67
TM7		0.7	0.51	0.91
Nitrospirae		0.19	0.6	0.17
Cyanobacteria		0.11	0.12	0.06
Armatimonadetes		0.06	0.06	0
	Fimbriimonadia	0.05	0.05	0
Chlamydiae		0.05	0.01	0
Elusimicrobia		0.01	0.05	0

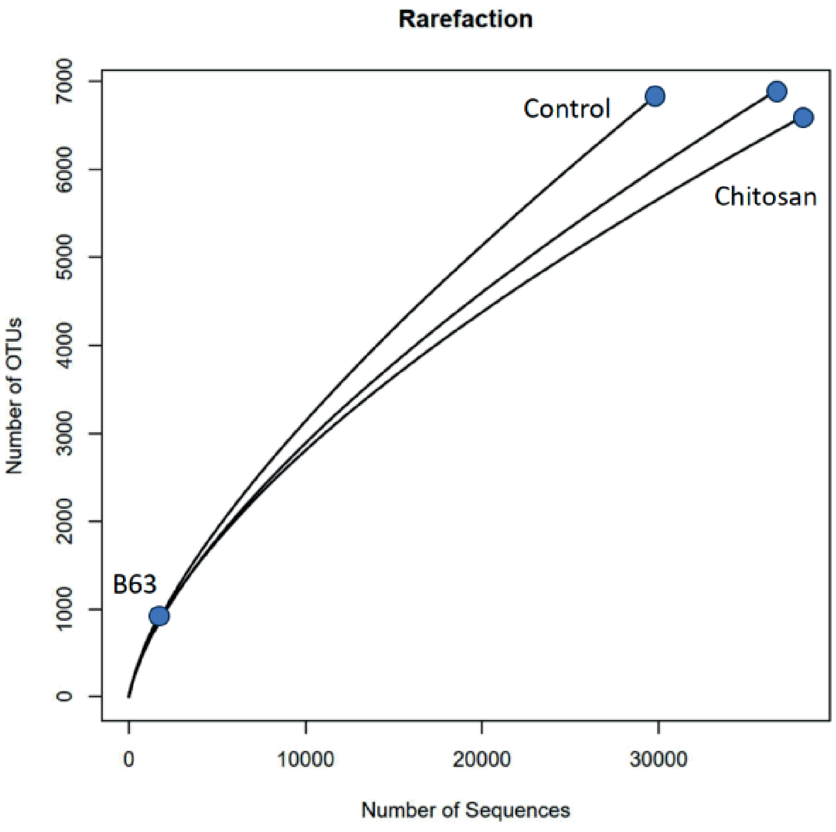

Figure S1. Rarefaction curve.