Supplementary Tables

Table S1: Selected bacterial strains belonging to *Pseudomonas* and *Bacillus* genera and their volatile organic compound-mediated pathogen suppression and plant growth-promotion.

Bacterial strains	Isolation source	Pathogen suppression (PS)	PS in the presence of activated charcoal	Plant growth promotion (PGP)	PGP in the presence of activated charcoal	PGP in the presence of $Ba(OH)_2$	Ammonia production	References
Pseudomonas fluorescens Q2-87	Wheat	+	-	+	-	+	-	Bangera and Thomashow, 1999
Pseudomonas fluorescens Phl1C2	Tomato	+	-	+	-	+	-	de la Fuente et al., 2006
Pseudomonas fluorescens Q8r1-96	Wheat	+	-	+	-	+	-	Raaijmakers and Weller, 1998
Pseudomonas fluorescens PF-5	Cotton	+	-	+	-	+	-	Howell and Stipanovic, 1979
Bacillus amyloliquefaciens SQR-9	Cucumber	+	-	+	-	+	-	Cao et al., 2011
Bacillus amyloliquefaciens NJN-6	Banana	+	-	+	-	+	-	Yuan et al., 2012
Bacillus amyloliquefaciens FZB42	Beet	+	-	+	-	+	-	Chen et al., 2007
Bacillus amyloliquefaciens T-5	Tomato	+	-	+	-	+	-	Tan et al., 2013

The involvement of ammonia in pathogen suppression was evaluated by ammonia production assay, which was conducted using a modified minimal salt medium amended with 1.5% sucrose, and 0.4% tryptone soy broth (w/v) according to a previous method (Weise et al., 2013), thereby mimicking the conditions used for volatile organic compound (VOC)-mediated functioning assays and VOC measurements later in the experiment. The involvement of CO_2 in plant growth-promotion by selected strains was determined using 0.1 M $Ba(OH)_2$ according to the method described previously (Kai and Piechulla, 2009). To further confirm that pathogen suppression and plant growth-promotion was only mediated by VOCs, 2 g of activated charcoal (Sicent General Material Co. Ltd., Beijing, China) that absorbs VOCs produced by each bacterial strain was used according to the method in our previous report (Raza et al., 2016). These experiments were done in triplicate using monocultures of each strain used in this study.

The results clearly show that all strains showed VOC-mediated pathogen suppression and plant growth promotion, but the use of activated charcoal which adsorbed VOCs, pathogen suppression and plant growth promotion was not found. In addition, with the use of $Ba(OH)_2$ that absorbed CO_2 produced during bacterial growth, plant growth promotion was still found, showing that VOCs were responsible for plant growth promotion. Ammonia production was also not found in any of the used strain under the assay conditions.

In the above table, "+" and "– "symbols denote for "have an effect" and "absence of effect", respectively.

Table S2: Experimental design showing the assembly of volatile organic compound-producing bacterial communities with different richness levels using four bacterial strains from two different genera. To balance the design, each strain was included thrice at each richness level except for richness levels 1 and 12. All the assays were done in triplicate for each community. Zeros and ones in the columns under different genera denote for the absence and presence of given strains from the communities, respectively.

Experiments	Richness	Strain 1	Strain 2	Strain 3	Strain 4
1	1	1	0	0	0
2	1	0	1	0	0
3	1	0	0	1	0
4	1	0	0	0	1
5	2	1	0	0	1
6	2	0	1	1	0
7	2	1	1	0	0
8	2	0	0	1	1
9	2	1	0	1	0
10	2	0	1	0	1
11	3	1	1	1	0
12	3	0	1	1	1
13	3	1	0	1	1
14	3	1	1	0	1
15	4	1	1	1	1

Table S3: Two models showing the relationship of community richness and strain identity based on the presence and absence of strains in monocultures and communities of *Pseudomonas* and *Bacillus* strains with pathogen suppression and plant growth promotion. Upward arrows denote positive effects.

Explanatory variables	**Pathogen suppression**			**Plant growth-promotion**		
	DF	**F**	**P**	**DF**	**F**	P
Pseudomonas strains						
Community richness	3	8.187↑	0.042	3	10.69↑	0.014
Q2-87		-	-	1	57.12↑	<0.0001
Phl1c2	1	21.10↑	<0.0001		-	-
Q8r1-96	1	46.66↑	<0.0001	1	29.00↑	<0.0001
PF-5	1	52.24↑	<0.0001	1	50.04↑	<0.0001
No. of residuals	38			38		
Model summary	R^2=0.76, AIC= 191.3			R^2=0.81, AIC= 334.8		
Bacillus strains						
Community richness	3	6.73↑	0.009	3	13.42↑	<0.0001
SQR-9	1	12.53↑	<0.0001	1	8.73↑	0.006
NJN-6	-	-	-	1	90.91↑	<0.0001
FZB42	-	-	-	1	38.55↑	<0.0001
T-5	1	10.19↑	0.001	-	-	-
No. of residuals	39			38		
Model summary	R^2=0.69, AIC= 217.1			R^2=0.89, AIC= 316.5		

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