Supplementary Material

Bioprospecting of beneficial bacteria traits associated with tomato root in greenhouse environment reveals that sampling sites impact more than the root compartment.

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1 Supplementary Figures and Tables

1.1 Supplementary Figures

1.1.1 **Figure S1.** Heat map obtained using two arbitrary scales to quantitative evaluate the antagonistic potential bacterial collected according to the farms and root compartment of isolation (E, endorhizosphere, RP, rhizoplane and, R, rhizosphere). For a quantitative evaluation of the bacterial strains antagonistic activity two arbitrary 0-3 scales were used. The antibacterial activity was scored based on the growth inhibition area size as: 0, no antagonism; 1, < 3 mm; 2, ≥ 3, <10 mm; 3, >10 mm. Antifungal activity was scored based on the percentage of growth inhibition against *Fol* (PGI) as follow: 0, no inhibition, 1, PGI <30%; 2, PGI 30- 60%; 3, PGI >60%.

1.2 Supplementary Table

1.2.1 **Table S1:** Phenotypic qualitative evaluation of the presence (1) or absence (0) of beneficial traits of bacteria isolated from rhizosphere (R), rhizoplane (RP), and endorhizosphere (E) .

1.2.2 **Table S2**: Principal Component Analysis (PCA) table of the full dataset on 424 bacteria, showing relationships between phenotypic traits (Gram reaction, fluorescence production, siderophore production, phosphate solubilisation, salt tolerance, antagonist activity against *Cmm*, *Pco*, *Pto*, *Xep*, and *Fol*) and bacterial isolates.

1.2.3 **Table S3:** Molecular identification of the endophytic bacteria based on the 16S rRNA gene sequence.

1.2.4 **Table S4:** Accession numbers of the sequences of the type strains used as references in the dendrogram in figure 6 in this study.

1.2.5 **Table S5:** Effect of the treatments by soil drenching of tomato plantlets grown in pots using bacterial endophytes belonging to the genus *Pseudomonas* and *Bacillus*. Plant height, fresh and dry weight of roots and shoots, dry matter and root/shoot ratio was measured 30 days after the treatment.

Figure S1: Heat map obtained using two arbitrary scales to quantitative evaluate the antagonistic potential bacterial collected according to the farms and root compartment of isolation (E, endorhizosphere, RP, rhizoplane and, R, rhizosphere). For a quantitative evaluation of the bacterial strains antagonistic activity two arbitrary 0-3 scales were used. The antibacterial activity was scored based on the growth inhibition area size as: 0, no antagonism; 1, < 3 mm; 2, ≥ 3, <10 mm; 3, >10 mm. Antifungal activity was scored based on the percentage of growth inhibition against *Fol* (PGI) as follow: 0, no inhibition, 1, PGI <30%; 2, PGI 30- 60%; 3, PGI >60%.

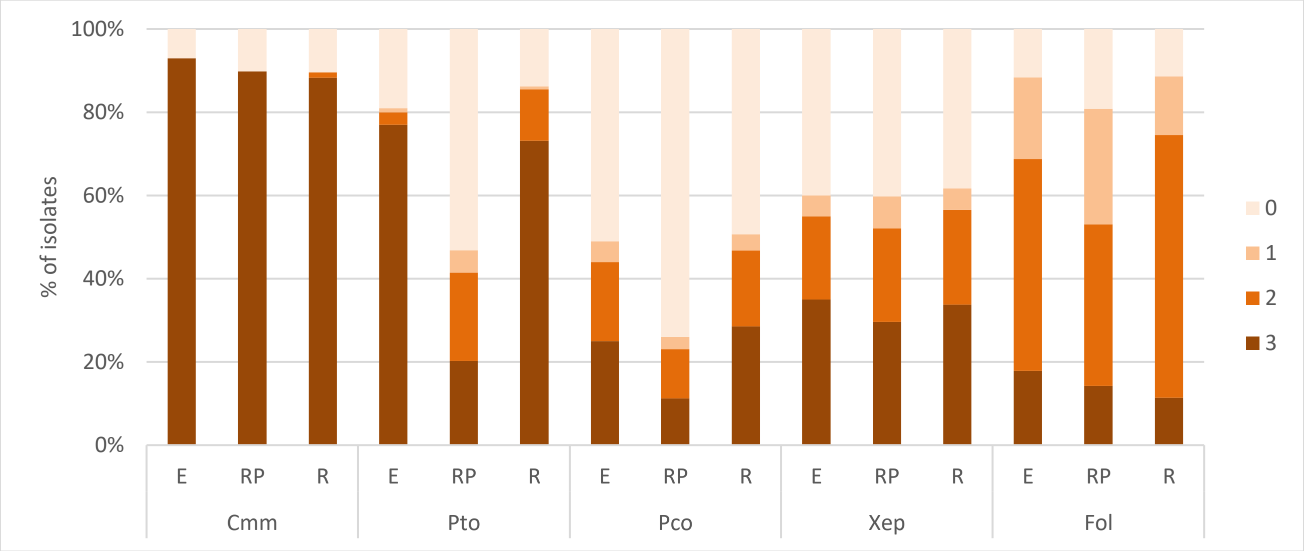

Table S1: Phenotypic qualitative evaluation of the presence (1) or absence (0) of beneficial traits of bacteria isolated from rhizosphere (R), rhizoplane (RP), and endorhizosphere (E).

Farm	**Root compartment**	**Name ID**	**Gram**	**Fluorescence**	**PGP activity**			**Antagonistic activity**				
					Siderophore production	**Phosphate solubilization**	**Salt tolerance (NaCl 8%)**	***Cmm***	***Pto***	***Pco***	***Xep***	***Fol***
1	RP	**1**	0	0	1	0	0	1	1	0	1	1
1	RP	**2**	0	0	1	0	1	1	1	0	1	1
1	RP	**3**	0	1	1	0	1	1	0	0	1	1
1	RP	**4**	0	0	1	0	1	1	0	0	1	1
1	RP	**5**	0	0	1	0	1	1	0	0	1	1
1	RP	**6**	0	0	1	0	1	1	0	0	1	1
1	RP	**7**	0	0	1	0	1	1	1	0	1	1
1	RP	**8**	0	0	1	0	0	1	1	0	1	1
1	RP	**9**	0	0	1	0	1	1	0	0	1	1
1	RP	**10**	0	0	0	0	1	1	0	0	1	1
1	RP	**11**	0	0	0	0	1	1	1	0	1	1
1	RP	**12**	0	0	0	0	1	1	0	0	1	1
1	RP	**13**	0	0	0	0	1	1	1	0	1	1
1	RP	**14**	0	0	0	0	1	1	0	0	0	1
1	RP	**15**	0	0	0	0	1	1	0	0	0	1
1	RP	**16**	0	0	1	0	1	1	1	0	0	1
1	RP	**17**	0	0	0	0	1	1	0	0	0	1
1	RP	**18**	0	0	0	0	1	1	1	0	0	1
1	R	**19**	0	0	0	0	1	1	1	0	0	1
1	RP	**20**	0	0	0	0	1	1	1	0	1	1
1	RP	**21**	0	0	0	0	1	1	1	0	1	1
1	RP	**22**	0	0	0	0	1	1	1	0	1	1
1	RP	**23**	0	0	0	0	1	1	1	0	1	1
1	RP	**24**	0	0	0	0	1	1	1	0	1	1
1	RP	**25**	0	0	1	0	1	0	1	0	1	0
1	RP	**26**	0	0	1	0	1	0	0	0	0	0
1	RP	**27**	0	0	0	0	1	1	1	0	1	1
1	RP	**28**	0	1	0	0	1	1	1	0	1	1
1	RP	**29**	0	0	0	0	1	1	1	0	1	1
1	RP	**30**	0	0	0	0	1	1	1	0	1	1
1	RP	**31**	0	0	0	0	1	0	0	0	0	1
1	RP	**32**	0	0	0	0	1	0	0	0	0	1
1	RP	**33**	0	0	0	0	1	1	0	0	0	1
1	RP	**34**	0	0	0	0	1	1	0	0	0	1
1	RP	**35**	0	1	0	0	1	1	0	0	0	1
1	RP	**36**	0	0	0	0	1	1	1	0	1	1
1	RP	**37**	0	1	0	0	1	1	1	0	1	1
1	RP	**38**	0	0	0	0	1	1	0	0	0	1
1	RP	**39**	0	0	0	0	1	1	1	0	1	1
1	RP	**40**	0	0	0	0	1	0	1	0	1	1
1	RP	**41**	0	0	0	0	1	1	1	0	1	1
1	RP	**42**	0	0	1	0	1	1	1	0	1	1
1	RP	**43**	0	0	1	0	1	1	1	0	1	1
1	RP	**44**	0	0	1	0	1	1	1	0	1	1
1	RP	**45**	0	0	0	0	1	1	1	0	1	1
1	RP	**46**	0	0	0	0	1	1	1	0	1	1

Farm	**Root compartment**	**Name ID**	**Gram**	**Fluorescence**	**PGP activity**			**Antagonistic activity**				
					Siderophore production	**Phosphate solubilization**	**Salt tolerance (NaCl 8%)**	***Cmm***	***Pto***	***Pco***	***Xep***	***Fol***
1	RP	**47**	0	0	1	0	1	1	1	0	1	1
1	E	**48**	0	0	1	0	1	1	1	0	1	1
1	E	**49**	0	0	0	1	1	1	0	0	1	1
1	R	**50**	0	0	0	1	1	1	1	0	1	1
1	R	**51**	0	0	0	1	1	1	0	0	1	1
1	R	**52**	0	0	1	1	1	1	1	0	1	1
1	R	**53**	0	0	1	1	1	1	1	0	1	1
1	R	**54**	0	0	1	1	1	1	1	0	1	1
1	R	**55**	0	0	1	1	1	1	1	0	1	1
1	R	**56**	0	0	1	1	1	1	1	1	1	1
1	R	**57**	0	0	0	1	1	1	1	0	1	1
1	R	**58**	0	0	0	1	1	1	1	0	1	1
1	R	**59**	0	0	0	1	0	1	1	0	1	1
1	R	**60**	0	0	0	1	0	1	1	0	1	1
1	R	**61**	0	0	0	1	1	1	1	0	1	1
1	R	**62**	0	0	0	1	0	1	1	0	1	1
1	RP	**63**	0	0	0	1	0	1	1	0	1	1
1	RP	**64**	0	0	1	1	0	1	1	0	1	1
1	RP	**65**	0	0	1	0	0	1	1	0	0	1
1	RP	**66**	0	0	0	0	0	1	1	0	0	1
1	R	**67**	0	0	1	1	0	0	1	0	0	1
1	R	**68**	0	0	0	1	0	0	1	0	0	1
1	R	**69**	0	0	0	1	0	1	1	0	0	1
1	R	**70**	0	0	0	1	0	0	1	0	0	1
2	R	**91**	0	0	0	1	1	1	1	0	0	1
2	R	**92**	0	0	0	1	1	1	1	1	1	1
2	R	**93**	0	0	0	0	1	1	1	1	1	1
2	R	**94**	1	0	0	0	1	1	1	1	0	1
2	R	**95**	0	0	0	0	1	1	1	1	1	1
2	R	**96**	0	0	0	1	1	1	1	1	0	1
2	R	**97**	1	0	0	1	0	1	1	1	1	1
2	R	**98**	0	0	0	1	0	1	1	1	1	1
2	R	**99**	1	0	0	1	1	1	1	1	1	1
2	R	**100**	0	0	0	0	1	1	1	0	1	1
2	R	**101**	0	0	0	0	0	1	1	0	1	1
2	R	**102**	0	0	0	0	0	1	1	1	0	1
2	R	**103**	0	0	0	0	1	1	1	0	1	1
2	R	**104**	0	0	0	0	1	1	1	1	1	1
2	R	**105**	0	0	0	1	1	1	1	1	1	1
2	R	**106**	0	0	0	0	0	1	1	0	0	1
2	RP	**107**	0	0	0	1	1	1	1	0	1	1
2	RP	**108**	0	0	0	0	0	1	1	0	1	1
2	RP	**109**	0	0	0	0	0	1	1	0	0	1
2	RP	**110**	0	0	0	0	1	1	1	0	0	1
2	RP	**111**	0	0	0	0	1	1	1	0	1	1
2	RP	**112**	1	0	0	0	1	1	1	0	0	1
2	RP	**113**	0	0	0	0	1	1	1	0	1	1
2	R	**114**	0	0	0	0	1	1	1	0	1	1

Farm	**Root compartment**	**Name ID**	**Gram**	**Fluorescence**	**PGP activity**			**Antagonistic activity**				
					Siderophore production	**Phosphate solubilization**	**Salt tolerance (NaCl 8%)**	***Cmm***	***Pto***	***Pco***	***Xep***	***Fol***
2	RP	**115**	0	0	0	1	1	1	1	1	0	1
2	RP	**116**	0	0	0	0	1	1	1	1	1	1
2	RP	**117**	0	0	0	0	1	1	1	1	1	1
2	RP	**118**	0	0	0	0	0	1	1	0	1	1
2	RP	**119**	0	0	0	0	1	1	1	0	1	1
2	RP	**120**	0	0	0	0	1	1	1	0	1	1
2	RP	**121**	1	0	0	0	1	1	1	0	0	0
2	RP	**122**	0	0	0	1	1	1	1	0	0	0
2	E	**123**	0	0	0	1	0	1	1	1	1	1
2	E	**124**	0	0	0	0	1	1	1	1	1	1
2	E	**125**	0	0	0	0	1	1	1	1	1	1
2	E	**126**	0	0	0	0	1	1	1	0	1	1
2	E	**127**	0	0	0	0	0	1	1	1	1	1
2	E	**128**	0	0	0	0	0	1	1	0	0	1
2	E	**129**	0	0	0	0	1	1	1	0	0	0
2	E	**130**	1	0	0	0	1	1	1	0	0	0
2	E	**131**	0	0	0	1	0	1	1	1	1	1
2	E	**132**	0	0	0	0	1	1	1	1	1	1
2	E	**133**	0	0	0	0	1	1	1	0	0	1
2	E	**134**	0	0	0	0	1	1	1	1	1	1
2	E	**135**	1	0	0	0	0	1	1	1	1	1
2	E	**136**	1	0	0	0	1	1	1	0	1	1
2	R	**137**	1	0	0	0	1	1	1	0	1	1
2	R	**138**	0	0	0	1	1	1	1	1	1	1
2	R	**139**	1	0	0	0	1	1	1	1	1	1
2	R	**140**	0	0	0	0	1	1	1	1	1	1
2	R	**141**	1	0	0	1	1	1	1	0	1	1
2	R	**142**	0	0	0	1	0	1	1	0	0	1
2	R	**143**	1	0	0	1	1	1	1	0	1	1
2	R	**144**	0	0	0	0	0	1	1	1	1	0
2	R	**145**	1	0	0	0	0	1	1	0	0	1
2	R	**146**	0	0	0	0	0	1	1	0	1	1
2	R	**147**	0	0	0	1	1	1	1	0	1	1
2	R	**148**	1	0	0	1	1	1	1	0	1	1
2	R	**149**	0	0	0	1	1	1	1	0	1	1
2	R	**150**	1	0	0	1	1	1	1	0	1	1
2	R	**151**	1	0	0	1	0	1	1	1	1	1
2	R	**152**	1	0	0	0	1	1	1	0	1	1
2	R	**153**	1	0	0	0	1	1	1	0	0	1
2	R	**154**	1	0	0	0	1	1	1	1	1	1
2	R	**155**	0	0	0	1	1	1	1	1	1	1
2	R	**156**	1	0	0	0	1	1	1	0	0	1
2	R	**157**	1	0	0	0	1	1	1	1	1	1
2	R	**158**	1	0	0	0	1	1	1	1	0	1
2	R	**159**	1	0	0	0	1	1	1	0	0	1
2	RP	**160**	1	0	0	0	1	1	1	0	1	1
2	RP	**161**	1	0	0	0	0	1	1	0	1	1
2	RP	**162**	1	0	0	0	1	1	1	1	1	1
2	RP	**163**	1	0	0	1	1	1	1	0	1	1

Farm	**Root compartment**	**Name ID**	**Gram**	**Fluorescence**	**PGP activity**			**Antagonistic activity**				
					Siderophore production	**Phosphate solubilization**	**Salt tolerance (NaCl 8%)**	***Cmm***	***Pto***	***Pco***	***Xep***	***Fol***
2	RP	**164**	1	0	0	1	1	1	1	0	0	1
2	RP	**165**	0	0	0	0	1	1	1	1	1	1
2	RP	**166**	1	0	0	0	1	1	1	1	1	1
2	RP	**167**	1	0	0	0	1	1	1	0	1	1
2	E	**168**	0	0	0	0	1	1	1	0	0	1
2	E	**169**	0	0	0	0	1	1	1	0	1	1
2	E	**170**	1	0	0	0	1	1	1	0	0	1
2	E	**171**	1	0	0	1	1	1	1	0	1	1
2	E	**172**	1	0	0	1	1	1	1	0	1	1
2	E	**173**	1	0	0	0	1	1	1	0	0	1
2	E	**174**	1	0	0	1	1	1	1	0	0	1
2	E	**175**	1	0	0	1	1	1	1	0	1	1
2	E	**176**	0	0	0	1	1	1	1	0	0	1
2	R	**177**	1	0	0	1	1	1	1	0	0	1
2	R	**178**	1	0	0	1	1	1	1	0	0	1
2	R	**179**	1	0	0	1	1	1	1	1	1	1
2	R	**180**	0	0	0	1	1	1	1	0	1	1
2	R	**181**	0	0	0	0	1	1	1	0	0	1
2	R	**182**	0	0	0	1	1	1	1	1	0	1
2	RP	**183**	0	0	0	1	1	1	1	0	1	1
2	RP	**184**	0	0	0	1	1	1	1	0	1	1
2	RP	**185**	0	0	0	1	1	1	1	1	1	1
2	RP	**186**	0	0	0	1	1	1	1	1	1	1
2	RP	**187**	1	0	0	1	1	1	1	0	0	0
2	RP	**188**	0	0	0	1	1	1	1	0	1	1
2	RP	**189**	0	0	0	1	1	1	1	0	1	1
2	RP	**190**	0	0	0	1	1	1	1	0	1	1
2	RP	**191**	0	0	0	1	1	1	1	1	1	1
2	RP	**192**	1	0	0	1	1	1	1	0	1	1
2	RP	**193**	0	0	0	1	1	1	1	0	1	1
2	RP	**194**	1	0	0	1	1	1	1	0	0	1
2	RP	**195**	0	0	0	1	1	1	1	0	0	1
2	E	**196**	0	0	0	1	1	1	1	0	1	1
2	E	**197**	0	0	0	1	1	1	1	0	0	1
2	E	**198**	0	0	0	1	1	1	1	0	0	1
2	E	**199**	0	0	0	1	1	1	1	0	0	1
2	E	**200**	0	0	0	1	1	1	1	0	1	1
2	E	**201**	1	0	0	1	1	1	1	0	0	1
2	E	**202**	0	0	0	1	1	1	1	0	1	1
2	E	**203**	1	0	0	1	1	1	1	1	1	0
2	E	**204**	0	0	0	1	1	1	1	1	1	0
2	E	**205**	0	0	0	1	1	1	1	1	1	1
2	E	**206**	0	0	0	1	1	1	1	0	0	1
2	E	**207**	1	0	0	1	0	1	1	0	0	1
2	E	**208**	0	0	0	1	0	1	1	1	1	1
2	RP	**F11**	0	0	0	1	1	1	1	0	0	1
2	R	**F13**	0	0	0	1	1	1	1	0	1	1
2	E	**F1**	0	1	0	1	1	1	1	1	0	1

Farm	**Root compartment**	**Name ID**	**Gram**	**Fluorescence**	**PGP activity**			**Antagonistic activity**				
					Siderophore production	**Phosphate solubilization**	**Salt tolerance (NaCl 8%)**	***Cmm***	***Pto***	***Pco***	***Xep***	***Fol***
2	E	**F2**	0	1	0	1	1	1	1	0	1	1
2	RP	**F3**	0	1	0	1	0	1	1	0	0	1
2	RP	**F4**	0	1	0	1	1	1	1	0	0	1
2	RP	**F5**	0	1	0	1	1	1	1	0	0	1
2	RP	**F6**	0	1	0	1	1	1	1	0	0	1
2	R	**F7**	0	0	0	1	1	1	1	0	0	1
2	R	**F8**	0	0	0	1	1	1	1	0	0	1
2	E	**F9**	0	1	0	1	0	1	1	0	1	1
2	E	**F10**	0	1	0	1	0	1	1	0	1	1
2	RP	**F12**	0	1	0	1	1	1	1	0	0	1
2	E	**F14**	0	1	0	1	0	1	1	1	0	1
3	RP	**209**	0	0	0	0	1	1	1	0	1	0
3	RP	**210**	0	0	0	0	1	1	1	0	0	0
3	RP	**211**	1	0	0	0	1	1	1	0	0	0
3	RP	**212**	0	0	0	0	1	1	1	0	1	1
3	RP	**213**	0	0	0	0	1	1	1	1	1	1
3	RP	**214**	0	0	0	0	1	1	1	1	1	1
3	RP	**215**	0	0	0	0	1	1	1	1	1	1
3	RP	**216**	0	0	0	0	1	1	1	1	1	1
3	RP	**217**	0	0	0	0	1	1	1	1	1	1
3	RP	**218**	0	0	0	0	1	1	1	1	1	1
3	RP	**219**	0	0	0	0	1	1	1	1	1	1
3	RP	**220**	1	0	0	0	1	1	1	1	1	1
3	RP	**221**	0	0	0	0	1	1	1	1	1	1
3	RP	**222**	0	0	0	0	1	1	1	1	1	1
3	RP	**223**	0	0	0	0	1	1	1	1	1	1
3	RP	**224**	0	0	0	0	1	1	1	1	1	1
3	RP	**225**	0	0	1	0	1	1	1	1	1	1
3	RP	**226**	1	0	0	0	1	1	1	1	1	1
3	RP	**227**	1	0	0	0	1	1	1	1	1	1
3	RP	**228**	0	0	0	0	1	1	1	0	0	0
3	RP	**229**	1	0	0	0	0	1	1	0	1	1
3	R	**230**	0	0	0	0	1	1	1	0	1	1
3	R	**231**	0	0	0	0	1	1	1	0	0	0
3	R	**232**	0	0	0	0	1	1	1	1	0	0
3	R	**233**	0	0	1	0	1	1	1	0	0	0
3	R	**234**	0	0	0	0	1	1	1	1	0	0
3	R	**235**	0	0	0	0	1	1	1	0	0	0
3	R	**236**	1	0	0	0	1	1	1	1	1	1
3	R	**237**	0	0	0	0	1	1	1	1	1	1
3	R	**238**	0	0	0	0	1	1	1	0	1	1
3	R	**239**	0	0	0	0	1	1	1	0	1	1
3	R	**240**	0	0	0	0	1	1	1	0	1	1
3	R	**241**	0	0	1	0	1	1	1	1	1	1
3	R	**242**	0	0	0	0	1	1	1	1	1	1
3	R	**243**	0	0	0	0	1	1	1	1	0	0
3	R	**244**	0	0	0	0	1	1	1	0	0	0
3	R	**245**	0	0	0	0	1	1	1	0	0	0
3	R	**246**	0	0	0	0	0	1	1	0	0	0

Farm	**Root compartment**	**Name ID**	**Gram**	**Fluorescence**	**PGP activity**			**Antagonistic activity**				
					Siderophore production	**Phosphate solubilization**	**Salt tolerance (NaCl 8%)**	***Cmm***	***Pto***	***Pco***	***Xep***	***Fol***
3	R	**247**	0	0	0	0	0	1	1	0	1	1
3	R	**248**	0	0	0	0	0	1	1	1	1	1
3	R	**249**	0	0	1	0	1	1	1	1	0	0
3	R	**250**	0	0	0	0	1	1	1	0	0	0
3	E	**251**	0	0	0	0	1	1	1	1	0	0
3	E	**252**	0	0	0	0	0	1	1	1	1	1
3	E	**253**	0	0	0	0	1	1	1	1	1	1
3	E	**254**	0	0	0	0	1	1	1	0	0	0
3	E	**255**	0	0	0	0	1	1	1	1	1	1
3	E	**256**	0	0	0	0	0	1	1	0	0	0
3	E	**257**	0	0	0	1	1	1	1	1	1	1
3	E	**258**	0	0	0	0	1	1	1	1	1	1
3	E	**259**	0	0	0	1	1	1	1	1	0	1
3	E	**260**	0	0	0	1	1	1	1	0	1	1
3	E	**261**	0	0	0	1	1	1	1	1	1	1
3	E	**262**	0	0	0	1	1	1	1	1	1	1
3	E	**263**	0	0	0	1	1	1	1	1	1	1
3	E	**264**	0	0	0	1	1	1	1	1	1	1
3	E	**265**	0	0	0	0	1	1	1	1	1	1
3	E	**266**	1	0	0	1	1	1	1	1	1	1
3	E	**267**	0	0	0	1	1	1	1	1	1	1
3	E	**268**	0	0	0	1	1	1	1	1	1	1
3	E	**269**	0	0	0	1	1	1	1	0	1	1
3	E	**270**	0	0	0	1	1	1	1	1	1	1
3	E	**F19**	0	0	0	1	1	1	1	1	1	1
3	E	**F21**	0	0	0	1	1	1	1	1	1	1
3	E	**F22**	0	0	0	1	1	1	1	1	0	0
3	E	**F24**	0	0	0	1	1	1	1	0	0	0
3	R	**F32**	0	0	0	1	1	1	1	0	0	0
3	R	**F38**	0	0	0	1	1	1	1	1	1	1
3	R	**F39**	0	0	0	1	1	1	1	1	1	1
3	E	**F16**	0	1	0	1	1	1	1	1	1	1
3	E	**F17**	0	1	0	1	1	1	1	1	0	0
3	E	**F18**	0	1	0	1	1	1	1	0	0	0
3	E	**F20**	0	1	0	1	1	1	1	1	0	0
3	RP	**F25**	0	1	0	1	1	1	1	1	0	0
3	RP	**F26**	0	1	0	1	1	1	1	0	0	0
3	RP	**F27**	0	1	0	1	1	1	1	1	1	1
3	RP	**F28**	0	1	0	1	1	1	1	1	0	0
3	RP	**F29**	0	1	0	1	1	1	1	1	1	1
3	RP	**F30**	0	1	0	1	1	1	1	1	0	0
3	RP	**F31**	0	1	0	1	1	1	1	1	0	0
3	R	**F32**	0	1	0	1	1	1	1	1	1	1
3	R	**F33**	0	1	0	1	1	1	1	1	1	1
3	R	**F34**	0	1	0	1	1	1	1	1	0	0
3	R	**F35**	0	1	0	1	1	1	1	1	0	0
3	R	**F36**	0	1	0	1	1	1	1	1	1	1
4	R	**271**	0	0	1	0		1	1	1	1	1

Farm	**Root compartment**	**Name ID**	**Gram**	**Fluorescence**	**PGP activity**			**Antagonistic activity**				
					Siderophore production	**Phosphate solubilization**	**Salt tolerance (NaCl 8%)**	***Cmm***	***Pto***	***Pco***	***Xep***	***Fol***
4	R	**272**	0	0	0	0	1	1	1	1	1	1
4	R	**273**	0	0	1	0	1	0	0	0	0	1
4	R	**274**	1	0	1	0	1	1	1	1	0	1
4	R	**275**	0	0	1	0	1	1	1	1	1	1
4	R	**276**	0	0	0	0	1	1	1	1	1	1
4	R	**277**	0	0	1	0	1	0	0	0	0	1
4	R	**278**	0	0	1	0	1	0	0	0	0	1
4	R	**279**	0	0	0	0	1	0	0	0	0	1
4	R	**280**	0	0	0	0	1	1	1	1	1	1
4	R	**281**	1	0	1	0	1	0	0	1	1	1
4	R	**282**	0	0	1	0	1	1	1	1	1	1
4	R	**283**	1	0	0	0	1	0	0	0	0	1
4	R	**284**	1	0	1	0	1	0	0	0	0	1
4	R	**285**	1	0	1	0	1	0	0	0	0	1
4	R	**286**	1	0	1	0	1	1	0	1	1	1
4	R	**287**	0	0	0	0	1	0	1	0	0	1
4	R	**288**	0	0	0	0	1	0	0	0	0	1
4	R	**289**	0	0	0	0	1	1	1	1	1	1
4	R	**290**	1	0	0	0	1	1	1	1	1	1
4	R	**291**	1	0	1	0	1	0	1	0	0	1
4	RP	**292**	0	0	1	0	1	0	0	0	0	1
4	RP	**293**	0	0	1	0	1	0	0	0	0	1
4	RP	**294**	0	0	1	0	1	0	0	0	0	1
4	RP	**295**	0	0	0	0	1	0	0	0	0	1
4	RP	**296**	0	0	0	0	1	1	0	1	1	1
4	RP	**297**	0	0	0	0	1	0	1	0	0	1
4	RP	**298**	0	0	0	0	1	0	0	0	0	1
4	RP	**299**	0	0	1	0	1	0	0	0	0	1
4	RP	**300**	0	0	1	0	1	0	0	0	0	1
4	RP	**301**	1	0	0	0	1	0	0	0	0	1
4	RP	**302**	0	0	1	0	1	0	0	0	0	1
4	E	**303**	0	0	1	0	1	0	0	0	0	1
4	E	**304**	0	0	1	0	1	1	0	1	1	1
4	E	**305**	1	0	0	0	1	1	1	1	1	1
4	E	**306**	1	0	1	0	1	1	1	1	1	1
4	E	**307**	0	0	0	0	1	0	1	0	0	1
4	E	**308**	0	0	0	0	1	0	0	0	0	1
4	E	**309**	0	0	1	0	1	0	0	0	0	1
4	E	**310**	0	0	1	0	1	1	0	1	1	1
4	R	**311**	0	0	1	0	1	1	1	1	1	1
4	R	**312**	1	0	1	0	1	1	1	1	1	1
4	R	**313**	0	0	0	0	1	1	1	1	1	1
4	R	**314**	1	0	1	0	1	0	1	0	0	1
4	R	**315**	0	0	0	0	1	1	1	1	1	1
4	R	**316**	0	0	0	0	1	1	1	1	1	1
4	R	**317**	1	0	0	0	1	1	1	1	1	1
4	R	**318**	0	0	1	0	1	0	1	1	0	1
4	R	**319**	0	0	1	1	1	1	1	1	1	1
4	R	**320**	1	0	1	1	1	1	1	1	1	1

Farm	**Root compartment**	**Name ID**	**Gram**	**Fluorescence**	**PGP activity**			**Antagonistic activity**				
					Siderophore production	**Phosphate solubilization**	**Salt tolerance (NaCl 8%)**	***Cmm***	***Pto***	***Pco***	***Xep***	***Fol***
4	R	**321**	1	0	1	1	1	1	1	1	1	1
4	R	**322**	1	0	1	1	1	1	1	1	1	1
4	R	**323**	0	0	1	1	1	1	0	0	0	1
4	R	**324**	1	0	1	1	1	0	1	1	1	1
4	R	**325**	1	0	1	1	1	1	0	0	1	1
4	R	**326**	1	0	1	1	1	1	0	0	1	1
4	R	**327**	1	0	1	1	1	0	1	1	1	1
4	R	**328**	0	0	1	1	1	0	1	1	1	1
4	R	**329**	0	0	1	1	1	1	1	1	1	1
4	R	**330**	1	0	1	1	1	1	1	1	1	1
4	RP	**331**	0	0	1	1	1	1	0	0	0	1
4	RP	**332**	0	0	1	1	1	1	0	0	1	1
4	RP	**333**	0	0	1	1	1	1	0	0	1	1
4	RP	**334**	1	0	1	1	1	1	1	1	1	1
4	RP	**335**	0	0	1	1	1	1	0	0	0	1
4	RP	**336**	0	0	1	1	1	1	1	1	0	1
4	RP	**337**	0	0	1	1	1	1	0	0	0	1
4	E	**338**	0	0	1	1	1	1	1	1	1	1
4	E	**339**	0	0	1	1	1	1	0	0	0	1
4	E	**340**	1	0	1	1	1	1	0	0	1	1
4	E	**341**	0	0	1	1	1	1	0	0	1	1
4	E	**342**	0	0	1	1	1	1	1	1	1	1
4	E	**343**	0	0	1	1	1	1	1	1	1	1
4	E	**344**	1	0	1	1	1	0	1	1		1
4	E	**345**	0	0	1	1	1	1	1	1	0	1
4	E	**346**	0	0	1	1	1	1	0	0	1	1
4	E	**347**	1	0	1	1	1	1	1	0	1	1
4	E	**348**	0	0	1	1	1	1	0	0	0	1
4	E	**349**	1	0	1	1	1	1	0	0	1	1
4	E	**350**	0	0	1	1	1	1	0	0	1	1
4	E	**351**	1	0	1	1	1	1	1	1	1	1
4	E	**352**	1	0	1	1	1	1	1	1	0	1
4	E	**353**	0	0	1	1	1	1	1	1	0	1
4	E	**354**	0	0	1	1	1	1	0	0	0	1
4	RP	**355**	0	0	1	1	1	1	1	0	1	1
4	RP	**356**	0	0	1	1	1	1	1	1	1	1
4	RP	**357**	0	0	1	1	1	1	1	1	1	1
4	RP	**358**	0	0	1	1	1	1	1	1	1	1
4	R	**359**	0	0	1	1	1	1	1	1	0	1
4	R	**360**	0	0	1	1	1	1	1	1	0	1
4	R	**361**	0	0	1	1	1	1	1	1	1	1
4	R	**362**	1	0	1	1	1	1	0	1	0	1
4	R	**363**	0	0	1	1	1	1	1	1	1	1
4	R	**364**	1	0	1	1	1	1	1	1	1	1
4	R	**365**	0	0	1	1	1	1	1	1	1	1
4	R	**366**	0	0	1	1	1	1	1	1	1	1
4	R	**367**	0	0	1	0	1	1	0	0	0	1
4	E	**368**	0	0	1	0	1	1	1	1	1	1

Farm	**Root compartment**	**Name ID**	**Gram**	**Fluorescence**	**PGP activity**			**Antagonistic activity**				
					Siderophore production	**Phosphate solubilization**	**Salt tolerance (NaCl 8%)**	***Cmm***	***Pto***	***Pco***	***Xep***	***Fol***
4	E	**369**	1	0	1	0	1	0	0	0	1	1
4	E	**370**	1	0	0	1	1	1	1	1	1	1
4	E	**371**	1	0	1	1	1	1	1	1	1	1
4	E	**372**	0	0	1	1	1	1	1	1	1	1
4	E	**373**	0	0	1	1	1	1	1	1	1	1
4	RP	**374**	0	0	0	0	1	1	1	1	1	1
4	RP	**375**	0	0	1	0	1	1	1	1	1	1
4	RP	**376**	0	0	1	0	1	1	1	1	1	1
4	RP	**377**	0	0	1	0	1	0	0	0	0	1
4	RP	**378**	0	0	1	1	1	1	1	0	1	1
4	RP	**379**	1	0	1	1	1	1	1	1	1	1
4	RP	**380**	0	0	0	1	1	1	1	1	1	1
4	RP	**381**	0	0	1	0	1	1	0	1	1	1
4	RP	**382**	0	0	1	0	0	0	0	0	0	1
4	RP	**F37**	0	0	1	0	1	1	0	1	0	1
4	RP	**F38**	0	0	1	0	1	1	0	0	0	1
4	RP	**F39**	0	0	1	0	1	1	0	0	0	1
4	RP	**F40**	0	0	1	0	1	1	0	0	0	1
4	RP	**F41**	0	1	1	0	0	1	0	0	0	1
4	E	**F42**	0	1	1	0	0	1	0	0	0	1
4	RP	**F43**	0	0	1	0	0	1	0	0	0	1
4	RP	**F44**	0	0	1	0	1	1	0	0	0	1
4	RP	**F45**	0	0	1	0	0	1	0	0	0	1
4	E	**F46**	0	1	1	0	1	1	0	0	0	1
4	RP	**F47**	0	0	1	0	1	1	0	0	0	1
4	E	**F48**	0	1	1	0	0	1	0	0	0	1
4	RP	**F49**	0	0	1	0	0	1	0	0	0	1
4	E	**F50**	0	1	1	0	0	1	0	0	0	1
4	RP	**F51**	0	0	1	0	0	1	0	0	0	1
4	E	**F52**	0	1	1	0	0	1	0	0	0	1
4	E	**F53**	0	1	1	0	0	1	0	0	0	1
4	E	**F54**	0	1	0	0	1	1	0	0	0	1
4	R	**F55**	0	1	1	1	1	0	0	0	0	1
4	E	**F56**	0	1	1	0	1	1	1	1	1	1
4	R	**F57**	0	1	1	0	1	1	0	0	0	1
4	E	**F58**	0	1	1	0	0	1	0	0	0	1
4	R	**F59**	0	1	1	0	1	1	0	0	0	1
4	E	**F60**	0	1	1	0	1	1	1	1	1	1

Table S2: Principal Component Analysis (PCA) table of the full dataset on 424 bacteria, showing relationships between phenotypic traits (Gram reaction, fluorescence production, siderophore production, phosphate solubilisation, salt tolerance, antagonist activity against *Cmm*, *Pco*, *Pto*, *Xep*, and *Fol*) and bacterial isolates.

Bacteria ID	PC1	PC2
1	-0.272	-0.295
2	-0.199	-0.4
3	-0.709	-0.643
4	-0.659	-0.708
5	-0.659	-0.708
6	-0.659	-0.708
7	-0.199	-0.4
8	-0.272	-0.295
9	-0.659	-0.708
10	-0.384	0.08
11	0.076	0.388
12	-0.384	0.08
13	0.076	0.388
14	-0.92	0.359
15	-0.92	0.359
16	-0.734	-0.121
17	-0.92	0.359
18	-0.459	0.667
19	-0.459	0.667
20	0.076	0.388
21	0.076	0.388
22	0.076	0.388
23	0.076	0.388
24	0.076	0.388
25	-0.456	-0.285
26	-1.451	-0.313
27	0.076	0.388
28	0.026	0.452
29	0.076	0.388
30	0.076	0.388
31	-1.144	0.255
32	-1.144	0.255
33	-0.92	0.359
34	-0.92	0.359
35	-0.97	0.424
36	0.076	0.388
37	0.026	0.452
38	-0.92	0.359
39	0.076	0.388
40	-0.149	0.284
41	0.076	0.388
42	-0.199	-0.4

Bacteria ID	PC1	PC2
43	-0.199	-0.4
44	-0.199	-0.4
45	0.076	0.388
46	0.076	0.388
47	-0.199	-0.4
48	-0.199	-0.4
49	-0.072	-0.033
50	0.389	0.275
51	-0.072	-0.033
52	0.114	-0.513
53	0.114	-0.513
54	0.114	-0.513
55	0.114	-0.513
56	0.624	-0.846
57	0.389	0.275
58	0.389	0.275
59	0.316	0.379
60	0.316	0.379
61	0.389	0.275
62	0.316	0.379
63	0.316	0.379
64	0.041	-0.409
65	-0.807	-0.016
66	-0.532	0.771
67	-0.719	-0.233
68	-0.444	0.554
69	-0.219	0.658
70	-0.444	0.554
91	-0.146	0.554
92	0.899	-0.058
93	0.586	0.055
94	0.142	0.237
95	0.586	0.055
96	0.364	0.221
97	0.917	-0.051
98	0.826	0.046
99	0.99	-0.155
100	0.076	0.388
101	0.003	0.492
102	-0.022	0.438
103	0.076	0.388
104	0.586	0.055
105	0.899	-0.058
106	-0.532	0.771
107	0.389	0.275
108	0.003	0.492
109	-0.532	0.771

Bacteria ID	PC1	PC2
110	-0.459	0.667
111	0.076	0.388
112	-0.368	0.57
113	0.076	0.388
114	0.076	0.388
115	0.364	0.221
116	0.586	0.055
117	0.586	0.055
118	0.003	0.492
119	0.076	0.388
120	0.076	0.388
121	-0.401	0.789
122	-0.179	0.773
123	0.826	0.046
124	0.586	0.055
125	0.586	0.055
126	0.076	0.388
127	0.514	0.159
128	-0.532	0.771
129	-0.491	0.886
130	-0.401	0.789
131	0.826	0.046
132	0.586	0.055
133	-0.459	0.667
134	0.586	0.055
135	0.604	0.063
136	0.167	0.291
137	0.167	0.291
138	0.899	-0.058
139	0.677	-0.042
140	0.586	0.055
141	0.48	0.178
142	-0.219	0.658
143	0.48	0.178
144	0.481	0.378
145	-0.441	0.675
146	0.003	0.492
147	0.389	0.275
148	0.48	0.178
149	0.389	0.275
150	0.48	0.178
151	0.917	-0.051
152	0.167	0.291
153	-0.368	0.57
154	0.677	-0.042
155	0.899	-0.058

Bacteria ID	PC1	PC2
156	-0.368	0.57
157	0.677	-0.042
158	0.142	0.237
159	-0.368	0.57
160	0.167	0.291
161	0.094	0.396
162	0.677	-0.042
163	0.48	0.178
164	-0.056	0.457
165	0.586	0.055
166	0.677	-0.042
167	0.167	0.291
168	-0.459	0.667
169	0.076	0.388
170	-0.368	0.57
171	0.48	0.178
172	0.48	0.178
173	-0.368	0.57
174	-0.056	0.457
175	0.48	0.178
176	-0.146	0.554
177	-0.056	0.457
178	-0.056	0.457
179	0.99	-0.155
180	0.389	0.275
181	-0.459	0.667
182	0.364	0.221
183	0.389	0.275
184	0.389	0.275
185	0.899	-0.058
186	0.899	-0.058
187	-0.088	0.676
188	0.389	0.275
189	0.389	0.275
190	0.389	0.275
191	0.899	-0.058
192	0.48	0.178
193	0.389	0.275
194	-0.056	0.457
195	-0.146	0.554
196	0.389	0.275
197	-0.146	0.554
198	-0.146	0.554
199	-0.146	0.554
200	0.389	0.275
201	-0.056	0.457
202	0.389	0.275

Bacteria ID	PC1	PC2
203	0.958	0.064
204	0.867	0.16
205	0.899	-0.058
206	-0.146	0.554
207	-0.129	0.562
208	0.826	0.046
F11	-0.146	0.554
F13	0.389	0.275
F1	0.314	0.285
F2	0.339	0.339
F3	-0.269	0.723
F4	-0.196	0.619
F5	-0.196	0.619
F6	-0.196	0.619
F7	-0.146	0.554
F8	-0.146	0.554
F9	0.266	0.444
F10	0.266	0.444
F12	-0.196	0.619
F14	0.241	0.39
209	0.044	0.607
210	-0.491	0.886
211	-0.401	0.789
212	0.076	0.388
213	0.586	0.055
214	0.586	0.055
215	0.586	0.055
216	0.586	0.055
217	0.586	0.055
218	0.586	0.055
219	0.586	0.055
220	0.677	-0.042
221	0.586	0.055
222	0.586	0.055
223	0.586	0.055
224	0.586	0.055
225	0.312	-0.733
226	0.677	-0.042
227	0.677	-0.042
228	-0.491	0.886
229	0.094	0.396
230	0.076	0.388
231	-0.491	0.886
232	0.019	0.553
233	-0.766	0.098
234	0.019	0.553

Bacteria ID	PC1	PC2
235	-0.491	0.886
236	0.677	-0.042
237	0.586	0.055
238	0.076	0.388
239	0.076	0.388
240	0.076	0.388
241	0.312	-0.733
242	0.586	0.055
243	0.019	0.553
244	-0.491	0.886
245	-0.491	0.886
246	-0.564	0.99
247	0.003	0.492
248	0.514	0.159
249	-0.256	-0.235
250	-0.491	0.886
251	0.019	0.553
252	0.514	0.159
253	0.586	0.055
254	-0.491	0.886
255	0.586	0.055
256	-0.564	0.99
257	0.899	-0.058
258	0.586	0.055
259	0.364	0.221
260	0.389	0.275
261	0.899	-0.058
262	0.899	-0.058
263	0.899	-0.058
264	0.899	-0.058
265	0.586	0.055
266	0.99	-0.155
267	0.899	-0.058
268	0.899	-0.058
269	0.389	0.275
270	0.899	-0.058
F19	0.899	-0.058
F21	0.899	-0.058
F22	0.332	0.44
F24	-0.179	0.773
F32	-0.179	0.773
F38	0.899	-0.058
F39	0.899	-0.058
F16	0.849	0.006
F17	0.282	0.504
F18	-0.229	0.837
F20	0.282	0.504

Bacteria ID	PC1	PC2
F25	0.282	0.504
F26	-0.229	0.837
F27	0.849	0.006
F28	0.282	0.504
F29	0.849	0.006
F30	0.282	0.504
F31	0.282	0.504
F32	0.849	0.006
F33	0.849	0.006
F34	0.282	0.504
F35	0.282	0.504
F36	0.849	0.006
271	0.239	-0.628
272	0.586	0.055
273	-1.419	-0.532
274	-0.133	-0.55
275	0.312	-0.733
276	0.586	0.055
277	-1.419	-0.532
278	-1.419	-0.532
279	-1.144	0.255
280	0.586	0.055
281	-0.283	-1.241
282	0.312	-0.733
283	-1.054	0.159
284	-1.328	-0.629
285	-1.328	-0.629
286	-0.058	-1.137
287	-0.684	0.563
288	-1.144	0.255
289	0.586	0.055
290	0.677	-0.042
291	-0.868	-0.321
292	-1.419	-0.532
293	-1.419	-0.532
294	-1.419	-0.532
295	-1.144	0.255
296	0.126	-0.253
297	-0.684	0.563
298	-1.144	0.255
299	-1.419	-0.532
300	-1.419	-0.532
301	-1.054	0.159
302	-1.419	-0.532
303	-1.419	-0.532
304	-0.149	-1.041

Bacteria ID	PC1	PC2
305	0.677	-0.042
306	0.402	-0.829
307	-0.684	0.563
308	-1.144	0.255
309	-1.419	-0.532
310	-0.149	-1.041
311	0.312	-0.733
312	0.402	-0.829
313	0.586	0.055
314	-0.868	-0.321
315	0.586	0.055
316	0.586	0.055
317	0.677	-0.042
318	-0.448	-0.557
319	0.624	-0.846
320	0.715	-0.943
321	0.715	-0.943
322	0.715	-0.943
323	-0.882	-0.542
324	0.491	-1.046
325	-0.256	-0.917
326	-0.256	-0.917
327	0.491	-1.046
328	0.4	-0.95
329	0.624	-0.846
330	0.715	-0.943
331	-0.882	-0.542
332	-0.346	-0.821
333	-0.346	-0.821
334	0.715	-0.943
335	-0.882	-0.542
336	0.089	-0.567
337	-0.882	-0.542
338	0.624	-0.846
339	-0.882	-0.542
340	-0.256	-0.917
341	-0.346	-0.821
342	0.624	-0.846
343	0.624	-0.846
344	-0.045	-0.767
345	0.089	-0.567
346	-0.346	-0.821
347	0.205	-0.61
348	-0.882	-0.542
349	-0.256	-0.917
350	-0.346	-0.821
351	0.715	-0.943

Bacteria ID	PC1	PC2
352	0.18	-0.663
353	0.089	-0.567
354	-0.882	-0.542
355	0.114	-0.513
356	0.624	-0.846
357	0.624	-0.846
358	0.624	-0.846
359	0.089	-0.567
360	0.089	-0.567
361	0.624	-0.846
362	-0.281	-0.971
363	0.624	-0.846
364	0.715	-0.943
365	0.624	-0.846
366	0.624	-0.846
367	-1.194	-0.428
368	0.312	-0.733
369	-0.793	-0.908
370	0.99	-0.155
371	0.715	-0.943
372	0.624	-0.846
373	0.624	-0.846
374	0.586	0.055
375	0.312	-0.733
376	0.312	-0.733
377	-1.419	-0.532
378	0.114	-0.513
379	0.715	-0.943
380	0.899	-0.058
381	-0.149	-1.041
382	-1.492	-0.428
F37	-0.684	-0.762
F38	-1.194	-0.428
F39	-1.194	-0.428
F40	-1.194	-0.428
F41	-1.317	-0.259
F42	-1.317	-0.259
F43	-1.267	-0.324
F44	-1.194	-0.428
F45	-1.267	-0.324
F46	-1.244	-0.364
F47	-1.194	-0.428
F48	-1.317	-0.259
F49	-1.267	-0.324
F50	-1.317	-0.259
F51	-1.267	-0.324

Bacteria ID	PC1	PC2
F52	-1.317	-0.259
F53	-1.317	-0.259
F54	-0.97	0.424
F55	-1.156	-0.581
F56	0.262	-0.668
F57	-1.244	-0.364
F58	-1.317	-0.259
F59	-1.244	-0.364
F60	0.262	-0.668

Table S3: Molecular identification of the endophytic bacteria based on the 16S rRNA gene sequence.

	Best hit (ref_seq)						This study GenBank accession No.
Strain ID	**Order**	**Family**	**Genus**	**Species**	**Ident. %**	**NCBI Acc. No.**	
124	Pseudomonadales	Moraxellaceae	*Acinetobacter*	*Acinetobacter baumannii*	100	CP050388.1	MW130753
170	Pseudomonadales	Moraxellaceae	*Acinetobacter*	*Acinetobacter baumannii*	100	CP050388.1	MW130754
123	Pseudomonadales	Moraxellaceae	*Acinetobacter*	*Acinetobacter baumannii*	100	MT256198.1	MW130755
307	Pseudomonadales	Moraxellaceae	*Acinetobacter*	*Acinetobacter baumannii*	100	MT256198.1	MW130756
263	Bacillales	Bacillaceae	*Bacillus*	*Bacillus velezensis*	100	MN559711.1	MW130757
373	Bacillales	Bacillaceae	*Bacillus*	*Bacillus subtilis*	100	CP051860.1	MW130758
306	Bacillales	Bacillaceae	*Bacillus*	*Bacillus velezensis*	100	CP051463.1	MW130759
341	Bacillales	Bacillaceae	*Bacillus*	*Bacillus velezensis*	100	KY927398.1	MW130760
268	Bacillales	Bacillaceae	*Bacillus*	*Bacillus megaterium*	99	KT883839.1	MW130761
261	Bacillales	Bacillaceae	*Bacillus*	*Bacillus velezensis*	99	CP051463.1	MW130762
304	Bacillales	Bacillaceae	*Bacillus*	*Bacillus velezensis*	100	CP051463.1	MW130763
305	Bacillales	Bacillaceae	*Bacillus*	*Bacillus velezensis*	100	CP051463.1	MW130764
255	Bacillales	Bacillaceae	*Bacillus*	*Bacillus velezensis*	100	MT365117.1	MW130765
265	Bacillales	Bacillaceae	*Bacillus*	*Bacillus velezensis*	100	MT365117.1	MW130766
351	Bacillales	Bacillaceae	*Bacillus*	*Bacillus amyloliquefaciens*	100	MK501609.1	MW130767
347	Bacillales	Bacillaceae	*Bacillus*	*Bacillus amyloliquefaciens*	100	MK501609.1	MW130768
374	Bacillales	Bacillaceae	*Bacillus*	*Bacillus velezensis*	100	KY927398.1	MW130769
257	Bacillales	Bacillaceae	*Bacillus*	*Bacillus amiloliquefaciens*	100	MK501609.1	MW130770
136	Bacillales	Bacillaceae	*Bacillus*	*Bacillus velezensis*	99	MN654121.1	MW130771
270	Bacillales	Bacillaceae	*Bacillus*	*Bacillus amiloliquefaciens*	100	MK501609.1	MW130772
372	Bacillales	Bacillaceae	*Bacillus*	*Bacillus subtilis*	100	MT081484.1	MW130773
260	Bacillales	Bacillaceae	*Bacillus*	*Bacillus subtilis*	100	KU729674.1	MW130774
338	Bacillales	Bacillaceae	*Bacillus*	*Bacillus sp.*	100	CP040881.1	MW130775
370	Bacillales	Bacillaceae	*Bacillus*	*Bacillus sp.*	100	CP040881.1	MW130776
269	Bacillales	Bacillaceae	*Bacillus*	*Bacilus velenzensis*	100	CP024922.1	MW130777
132	Enterobacteriales	Enterobacteriaceae	*Lelliottia*	*Lelliottia sp.*	97	JN853247.1	MW130778
127	Enterobacteriales	Enterobacteriaceae	*Lelliottia*	*Lelliottia sp.*	97	JN853247.1	MW130779
198	Enterobacteriales	Enterobacteriaceae	*Lelliottia*	*Lelliottia sp.*	97	JN853247.1	MW130780
135	Enterobacteriales	Enterobacteriaceae	*Lelliottia*	*Lelliottia sp.*	97	JN853247.1	MW130781
267	Enterobacteriales	Enterobacteriaceae	*Enterobacter*	*Enterobacter cancerogenus*	97	FJ976582.1	MW130782
f20	Enterobacteriales	Enterobacteriaceae	*Enterobacter*	*Enterobacter cancerogenus*	97	FJ976582.1	MW130783
f21	Enterobacteriales	Enterobacteriaceae	*Enterobacter*	*Enterobacter cancerogenus*	97	FJ976582.1	MW130784
f18	Enterobacteriales	Enterobacteriaceae	*Enterobacter*	*Enterobacter cancerogenus*	97	FJ976582.1	MW130785
252	Enterobacteriales	Enterobacteriaceae	*Enterobacter*	*Enterobacter cancerogenus*	97	FJ976582.1	MW130786
f17	Enterobacteriales	Enterobacteriaceae	*Enterobacter*	*Enterobacter mori*	97	KJ589489.1	MW130787
f19	Enterobacteriales	Enterobacteriaceae	*Enterobacter*	*Enterobacter cancerogenus*	97	FJ976582.1	MW130788
254	Enterobacteriales	Enterobacteriaceae	*Enterobacter*	*Enterobacter cancerogenus*	97	FJ976582.1	MW130789

	Best hit (ref_seq)						**This study GenBank accession No.**
Strain ID	**Order**	**Family**	**Genus**	**Species**	**Ident. %**	**NCBI Acc. No.**	
266	Enterobacteriales	Enterobacteriaceae	*Enterobacter*	*Enterobacter cancerogenus*	97	FJ976582.1	MW130790
128	Enterobacteriales	Enterobacteriaceae	*Lelliottia*	*Lelliottia sp.*	97	JN853247.1	MW130791
f52	Enterobacteriales	Enterobacteriaceae	*Enterobacter*	*Enterobacter tabaci*	97	MF682952.1	MW130792
126	Enterobacteriales	Enterobacteriaceae	*Lelliottia*	*Lelliottia sp.*	97	JN853247.1	MW130793
200	Enterobacteriales	Enterobacteriaceae	*Lelliottia*	*Lelliottia sp.*	96	JN853247.1	MW130794
202	Enterobacteriales	Enterobacteriaceae	*Lelliottia*	*Lelliottia sp.*	97	JN853247.1	MW130795
259	Enterobacteriales	Enterobacteriaceae	*Lelliottia*	*Lelliottia sp.*	97	JN853247.1	MW130796
176	Enterobacteriales	Enterobacteriaceae	*Lelliottia*	*Lelliottia sp.*	97	JN853247.1	MW130797
310	Enterobacteriales	Enterobacteriaceae	*Enterobacter*	*Enterobacter cancerogenus*	97	FJ976582.1	MW130798
49	Enterobacteriales	Enterobacteriaceae	*Ewingella*	*Ewingella americana*	100	MT101745.1	MW130799
48	Enterobacteriales	Enterobacteriaceae	*Ewingella*	*Ewingella americana*	99	MT101745.1	MW130800
35	Enterobacteriales	Enterobacteriaceae	*Ewingella*	*Ewingella americana*	99	KY126991.1	MW130801
346	Enterobacteriales	Enterobacteriaceae	*Pantoea*	*Pantoea sp.*	97	MK229045.1	MW130802
353	Enterobacteriales	Enterobacteriaceae	*Pantoea*	*Pantoea sp.*	97	MH884045.1	MW130803
264	Enterobacteriales	Enterobacteriaceae	*Enterobacter*	*Enterobacter cancerogenus*	97	FJ976582.1	MW130804
344	Enterobacteriales	Enterobacteriaceae	*Pantoea*	*Pantoea sp.*	97	MK229045.1	MW130805
345	Enterobacteriales	Enterobacteriaceae	*Pantoea*	*Pantoea sp.*	97	MK229045.1	MW130806
342	Enterobacteriales	Morganellaceaea	*Providencia*	*Providencia vermicola*	99	KX394623.1	MW130807
350	Enterobacteriales	Morganellaceaea	*Providencia*	*Providencia vermicola*	99	MK942706.1	MW130808
349	Enterobacteriales	Morganellaceaea	*Providencia*	*Providencia vermicola*	99	MK942706.1	MW130809
f1	Pseudomonadales	Pseudomonadaceae	*Pseudomonas*	*Pseudomonas citronellolis*	100	KM210226.1	MW130810
172	Pseudomonadales	Pseudomonadaceae	*Pseudomonas*	*Pseudomonas plecoglossicida*	100	MT367715.1	MW130811
f14	Pseudomonadales	Pseudomonadaceae	*Pseudomonas*	*Pseudomonas putida*	100	LN866622.1	MW130812
f53	Pseudomonadales	Pseudomonadaceae	*Pseudomonas*	*Pseudomonas monteilii*	100	MH603875.1	MW130813
125	Pseudomonadales	Pseudomonadaceae	*Pseudomonas*	*Pseudomonas plecoglossicida*	100	MT367715.1	MW130814
201	Pseudomonadales	Pseudomonadaceae	*Pseudomonas*	*Pseudomonas plecoglossicida*	100	MT367715.1	MW130815
168	Pseudomonadales	Pseudomonadaceae	*Pseudomonas*	*Pseudomonas plecoglossicida*	100	KJ819579.1	MW130816
169	Pseudomonadales	Pseudomonadaceae	*Pseudomonas*	*Pseudomonas plecoglossicida*	100	MT367715.1	MW130817
174	Pseudomonadales	Pseudomonadaceae	*Pseudomonas*	*Pseudomonas plecoglossicida*	100	MT367715.1	MW130818
352	Pseudomonadales	Pseudomonadaceae	*Pseudomonas*	*Pseudomonas plecoglossicida*	100	MT367715.1	MW130819
173	Pseudomonadales	Pseudomonadaceae	*Pseudomonas*	*Pseudomonas plecoglossicida*	100	MT367715.1	MW130820
f2	Pseudomonadales	Pseudomonadaceae	*Pseudomonas*	*Pseudomonas plecoglossicida*	100	MT367715.1	MW130821
f10	Pseudomonadales	Pseudomonadaceae	*Pseudomonas*	*Pseudomonas plecoglossicida*	100	MT367715.1	MW130822
f56	Pseudomonadales	Pseudomonadaceae	*Pseudomonas*	*Pseudomonas plecoglossicida*	100	MT367715.1	MW130823
f60	Pseudomonadales	Pseudomonadaceae	*Pseudomonas*	*Pseudomonas plecoglossicida*	100	MT367715.1	MW130824
f42	Pseudomonadales	Pseudomonadaceae	*Pseudomonas*	*Pseudomonas putida*	100	CP026115.2	MW130825
f48	Pseudomonadales	Pseudomonadaceae	*Pseudomonas*	*Pseudomonas putida*	100	CP026115.2	MW130826

	Best hit (ref_seq)						**This study GenBank accession No.**
Strain ID	**Order**	**Family**	**Genus**	**Species**	**Ident. %**	**NCBI Acc. No.**	
171	Pseudomonadales	Pseudomonadaceae	*Pseudomonas*	*Pseudomonas plecoglossicida*	100	MT367715.1	MW130827
f9	Pseudomonadales	Pseudomonadaceae	*Pseudomonas*	*Pseudomonas plecoglossicida*	100	MT367715.1	MW130828
f46	Pseudomonadales	Pseudomonadaceae	*Pseudomonas*	*Pseudomonas putida*	100	LN866622.1	MW130829

Table S4: Accession numbers of the sequences of the type strains used as references in the dendrogram in Figure 6 in this study.

Species	Type Strain	Sequence accession no. (16S rRNA gene)
Bacillus subtilis	ATCC 6051^T	AJ276351
B. pumilus	ATCC 7061^T	AY876289
B. megaterium	ATCC 14581^T	D16273
B. siamensis	KCTC 13613^T	GQ281299
B. mojavensis	ATCC 51516^T	AB021191
B. amyloliquefaciens	ATCC 23350^T	AB006920
B. velezensis	CCUG 50740^T	AY603658
B. thuringiensis	ATCC 10792^T	D16281
B. cereus	ATCC 14579^T	AE016877
Acinetobacter baumannii	DSM 30007^T	NR_117677
Pseudomonas citronellolis	ATCC 13674^T	Z76659
P. plecoglossicida	ATCC 700383^T	AB009457
P. putida	ATCC 12633^T	D84020
P. monteilii	ATCC 700476^T	AF064458
P. mosselii	CIP 105259^T	AF072688
P. entomophila	CCUG 61470^T	AY907566
P. parafulva	DSM 17004^T	AB060132
P. fulva	DSM 17717^T	AB060136
P. syingae pv. syingae	NCPPB 281^T	DQ318866
P. fluorescens	DSM 50090^T	D84013
P. aeruginosa	DSM 50071^T	HE978771
Enterobacter cancerogenus	LMG 2693^T	NR 116756.1
E. mori	LMG 25706^T	NZ_GL890774
E. tabaci	KACC 17832^T	NR_146667
Ewingella americana	ATCC 33852^T	JMPJ01000013
Providencia vermicola	DSM 17385^T	NR_042415
Lelliottia amnigena	ATCC 33731^T	AB004749
L. nimipressuralis	DSM 18955^T	KF516260
Pantoea agglomerans	DSM 3493^T	NR_041978

Table S5: Effect of the treatments by soil drenching of tomato plantlets grown in pots using bacterial endophytes belonging to the genus *Pseudomonas* and *Bacillus*. Plant height, fresh and dry weight of roots and shoots, dry matter and root/shoot ratio was measured 30 days after the treatment.

Bacterial strains	Plant height		Root			Shoot			R/S
	T30	Gain (%)	fw	dw	DM	fw	dw	DM	
P. plecoglossicida _171	29.33±1.15 abc	11.36	0.70 ab	0.57 a	83.41 c	4.20 a	1.84 a	44.06 a	0.31 ab
P. plecoglossicida _172	29.83±1.89 abc	12.85	0.90 ab	0.53 a	60.14 ab	5.10 a	2.23 b	43.71 a	0.24 ab
*P. citronellolis*_f1	31.33±3.06 bc	17.02	1.13 b	0.63 a	56.00 a	5.13 a	2.23 b	44.62 a	0.29 ab
*P. monteilii*_f53	29.00±1.00 abc	10.4	0.93 ab	0.59 a	62.81 ab	4.63 a	1.73 a	37.82 a	0.34 b
*P. plecoglossicida*_f56	32.33±1.15 bc	19.59	0.66 a	0.58 a	87.22 c	5.36 a	2.26 b	42.41 a	0.25 ab
B. velezensis _261	31.67±2.52 bc	17.89	1.08 ab	0.54 a	54.42 a	5.03 a	2.22 b	46.18 a	0.24 ab
*B. velezensis*_263	30.33±0.58 abc	14.29	0.63 a	0.49 a	76.98 bc	4.90 a	2.19 b	44.76 a	0.22 a
B. velezensis _265	27.67±1.53 ab	6.02	1.13 b	0.65 a	57.77 ab	5.03 a	1.91 ab	37.98 a	0.35 b
*B. megaterium*_268	26.33±1.53 a	1.27	0.90 ab	0.62 a	70.00 abc	4.80 a	2.26 b	47.47 a	0.28 ab
B. velezensis _306	33.33±1.15 bc	22.00	1.00 ab	0.54 a	53.94 a	4.20 a	1.84 a	45.01 a	0.25 ab
Control	26.00±1.73 a	/	0.80 ab	0.53 a	62.91 ab	5.10 a	2.23 b	52.11 a	0.24 ab

fw, fresh weight, dw, dry weight; DM dry matter; R/S, root to shoot dry weight ratio.

Gain%: the effect of bacterial treatments on plant height was assessed as relative percentage change in comparison to the control. Means in a column followed by the same letter are not significantly different according to Student–Newman–Keuls test (P≤ 0.05)