

Supplementary material

TABLE S1. Taxonomic characterization of banana-associated strains based on partial 16S rRNA/ITS gene sequences obtained from SSCP gels

Band No.	Closet database match	Identity	Accession No.	Taxonomic affiliation
1.1	<i>Flavobacterium micromati</i>	97%	NR_029010.1	Flavobacteria
2.1	<i>Delftia tsuruhatensis</i>	99%	NR_024786	Betaroteobacteria
3.1	<i>Buttiauxella warmboldiae</i>	99%	NR_028893	Gammaproteobacteria
3.2	<i>Brevundimonas nasdae</i>	99%	NR_028633	Alphaproteobacteria
4.1	<i>Herbaspirillum seropedicae</i>	98%	NR_02932	Betaroteobacteria
4.2	<i>Serratia fonticola</i>	98%	NR_025339	Gammaproteobacteria
6.1	<i>Acidovorax temperans</i>	99%	NR_028715	Betaroteobacteria
7.1	<i>Delftia tsuruhatensis</i>	98%	NR_024786	Betaroteobacteria
7.2	<i>Azoarcus communis</i>	93%	NR_024850	Betaroteobacteria
7.3.	<i>Flavobacterium frigoris</i>	96%	NR_025597	Flavobacteria
7.4	<i>Brevundimonas nasdae</i>	99%	NR_028633	Alphaproteobacteria
8.1	<i>Flavobacterium micromati</i>	95%	NR_029010	Flavobacteria
10.1	<i>Flavobacterium xinjiangense</i>	96%	NR_025201	Flavobacteria
10.2	<i>Brevundimonas nasdae</i>	98%	NR_028633	Alphaproteobacteria
11.1	<i>Herbaspirillum seropedicae</i>	98%	NR_029329	Betaroteobacteria
12.1	<i>Pseudomonas cichorii</i>	98%	NR_026532	Gammaproteobacteria
13.1	<i>Flavobacterium frigoris</i>	94%	NR_025597	Flavobacteria
13.2	<i>Flavobacterium micromati</i>	96%	NR_029010	Flavobacteria
14.1	<i>Diaphorobacter nitroreducens</i>	98%	NR_024782	Betaroteobacteria
14.2	<i>Shingobacterium faecium</i>	93%	NR_025537	Sphingobacteria
15.1	<i>Flavobacterium frigidarium</i>	95%	NR_025020	Flavobacteria
16.1	<i>Delftia tsuruhatensis</i>	99%	NR_024786	Betaroteobacteria
R1.1	<i>Lepista sordida</i>	77%	FJ770391.1	Basidiomycota
R4.1	<i>Tulostoma melanocyclum</i>	80%	EU784436.1	Basidiomycota
R4.2	<i>Geastrum corollinum</i>	92%	EU784222.1	Basidiomycota
R5.1	<i>Macrolepiota clelandii</i>	80%	AY083203.1	Basidiomycota
R6.1	<i>Pluteus albostipitatus</i>	96%	HM562106.1	Basidiomycota
R7.2	<i>Geastrum corollinum</i>	88%	EU784222.1	Basidiomycota
R8.1	<i>Ampulloclitocybe clavipes</i>	87%	AB301607.1	Basidiomycota
R9.1	<i>Macrolepiota clelandii</i>	79%	AY083203.1	Basidiomycota
R11.1	<i>Agaricus bisporus</i>	90%	HM561978.1	Basidiomycota
R13.1	<i>Hyphodontia nothofagi</i>	94%	GQ411524.1	Basidiomycota
E2.1	<i>Coprinus fissolanatus</i>	96%	AF345812.1	Basidiomycota
E2.2	<i>Bullera oryzae</i>	99%	AF444413.1	Basidiomycota
E5.1	<i>Musa acuminata x Musa schizocarpa</i>	98%	FR727963.1	Plant DNA
E5.2	<i>Cryptococcus zaeae</i>	97%	AJ965481.1	Basidiomycota
E8.1	<i>Hypochnicium vellereum</i>	82%	AY787674.2	Basidiomycota

TABLE S2. Bacterial isolates with the highest antagonistic activity: origin, activity and identity

No.	Isolat No.	Origin ^a	Antagonistic activity ^b			Identification			
			<i>C. m.</i>	<i>F. c.</i>	<i>F. o.</i>	ARDRA group	Species	Similarity	Accession No.
1	R1R2A2.3	R: 1	++	+	++	1			
2	S3MC4.4	S: 3a	+++	++	-	1	<i>Burkholderia multivorans</i>	99%	NR_029358.1
3	S3MC4.7	S: 3a	++	++	++	1	<i>B. cepacia</i>	99%	NR_029209.1
4	E1SNA2.9	E: 1	+++	+++	++	1	<i>B. plantarii</i>	99%	NR_037064.1
5	E1SNA2.12	E: 1	+++	+++	++	1			
6	E1SNA2.13	E: 1	+++	+++	++	1			
7	E1SNA2.14	E: 1	+++	+++	++	1			
8	E3KB1.6	E: 3a	+	+	-	2	<i>Serratia marcescens</i>	99%	NR_036886.1
9	S2MC1.5	S: 2	+++	+	-	2	<i>S. marcescens</i>	99%	NR_036886.1
10	S4MC4.2	S: 3b	++	+	-	2			
11	S4MC4.3	S: 3b	+	+	-	2	<i>S. marcescens</i>	99%	NR_036886.1
12	S4KB1.8	S: 3b	+	+	-	2	<i>S. marcescens</i>	99%	NR_036886.1
13	S2R2A2.5	S: 2	+	+	-	2			
14	S3R2A1.6	S: 3a	+	+	-	2	<i>S. marcescens</i>	100%	NR_036886.1
15	R1KB1.8	R: 1	++	+	+	3	<i>Pseudomonas fluorescens</i>	99%	DQ073039.1
16	R1KB2.1	R: 1	+	+	+	3	<i>P. putida</i>	94%	HQ259593.1
17	R1KB2.3	R: 1	+	+	-	3			
18	R4KB1.1	R: 3b	+++	++	+	3	<i>P. cichorii</i>	98%	NR_026532.1
19	R4KB3.1	R: 3b	++	+	-	3			
20	E1MC1.8	E: 1	+	+	-	3			
21	E1MC2.1	E: 1	+++	+	-	3			
22	E1MC2.7	E: 1	+++	++	-	3			
23	E1KB2.1	E: 1	+++	++	++	3	<i>P. palleroniana</i>	99%	NR_029050.1
24	E1KB2.5	E: 1	+++	++	++	3	<i>P. palleroniana</i>	99%	NR_029050.1
25	E1KB2.8	E: 1	+	++	++	3	<i>P. palleroniana</i>	99%	NR_029050.1
26	E2KB1.7	E: 2	+	+	-	3			
27	S2MC2.5	S: 2	+++	++	++	3	<i>P. putida</i>	99%	HM439953.1
28	R3MC3.6	R: 3a	++	++	+	4			
29	R3R2A4.6	R: 3a	++	++	-	4			
30	R4R2A1.6	R: 3b	+	+	++	4			
31	S1R2A1.2	S: 1	+	+	+	4			
32	S1R2A2.2	S: 1	+	+	-	4			
33	S1R2A2.5	S: 1	+	+	-	4			
34	S2R2A3.7	S: 2	+	+	-	4	<i>Bacillus weihenstephanensis</i>	98%	NR_024697
35	S2R2A4.4	S: 2	+	+	+	4			
36	S4R2A4.6	S: 3b	+	+	+	4			
37	S3R2A4.4	S: 3a	+	+	-	5	<i>Bacillus indicus</i>	96%	NR_029022.1

^a S=soil, R=rhizosphere and E=endosphere

^b *C.m* =*Colletotrichum musae*, *F.c* =*Fusarium chlamydosporum*, *F.o* =*Fusarium oxysporum*

TABLE S3. Fungal isolates with the highest antagonistic activity: origin, activity and identity

No.	Isolat No.	Origin ^a	Antagonistic activity ^b			ARDRA group	Identification		Accession No.
			C. m.	F. c.	F. o.		Species	Similarity	
1	R3SNA4.1	R: 3a	+	+	-	1		<i>Penicillium janthinellum</i>	97%
2	R3SNA4.3	R: 3a	+	+	-	1	1	<i>Penicillium janthinellum</i>	99%
3	R4SNA1.10	R: 3b	++	+	+	2	1	<i>Penicillium phialosporum</i>	87%
4	R4SNA1.11	R: 3b	++	+	-	2	1	<i>Penicillium brevicompactum</i>	99%
5	R4SNA1.14	R: 3b	++	+	-	2	1	<i>Penicillium brevicompactum</i>	99%
6	S3SNA1.5	S: 3a	+	+	-	3	1	<i>Penicillium</i> sp.	99%
7	S3SNA2.1	S: 3a	+	+	-	3	1	-	
8	S3SNA4.7	S: 3a	+	+	-	3	n.d.	<i>Penicillium</i> sp.	99%
9	R2SNA1.12	R: 2	+	+	-	3	n.d.	<i>Penicillium brevicompactum</i>	94%
10	S1SNA1.9	S: 1	+	+	-	4	n.d.	<i>Mortierella</i> sp.	99%
11	S1SNA1.12	S: 1	+	+	-	4	2	<i>Mortierella</i> sp.	99%
12	R4SNA4.10	R: 3b	+	+	-	4	2	<i>Mortierella</i> sp.	99%
13	S3SNA2.2	S: 3a	+	+	+	5	2	<i>Penicillium</i> sp.	99%
14	S3SNA4.8	S: 3a	+	+	-	5	1	<i>Penicillium</i> sp.	100%
15	S3SNA1.4	S: 3a	++	+	-	6	1	<i>Penicillium</i> sp.	98%
16	S3SNA2.5	S: 3a	+	+	-	6	3	<i>Penicillium chrysogenum</i>	98%
17	S1SNA1.2	S: 1	++	+	-	7	3	<i>Fusarium solani</i>	99%
18	S1SNA3.1	S: 1	+++	+	-	8	4	<i>Penicillium coprobium</i>	100%
19	S2SNA1.7	S: 1	++	+	+	9	3	<i>Fusarium</i> sp.	99%
20	S2SNA2.3	S: 2	++	+	-	10	4	-	
21	S2SNA4.14	S: 2	++	+	-	11	5	<i>Bionectria pityrodes</i>	99%
22	S3SNA1.6	S: 3a	+	+	+	12	5	-	
23	S4SNA3.3	S: 3b	+	+	++	13	n.d.	-	
24	S1TSM3.3	S: 1	++	+	++	14	4	<i>Hypocrea lixi</i>	99%
25	R2SNA3.11	R: 2	+	+	-	15	6	<i>Paecilomyces lilacinus</i>	100%
26	R2SNA4.3	R: 2	+	+	+	16	5	<i>Paecilomyces lilacinus</i>	100%
27	R3SNA1.4	R: 3a	++	+	-	17	5	<i>Penicillium</i> sp.	99%
28	R3SNA1.9	R: 3a	++	+	-	18	1	<i>Penicillium</i> sp.	99%
29	R3SNA2.1	R: 3a	++	+	+	19	1	<i>Fusarium</i> sp.	99%
30	R3SNA3.5	R: 3a	+	+	-	20	4	<i>Paecilomyces marquandii</i>	99%
31	R4SNA1.12	R: 3b	++	+	-	21	7	<i>Penicillium brevicompactum</i>	100%
32	R4SNA4.2	R: 3b	++	+	-	22	3	<i>Penicillium</i>	99%

33	E1SNA4.5	E: 1	++	+	+	23	8	<i>janthinellum</i> <i>Fusarium oxysporum</i>	99%
34	E1SNA4.18	E: 1	+	+	-	24	9	<i>Penicillium</i> sp.	99%
35	E2SNA1.6	E: 2	+	+	-	25	n.d.	<i>Paecilomyces lilacinus</i>	99%
36	E2SNA3.14	E: 2	+++	++	++	26	5	<i>Faurelina elongata</i>	99%

^a S=soil, R=rhizosphere and E=endosphere

^b *C.m* =*Colletotrichum musae*, *F.c* =*Fusarium chlamydosporum*, *F.o* =*Fusarium oxysporum*

Fig. S1. Bacterial abundances presented as $\log_{10} \text{g}^{-1}$ values per gram fresh weight for rhizosphere (R), endosphere (E) and soil (S) determined on A) R2A medium, B) King's B medium C) MacConkey medium and, D) fungal abundances on SNA medium from the different field sites: 1: Field 1 no herbicide treatment, 2: Field 2 intensive herbicide treatment, 3a: Field 3a no herbicide treatment, agro-forest, 3b: Field 3b no herbicide treatment, no agro-forest. Bars represent confidence intervals at $P=0.05$.

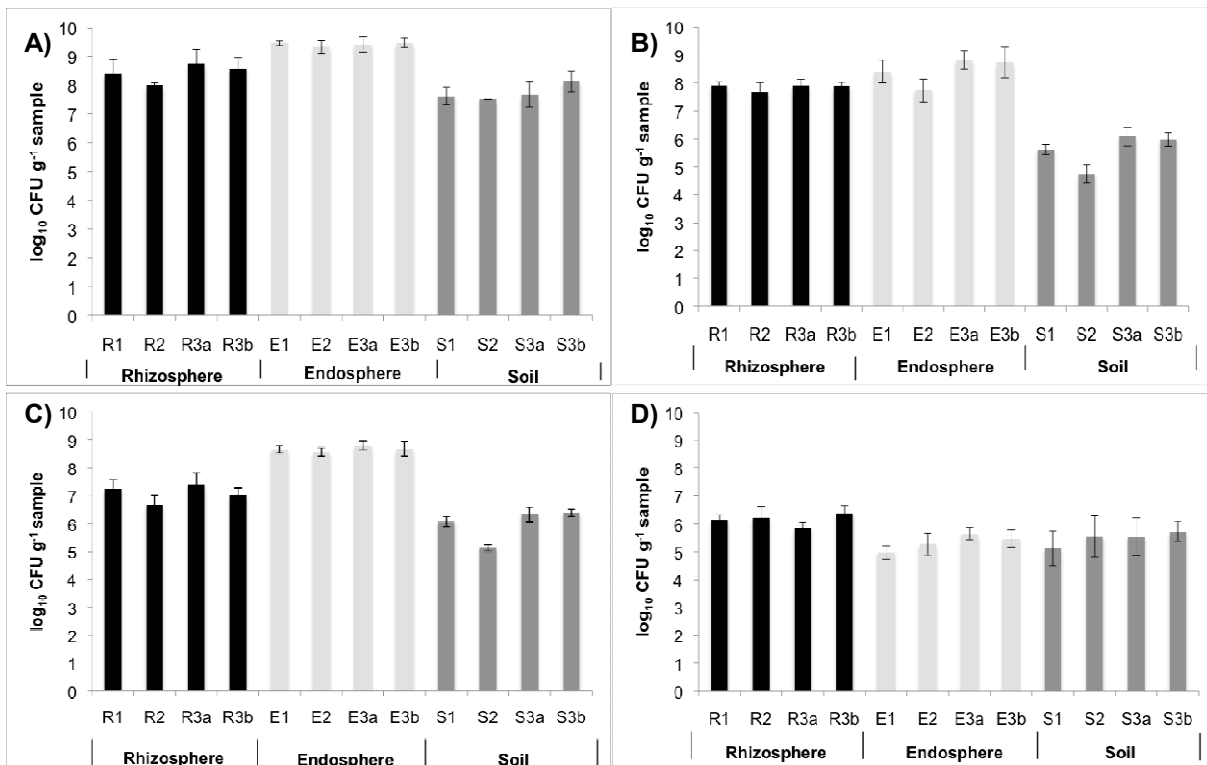


Fig. S2. Rarefaction curves obtained for enterics by amplicon sequencing for the rhizosphere (rhizo, 3a: no herbicide treatment, agro-forest, 3b: no herbicide treatment), the endosphere (endo) and soil.

