

Table S1. Effect of 0 (C), selected bioinoculum (I), 200 mM NaCl (S) and their interactions on plant height (PH), root length (RL), shoot length (SL), root/shoot ratio (R/S), root fresh weight (RFW), shoot fresh weight (SFW), total fresh weight (TFW) of *Solanum melongena* L. plant 66 days after sowing. Values are means \pm SD based on triplicate independent determinations, and different letters means significant difference as evaluated by Duncan's multiple comparison test ($p < 0.05$).

Treatment	Growth parameters						
	PH (cm)	RL (cm)	SL (cm)	R/S	RFW (g plant ⁻¹)	SFW (g plant ⁻¹)	TFW (g plant ⁻¹)
C	73.50 ^a \pm 5.20	22.50 ^a \pm 3.91	51.0 ^a \pm 7.76	0.45 ^{bc} \pm 0.15	34.17 ^a \pm 0.76	45.18 ^a \pm 13.40	79.35 ^a \pm 12.65
I	73.83 ^a \pm 13.05	22.0 ^a \pm 4.82	51.83 ^a \pm 9.70	0.43 ^c \pm 0.09	13.57 ^b \pm 4.08	42.50 ^a \pm 5.96	56.07 ^b \pm 1.90
S	56.17 ^b \pm 5.58	26.0 ^a \pm 2.65	30.17 ^b \pm 3.25	0.86 ^a \pm 0.06	1.41 ^d \pm 0.16	7.22 ^b \pm 0.16	8.62 ^d \pm 0.30
S+I	59.83 ^{ab} \pm 1.53	24.17 ^a \pm 4.25	35.67 ^b \pm 3.01	0.69 ^{ab} \pm 0.18	8.79 ^c \pm 2.35	21.66 ^b \pm 5.15	30.46 ^c \pm 7.47

Table S2. Effect of 0 (C), selected bioinoculum (I), 200 mM NaCl (S) and their interactions on root dry weight (RDW), shoot dry weight (SDW), total dry weight (TDW), root water content (RWC), shoot water content (SWC), total water content (TWC), and leaf area(LA) of *Solanum melongena* L. plant 66 days after sowing. Values are means \pm SD based on triplicate independent determinations, and different letters means significant difference as evaluated by Duncan's multiple comparison test ($p < 0.05$).

Treatment	Growth parameters						
	RDW (g plant ⁻¹)	SDW (g plant ⁻¹)	TDW (g plant ⁻¹)	RWC (g plant ⁻¹)	SWC (g plant ⁻¹)	TWC (g plant ⁻¹)	LA (cm ² /plant)
C	11.35 ^a \pm 0.75	7.95 ^a \pm 2.25	19.31 ^a \pm 3.0	22.81 ^a \pm 1.49	37.23 ^a \pm 11.15	60.04 ^a \pm 9.66	136.5 ^a \pm 25.45
I	3.62 ^b \pm 0.76	6.88 ^{ab} \pm 0.74	10.50 ^b \pm 0.61	9.94 ^b \pm 3.35	35.62 ^a \pm 5.40	45.56 ^b \pm 2.20	122.0 ^a \pm 21.35
S	0.42 ^c \pm 0.07	1.34 ^c \pm 0.17	1.76 ^d \pm 0.23	0.99 ^c \pm 0.10	5.88 ^b \pm 0.15	6.87 ^d \pm 0.17	55.78 ^b \pm 9.38
S+I	2.47 ^b \pm 0.85	4.52 ^b \pm 1.08	6.99 ^c \pm 1.93	6.32 ^b \pm 1.50	17.14 ^b \pm 4.08	23.47 ^c \pm 5.56	108.6 ^a \pm 32.64

Table S3: Similarity percentages and accession numbers obtained after comparing the sequence of the tested strain (B1SRZS) to the submitted sequences in Gene Bank

Description	Max Score	Total Score	Query Cover	E value	Per. Ident	Accession
<i>Bacillus subtilis subsp. stercoris</i>	1249	1249	52%	0.0	99.71%	MT214144.1
<i>Bacillus subtilis</i>	1249	1249	52%	0.0	99.71%	MT673811.1
<i>Bacillus subtilis</i>	1254	1254	53%	0.0	99.71%	AY973269.1
<i>Bacillus subtilis</i>	1253	1253	53%	0.0	99.56%	MT111030.1
<i>Bacillus siamensis</i>	1256	1256	53%	0.0	99.71%	KX660755.1

Description	Max Score	Total Score	Query Cover	E value	Per. Ident	Accession
<i>Bacillus subtilis</i>	1254	1254	53%	0.0	99.71%	MT1111001.1
<i>Bacillus velezensis</i>	1254	1254	53%	0.0	99.71%	MT078629.1
<i>Bacillus amyloliquefaciens</i>	1253	1253	53%	0.0	99.56%	MT081100.1
<i>Bacillus subtilis</i>	1253	1253	53%	0.0	99.56%	MN227486.1
<i>Bacillus tequilensis</i>	1253	1253	53%	0.0	99.56%	MF077125.1
<i>Uncultured bacterium</i>	1253	1253	53%	0.0	99.56%	KP843085.1
<i>Bacillus siamensis</i>	1253	1253	52%	0.0	99.71%	MW474847.1
<i>Bacillus subtilis</i>	1251	1251	52%	0.0	99.71%	MH359177.1
<i>Bacillus sp.</i>	1251	1251	52%	0.0	99.71%	MH769161.1
<i>Bacillus sp.</i>	1251	1251	52%	0.0	99.71%	MH769061.1
<i>Geobacillus sp.</i>	1251	1251	52%	0.0	99.71%	KP792636.1
<i>Bacillus subtilis</i>	1251	1251	52%	0.0	99.71%	MH210872.1
<i>Bacillus sp.</i>	1251	1251	53%	0.0	99.56%	MN826383.1
<i>Bacillus subtilis</i>	1251	1251	52%	0.0	99.71%	MN330078.1
<i>Bacillus amyloliquefaciens</i>	1251	1251	52%	0.0	99.71%	JF899282.1
<i>Bacillus licheniformis</i>	1249	1249	52%	0.0	99.71%	MT525234.1
<i>Bacillus subtilis</i>	1249	1249	52%	0.0	99.71%	MT372156.1
<i>Bacillus velezensis</i>	1249	1249	52%	0.0	99.71%	MT365117.1
<i>Bacillus subtilis subsp. stercoris</i>	1249	1249	52%	0.0	99.71%	MT332715.1
<i>Bacillus velezensis</i>	1249	1249	52%	0.0	99.71%	MT124527.1
<i>Bacillus amyloliquefaciens</i>	1249	1249	52%	0.0	99.71%	MK743994.1
<i>Bacillus sp.</i>	1249	1249	52%	0.0	99.71%	MN826422.1
<i>Bacillus sp.</i>	1249	1249	52%	0.0	99.71%	MN826418.1
<i>Bacillus sp.</i>	1249	1249	52%	0.0	99.71%	MN826404.1
<i>Bacillus subtilis</i>	1245	1245	52%	0.0	99.56%	MW513386.1
<i>Bacillus subtilis</i>	1249	1249	52%	0.0	99.71%	MT898543.1

Table S4: Similarity percentages and accession numbers obtained after comparing the sequence of the tested strain (**B4SRZS**) to the submitted sequences in Gene Bank

Description	Max Score	Total Score	Query Cover	E value	Per. Ident	Accession
<i>Bacillus subtilis</i>	1256	1256	99%	0.0	99.28%	MH359177.1
<i>Bacillus subtilis</i>	1258	1258	99%	0.0	99.28%	AY162133.1

Description	Max Score	Total Score	Query Cover	E value	Per. Ident	Accession
<i>Bacillus subtilis</i>	1256	1256	99%	0.0	99.14%	MT111030.1
<i>Bacillus siamensis</i>	1262	1262	99%	0.0	99.28%	KX660755.1
<i>Bacillus sp.</i>	1260	1260	99%	0.0	99.42%	GU374120.1
<i>Bacillus subtilis</i>	1260	1260	99%	0.0	99.28%	AY973269.1
<i>Bacillus amyloliquefaciens</i>	1258	1258	99%	0.0	99.14%	MT081100.1
<i>Bacillus velezensis</i>	1256	1256	99%	0.0	99.28%	MT103089.1
<i>Bacillus subtilis</i>	1256	1256	99%	0.0	99.14%	MN227486.1
<i>Bacillus subtilis subsp. stercoris</i>	1256	1256	99%	0.0	99.28%	MN704447.1
<i>Bacillus sp.</i>	1256	1256	99%	0.0	99.28%	MK685119.1
<i>Bacillus subtilis</i>	1256	1256	99%	0.0	99.28%	MH210872.1
<i>Bacillus subtilis</i>	1256	1256	98%	0.0	99.42%	MF061811.1
<i>Bacillus subtilis</i>	1256	1256	98%	0.0	99.42%	MF581448.1
<i>Bacillus subtilis</i>	1256	1256	99%	0.0	99.28%	KX467568.1
<i>Bacillus sonorensis</i>	1256	1256	99%	0.0	99.28%	KT986188.1
Uncultured <i>bacterium</i>	1256	1256	99%	0.0	99.14%	KP843085.1
<i>Bacillus sp.</i>	1256	1256	99%	0.0	99.28%	KM823924.1
<i>Bacillus amyloliquefaciens</i>	1254	1254	99%	0.0	99.28%	MT613661.1
<i>Bacillus subtilis subsp. subtilis</i>	1254	1254	99%	0.0	99.28%	MT605298.1
<i>Bacillus subtilis subsp. subtilis</i>	1254	1254	99%	0.0	99.28%	MT605295.1
<i>Bacillus subtilis subsp. subtilis</i>	1254	1254	99%	0.0	99.28%	MT605293.1
<i>Bacillus subtilisstraine</i>	1254	1254	99%	0.0	99.28%	MT111083.1
<i>Bacillus subtilis subsp. stercoris</i>	1254	1254	99%	0.0	99.28%	MN704479.1
<i>Bacillus subtilis subsp. stercoris</i>	1254	1254	99%	0.0	99.28%	MN704475.1
<i>Bacillus sp.</i>	1254	1254	99%	0.0	99.28%	MN493914.1
<i>Bacillus sp.</i>	1254	1254	99%	0.0	99.28%	MN493892.1
<i>Bacillus sp.</i>	1254	1254	99%	0.0	99.28%	MN396123.1
<i>Bacillus sp.</i>	1254	1254	99%	0.0	99.28%	MN826347.1
<i>Bacillus sp.</i>	1254	1254	99%	0.0	99.28%	MT950329.1
<i>Bacillus subtilis</i>	1254	1254	99%	0.0	99.28%	MK878625.1
<i>Bacillus subtilis</i>	1253	1253	98%	0.0	99.42%	HG764607.1

Description	Max Score	Total Score	Query Cover	E value	Per. Ident	Accession
<i>Bacillus subtilis</i>	1251	1251	99%	0.0	99.14%	MW513386.1

Table S5: Similarity percentages and accession numbers obtained after comparing the sequence of the tested strain (**B7SRZS**) to the submitted sequences in Gene Bank

Description	Max Score	Total Score	Query Cover	E value	Per. Ident	Accession
<i>Pseudomonas sp.</i>	1258	1258	76%	0.0	99.57%	KR054995.1
<i>Pseudomonas putida</i>	1258	1258	76%	0.0	99.57%	JQ910873.1
<i>Pseudomonas putida</i>	1264	1264	76%	0.0	99.71%	MT271893.1
<i>Pseudomonas sp. s</i>	1264	1264	76%	0.0	99.71%	MT192506.1
<i>Pseudomonas sp.</i>	1264	1264	76%	0.0	99.71%	MT192454.1
<i>Pseudomonas sp.</i>	1264	1264	76%	0.0	99.71%	MT192448.1
<i>Pseudomonas japonica</i>	1264	1264	76%	0.0	99.71%	MH712954.1
<i>Pseudomonas putida</i>	1264	1264	77%	0.0	99.57%	MF952434.1
<i>Pseudomonas sp. s</i>	1264	1264	76%	0.0	99.71%	MH388435.1
<i>Pseudomonas qingdaonensis</i>	1264	1264	76%	0.0	99.71%	MG589917.1
<i>Pseudomonas putida</i>	1264	1264	76%	0.0	99.71%	MF276640.1
<i>Pseudomonas japonica</i>	1264	1264	76%	0.0	99.71%	KX588594.1
<i>Pseudomonas kilonensis</i>	1264	1264	76%	0.0	99.71%	LC005849.1
<i>Pseudomonas sp.</i>	1264	1264	76%	0.0	99.71%	KF896129.1
<i>Pseudomonas sp.</i>	1264	1264	76%	0.0	99.71%	JN886725.1
<i>Pseudomonas sp.</i>	1264	1264	76%	0.0	99.71%	HE979862.1
<i>Pseudomonas japonica</i>	1264	1264	76%	0.0	99.71%	MT658656.1
Uncultured bacterium	1264	1264	76%	0.0	99.71%	HQ121069.1
<i>Pseudomonas putida</i>	1264	1264	76%	0.0	99.71%	AB680123.1
<i>Pseudomonas putida</i>	1264	1264	76%	0.0	99.71%	EU439423.1
<i>Pseudomonas putida</i>	1264	1264	76%	0.0	99.71%	AM411059.1
<i>Pseudomonas kilonensis</i>	1260	1260	76%	0.0	99.57%	LC005850.1
<i>Pseudomonas japonica</i>	1260	1260	76%	0.0	99.57%	MT645252.1
<i>Pseudomonas japonica</i>	1260	1260	76%	0.0	99.57%	MT645250.1

Description	Max Score	Total Score	Query Cover	E value	Per. Ident	Accession
<i>Pseudomonas japonica</i>	1260	1260	76%	0.0	99.57%	MT645248.1
<i>Pseudomonas putida</i>	1258	1258	76%	0.0	99.57%	MH379722.1
Uncultured <i>Pseudomonas</i> sp.	1258	1258	76%	0.0	99.57%	LN875100.1
<i>Pseudomonas putida</i>	1258	1258	76%	0.0	99.57%	AB681704.1
<i>Pseudomonas</i> sp.	1258	1258	76%	0.0	99.57%	MT672631.1
Uncultured <i>bacterium</i>	1258	1258	76%	0.0	99.57%	GU553791.1
<i>Pseudomonas putida</i>	1258	1258	76%	0.0	99.57%	FJ430676.1
<i>Pseudomonas</i> sp.	1256	1256	76%	0.0	99.42%	LC107147.1
<i>Pseudomonas putida</i>	1258	1258	76%	0.0	99.71%	HM641753.1