

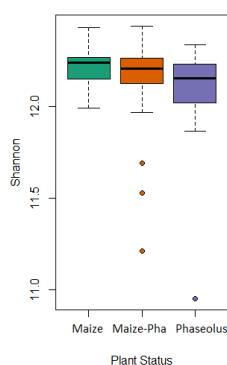
## Supplementary material

**Table S1. Physical/chemical characteristics of the soil.** The ratings are expressed according to the classifications published by the United States Department of Agriculture and the Italian Association of Public Agrochemical Laboratories. Soil analyses were performed by the Regional Agrochemical Centre Analysis Laboratory using standard operational procedures.

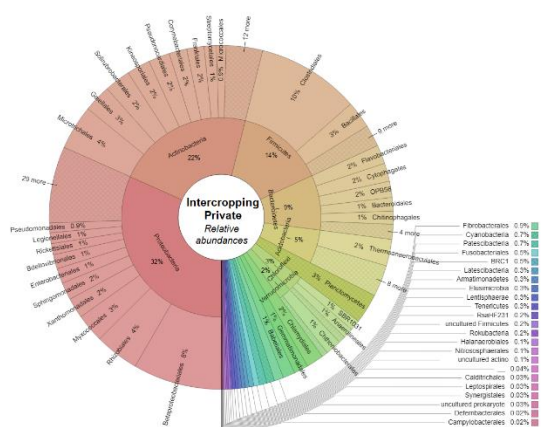
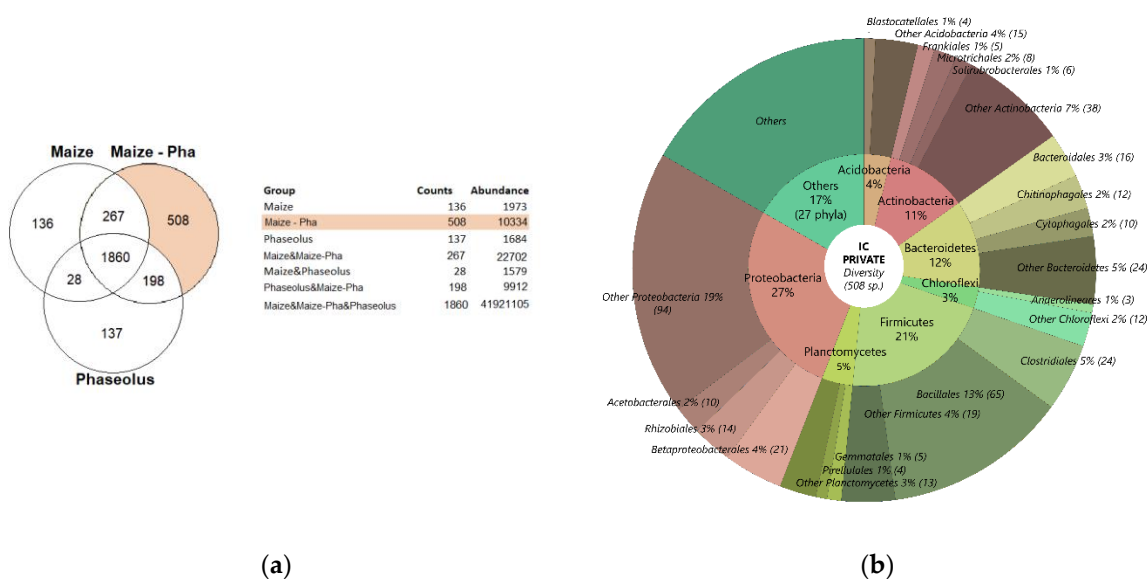
Physiochemical properties of the soils		Ratings
pH	8.22	alkaline
Soil texture		tending clayey
Sand (g/Kg)	178	
Silt (g/Kg)	425	
Clay (g/Kg)	397	
Active limestone (g/Kg)	126	very high
Total limestone (g/Kg)	234	moderately calcareous
Assimilable phosphorus (mg/Kg)	9.5	low
Exchangeable sodium (mg/Kg)	40	
Exchangeable calcium (mg/Kg)	5467	
Cation exchange capacity (meq/100g)	23.5	high
Assimilable iron (mg/Kg)	8.6	low
Assimilable manganese (mg/Kg)	3.3	very low
Assimilable zinc (mg/Kg)	0.43	low
Assimilable copper (mg/Kg)	3.4	medium
Soluble boron (mg/Kg)	0.25	low
C/N	9.3	regular
Organic matter		low
Total nitrogen	1.05	medium
Mg/K	6.1	
Exchangeable magnesium (mg/Kg)	389	high
Exchangeable phosphorus (mg/Kg)	204	high

**Table S2. Anova on Alpha-diversity indexes for Plant status and Cropping system.** Results of Anova applied to Chao1 and Shannon index values to test the effect of Cropping System and Plant Status.

Chao1	Df	Sum Sq	Mean Sq	F value	Pr(>F)
Year	1	178667	178667	0.549	0.461
Replicates	2	299654	149827	0.46	0.633
Cropping system	1	134212	134212	0.412	0.523
Plant status	1	1349759	1349759	4.144	0.045*
Residuals	89	28988579	325714		
Shannon	Df	Sum Sq	Mean Sq	F value	Pr(>F)
Year	1	0.07	0.069	1.666	0.200
Replicates	2	0.089	0.045	1.072	0.347
Cropping system	1	0.009	0.009	0.216	0.643
Plant status	1	0.177	0.177	4.245	0.042*
Residuals	89	3.715	0.042		



**Figure S1. Means of Shannon diversity index for Plant Status.** Boxplots of Shannon diversity index values for means of maize and beans in SC and for the IC condition (Plant Status).

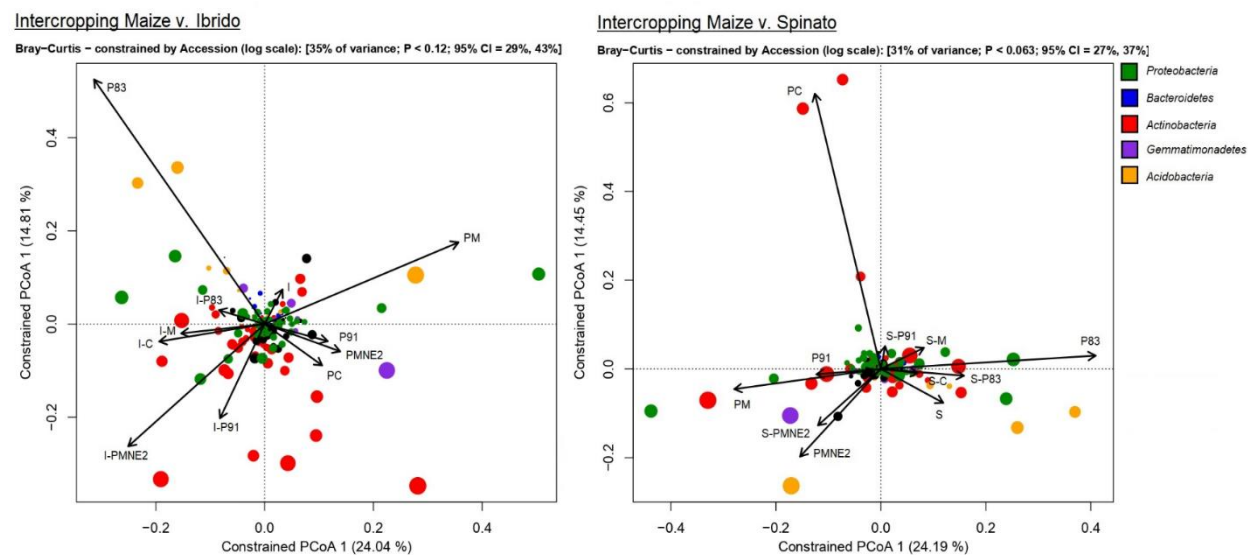


(c)

**Figure S2. Diversity and composition of private bacterial members of IC condition.** (A) Venn diagram of bacterial species belonging to each subset with number of taxa and total reads for each subset. (B) Doughnut plot of total bacterial diversity for private members of IC condition with percentages of phyla in the inner circle and orders in the outer circle. (C) Krona plot of relative abundances of the bacterial members that are private of the IC condition.

**Table S3. Multi-factorial Anova on Chao1 index to test the effect of genotypes combinations in IC.** Results of the multi-factorial Anova applied to Chao1 diversity index values.

	Df	Sum Sq	Mean Sq	F value	Pr(>F)
Year	1	22171	22171	0.069	0.793
Replicates	2	771458	385729	1.202	0.305
Environment	4	1461652	365413	1.138	0.343
Replicates:Environment	8	3101719	387715	1.208	0.303
Environment:Accession	23	14361557	624416	1.945	0.013 *
Year:Replicates	2	752579	376290	1.172	0.314
Year:Replicates:Environment	12	5332940	444412	1.384	0.187
Year:Replicates:Environment:Accession	49	14752634	301074	0.938	0.591
Residuals	95	30495176	321002		



**Figure S3. CPcoA for IC combinations with maize I and S.** Constrained Principal Coordinate analysis (PcoA) and biplot of phyla scores of PcoA analysis based on Bray-Curtis distances of rhizosphere samples IC systems of S and I, constrained by “Accessions” including maize and beans in SC and different IC combination with the maize line. The percentage of variation explained by each axis refers to the fraction of the total variance of the data explained by the constrained factor (35% and 31% for I and S systems, respectively). CAP analysis failed to show a significant effect on sample clustering by “Accessions” ( $p < 0.12$  and  $p < 0.063$  in I and S, respectively). The arrows point to the centroid of the constrained factor.

Circle size depicts the relative abundance of phyla (log scale) that were more contributing in clustering samples. Colors illustrate different phyla as reported in the legend.

**Table S4. p-values and LDA scores of LefSE analysis.** Table showing results derived by the Linear discriminant analysis Effect Size (LEfSe) for the bacterial communities at genus level identifying biomarkers between Maize and Phaseolus in SC and Maize – Phaseolus in IC.

Taxa	Group	pvalue	LDA
k_Bacteria p_Proteobacteria c_Gammaproteobacteria o_Betaproteobacteriales	Maize	0.04011	3.986829
k_Bacteria p_Proteobacteria c_Gammaproteobacteria o_Betaproteobacteriales f_Burkholderiaceae	Maize	0.04692	3.946383
k_Bacteria p_Proteobacteria c_Gammaproteobacteria o_Betaproteobacteriales f_Nitrosomonadaceae	Phaseolus	0.00342	3.891149
k_Bacteria p_Proteobacteria c_Gammaproteobacteria o_Betaproteobacteriales f_Nitrosomonadaceae g_MND1	Phaseolus	0.00484	3.868153
k_Bacteria p_Actinobacteria c_Actinobacteria	Maize-Pha	0.01247	3.839024
k_Bacteria p_Actinobacteria c_Actinobacteria o_Propionibacteriales f_Nocardioidaceae g_Nocardioides	Maize-Pha	0.00349	3.528047
k_Bacteria p_Actinobacteria c_Actinobacteria o_Propionibacteriales	Maize-Pha	0.00615	3.495445
k_Bacteria p_Actinobacteria c_Actinobacteria o_Propionibacteriales f_Nocardioidaceae	Maize-Pha	0.00615	3.495445
k_Bacteria p_Actinobacteria c_Actinobacteria o_Streptomycetales	Maize-Pha	0.02654	3.486422
k_Bacteria p_Actinobacteria c_Actinobacteria o_Streptomycetales f_Streptomycetaceae	Maize-Pha	0.02654	3.486422
k_Bacteria p_Actinobacteria c_Actinobacteria o_Streptomycetales f_Streptomycetaceae g_Streptomyces	Maize-Pha	0.02654	3.486422
k_Bacteria p_Proteobacteria c_Deltaproteobacteria o_Myxococcales f_Haliangiaceae	Phaseolus	0.04737	3.472508
k_Bacteria p_Proteobacteria c_Deltaproteobacteria o_Myxococcales f_Haliangiaceae g_Haliangium	Phaseolus	0.04737	3.472508
k_Bacteria p_Actinobacteria c_Actinobacteria o_Micrococcales	Maize	0.01431	3.411162
k_Bacteria p_Verrucomicrobia	Maize	0.02435	3.293216
k_Bacteria p_Verrucomicrobia c_Verrucomicrobiae	Maize	0.02435	3.293216
k_Bacteria p_Verrucomicrobia c_Verrucomicrobiae o_Pedosphaerales	Maize	0.02332	3.199208
k_Bacteria p_Verrucomicrobia c_Verrucomicrobiae o_Pedosphaerales f_Pedosphaeraceae	Maize	0.02332	3.199208
k_Bacteria p_Proteobacteria c_Deltaproteobacteria o_NB1-j	Phaseolus	0.02816	3.190599
k_Bacteria p_Actinobacteria c_Actinobacteria o_Pseudonocardiales f_Pseudonocardiaceae g_Lechevalieria	Maize	0.01147	3.162907
k_Bacteria p_Actinobacteria c_Actinobacteria o_Micrococcales f_Micrococcaceae	Maize	0.00929	3.072155
k_Bacteria p_Entotheonellaeota	Maize-Pha	0.01402	3.058515
k_Bacteria p_Entotheonellaeota c_Entotheonellia	Maize-Pha	0.01402	3.058515
k_Bacteria p_Entotheonellaeota c_Entotheonellia o_Entotheonellales f_Entotheonellaceae	Maize-Pha	0.01402	3.058515
k_Bacteria p_Entotheonellaeota c_Entotheonellia o_Entotheonellales	Maize-Pha	0.01402	3.058515
k_Bacteria p_Actinobacteria c_Actinobacteria o_Micrococcales f_Microbacteriaceae g_Agromyces	Maize-Pha	0.02815	3.017008
k_Bacteria p_Actinobacteria c_Actinobacteria o_Micrococcales f_Microbacteriaceae	Maize-Pha	0.02815	3.017008
k_Bacteria p_Proteobacteria c_Gammaproteobacteria o_Pseudomonadales	Maize	0.02981	3.016641
k_Bacteria p_Proteobacteria c_Gammaproteobacteria o_Pseudomonadales f_Pseudomonadaceae g_Pseudomonas	Maize	0.02981	3.016641
k_Bacteria p_Proteobacteria c_Gammaproteobacteria o_Pseudomonadales f_Pseudomonadaceae	Maize	0.02981	3.016641
k_Bacteria p_Actinobacteria c_Actinobacteria o_Corynebacteriales	Maize-Pha	0.04192	2.963743
k_Bacteria p_Verrucomicrobia c_Verrucomicrobiae o_Verrucomicrobiales f_Rubritaleaceae	Maize	0.00047	2.93693
k_Bacteria p_Verrucomicrobia c_Verrucomicrobiae o_Verrucomicrobiales	Maize	0.00047	2.93693
k_Bacteria p_Verrucomicrobia c_Verrucomicrobiae o_Verrucomicrobiales f_Rubritaleaceae g_Luteolibacter	Maize	0.00047	2.93693
k_Bacteria p_Proteobacteria c_Deltaproteobacteria o_Myxococcales f_Archangiaceae	Maize-Pha	0.04081	2.734768
k_Bacteria p_Actinobacteria c_Actinobacteria o_Micrococcales f_Intrasporangiaceae	Maize-Pha	0.01	2.733414
k_Bacteria p_Cyanobacteria c_Oxyphotobacteria o_Chloroplast f_Phaseolus acutifolius (tepary bean)	Phaseolus	0.01608	2.604061
k_Bacteria p_Cyanobacteria c_Oxyphotobacteria o_Chloroplast f_Phaseolus acutifolius (tepary bean) g_Phaseolus acutifolius (tepary bean)	Phaseolus	0.01608	2.604061
k_Bacteria p_Cyanobacteria c_Oxyphotobacteria o_Chloroplast f_Phaseolus acutifolius (tepary bean) g_Phaseolus acutifolius (tepary bean) s_Phaseolus acutifolius (tepary bean)	Phaseolus	0.01608	2.604061









## Comparison in Maize v. Ibrido



**Figure S4. Bacterial genera differentially expressed in IC combinations.** Log2 Fold Changes and average expressions of bacterial genera differentially expressed obtained with the FitZig model applied at “Accession” level on log transformed counts for each “Environment” (A. Biancoperla, B. Ottofile, C. Spinato, D. Ibrido). Bacterial genera are grouped by phyla and all genera differentially expressed are reported. Intersection plots showing genera differentially expressed and up and down regulated in each comparison are reported. Blue dots are reported in correspondence of bacterial genera that properly belong to the intercropping system.

### IC combinations with Maize Ottofile

