

S1. Supplementary Material: Cultivable Endophytic and Rhizosphere Bacteria from *Cannabis sativa* L. as Candidates for Agricultural Bio-Inputs

Table S1.1. Taxonomic assignment of the bacterial isolates in the collection, indicating sequence length, genus and species, percentage of identity, and NCBI accession number of the best BLAST alignment.

Microhabitat	Isolate	Sequence length	Genus	Species	Identity (%)	NCBI accession number
Rhizosphere	Rh1	839	<i>Parabulkholderia</i>	<i>phytofirmans</i>	99.76%	OQ236374.1
	Rh2	799	<i>Flavobacterium</i>	<i>hauense</i>	98.12%	MW089115.1
	Rh3	169	<i>Bacillus</i>	<i>sp.</i>	100.00%	KT957312.1
	Rh4	819	<i>Pseudomonas</i>	<i>reinekei</i>	100.00%	LT838073.1
	Rh5	839	<i>Bacillus</i>	<i>thuringiensis</i>	100.00%	CP050183.1
	Rh6	829	<i>Bacillus</i>	<i>mobilis</i>	100.00%	MT515806.1
	Rh7	nd	nd	nd	nd	nd
	Rh8	769	<i>Bacillus</i>	<i>anthracis</i>	100.00%	CP054816.1
	Rh9	778	<i>Bacillus</i>	<i>thuringiensis</i>	100.00%	CP019230.1
Root	Rt1*	830	<i>Burkholderia</i>	<i>sp.</i>	100.00%	MG452786.1
	Rt2*	828	<i>Pseudomonas</i>	<i>sp.</i>	99.88%	DQ300313.1
	Rt3*	800	<i>Bacillus</i>	<i>sp.</i>	99.62%	OR131050.1
	Rt4*	820	<i>Parabulkholderia</i>	<i>sp.</i>	100.00%	MH844876.1
	Rt5*	810	<i>Massilia</i>	<i>sp.</i>	100.00%	PP837887.1
	Rt6*	810	<i>Pseudomonas</i>	<i>mediterranea</i>	100.00%	KF054768.1
	Rt7*	839	<i>Pseudomonas</i>	<i>mediterranea</i>	99.88%	CP102176.1
	Rt8*	838	<i>Pseudomonas</i>	<i>sp.</i>	100.00%	ON419205.1
	Rt9*	818	<i>Pseudomonas</i>	<i>sp.</i>	100.00%	ON419205.2
	Rt10*	839	<i>Bacillus</i>	<i>bacterium</i>	99.76%	MT799960.1
	Rt11*	598	<i>Kosakonia</i>	<i>sp.</i>	100.00%	KR189886.1
	Rt12	850	<i>Priestia sp.</i>	<i>megaterium</i>	100.00%	KY316462.1
	Rt13	819	<i>Pseudomonas</i>	<i>fulva</i>	99.88%	KT253977.1
	Rt14	819	<i>Pseudomonas</i>	<i>sp.</i>	100.00%	ON419226.1
	Rt15	810	<i>Pseudomonas</i>	<i>nitroreducens</i>	100.00%	MT472129.1
	Rt16	808	<i>Nocardioides</i>	<i>sp.</i>	99.88%	MT936121.1
	Rt17	808	<i>Klebsiella</i>	<i>sp.</i>	100.00%	KF896101.1
	Rt18	818	<i>Pseudomonas</i>	<i>sp.</i>	100.00%	MN944909.1
	Rt19	829	<i>Pseudomonas</i>	<i>aeruginosa</i>	100.00%	JQ659966.1
	Rt20	789	<i>Burkholderia</i>	<i>sp.</i>	100.00%	AB921271.1
	Rt21	819	<i>Burkholderia</i>	<i>sp.</i>	100.00%	AB921271.2
Inflorescence	Inf1*	nd	nd	nd	nd	nd
	Inf2*	869	<i>Bacillus</i>	<i>sp.</i>	100.00%	GU458276.1
	Inf3*	870	<i>Bacillus</i>	<i>sp.</i>	100.00%	MN410651.1
	Inf4*	843	<i>Pantoea</i>	<i>sp.</i>	100.00%	MT557009.1
	Inf5*	868	<i>Bacillus</i>	<i>sp.</i>	100.00%	KC466249.1
	Inf6*	758	<i>Bacillus</i>	<i>amyloliquefaciens</i>	99.87%	OL847641.1
	Inf7*	843	<i>Pseudomonas</i>	<i>sp.</i>	100.00%	KX645738.1
	Inf8	779	<i>Bacillus</i>	<i>proteolyticus</i>	100.00%	MN448444.1
	Inf9	850	<i>Pseudomonas</i>	<i>sp.</i>	100.00%	JX067668.1
	Inf10	853	<i>Pseudomonas</i>	<i>oryzihabitans</i>	99.65%	PQ160418.1

Table S1.1. (Continued) Taxonomic assignment of the bacterial isolates in the collection, indicating sequence length, genus and species, percentage of identity, and NCBI accession number of the best BLAST alignment.

Microhabitat	Isolate	Sequence length	Genus	Species	Identity (%)	NCBI accession number
Leaf	Lf1	842	<i>Kosakonia</i>	<i>sp.</i>	100.00%	MN648222.1
	Lf2	nd	nd	nd	nd	nd
	Lf3	nd	nd	nd	nd	nd
	Lf4	768	<i>Bacillus</i>	<i>velezencis</i>	99.87%	HQ238543.1
	Lf5	160	<i>Bacillus</i>	<i>sp.</i>	100.00%	MT415999.1
	Lf6	418	<i>Bacillus</i>	<i>amyloliquefaciens</i>	97.61%	JQ420832.1
	Lf7	799	<i>Bacillus</i>	<i>sp.</i>	100.00%	MG470705.1
	Lf8	829	<i>Bacillus</i>	<i>zanthoxyli</i>	100.00%	QQ410708.1
Stem	St1	818	<i>Bacillus</i>	<i>thuringiensis</i>	99.88%	MT799960.1
	St2	810	<i>Brachybacterium</i>	<i>sp.</i>	100.00%	OP989961.1
	St3	229	<i>Bacillus</i>	<i>sp.</i>	99.56%	MT664693.1
	St4	819	<i>Bacillus</i>	<i>pumilus</i>	100.00%	OM981306.1
	St5	778	<i>Microbacterium</i>	<i>sp.</i>	100.00%	MH127624.1
	St6	635	<i>Bacillus</i>	<i>cereus</i>	100.00%	MN966874.1
	St7	779	<i>Bacillus</i>	<i>thuringiensis</i>	100.00%	CP050183.1
	St8	839	<i>Bacillus</i>	<i>cereus</i>	100.00%	HF584764.1
	St9	nd	nd	nd	nd	nd
	St10	800	<i>Microbacterium</i>	<i>sp.</i>	100.00%	KR906156.1
	St11	nd	nd	nd	nd	nd
	St12	838	<i>Pantoea</i>	<i>sp.</i>	99.88%	KY440053.1
	St13*	818	<i>Bacillus</i>	<i>zhangzhouensis</i>	100.00%	MW405674.1
	St14*	789	<i>Curtobacterium</i>	<i>sp.</i>	100.00%	MW131580.1
	St15*	838	<i>Bacillus</i>	<i>sp.</i>	99.76%	JQ943617.1

Table S1.2. Results of the *in vitro* characterization related to plant colonization traits (cellulase activity and pectinase activity) together with the PCi index. calculated for each bacterial isolate in the collection.

Microhabitat	Isolate	Taxonomy	Cellulase	Pectinase	PCi
Rhizosphere	Rt1*	<i>Burkholderia</i>	(-)	(-)	0
	Rt2*	<i>Pseudomonas</i>	(-)	(-)	0
	Rt3*	<i>Bacillus</i>	(-)	(-)	0
	Rt4*	<i>Paraburkholderia</i>	(-)	(-)	0
	Rt5*	<i>Massilia</i>	(+)	(+)	1
	Rt6*	<i>Pseudomonas</i>	(-)	(+)	0.5
	Rt7*	<i>Pseudomonas</i>	(-)	(+)	0.5
	Rt8*	<i>Pseudomonas</i>	(-)	(-)	0
	Rt9*	<i>Pseudomonas</i>	(+)	(+)	1
Root	Rt10*	<i>Bacillus</i>	(-)	(+)	0.5
	Rt11*	<i>Kosakonia</i>	(-)	(-)	0
	Rt12	<i>Priestia sp.</i>	(-)	(-)	0
	Rt13	<i>Pseudomonas</i>	(+)	(-)	0.5
	Rt14	<i>Pseudomonas</i>	(-)	(+)	0.5
	Rt15	<i>Pseudomonas</i>	(-)	(-)	0
	Rt16	<i>Nocardioides</i>	(-)	(-)	0
	Rt17	<i>Klebsiella</i>	(+)	(+)	1
	Rt18	<i>Pseudomonas</i>	(-)	(-)	0
	Rt19	<i>Pseudomonas</i>	(-)	(-)	0
	Rt20	<i>Burkholderia</i>	(-)	(-)	0
	Rt21	<i>Burkholderia</i>	(-)	(-)	0
	Rh1	<i>Paraburkholderia</i>	(-)	(-)	0
	Rh2	<i>Flavobacterium</i>	(+)	(-)	0.5
	Rh3	<i>Bacillus</i>	(+)	(-)	0.5
	Rh4	<i>Pseudomonas</i>	(-)	(-)	0
	Rh5	<i>Bacillus</i>	(-)	(-)	0
	Rh6	<i>Bacillus</i>	(+)	(+)	1
	Rh7	nd	(+)	(+)	1
	Rh8	<i>Bacillus</i>	(+)	(+)	1
	Rh9	<i>Bacillus</i>	(+)	(-)	0.5
Inflorescence	Inf1*	nd	(-)	(-)	0
	Inf2*	<i>Bacillus</i>	(-)	(-)	0
	Inf3*	<i>Bacillus</i>	(+)	(-)	0.5
	Inf4*	<i>Pantoea</i>	(-)	(-)	0
	Inf5*	<i>Bacillus</i>	(-)	(-)	0
	Inf6*	<i>Bacillus</i>	(+)	(+)	1
	Inf7*	<i>Pseudomonas</i>	(+)	(-)	0.5
	Inf8	<i>Bacillus</i>	(-)	(-)	0
	Inf9	<i>Pseudomonas</i>	(+)	(-)	0.5
	Inf10	<i>Pseudomonas</i>	(+)	(+)	1

Table S1.2. (Continued) Results of the *in vitro* characterization related to plant colonization traits (cellulase activity and pectinase activity) together with the PCi index. calculated for each bacterial isolate in the collection.

Microhabitat	Isolate	Taxonomy	Cellulase	Pectinase	PCi
Leaf	Lf1	<i>Kosakonia</i>	(+)	(+)	1
	Lf2	nd	(-)	(-)	0
	Lf3	nd	(-)	(-)	0
	Lf4	<i>Bacillus</i>	(-)	(-)	0
	Lf5	<i>Bacillus</i>	(+)	(-)	0.5
	Lf6	<i>Bacillus</i>	(-)	(-)	0
	Lf7	<i>Bacillus</i>	(-)	(-)	0
	Lf8	<i>Bacillus</i>	(+)	(+)	1
Stem	St1	<i>Bacillus</i>	(+)	(-)	0.5
	St2	<i>Brachybacterium</i>	(+)	(-)	0.5
	St3	<i>Bacillus</i>	(-)	(-)	0
	St4	<i>Bacillus</i>	(+)	(-)	0.5
	St5	<i>Microbacterium</i>	(+)	(-)	0.5
	St6	<i>Bacillus</i>	(-)	(+)	0.5
	St7	<i>Bacillus</i>	(-)	(-)	0
	St8	<i>Bacillus</i>	(+)	(+)	1
	St9	nd	(-)	(-)	0
	St10	<i>Microbacterium</i>	(+)	(-)	0.5
	St11	nd	(+)	(+)	1
	St12	<i>Pantoea</i>	(-)	(-)	0
	St13*	<i>Bacillus</i>	(-)	(-)	0
	St14*	<i>Curtobacterium</i>	(-)	(-)	0
	St15*	<i>Bacillus</i>	(+)	(+)	1

Table S1.3. (Continued) Results of the *in vitro* characterization related to plant colonization capacity (PCi) and traits related to antagonistic activity (amylase, chitinase, protease and lipase activities, and inhibition of radial growth of phytopathogenic fungi), along with the ECiA, PIRG, APi and BPi indices calculated for each bacterial isolate in the collection.

[illegible]

Table S1.4. Results of the *in vitro* characterization related to plant colonization capacity (PCi) and plant growth-promoting traits (phosphate solubilization and biological nitrogen fixation), along with the PSE, PSi, BNF, PGPi and PGPPi indices calculated for each bacterial isolate in the collection.

Isolate	PCi	Phosphorus solubilization	PSE	PSi	BNF (LGI)	BNF (NFb)	BNF	PGPi	PGPPi
Rt1*	0.00	(+++)	1.75	0.88	(+)	(+)	1	0.9375	0.9375
Rt2*	0.00	(+)	0.10	0.05	(-)	(-)	0	0.025	0.025
Rt3*	0.00	(++)	0.36	0.18	(-)	(+)	1	0.59	0.59
Rt4*	0.00	(++)	0.15	0.08	(+)	(+)	1	0.5375	0.5375
Rt5*	1.00	(+)	0.10	0.05	(+)	(+)	1	0.525	1.025
Rt6*	0.50	(+)	0.10	0.05	(-)	(-)	0	0.025	0.275
Rt7*	0.50	(+)	0.10	0.05	(-)	(-)	0	0.025	0.275
Rt8*	0.00	(+)	0.10	0.05	(-)	(-)	0	0.025	0.025
Rt9*	1.00	(-)	nd	0.00	(+)	(+)	1	0.5	1
Rt10*	0.50	(+)	0.10	0.05	(-)	(+)	1	0.525	0.775
Rt11*	0.00	(+++)	1.85	0.93	(-)	(-)	0	0.4625	0.4625
Rt12	0.00	(+)	0.10	0.05	(-)	(+)	1	0.525	0.525
Rt13	0.50	(++)	0.16	0.08	(+)	(+)	1	0.54	0.79
Rt14	0.50	(+)	0.10	0.05	(-)	(+)	1	0.525	0.775
Rt15	0.00	(++)	0.36	0.18	(+)	(-)	1	0.59	0.59
Rt16	0.00	(+)	0.10	0.05	(+)	(+)	1	0.525	0.525
Rt17	1.00	(+)	0.10	0.05	(+)	(+)	1	0.525	1.025
Rt18	0.00	(-)	nd	0.00	(-)	(-)	0	0	0
Rt19	0.00	(++)	1.22	0.61	(+)	(+)	1	0.805	0.805
Rt20	0.00	(++)	1.42	0.71	(+)	(+)	1	0.855	0.855
Rt21	0.00	(+++)	1.42	0.71	(+)	(-)	1	0.855	0.855
Rh1	0.00	(+)	0.10	0.05	(+)	(+)	1	0.525	0.525
Rh2	0.50	(-)	nd	0.00	(-)	(-)	0	0	0.25
Rh3	0.50	(++)	0.74	0.37	(+)	(-)	1	0.685	0.935
Rh4	0.00	(-)	nd	0.00	(+)	(-)	1	0.5	0.5
Rh5	0.00	(-)	nd	0.00	(+)	(-)	1	0.5	0.5
Rh6	1.00	(++)	0.45	0.23	(+)	(+)	1	0.6125	1.1125
Rh7	1.00	(-)	nd	0.00	(+)	(+)	1	0.5	1
Rh8	1.00	(++)	0.43	0.22	(-)	(-)	0	0.1075	0.6075
Rh9	0.50	(-)	nd	0.00	(+)	(+)	1	0.5	0.75
Inf1*	0.00	(++)	1.14	0.57	(+)	(-)	1	0.785	0.785
Inf2*	0.00	(-)	nd	0.00	(+)	(+)	1	0.5	0.5
Inf3*	0.50	(++)	0.75	0.38	(+)	(+)	1	0.6875	0.9375
Inf4*	0.00	(++)	0.79	0.40	(-)	(-)	0	0.1975	0.1975
Inf5*	0.00	(++)	0.5	0.25	(+)	(-)	1	0.625	0.625
Inf6*	1.00	(+)	0.10	0.05	(-)	(+)	1	0.525	1.025
Inf7*	0.50	(++)	0.78	0.39	(-)	(+)	1	0.695	0.945
Inf8	0.00	(+)	0.10	0.05	(+)	(+)	1	0.525	0.525
Inf9	0.50	(++)	0.15	0.08	(+)	(+)	1	0.5375	0.7875
Inf10	1.00	(+)	0.10	0.05	(+)	(+)	1	0.525	1.025

Table S1.4. (Continued) Results of the *in vitro* characterization related to plant colonization capacity (PCi) and plant growth-promoting traits (phosphate solubilization and biological nitrogen fixation). along with the PSE, PSi, BNF, PGPi and PGPPi indices calculated for each bacterial isolate in the collection.

Isolate	PCi	Phosphorus solubilization	PSE	PSi	BNF (LGI)	BNF (NFb)	BNF	PGPi	PGPPi
Lf1	1.00	(+++)	0.25	0.13	(-)	(-)	0	0.0625	0.5625
Lf2	0.00	(+++)	2.00	1.00	(-)	(-)	0	0.5	0.5
Lf3	0.00	(+)	0.10	0.05	(+)	(+)	1	0.525	0.525
Lf4	0.00	(+++)	0.85	0.43	(-)	(-)	0	0.2125	0.2125
Lf5	0.50	(+++)	0.60	0.30	(-)	(-)	0	0.15	0.4
Lf6	0.00	(+)	0.10	0.05	(+)	(+)	1	0.525	0.525
Lf7	0.00	(+)	0.10	0.05	(+)	(-)	1	0.525	0.525
Lf8	1.00	(+)	0.10	0.05	(+)	(+)	1	0.525	1.025
St1	0.50	(-)	nd	0.00	(+)	(+)	1	0.5	0.75
St2	0.50	(+)	0.10	0.05	(+)	(+)	1	0.525	0.775
St3	0.00	(-)	ND	0.00	(+)	(+)	1	0.5	0.5
St4	0.50	(+)	0.10	0.05	(+)	(-)	1	0.525	0.775
St5	0.50	(+++)	0.10	0.05	(-)	(-)	0	0.025	0.275
St6	0.50	(-)	nd	0.00	(+)	(+)	1	0.5	0.75
St7	0.00	(+)	0.10	0.00	(+)	(+)	0	0	0
St8	1.00	(+)	0.10	0.05	(-)	(-)	0	0.025	0.525
St9	0.00	(-)	nd	0.00	(-)	(-)	0	0	0
St10	0.50	(-)	nd	0.00	(+)	(-)	1	0.5	0.75
St11	1.00	(+)	0.10	0.05	(+)	(+)	1	0.525	1.025
St12	0.00	(+++)	0.44	0.22	(-)	(-)	0	0.11	0.11
St13*	0.00	(-)	nd	0.00	(+)	(-)	0	0	0
St14*	0.00	(-)	nd	0.00	(+)	(-)	1	0.5	0.5
St15*	1.00	(+)	0.10	0.05	(+)	(+)	1	0.525	1.025

Table S1.5. Bacterial population counts (CFU g⁻¹) and their log-transformed values for each sample. specifying the microhabitat of origin and whether they represent total bacteria or endophytes (surface-disinfected tissues).

Microhabitat	Population	Count (UFC/gr)	Log (UFC/gr)
Rhizosphere	Total	2.88E+07	7.46
Rhizosphere	Total	2.70E+07	7.43
Root	Endophyte	3.28E+05	5.52
Root	Endophyte	1.08E+07	7.03
Root	Total	1.66E+08	8.22
Root	Total	4.00E+07	7.60
Stem	Endophyte	2.67E+01	1.43
Stem	Endophyte	4.48E+01	1.65
Stem	Total	3.71E+02	2.57
Stem	Total	4.38E+02	2.64
Leaf	Endophyte	nd	nd
Leaf	Endophyte	nd	nd
Leaf	Total	2.29E+02	2.36
Leaf	Total	1.84E+02	2.27
Inflorescence	Endophyte	3.91E+02	2.59
Inflorescence	Endophyte	1.47E+02	2.17
Inflorescence	Total	1.90E+04	4.28
Inflorescence	Total	3.19E+03	3.50

Análisis de la varianza

Variable	N	R ²	R ² Aj	CV
Log (UFC/gr)	10	0.99	0.98	6.53

Cuadro de Análisis de la Varianza (SC tipo III)

F.V.	SC	gl	CM	F	p-valor
Modelo	57.00	4	14.25	142.92	<0.0001
Microhabitat	57.00	4	14.25	142.92	<0.0001
Error	0.50	5	0.10		
Total	57.50	9			

Test:Tukey Alfa=0.05 DMS=1.26675

Error: 0.0997 gl: 5

Microhabitat	Medias	n	E.E.
Lf	2.31	2	0.22 A
St	2.61	2	0.22 A
Inf	3.89	2	0.22 B
Rh	7.45	2	0.22 C
Rt	7.91	2	0.22 C

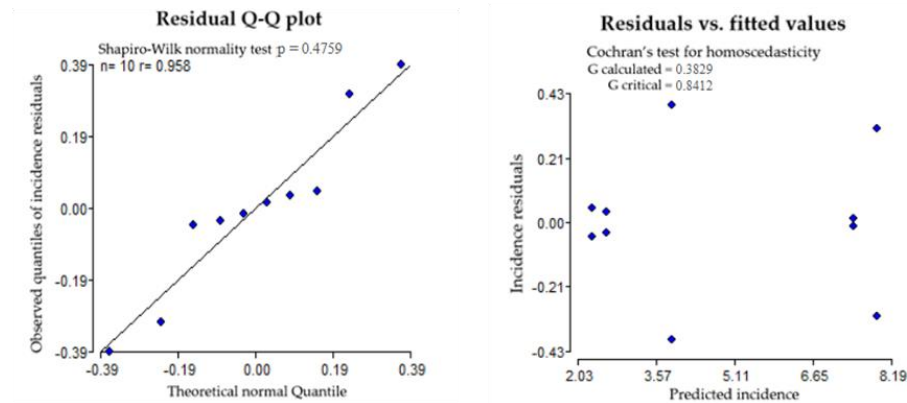


Figure S1.1. InfoStat output for the one-way analysis of variance of total cultivable bacterial population densities (log CFU g⁻¹) across microhabitats associated with *Cannabis sativa* L.: analysis of variance table, Tukey's mean comparison test ($\alpha = 0.05$), and verification of model assumptions by the modified Shapiro–Wilk test for normality of residuals and Cochran's test for homoscedasticity. Rh, rhizosphere; Rt, root; St, stem; Lf, leaf; Inf, inflorescence.

Análisis de la varianza

Variable	N	R ²	R ² Aj	CV
Log (UFC/gr)	12	0.97	0.95	13.21

Cuadro de Análisis de la Varianza (SC tipo III)

F.V.	SC	gl	CM	F	p-valor
Modelo	62.10	5	12.42	42.32	0.0001
Microhabitat	56.00	2	28.00	95.41	<0.0001
Preliminary disinfection	5.92	1	5.92	20.17	0.0041
Microhabitat*Preliminary d..	0.18	2	0.09	0.31	0.7475
Error	1.76	6	0.29		
Total	63.86	11			

Test:Tukey Alfa=0.05 DMS=1.17538

Error: 0.2935 gl: 6

Microhabitat	Medias	n	E.E.
St	2.07	4	0.27 A
Inf	3.14	4	0.27 A
Rt	7.09	4	0.27 B

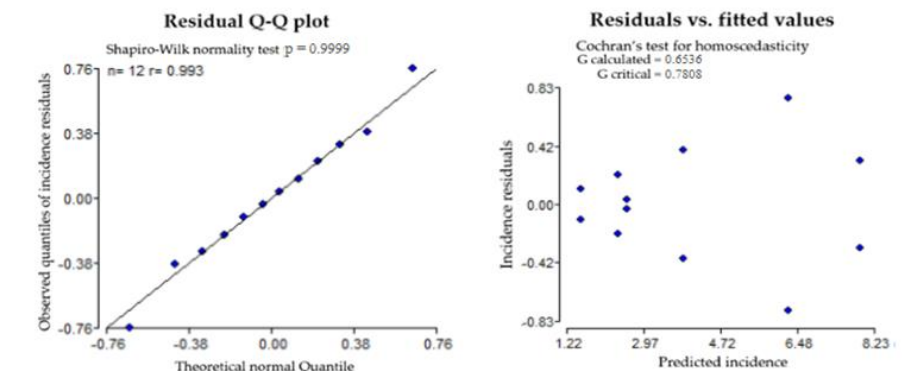


Figure S1.2. InfoStat output for the two-way analysis of variance of cultivable bacterial population densities (log CFU g⁻¹) in *Cannabis sativa* L. tissues, with microhabitat (Rt, root; St, stem; Inf, inflorescence) and preliminary surface disinfection (non-disinfected, total population; disinfected, endophytic population) as fixed factors: analysis of variance table including the interaction term, Tukey's mean comparison test for the microhabitat factor ($\alpha = 0.05$), and verification of model assumptions by the modified Shapiro–Wilk test for normality of residuals and Cochran's test for homoscedasticity. Leaves were excluded owing to the absence of colony growth in surface-disinfected samples.

Table S1.6. Percentage of rooted cuttings across treatments.

Treatment	Percentage of rooted (%)
Control	82.35
Control	66.67
Rt1*	94.12
Rt1*	88.24
Inf6*	70.59
Inf6*	82.35
PG	66.67
PG	72.22
BG	88.24
BG	88.24

Table S1.7. Model adequacy diagnostics for the quasi-binomial generalized linear model fitted to the number of rooted cuttings per experimental unit. The dispersion parameter (ϕ) was estimated as the Pearson χ^2 divided by the residual degrees of freedom; values below unity indicate under dispersion relative to the nominal binomial variance. Goodness of fit was assessed by comparing the residual deviance against a χ^2 distribution with the corresponding degrees of freedom.

Diagnostic	Value
Residual degrees of freedom	5
Pearson χ^2	2.277
Residual deviance	2.307
Dispersion parameter ($\phi = \chi^2/\text{df}$)	0.455
Goodness-of-fit (χ^2 test)	p = 0.810
Log-likelihood	-15.062
AIC	40.13

Table S1.8. One-sided Dunnett comparisons of each bacterial treatment against the uninoculated control, derived from the quasi-binomial generalized linear model. Contrasts are expressed on the logit scale (log-OR) and back-transformed as odds ratios with 95% confidence intervals. Unadjusted p -values are two-sided; Dunnett p -values are one-sided and adjusted for the four simultaneous comparisons against a common control, obtained by simulation from the corresponding multivariate t distribution (10^6 replicates). The significance level was declared a priori at $\alpha = 0.10$ (one-sided critical value $t = 2.299$). Rt1*, root endosphere isolate; Inf6*, inflorescence endosphere isolate; PG, *Paraburkholderia tropica* Mto-293 + *Gluconacetobacter diazotrophicus* PAL5; BG, *Bacillus velezensis* TM30 + *G. diazotrophicus* PAL5.

Contrast	log-OR	SE	t	p unadjusted	p Dunnett (one-sided)	OR (95% CI)
Rt1* vs Control	1.2745	0.4843	2.632	0.023	0.068	3.58 (1.03 – 12.42)
BG vs Control	0.9540	0.4440	2.149	0.042	0.119	2.60 (0.83 – 8.13)
Inf6* vs Control	0.1178	0.3775	0.312	0.384	0.721	1.13 (0.43 – 2.97)
PG vs Control	-0.2399	0.3574	-0.671	0.734	0.955	0.79 (0.31 – 1.97)

Frecuencias absolutas
En columnas: root quality

treatment	abundant	good	poor	Total
BG	5	8	7	20
Control	7	7	6	20
Inf6*	4	7	9	20
PG	4	7	9	20
Rt1*	7	11	2	20
Total	27	40	33	100

Prueba de Kruskal Wallis

Variable	treatment	N	Medias	D.E.	Medianas	gl	H	p
root quality	BG	20	1.90	0.79	2.00	4	5.45	0.1855
root quality	Control	20	2.05	0.83	2.00			
root quality	Inf6*	20	1.75	0.79	2.00			
root quality	PG	20	1.75	0.79	2.00			
root quality	Rt1*	20	2.25	0.64	2.00			

Figure S1.3. Root system quality of cannabis cuttings at the end of the rooting assay. Absolute frequencies of root systems assigned to each qualitative category (abundant, good, poor) per treatment (n = 20 rooted cuttings per treatment), and Kruskal–Wallis test comparing the ordinal quality scores among treatments (H = 5.45; df = 4; $p = 0.1855$). Categories were coded as ordinal scores for the analysis (poor = 1, good = 2, abundant = 3). Rt1*, root endosphere isolate; Inf6*, inflorescence endosphere isolate; PG, *Paraburkholderia tropica* Mto-293 + *Gluconacetobacter diazotrophicus* PAL5; BG, *Bacillus velezensis* TM30 + *G. diazotrophicus* PAL5.