

Table S1. Numbers of bacterial sequences and OTUs identified by 16S rRNA gene sequencing

Samples	Planting pattern	Number of raw sequences	Number of final sequences	Number of OTUs
A13	Maize	39469	19486	4031
A14	Maize	34817	26024	2558
A15	Maize	41221	21692	3503
A16	Maize	39801	34770	1495
A17	Mushroom	40183	31616	1204
A18	Mushroom	38418	33949	1030
A19	Mushroom	38265	33724	940
A20	Mushroom	36860	30459	895
A21	Intercropping	36951	31085	806
A22	Intercropping	39826	34412	730
A23	Intercropping	39831	30123	696
A24	Intercropping	37171	32001	631

Table S2. Pearson's correlation coefficients between relative abundances of dominant bacterial phyla and soil properties

	TN	AN	NO ₃ ⁻ -N	NH ₄ ⁺ -N	SOM	Chao1 index	Shanno n index	Proteob acteria	Chlorof lexi	Acidob acteria	Actinob acteria	Firmicu tes	Gemma timona detes	Cyanob acteria	Sacchar ibacteri a	Bactero idetes	Nitrosp irae	Plancto mycete s	Verruc omicro bia	Parcub acteria
pH	0.303	-0.817**	-0.914**	-0.900**	0.537	0.913**	0.788**	-0.458	0.869**	0.845**	0.082	-0.394	0.384	0.296	0.209	0.483	0.629*	0.842**	0.789**	0.780**
TN		-0.103	-0.112	-0.004	-0.053	0.100	0.349	0.387	0.150	0.301	0.426	-0.496	0.563	-0.372	0.216	-0.021	0.345	0.166	-0.058	0.041
AN			0.894**	0.900**	-0.673*	-0.809**	-0.794**	0.331	0-.821**	-0.643*	-0.143	0.499	-0.376	-0.519	-0.461	-0.714**	-0.257	-0.621*	-0.628*	-0.640*
NO ₃ ⁻ -N				0.989**	-0.618*	-0.866**	-0.789**	0.543	-0.839**	-0.735**	-0.123	0.334	-0.357	-0.421	-0.318	-0.617*	-0.400	-0.729**	-0.718**	-0.727**
NH ₄ ⁺ -N					-0.632*	-0.862**	-0.737**	0.614*	-0.836**	-0.713**	-0.017	0.260	-0.268	-0.446	-0.332	-0.646*	-0.370	-0.715**	-0.726**	-0.732**
SOM						0.634*	0.663*	-0.187	0.705*	0.478	0.238	-0.434	0.241	-0.009	0.553	0.483	0.382	0.643*	0.560	0.536
Chao1 index							0.857**	-0.377	0.958**	0.918**	0.188	-0.498	0.452	0.389	0.041	0.324	0.693*	0.913**	0.840**	0.839**
Shannon index								0.024	0.898**	0.773**	0.585*	-0.816**	0.734**	0.279	0.169	0.420	0.580*	0.846**	0.703*	0.756**
Proteobacteria									-0.313	-0.320	0.676*	-0.577*	0.430	-0.253	-0.087	-0.259	-0.144	-0.203	-0.412	-0.372
Chloroflexi										0.886**	0.225	-0.563	0.515	0.296	0.120	0.376	0.713**	0.891**	0.836**	0.897**
Acidobacteria											0.159	-0.472	0.469	0.235	-0.030	0.080	0.789**	0.855**	0.719**	0.715**
Actinobacteria												-0.818**	0.846**	-0.044	-0.010	-0.037	0.198	0.325	0.027	0.096
Firmicutes													-0.832**	-0.140	-0.121	-0.195	-0.382	-0.568	-0.328	-0.372
Gemmatimonadetes														0.037	-0.012	0.003	0.458	0.492	0.188	0.377
Cyanobacteria															-0.228	0.265	-0.121	0.175	0.410	0.226
Saccharibacteria																0.672*	-0.265	-0.012	-0.139	-0.099
Bacteroidetes																	-0.240	0.241	0.313	0.355
Nitrospirae																		0.793**	0.692*	0.706*
Planctomycetes																			0.849**	0.809**
Verrucomicrobia																				0.878**

Notes: Significance codes: '***' and '**' indicate significant difference at $P < 0.01$ and 0.05 level, respectively.

Table S3. The environmental vectors onto two ordination of redundancy analysis

Environmental variables	RDA1	RDA2	r ²	Pr(>r)
pH	0.902	-0.431	0.708	0.006**
TN	-0.392	-0.920	0.104	0.622
AN	-0.995	-0.103	0.384	0.118
NO ₃ ⁻ -N	-0.984	0.178	0.527	0.042*
NH ₄ ⁺ -N	-0.989	0.146	0.545	0.033*
SOM	0.330	-0.944	0.209	0.349

Notes: The projections of points onto vectors have maximum correlation with corresponding environmental variables, and the factors show the averages of factor levels. Significance codes: '***' and '**' indicate significant difference at $P < 0.01$ and 0.05 level, respectively. The number of permutations is 1000.

Table S4. The analysis of variance of the KEGG metabolic pathway

Metabolic pathway	Treatments		
	Maize	Mushroom	Intercropping
Xenobiotics	0.0345a	0.0332a	0.0336a
Nucleotide	0.0318a	0.0314a	0.0314a
Terpenoids and polyketides	0.0198b	0.0209a	0.0203ab
Amino acid	0.1020a	0.1022a	0.1051a
Cofactors and vitamins	0.0408b	0.0449a	0.0416ab
Lipid	0.0355a	0.0348a	0.0362a
Glycan	0.0198b	0.0213a	0.0213a
Enzyme families	0.0200a	0.0220a	0.0204a
Energy	0.0551b	0.0662a	0.0564b
Carbohydrate	0.0916b	0.0956ab	0.0995a
Other secondary metabolites	0.0087b	0.0106a	0.0104a

Note: Different lowercases indicate significant difference at $P < 0.05$ level.