

Supplementary data

Unraveling the Mechanisms of Cannabis Growth Promotion by *Bacillus velezensis* S141

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Table S1 Bacterial strains used in this study.

Bacterial Strains	Relevant Genotype or Description	References
<i>Bacillus velezensis</i> S141	Wild type	Sibponkrung, S.; Kondo, T.; Tanaka, K.; Tittabutr, P.; Boonkerd, N.; Yoshida, K.-i.; Teaumroong, N. Co-inoculation of <i>Bacillus velezensis</i> strain S141 and <i>Bradyrhizobium</i> strains promotes nodule growth and nitrogen fixation. <i>Microorganisms</i> 2020, 8, 678.
<i>B. velezensis</i> S141 Δ <i>dhaS</i>	<i>dhaS</i> deletion, Δ <i>dhaS</i> :: <i>erm</i> ^r	
<i>B. velezensis</i> S141 Δ <i>yhcX</i>	<i>yhcX</i> deletion, Δ <i>yhcX</i> :: <i>kan</i> ^r	
<i>B. velezensis</i> S141 Δ IPyAD	IPyAD deletion, Δ IPyAD:: <i>spm</i> ^r	
<i>B. velezensis</i> S141 Δ <i>ipt</i>	<i>IPT</i> deletion, Δ <i>ipt</i> :: <i>phle</i> ^r	
<i>B. velezensis</i> S141 Δ <i>ipi</i>	<i>IPI</i> deletion, Δ <i>ipi</i> :: <i>kan</i> ^r	

Table S2 The greenhouse experimental conditions.

Conditions	Non-treated soil normal fertilizer	Non-treated soil lower fertilizer	Boiled water- treated soil normal fertilizer	Boiled water- treated soil lower fertilizer
Pretreatment	-	-	Portions of the soil were subjected to addition by pouring through the soil volumes of boiled water (100 °C) at a ratio of 0.5 L boiled water per 1 kg of soil References Saied, M., <i>Evaluation of hot water soil treatment against cucumber root rot disease under greenhouse conditions</i> . Research Journal of Agriculture and Biological Sciences, 2011. 7(2): p. 212-222.	
Planting materials	- Loam soil -Coco husk chips -Rice husk-based charcoal -Manure			
plant pots	-Pot Size 30 L -Pot Diameter (Base) 13 inches - Pot Diameter 17 INCHES -Pot Height 15 INCHES			
Watering	every morning 1.5 - 2 L / plant			
Humidity	- 40 - 60% - 9 - 11 hr.			
Temperature	30 - 37 °C			
Urea Fertilizer 46-0-0-0	10 g / plant / week			
AB Fertilizer EC:1.8-2 mS/cm pH 6.5 - 7	2 L / 2 times / week	1 L / 2 times / week	2 L / 2 times / week	1 L / 2 times / week

Table S3 Elemental analysis of planting material

Sample	EC (ds/m) 1:5	pH 1:5	% OM	% N	% P	% K	% Ca	% Mg
Planting material	2.21	6.84	33.66	1.18	0.72	0.08	1.56	0.62

Table S4 Summary of primers for qRT-PCR used in this study.

Primers	Accession	Sequence (5'to3')	Annealing temperature (°C)	Experiment
Actin -F	XM_030632129.2	TTGCTGGTCGTGATCTTACTG	60	Internal control
Actin -R		GTCTCCATCTCCTGCTCAAAG	60	
THCAS-F	XM_030649882.2	GCTCTCTTCGTTGCTGGACT	60	qRT-PCR
THCAS-R		TGTTCCCACCTCTATGCCCA	60	
CBDAS-F	XM_030623918.2	CTTAGTTTGGCGGCTGGGTA	60	
CBDAS-R		CTTTGGGACAGCAACCAGTCT	60	
SAUR50-F	XM_030643469.2	GCTCTCTTCGTTGCTGGACT	60	
SAUR50-R		TGTTCCCACCTCTATGCCCA	60	
XEHP25-F	XM_030654082.2	CTTAGTTTGGCGGCTGGGTA	60	
XEHP25-R		CTTTGGGACAGCAACCAGTCT	60	
GLP2-1-F	XM_030625170.2	AGGCCTTGGGACTTGCTTTC	60	
GLP2-1-R		GACCGTGTACAAGAGCAGCT	60	
ABC29-F	XM_030635527.2	TGGATGGTGCTCCTTTTCTTCG	60	
ABC29-R		AGGCTCCAGACCAAATCCCA	60	
CBL120-F	XM_030646708.2	TGTGTGGACTCCTCAACTCCA	60	
CBL120-R		ACTCAAACATGCGACCACGT	60	
GTLS-F	XM_030629393.2	AGCTGTGACGGGTCAACTTC	60	
GTLS-R		AGAGATTGGGCCGATTGGTG	60	
LRLK4-F	XM_061114175.1	AGAAGCTAAGGCACCTGCAG	60	
LRLK4-R		CGGTATGGACTTGGTGCAGT	60	
PRP-1A-F	XM_030629932.1	TGGATGGTGCTCCTTTTCTTCG	60	
PRP-1A-R		AGGCTCCAGACCAAATCCCA	60	
EIX1-F	XM_030640350.1	TGTGTGGACTCCTCAACTCCA	60	
EIX1-R		ACTCAAACATGCGACCACGT	60	
CRF5-F	XM_030632056.1	AGCTGTGACGGGTCAACTTC	60	
CRF5-R		AGAGATTGGGCCGATTGGTG	60	
CAO -F	XM_030634090.1	AGAAGCTAAGGCACCTGCAG	60	
CAO -R		CGGTATGGACTTGGTGCAGT	60	
IAA-2-F	XM_030653759.2	GACACTTGGTGGTTTGCG	60	
IAA-2-R		TGCCCCGAGTTACCTGAAT	60	
ARR5-F	XM_030639807.2	CAGGGATGACAGGATATGAGCTTC	60	
ARR5-R		GACGATTGTGACGACAACACG	60	
ARR12-F	XM_030637161.2	TGTGTGGACTCCTCAACTCCA	60	
ARR12-R		ACTCAAACATGCGACCACGT	60	
UDP -F	XM_030628925.1	TGGATGGTGCTCCTTTTCTTCG	60	
UDP -R		AGGCTCCAGACCAAATCCCA	60	
ERFC3 -F	XM_030647537.1	TGTGTGGACTCCTCAACTCCA	60	
ERFC3 -R		ACTCAAACATGCGACCACGT	60	
S141-F	AP018402	TGATTGCCGGCACAGAAAATAACAGG	60	Bacterial copy number
S141-R		GGTTTCCGGTACCACGTCTGTC	60	

Table S5. Sequencing data analysis RNA sequencing (RNA-Seq) was analyzed and indicated of percent of GC, Q20 and Q30 of each sample.

#SampleID	Total Reads	Mapped Reads	GC (%)	Q20(%)	Q30(%)
CBRC1	41,813,660	37,584,995 (89.89%)	43.40	97.89	95.97
CBRC2	40,907,318	37,014,927 (90.48%)	43.63	97.82	95.78
CBRC3	40,852,224	36,650,102 (89.71%)	43.71	96.72	94.24
CBRI1	46,624,092	41,736,266 (89.52%)	43.59	96.88	94.54
CBRI2	42,244,200	37,838,633 (89.57%)	43.56	96.87	94.45
CBRI3	41,335,878	37,093,945 (89.74%)	43.53	96.80	94.39