

Table S1. Number of OTUs of culture-dependent endophytes of endo-phylosphere of maize obtained for all tested culture media in three replicates, and for the original mother culture medium (culture-independent).

Sample Code	Culture media	DNA conc. (ng/μl)	Quality (260/280 nm)	Total number of OTUs	Average number of OTUs
MPh-YsH 1	Sunflower broth 25 ml	39.8	2.1	82529	89461
MPh-YsH 2	Sunflower broth 25 ml	23.0	2.0	91134	
MPh-YsH 3	Sunflower broth 25 ml	35.6	2.1	94721	
MPh-YsL 1	Sunflower broth 5 ml	12.9	2.0	51004	83325
MPh-YsL 2	Sunflower broth 5 ml	9.71	2.0	101202	
MPh-YsL 3	Sunflower broth 5 ml	11.3	2.1	97769	
MPh-YmH 1	Maize broth 25 ml	40.3	2.0	82719	80390
MPh-YmH 2	Maize broth 25 ml	25.2	2.0	86018	
MPh-YmH 3	Maize broth 25 ml	18.7	2.1	72432	
MPh-YmL 1	Maize broth 5 ml	26.9	2.0	81959	70464
MPh-YmL 2	Maize broth 5 ml	18.2	2.1	84137	
MPh-YmL 3	Maize broth 5 ml	26.4	2.1	45297	
MPh-2A 1	R2A1/10	34.3	2.1	82014	85453
MPh-2A 2	R2A1/10	30.9	2.0	90193	
MPh-2A 3	R2A1/10	43.2	2.1	84152	
ML 2	Mother culture (plant leaves)	48.1	1.8	82910	89201
ML 3	Mother culture (plant leaves)	91.1	na	95492	

Table S2. Nutritional profile of the dehydrated powders of tested maize (*Zea mays* L.) and sunflower plants (*Helianthus annuus* L.).

Between brackets are % increase for sunflower values over those of maize

Parameters	<i>Zea mays</i> L.	<i>Helianthus annuus</i> L.
Total crude protein (%)	11.15	24.1 (116 %)
Total crude Fiber (%)	21.3	7.96
Total ash (%)	6.6	16.6 (151.5 %)
Total carbohydrates (%)	72.58	50.31
Amino Acids (%)		
Aspartic	1.24	2.13 (71.8 %)
Therionine	0.62	1.09 (75.8 %)
Serine	0.64	0.84 (31.3 %)
Glutamic	1.59	2.47 (55.3 %)
Proline	0.74	0.92 (24.3 %)
Glycine	0.75	1.21 (61.3 %)
Alanine	1.09	1.59 (45.9 %)
Valine	0.99	1.61 (62.6 %)
Methionine	0.35	0.57 (62.9 %)
Isoleucine	0.58	0.94 (62.1 %)
Leucine	1.12	1.88 (67.9 %)
Tyrosine	0.69	1.07 (55.1 %)
Phenylalanine	0.75	1.29 (72 %)
Histidine	0.25	0.36 (44 %)
Lysine	0.72	0.96 (33.3 %)
Argnine	0.43	1.16 (169.8 %)
Cysteine	0.19	0.29 (52.6 %)
Macro-nutrients (ppm)		
Ca	0.66	2.49
Mg	0.21	0.22
Na	1.35	1.89
K	1.84	2.09
P (%)	0.12	0.29
Micro-nutrients (ppm)		
Cu	1.06	2.52
Zn	0.34	0.39
Fe	0.96	0.31
Mn	1.16	1.34
Se (ppb)	31.08	68.72
Pb (ppb)	0.21	0.23

Parameter	Maize	Sunflower	
Total crude protein (%)	11.15	24.1	6
Total crude Fiber (%)	21.3	7.96	24
Total ash (%)	6.6	16.6	50
Total carbohydrates (%)	72.58	50.31	72
Macro-nutrients (ppm)			
Ca	0.66	2.49	0.1
Mg	0.21	0.22	0.6
Na	1.35	1.89	1.3
K	1.84	2.09	1.8
P	0.12	0.29	2
Micro-nutrients (ppm)			
Cu	1.06	2.52	0.2
Zn	0.34	0.39	0.3
Fe	0.96	0.31	1.3
Mn	1.16	1.34	31
Se	31.08	68.72	68
Pb	0.21	0.23	
Amino Acids (%)			
Aspartic	1.24	2.13	
Therionine	0.62	1.09	
Serine	0.64	0.84	
Glutamic	1.59	2.47	
Proline	0.74	0.92	0.1
Glycine	0.75	1.21	0.9
Alanine	1.09	1.59	1.1
Valine	0.99	1.61	1.6
Methionine	0.35	0.57	1.8
Isoleucine	0.58	0.94	2
Leucine	1.12	1.88	
Tyrosine	0.69	1.07	
Phenylalanine	0.75	1.29	
Histidine	0.25	0.36	
Lysine	0.72	0.96	
Argnine	0.43	1.16	
Cysteine	0.19	0.29	

Table S3. Two-way ANOVA analysis of log numbers of CFUs (data are log means \pm standard error [SE], n=5) of culturable endophytes of endo-rhizosphere and endo-phyllosphere of maize developed on the various culture media

Culture media	Two-way interactions (plant sphere x culture media)			
	Log No. CFUs g ⁻¹ DW			
	Total colonies		Micro-colonies	
	Endo-rhizosphere	Endo-phyllosphere	Endo-rhizosphere	Endo-phyllosphere
R2A	7.55 \pm 0.021 ^d	7.39 \pm 0.022 ^e	4.68 \pm 0.627 ^b	1.02 \pm 0.560 ^d
MPhYsH	.810 \pm 0.073 ^a	7.09 \pm 0.027 ^f	4.96 \pm 0.837 ^b	1.29 \pm 0.599 ^d
MPhYsL	7.86 \pm 0.072 ^b	6.85 \pm 0.026 ^g	6.56 \pm 0.504 ^a	3.80 \pm 0.653 ^{bc}
MPhYmH	7.57 \pm 0.035 ^d	6.01 \pm 0.028 ^h	7.34 \pm 0.088 ^a	2.86 \pm 0.605 ^c
MPhYmL	7.76 \pm 0.075 ^c	5.99 \pm 0.035 ^h	7.15 \pm 0.063 ^a	4.49 \pm 0.456 ^b
LSD (<i>p</i> value \leq 0. 05)	0.07		1.33	

*Statistically significant differences are designated by different letters ($P \leq 0.05$, n =5)

R2A, Reasoner's 2A agar; **MPhYmH**, culture-dependent on homologous maize broth 25mL-1; **MPhYmL**, culture-dependent on homologous maize broth 5mL-1; **MPhYsH** culture-dependent on heterologous sunflower broth 25mL-1; **MPhYsL**, culture-dependent on heterologous sunflower broth 5mL.

Table S4. Relative abundance ^a of dominant phyla, classes and orders in all tested culture-independent and culture-dependent samples ^b (average \pm standard error of the mean).

Phylum	Class	Order	ML	MPh2A	MPhYm H	MPhYmL	MPhYsH	MPhYs L
Proteobacter ia			94.81 \pm 2.16 ^{ab}	94.76 \pm 1.32 _{ab}	98.26 \pm 0.2 _{5a}	98 \pm 0.41 ^{ab}	95.27 \pm 2.26 _{ab}	94.32 \pm 0.82 _b
	Gammaproteobacteria		66.06 \pm 12.71 ^b	79.61 \pm 1.55 _{ab}	85.8 \pm 2.73 _a	84.78 \pm 3.85 _a	77.02 \pm 1.39 _{ab}	72.45 \pm 3.06 _b
		Pseudomonadales	38.24 \pm 4.92 ^c	72.78 \pm 2.2 ^{ab}	77.24 \pm 3.6 _{1a}	78.37 \pm 0.59 _a	71.98 \pm 1.11 _{ab}	66.99 \pm 3.51 _b
		Enterobacteriales	22.68 \pm 7.92 ^a	4.6 \pm 0.84 ^b	5.84 \pm 0.72 _b	3.37 \pm 3.69 ^b	2.81 \pm 1.74 ^b	2.94 \pm 1.2 _b
		Gammaproteobacteria_unclassif ied	1.05 \pm 0.07 ^b	2.21 \pm 0.18 ^{ab}	2.72 \pm 0.19 _a	3.03 \pm 0.62 ^a	2.05 \pm 0.25 ^{ab}	2.47 \pm 0.56 _a
		Xanthomonadales	4.09 \pm 0.2 ^a	0.01 \pm 0.01 ^b	0.01 \pm 0 ^b	0.01 \pm 0 ^b	0.17 \pm 0.27 ^b	0.05 \pm 0.02 _b
	Alphaproteobacteria		21.34 \pm 4.12 ^a	14.75 \pm 1.1 ^{ab}	12.35 \pm 2.8 _{2b}	12.49 \pm 4.33 _b	16.98 \pm 0.83 _{ab}	18.43 \pm 2.16 _{ab}
		Rhizobiales	15.21 \pm 4.58 ^a	0.45 \pm 0.35 ^b	0.14 \pm 0.16 _b	1.91 \pm 3.11 ^b	0.76 \pm 0.51 ^b	1.3 \pm 0.73 _b
		Sphingomonadales	6.11 \pm 0.46 ^{bc}	14.12 \pm 1.2 ^{ab}	11.96 \pm 2.3 _{ab}	10.55 \pm 3.78 _{bc}	16.17 \pm 0.88 _a	17.09 \pm 2.14 _a
		Alphaproteobacteria_unclassif ied	0.02 \pm 0	0.03 \pm 0	0.03 \pm 0.01	0.02 \pm 0.01	0.04 \pm 0	0.04 \pm 0.01
		Caulobacteriales	0 \pm 0	0.13 \pm 0.23	0 \pm 0	0 \pm 0	0.01 \pm 0.01	0 \pm 0
		Rhodobacterales	0 \pm 0	0.01 \pm 0.01	0.22 \pm 0.37	0.01 \pm 0	0.01 \pm 0.01	0 \pm 0
	Betaproteobacteria		7.3 \pm 6.42 ^a	0.3 \pm 0.51 ^b	0 \pm 0 ^b	0.6 \pm 0.54 ^b	1.16 \pm 0.92 ^a _b	3.33 \pm 1.58 _{ab}
		Burkholderiales	7.24 \pm 6.35 ^a	0.29 \pm 0.5 ^b	0 \pm 0 ^b	0.59 \pm 0.53 ^b	1.15 \pm 0.91 ^a _b	3.3 \pm 1.58 _{ab}
		Betaproteobacteria_unclassifie d	0.06 \pm 0.07	0 \pm 0.01	0 \pm 0	0.01 \pm 0.01	0.01 \pm 0.01	0.03 \pm 0.01
	Proteobacteria_unclassi fied		0.11 \pm 0.02	0.1 \pm 0.01	0.1 \pm 0.01	0.12 \pm 0.03	0.1 \pm 0	0.11 \pm 0.02
		Proteobacteria_unclassified	0.11 \pm 0.02	0.1 \pm 0.01	0.1 \pm 0.01	0.12 \pm 0.03	0.1 \pm 0	0.11 \pm 0.02
Firmicutes			1.63 \pm 0.38 ^{bc}	3.73 \pm 0.5 _a	1.25 \pm 0.22	1.43 \pm 0.32 ^c	3.25 \pm 0.8 ^{ab}	3.34 \pm 0.6

					c			a
	Bacilli		1.47±0.15 ^b	3.73±0.5 ^a	1.25±0.22 ^b	1.43±0.32 ^b	3.25±0.8 ^a	3.33±0.6 ^{2a}
		Bacillales	1.47±0.15	3.73±0.5	1.25±0.22	1.43±0.32	3.25±0.8	3.33±0.6 ²
	Clostridia		0.16±0.23	0 ± 0	0 ± 0	0 ± 0	0 ± 0	0 ± 0
		Clostridiales	0.16±0.23	0 ± 0	0 ± 0	0 ± 0	0 ± 0	0 ± 0
Bacteroidetes			3.09±2.82	0.96 ± 1.66	0 ± 0	0.01 ± 0.01	0.92 ± 1.49	1.58 ± 0.4
	Flavobacteriia		3.09±2.82	0.95 ± 1.65	0 ± 0	0 ± 0	0.87 ± 1.4	1.53 ± 0.43
	Saprospirae		0±0	0 ± 0	0 ± 0	0 ± 0	0.05 ± 0.08	0 ± 0
	Sphingobacteriia		0±0	0 ± 0	0 ± 0	0 ± 0	0 ± 0	0.05 ± 0.09
Actinobacteria			0.11±0.15	0.12 ± 0.09	0.06 ± 0.04	0.07 ± 0.03	0.17 ± 0.19	0.34 ± 0.29
	Actinobacteria		0.11±0.15	0.12 ± 0.09	0.06 ± 0.04	0.07 ± 0.03	0.17 ± 0.19	0.34 ± 0.29
		Actinomycetales	0.11±0.15	0.12 ± 0.09	0.06 ± 0.04	0.07 ± 0.03	0.17 ± 0.19	0.34 ± 0.29

^a Number shows the average percentage followed by ± standard deviation. Treatments sharing the same letters are non-significantly different ($p < 0.05$, ANOVA under generalized linear model followed by Tukey's Honest Significant Detection test). Significant increases in abundance compared to the ML are highlighted in green, while significant decreases are highlighted in red.

^b ML, culture-independent mother leaf; MPh2A, culture-dependent of R2A culture medium; MPhYmH, culture-dependent on homologous maize broth 25mL⁻¹; MPhYmL, culture-dependent on homologous maize broth 5mL⁻¹; MPhYsH culture-dependent on heterologous sunflower broth 25mL⁻¹; MPhYsL, culture-dependent on heterologous sunflower broth 5mL⁻¹.

Table S5. Relative abundance^a of dominant families and genera in all tested culture-independent and culture-dependent samples ^b (average \pm standard error of the mean).

Family	Genera	ML	MPh2A	MPhYmH	MPhYmL	MPhYsH	MPhYsL
Enterobacteriaceae		22.68 \pm 7.92 ^a					
	Family		4.6 \pm 0.84 ^b	5.84 \pm 0.72 ^b	3.37 \pm 3.69 ^b	2.81 \pm 1.74 ^b	2.94 \pm 1.2 ^b
	Enterobacteriaceae unclassified	22.4 \pm 8.24 ^a	0.16 \pm 0.01 ^b	0.17 \pm 0.03 ^b	0.16 \pm 0.1 ^b	0.11 \pm 0.04 ^b	0.12 \pm 0.02 ^b
	Erwinia	0.28 \pm 0.32	4.43 \pm 0.84	5.67 \pm 0.72	3.21 \pm 3.6	2.71 \pm 1.7	2.83 \pm 1.21
Sphingomonadaceae							
	Family	6.1 \pm 0.46 ^c	14.12 \pm 1.2 ^{ab}	11.96 \pm 2.3 ^{abc}	10.55 \pm 3.78 ^{bc}	16.17 \pm 0.88 ^{ab}	17.09 \pm 2.14 ^a
	Sphingomonadaceae unclassified	0.01 \pm 0 ^b	0.04 \pm 0.01 ^{ab}	0.03 \pm 0.01 ^{ab}	0.03 \pm 0 ^{ab}	0.04 \pm 0.01 ^{ab}	0.05 \pm 0.01 ^a
	Sphingomonas	6.09 \pm 0.46 ^c	14.08 \pm 1.19 ^{ab}	11.93 \pm 2.29 ^{abc}	10.53 \pm 3.78 ^{bc}	16.13 \pm 0.87 ^{ab}	17.04 \pm 2.14 ^a
Rhizobiaceae							
	Family	15.04 \pm 4.54 ^a	0.18 \pm 0.26 ^b	0.03 \pm 0.02 ^b	1.84 \pm 3.14 ^b	0.32 \pm 0.29 ^b	1.02 \pm 0.53 ^b
	Agrobacterium	14.93 \pm 4.52 ^a	0.17 \pm 0.25 ^b	0.02 \pm 0.02 ^b	1.81 \pm 3.08 ^b	0.3 \pm 0.28 ^b	0.99 \pm 0.51 ^b
	Rhizobiaceae unclassified	0.12 \pm 0.03 ^a	0 \pm 0 ^b	0 \pm 0 ^b	0.04 \pm 0.06 ^{ab}	0.01 \pm 0.01 ^b	0.02 \pm 0.01 ^b
	Shinella	0 \pm 0 ^b	0 \pm 0 ^b	0 \pm 0 ^b	0 \pm 0 ^b	0 \pm 0 ^b	0.01 \pm 0.01 ^a
Moraxellaceae							
	Family	15.46 \pm 15.16 ^b	54.09 \pm 1.8 ^a	55.62 \pm 0.2 ^a	52.01 \pm 2.24 ^a	50.48 \pm 2.65 ^a	46.02 \pm 1.83 ^a
	Acinetobacter	23.12 \pm 4.33 ^c	50.29 \pm 1.63 ^a	50.84 \pm 0.4 ^a	46.6 \pm 2.97 ^{ab}	46.93 \pm 2.96 ^{ab}	41.63 \pm 2.15 ^b
Pseudomonadaceae							
	Family	15.12 \pm 9.25 ^b	22.49 \pm 2.05 ^{ab}	26.4 \pm 3.21 ^{ab}	31.76 \pm 2.75 ^a	25.04 \pm 3.39 ^{ab}	25.35 \pm 5.44 ^{ab}
	Pseudomonas	14.87 \pm 8.95 ^b	22.42 \pm 2.05 ^{ab}	26.31 \pm 3.21 ^{ab}	31.66 \pm 2.74 ^a	22.32 \pm 1.17 ^{ab}	24.64 \pm 5.43 ^{ab}
Xanthomonadaceae							
	Family	4.09 \pm 0.2 ^a	0.01 \pm 0.01 ^b	0.01 \pm 0 ^b	0.01 \pm 0 ^b	0.17 \pm 0.27 ^b	0.05 \pm 0.02 ^b
	Stenotrophomonas	4.01 \pm 0.18 ^a	0 \pm 0 ^b	0 \pm 0 ^b	0.01 \pm 0 ^b	0 \pm 0 ^b	0.02 \pm 0.02 ^b
Comamonadaceae	Family	7.21 \pm 6.34 ^a	0.29 \pm 0.5 ^b	0 \pm 0 ^b	0.59 \pm 0.53 ^b	0.98 \pm 0.97 ^b	0.53 \pm 0.35 ^b

	Comamonadaceae unclassified	7.21 ± 6.34 ^a	0.29 ± 0.5 ^b	0 ± 0 ^b	0.59 ± 0.53 ^b	0.98 ± 0.97 ^b	0.53 ± 0.35 ^b
Gammaproteobacteria_unclassified	Family	1.05 ± 0.07 ^b	2.21 ± 0.18 ^{ab}	2.72 ± 0.19 ^a	3.03 ± 0.62 ^a	2.05 ± 0.25 ^{ab}	2.47 ± 0.56 ^a
	Gammaproteobacteria unclassified	1.05 ± 0.0 ^b	2.21 ± 0.18 ^{ab}	2.72 ± 0.19 ^a	3.03 ± 0.62 ^a	2.05 ± 0.25 ^{ab}	2.47 ± 0.56 ^a
Bacillaceae	Family	0 ± 0 ^d	2.35 ± 0.19 ^a	1 ± 0.38 ^{cd}	1.34 ± 0.29 ^{abc}	2.45 ± 0.46 ^{ab}	1.51 ± 0.66 ^{abc}
	Bacillus	0 ± 0 ^d	2.35 ± 0.19 ^a	1 ± 0.38 ^{cd}	1.34 ± 0.29 ^{abc}	2.45 ± 0.46 ^{ab}	1.51 ± 0.66 ^{abc}
Paenibacillaceae	Family	1.46 ± 0.15 ^a	1.36 ± 0.63 ^a	0.22 ± 0.13 ^{bc}	0.09 ± 0.04 ^b	0.78 ± 0.35 ^{bc}	1.8 ± 0.2 ^a
	Paenibacillus	1.46 ± 0.16 ^a	0.81 ± 0.63 ^{abc}	0 ± 0 ^c	0.01 ± 0.01 ^c	0.74 ± 0.34 ^{abc}	1.62 ± 0.3 ^{ab}
Rhizobiales_unclassified	Family	0.09 ± 0.05 ^a	0 ± 0 ^b	0 ± 0 ^b	0 ± 0 ^b	0 ± 0 ^b	0.01 ± 0.01 ^b
	Rhizobiales unclassified	0.09 ± 0.05 ^a	0 ± 0 ^b	0 ± 0 ^b	0 ± 0 ^b	0 ± 0 ^b	0.01 ± 0.01 ^b
Alcaligenaceae	Family	0.01 ± 0.01 ^b	0 ± 0 ^b	0 ± 0 ^b	0 ± 0 ^b	0.17 ± 0.21 ^b	2.76 ± 1.77 ^a
	Achromobacter	0.01 ± 0.01 ^b	0 ± 0 ^b	0 ± 0 ^b	0 ± 0 ^b	0.17 ± 0.21 ^b	2.73 ± 1.74 ^a

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^b ML, culture-independent mother leaf; MPh2A, culture-dependent of R2A culture medium; MPhYmH, culture-dependent on homologous maize broth 25mL⁻¹; MPhYmL, culture-dependent on homologous maize broth 5mL⁻¹; MPhYsH culture-dependent on heterologous sunflower broth 25mL⁻¹; MPhYsL, culture-dependent on heterologous sunflower broth 5mL⁻¹.