

Supplementary Material for

Changes of microbiome in response to sugars in a wilt pathogen-infested soil

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Table S1 High quality reads number.

Sample	High quality reads number
T0-CK	18,162±1,394
T0-FON	22,020±1,171
Subtotal	120,547
1d-CK	21,581±935
1d-Gluc	31,624±287
1d-Fruc	28,374±871
1d-Suc	26,333±2,357
1d-Mal	23,402±878
1d-FON	25,349±2,883
1d-FON+Gluc	29,001±11,264
1d-FON+Fruc	22,412±1,201
1d-FON+Suc	22,103±1,412
1d-FON+Mal	24,863±2,987
Subtotal	765,132
3d-CK	19,194±316
3d-Gluc	24,024±2,253
3d-Fruc	23,902±1,144
3d-Suc	26,003±965
3d-Mal	22,574±798
3d-FON	19,895±1,162
3d-FON+Gluc	30,718±5,035
3d-FON+Fruc	28,035±1,962
3d-FON+Suc	21,221±725
3d-FON+Mal	20,829±247
Subtotal	709,186
5d-CK	17,273±321
5d-Gluc	21,281±2,704
5d-Fruc	22,130±10,251
5d-Suc	25,252±3,988
5d-Mal	22,441±4,243
5d-FON	29,994±1,883
5d-FON+Gluc	23,973±4,959
5d-FON+Fruc	24,739±2,665
5d-FON+Suc	21,893±4,621
5d-FON+Mal	28,549±4,118
Subtotal	712,579
9d-CK	18,431±2,171
9d-Gluc	22,904±1,730
9d-Fruc	20,442±1,352
9d-Suc	21,853±1,830
9d-Mal	28,832±2,885
9d-FON	24,318±2,554

9d-FON+Gluc	26,296±1,484
9d-FON+Fruc	26,193±661
9d-FON+Suc	19,823±1,992
9d-FON+Mal	18,936±1,931
Subtotal	684,082
<hr/>	
42d-CK	17,708±193
42d-Gluc	19,977±1,251
42d-Fruc	21,917±3,590
42d-Suc	19,765±349
42d-Mal	17,766±804
42d-FON	21,295±1,920
42d-FON+Gluc	26,829±4,390
42d-FON+Fruc	26,711±2,690
42d-FON+Suc	27,172±1,726
42d-FON+Mal	27,576±1,034
Subtotal	680,142
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Total	3,671,668
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Mean	23,536
Max	41,966
Min	10,295
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CK, Gluc, Fruc, and Mal indicate the soil with the addition with H₂O, glucose, fructose, sucrose, and maltose solutions, respectively. FON indicates the soil was inoculated with *Fusarium oxysporum* f. sp. *niveum* (FON). FON+Gluc, FON+Fruc, FON+Suc, FON+Mal indicate that the soil was subjected to FON inoculation and supplied with glucose, fructose, sucrose, maltose solutions, respectively. T0 denotes zero time and 1d, 3d, 5d, 9d, and 42d indicate that the samples were collected from the soil microcosms after 1 day, 3 days, 5 days, 9 days, and 42 days of incubation. Data shown are the mean value of three replicates ± the standard deviation. Min and Max represent minimum and maximum sequence reads number, respectively.

Table S2 Significant tests using three statistical methods to assess the effects of sugars on the bacterial community structure.

Compared group	adonis ^a		ANOSIM ^b		MRPP ^c	
	<i>F</i>	<i>P</i> ^d	<i>R</i>	<i>P</i> ^d	δ	<i>P</i> ^d
1d						
Sugar effect in Low-FON soil						
CK vs. Gluc	31.259	0.039	1	0.040	0.216	0.038
CK vs. Fruc	38.570	0.042	1	0.041	0.201	0.039
CK vs. Suc	42.304	0.043	1	0.039	0.203	0.039
CK vs. Mal	32.401	0.041	1	0.038	0.214	0.043
Gluc vs. Fruc	2.490	0.173	0.667	0.164	0.150	0.115
Gluc vs. Suc	4.065	0.148	0.971	0.105	0.152	0.118
Gluc vs. Mal	4.660	0.152	0.971	0.103	0.164	0.109
Fruc vs. Suc	4.744	0.159	0.963	0.108	0.137	0.113
Fruc vs. Mal	7.896	0.150	0.971	0.109	0.149	0.105
Suc vs. Mal	4.833	0.141	0.971	0.111	0.151	0.121
Sugar effect in High-FON soil						
FON vs. FON+Gluc	26.846	0.039	1	0.034	0.239	0.041
FON vs. FON+Fruc	34.892	0.042	1	0.043	0.206	0.039
FON vs. FON+Suc	45.513	0.037	1	0.043	0.191	0.041
FON vs. FON+Mal	28.550	0.038	1	0.042	0.214	0.043
FON+Gluc vs. FON+Fruc	1.726	0.201	0.407	0.185	0.193	0.114
FON+Gluc vs. FON+Suc	3.333	0.162	0.556	0.172	0.178	0.107
FON+Gluc vs. FON+Mal	6.224	0.143	0.982	0.101	0.200	0.102
FON+Fruc vs. FON+Suc	3.579	0.157	0.963	0.103	0.145	0.115
FON+Fruc vs. FON+Mal	7.328	0.160	0.982	0.110	0.168	0.109
FON+Suc vs. FON+Mal	8.808	0.138	0.982	0.113	0.153	0.117
3d						
Sugar effect in Low-FON soil						
CK vs. Gluc	27.477	0.040	1	0.039	0.250	0.038
CK vs. Fruc	24.278	0.042	1	0.044	0.245	0.035
CK vs. Suc	25.743	0.040	1	0.046	0.241	0.039
CK vs. Mal	16.677	0.044	1	0.037	0.284	0.044
Gluc vs. Fruc	1.593	0.226	0.074	0.322	0.215	0.116
Gluc vs. Suc	1.259	0.284	-0.056	0.702	0.211	0.302
Gluc vs. Mal	1.648	0.203	0.037	0.502	0.254	0.182
Fruc vs. Suc	1.239	0.304	0.148	0.201	0.206	0.295
Fruc vs. Mal	1.542	0.218	0.185	0.205	0.249	0.230
Suc vs. Mal	0.946	0.381	0	0.395	0.245	0.511
Sugar effect in High-FON soil						
FON vs. FON+Gluc	24.872	0.034	1	0.039	0.249	0.038
FON vs. FON+Fruc	32.228	0.044	1	0.037	0.218	0.040
FON vs. FON+Suc	42.934	0.035	1	0.042	0.202	0.038
FON vs. FON+Mal	30.837	0.044	1	0.038	0.220	0.045

FON+Gluc vs. FON+Fruc	1.018	0.380	0.148	0.336	0.204	0.413
FON+Gluc vs. FON+Suc	2.613	0.168	0.482	0.171	0.188	0.102
FON+Gluc vs. FON+Mal	0.902	0.618	0.148	0.196	0.206	0.394
FON+Fruc vs. FON+Suc	5.764	0.143	0.963	0.108	0.157	0.110
FON+Fruc vs. FON+Mal	1.977	0.191	0.741	0.144	0.175	0.109
FON+Suc vs. FON+Mal	4.184	0.157	0.982	0.112	0.159	0.102

5d

Sugar effect in Low-FON soil

CK vs. Gluc	17.135	0.040	1	0.044	0.284	0.041
CK vs. Fruc	24.520	0.038	1	0.040	0.227	0.042
CK vs. Suc	29.746	0.036	1	0.038	0.236	0.039
CK vs. Mal	18.194	0.042	1	0.043	0.274	0.039
Gluc vs. Fruc	0.528	0.877	-0.333	0.788	0.252	0.560
Gluc vs. Suc	0.841	0.573	0.074	0.300	0.257	0.473
Gluc vs. Mal	0.594	0.526	-0.185	0.788	0.295	0.512
Fruc vs. Suc	1.398	0.198	0.167	0.407	0.195	0.198
Fruc vs. Mal	0.766	0.691	-0.083	0.707	0.241	0.525
Suc vs. Mal	1.074	0.403	0.111	0.312	0.248	0.389

Sugar effect in High-FON soil

FON vs. FON+Gluc	17.117	0.039	1	0.036	0.244	0.040
FON vs. FON+Fruc	33.833	0.040	1	0.045	0.222	0.040
FON vs. FON+Suc	14.810	0.035	1	0.048	0.264	0.046
FON vs. FON+Mal	12.467	0.040	1	0.034	0.308	0.039
FON+Gluc vs. FON+Fruc	4.035	0.141	0.917	0.115	0.200	0.116
FON+Gluc vs. FON+Suc	1.411	0.300	0.250	0.186	0.251	0.182
FON+Gluc vs. FON+Mal	0.648	0.509	0	0.526	0.303	0.409
FON+Fruc vs. FON+Suc	7.321	0.146	0.963	0.107	0.228	0.102
FON+Fruc vs. FON+Mal	1.115	0.504	0.074	0.315	0.272	0.401
FON+Suc vs. FON+Mal	1.557	0.287	0.222	0.304	0.314	0.298

9d

Sugar effect in Low-FON soil

CK vs. Gluc	22.415	0.045	1	0.034	0.260	0.042
CK vs. Fruc	33.059	0.039	1	0.040	0.212	0.038
CK vs. Suc	18.654	0.042	1	0.041	0.263	0.039
CK vs. Mal	21.778	0.043	1	0.039	0.258	0.037
Gluc vs. Fruc	0.919	0.611	0.259	0.199	0.191	0.201
Gluc vs. Suc	1.502	0.188	0.037	0.420	0.243	0.195
Gluc vs. Mal	0.596	0.691	-0.185	0.798	0.237	0.693
Fruc vs. Suc	3.363	0.152	0.556	0.173	0.194	0.106
Fruc vs. Mal	1.470	0.299	0.222	0.306	0.189	0.282
Suc vs. Mal	1.167	0.416	-0.111	0.807	0.241	0.389

Sugar effect in High-FON soil

FON vs. FON+Gluc	25.529	0.040	1	0.036	0.229	0.034
FON vs. FON+Fruc	14.921	0.036	1	0.044	0.283	0.044
FON vs. FON+Suc	11.946	0.040	1	0.040	0.315	0.042
FON vs. FON+Mal	16.735	0.038	1	0.034	0.276	0.042

FON+Gluc vs. FON+Fruc	0.939	0.646	0.111	0.295	0.240	0.413
FON+Gluc vs. FON+Suc	1.147	0.289	0.037	0.433	0.271	0.289
FON+Gluc vs. FON+Mal	0.973	0.497	-0.037	0.623	0.232	0.442
FON+Fruc vs. FON+Suc	0.819	0.402	-0.185	0.807	0.325	0.611
FON+Fruc vs. FON+Mal	0.740	0.627	-0.074	0.600	0.287	0.605
FON+Suc vs. FON+Mal	0.554	0.790	-0.259	1	0.318	0.808

42d

Sugar effect in Low-FON soil

CK vs. Gluc	9.732	0.042	1	0.043	0.272	0.039
CK vs. Fruc	10.849	0.037	1	0.043	0.288	0.041
CK vs. Suc	11.157	0.038	1	0.042	0.264	0.043
CK vs. Mal	11.267	0.046	1	0.041	0.249	0.045
Gluc vs. Fruc	1.729	0.207	0.333	0.204	0.284	0.185
Gluc vs. Suc	2.298	0.182	0.926	0.111	0.260	0.107
Gluc vs. Mal	2.654	0.167	0.852	0.116	0.244	0.108
Fruc vs. Suc	1.145	0.314	0.296	0.188	0.276	0.215
Fruc vs. Mal	2.061	0.184	0.667	0.162	0.261	0.116
Suc vs. Mal	1.835	0.195	0.741	0.135	0.237	0.115

Sugar effect in High-FON soil

FON vs. FON+Gluc	8.892	0.040	1	0.036	0.268	0.036
FON vs. FON+Fruc	8.584	0.043	1	0.036	0.266	0.039
FON vs. FON+Suc	11.930	0.049	1	0.034	0.239	0.041
FON vs. FON+Mal	12.289	0.045	1	0.042	0.240	0.041
FON+Gluc vs. FON+Fruc	1.084	0.509	-0.037	0.598	0.279	0.490
FON+Gluc vs. FON+Suc	1.291	0.197	0.370	0.193	0.252	0.119
FON+Gluc vs. FON+Mal	1.447	0.289	0.407	0.183	0.253	0.117
FON+Fruc vs. FON+Suc	1.542	0.184	0.482	0.177	0.251	0.109
FON+Fruc vs. FON+Mal	1.664	0.111	0.556	0.174	0.251	0.113
FON+Suc vs. FON+Mal	1.758	0.206	0.963	0.112	0.224	0.116

The soil inoculated or un-inoculated with *F. oxysporum* f. sp. *niveum* (FON) was referred to as High-FON soil or Low-FON soil, respectively. CK, Gluc, Fruc, Suc, and Mal denote the soil with the addition of H₂O, glucose, fructose, sucrose, and maltose solutions, respectively. FON indicates that the soil was subjected to FON inoculation. FON+Gluc, FON+Fruc, FON+Suc, and FON+Mal denote that the soil was not only inoculated with FON but also supplied with glucose, fructose, sucrose, and maltose solutions, respectively. T0 denotes zero time, and 1d, 3d, 5d, 9d, and 42d denote samples collected after 1 day, 3 days, 5 days, 9 days, and 42 days of microcosm incubation. These three tests are non-parametric multivariate analyses based on dissimilarities between samples.

^a Permutational multivariate analysis of variance using distance matrices. Significances were obtained with *F*-tests based on sequential sums of squares from permutations of the raw data.

^b Analysis of similarities. R was obtained based on the difference in the mean ranks between groups and within groups. The significance was determined by permuting the grouping vector to obtain the empirical distribution of R under the null model.

^c Multi-response permutation procedure. The δ is the overall weighted mean of within-group means of the pairwise dissimilarities among sampling units. The significance test indicates the fraction of permuted δ that is less than the observed δ .

^d Bonferroni correction of the P value was applied.

Table S3 Network topological properties.

Treatment	Threshold	Total nodes	Total links	Average degree (avgK)	Average clustering coefficient (avgCC)	Average path distance (GD)	Density (D)	Harmonic geodesic distance (HD)	Positive link %	R square of power-law
0-42d-CK	0.80	368	1434	7.804	0.244	3.092	0.021	2.823	87%	0.89
1d-Sugar	0.80	248	1795	14.476	0.360	2.480	0.059	2.250	75%	0.77
3d-Sugar	0.80	266	1877	14.113	0.345	2.492	0.053	2.274	77%	0.80
5d-Sugar	0.80	261	2377	18.215	0.347	2.343	0.070	2.139	79%	0.72
9d-Sugar	0.80	288	2264	15.722	0.364	2.445	0.055	2.238	76%	0.72
42d-Sugar	0.75	387	4897	25.307	0.353	2.230	0.066	2.068	81%	0.77
0-42d-FON	0.80	330	994	6.024	0.162	3.330	0.018	3.028	80%	0.83
1d-FON-Sugar	0.80	263	1973	15.004	0.369	2.468	0.057	2.249	76%	0.79
3d-FON-Sugar	0.80	276	2592	18.783	0.347	2.308	0.068	2.117	82%	0.72
5d-FON-Sugar	0.80	289	2985	20.657	0.358	2.279	0.072	2.092	69%	0.79
9d-FON-Sugar	0.80	323	2783	17.232	0.386	2.441	0.054	2.240	79%	0.78
42d-FON-Sugar	0.80	407	4836	23.764	0.408	2.295	0.059	2.123	85%	0.79

The designations CK and Sugar indicate that the soil was supplied with water and sugars (i.e., glucose, fructose, sucrose, and maltose), respectively. The designation FON represents the soil inoculated with FON. The 0, 1d, 3d, 5d, 9d, and 42d indicate that the samples were collected after 0 day (i.e., zero time), 1 day, 3 days, 5 days, 9 days, and 42 days of microcosm incubation, respectively.

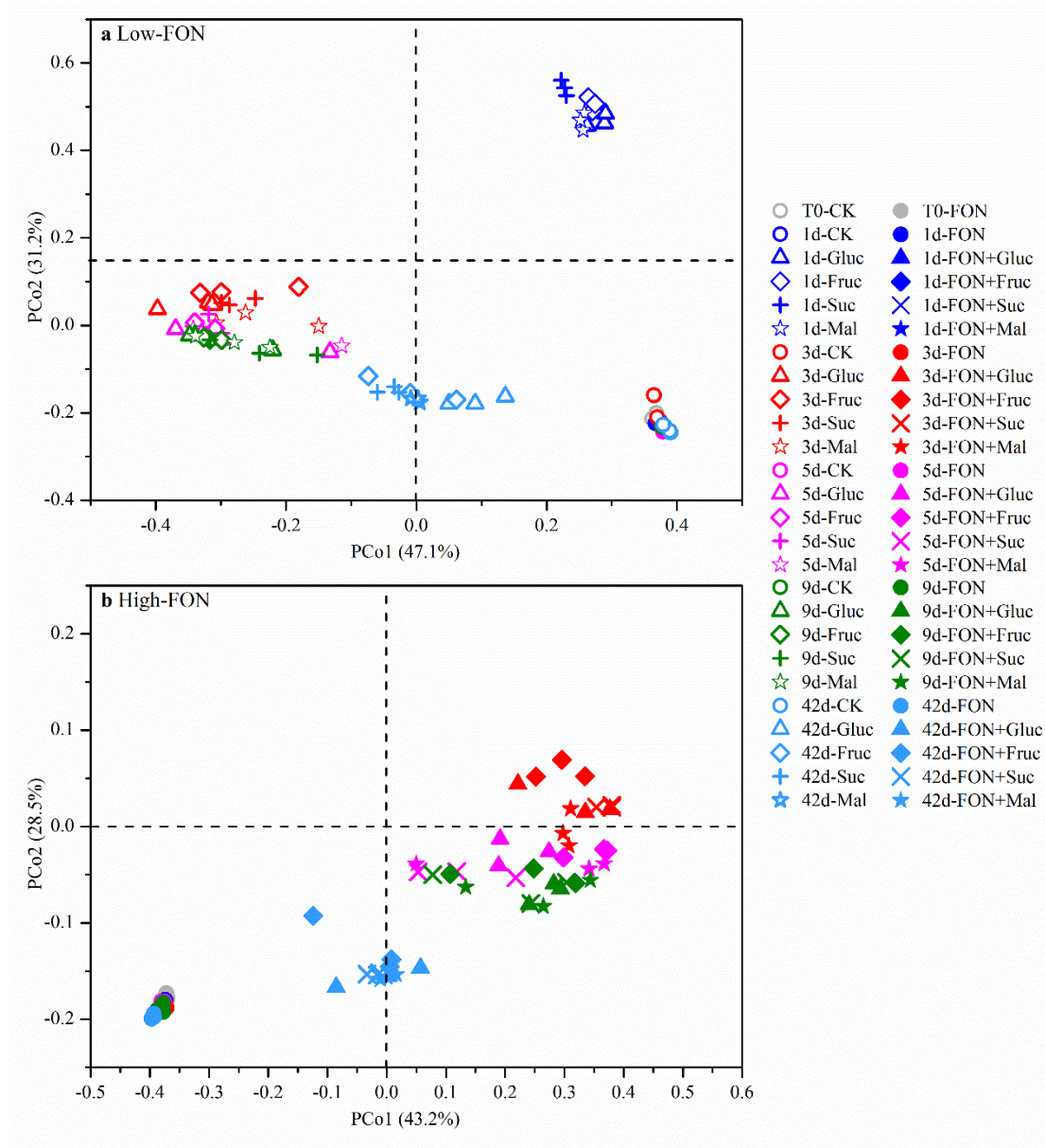


Fig. S1 Principal coordinates analysis (PCoA) of bacterial communities in Low-FON (a) and High-FON (b) soils. The Low-FON soil denotes the FON-uninoculated soil and the High-FON soil denotes the FON-inoculated soil. The percent in bracket represents the proportion of variation explained by each ordination axis. All other designations are the same as those in Table S1.

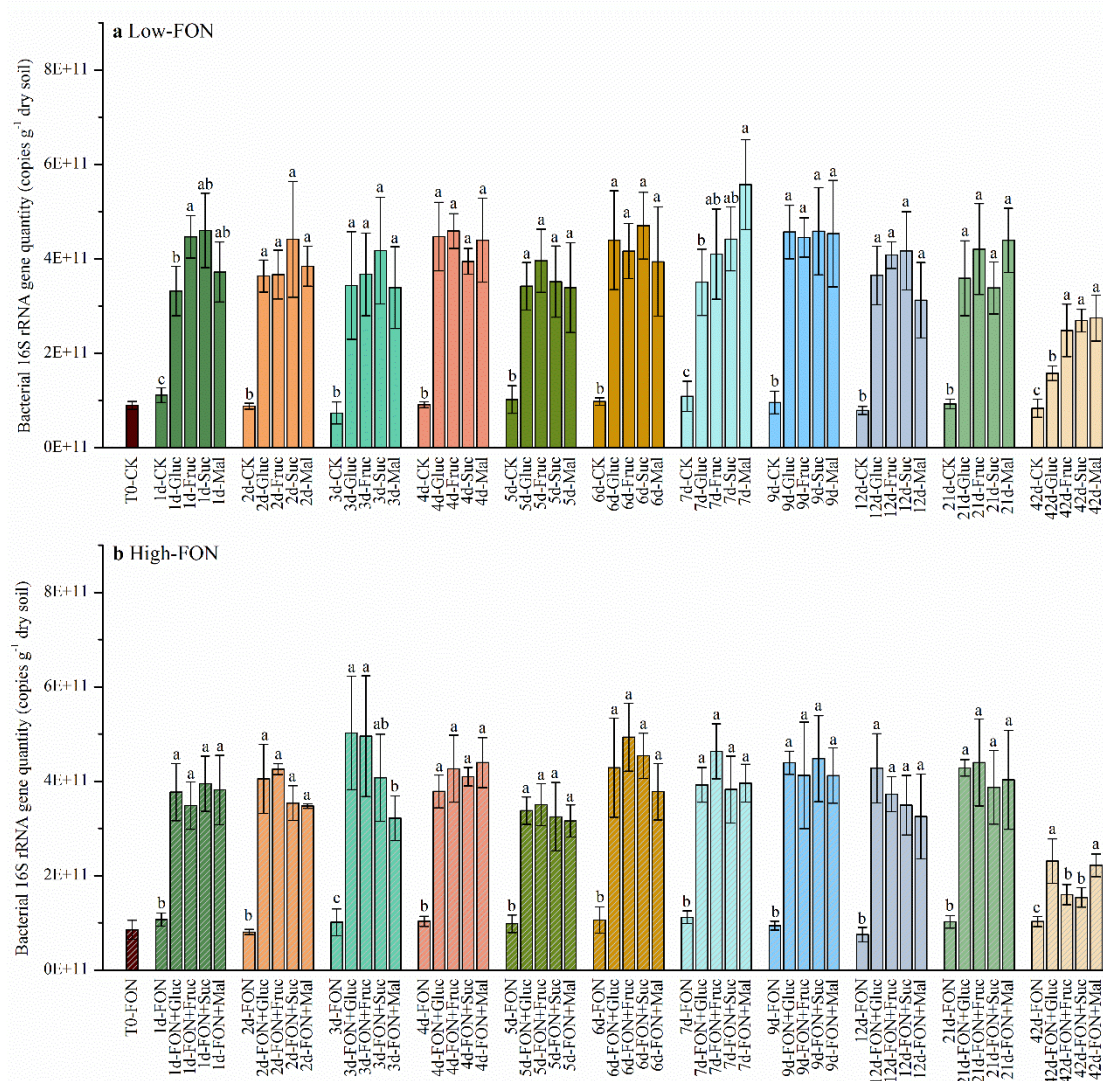


Fig. S2 Bacterial 16S rRNA gene copy number in Low-FON and High-FON soils determined by real-time PCR. The Low-FON soil represents the FON-uninoculated soil and the High-FON soil represents the FON-inoculated soil. T0 represents zero time and 1d, 2d, 3d, ...42d represent samples collected after 1 day, 2 days, 3 days, ...42 days of incubation. Different letters represent significant differences by Duncan's multiple range test ($P < 0.05$). The error bars represent the standard deviation of the means. All the other designations are the same as those in Table S1.

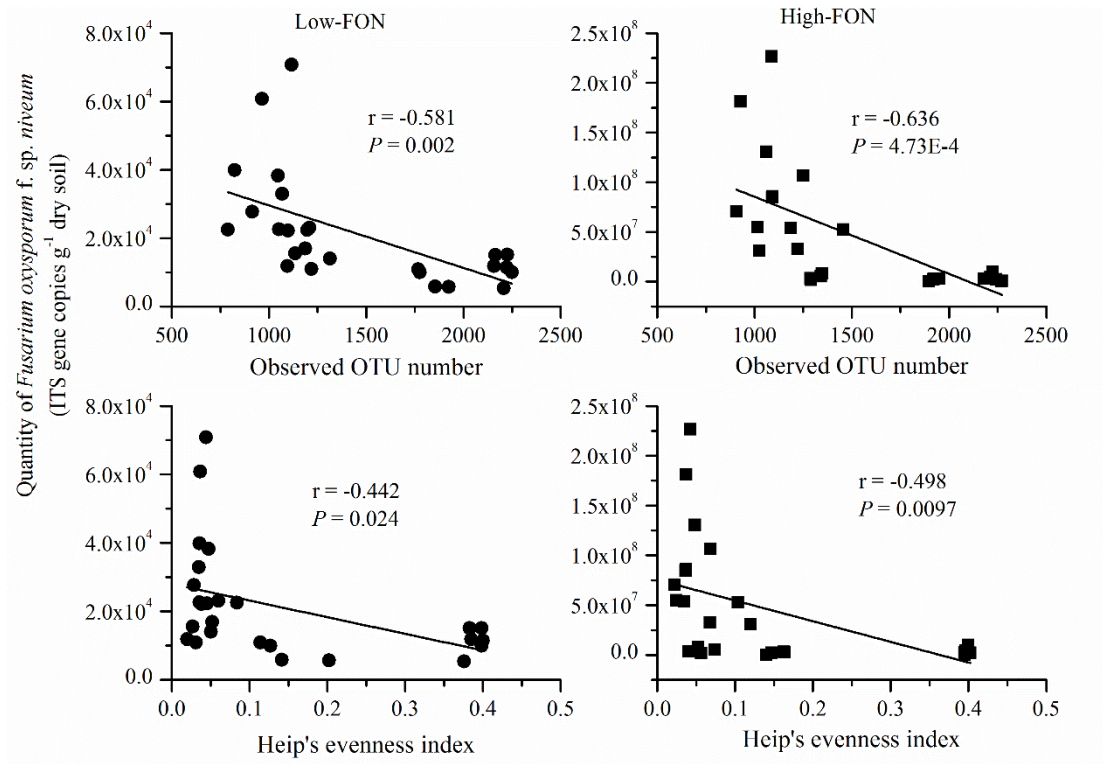


Fig. S3 Correlation analyses between observed OTU number and *Fusarium oxysporum* f. sp. *niveum* quantity or between Heip's evenness index and *Fusarium oxysporum* f. sp. *niveum* quantity in Low-FON and High-FON soils. The Low-FON denotes the FON-uninoculated soil and the High-FON denotes the FON-inoculated soil. The r-values denote the Pearson correlation coefficient.

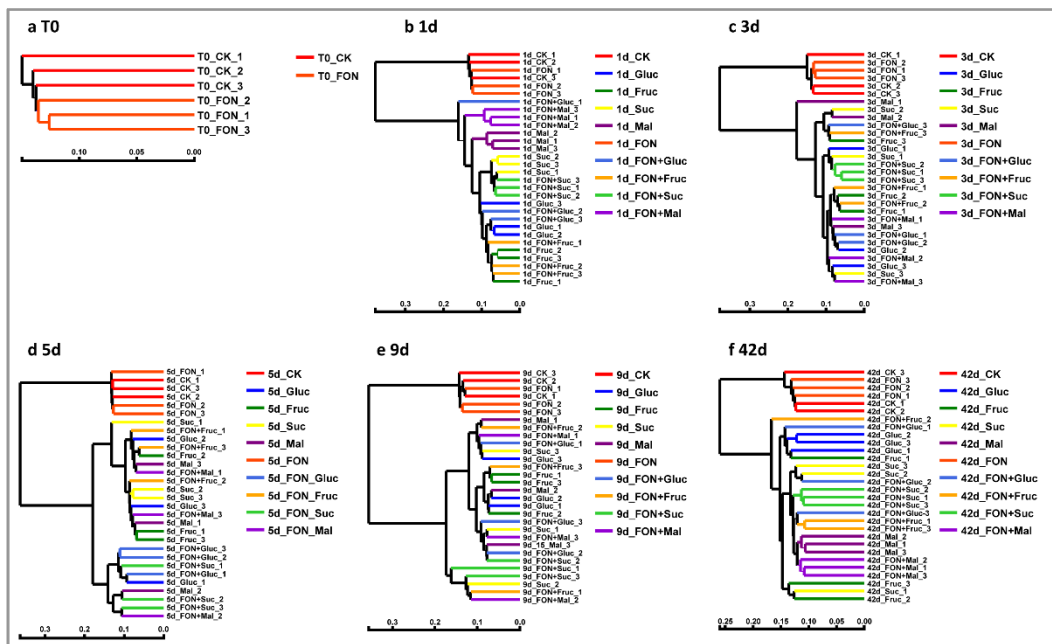


Fig. S4 Hierarchical clustering dendrograms based on the Bray-Curtis distance. Replicates for each treatment are indicated by the symbols “1”, “2”, and “3”. All other designations are the same as those in Table S1.

a	Abundance of phylotypes at the phylum/class level ($\times 10^8$ copies g^{-1} dry soil)															
	Alphaprot	Betaprote	Deltaprot	Gammapr	Firmicutes	Acidobact	Actinobact	Bacteroid	Chlorofle	Planctomy	Gemmati	Nitrospi	Cyanobact	Latescibac	Ignavibact	
	eobacteria	obacteria	eobacteria	oteobacte		eria	eria	etes	xi	cetes	monadete	rae	eria	teria	eriae	
	1	2	3	4	5	6	7	8	9	10	11	12	13	14	15	
1d	CK	120=3 a	96.9=7.1 a	53.2=0.9 a	117=8 d	64.7=3.7 d	180=3 a	114=14 c	58.0=10.3 ab	91.1=4.9 a	68.4=3.2 a	40.0=1.3 a	33.1=1.8 a	20.9=4.3 a	9.4=0.54 a	5.26=0.74 a
	Gluc	125=3 a	80.8=15.0 ab	37.8=4.9 b	223=19 c	2,295=112 c	106=12 b	148=5 b	35.8=6.3 c	64.2=4.0 b	52.0=2.6 b	28.7=4.2 b	21.2=3.2 b	16.8=0.9 a	7.89=0.68 b	2.58=0.46 b
	Fruc	128=3 a	81.1=3.6 b	42.7=7.1 b	317=35 b	3,277=110 b	128=2 b	206=46 a	45.4=7.1 bc	65.9=6.1 b	55.8=7.0 b	21.9=2.1 c	20.5=2.0 b	16.2=2.8 a	7.95=1.00 ab	2.60=0.75 bc
	Suc	95.7=9.4 b	76.9=19.0 ab	27.9=1.8 c	448=18 a	3,507=94 a	106=25 b	124=9 c	35.5=4.8 c	56.2=8.0 b	54.3=8.5 b	22.7=1.1 c	16.5=3.5 b	8.94=0.63 b	6.48=0.95 b	1.57=0.32 c
Mal	116=8 a	93.6=5.9 a	35.2=2.4 b	371=67 ab	2,536=141 c	122=14 b	146=26 abc	65.7=6.5 a	62.3=10.4 b	53.3=8.5 b	27.0=3.4 bc	21.2=5.2 b	17.0=0.5 a	8.55=1.71 ab	4.70=0.51 a	
3d	CK	86.8=4.0 b	77.3=9.2 b	38.6=0.9 b	90.3=3.3 c	43.6=11.4 c	140=9 a	103=13 c	37.8=6.2 c	73.7=7.0 a	52.5=3.8 a	36.5=2.3 a	24.1=1.1 a	15.5=1.4 b	8.35=0.64 a	3.78=0.90 b
	Gluc	143=28 a	70.6=14.6 b	48.2=4.2 a	2,478=65 b	365=26 b	83.1=21.0 c	170=15 b	107=25 ab	42.5=12.1 b	34.1=0.7 c	20.5=4.0 b	10.1=2.2 c	10.8=2.9 c	4.06=0.75 b	1.77=0.50 b
	Fruc	137=22 a	144=22 a	43.9=9.8 ab	2,280=309 b	494=97 a	88.5=12.3 c	161=27 b	98.2=10.6 b	39.9=0.0 b	41.5=2.8 b	21.7=1.5 b	25.1=4.3 ab	9.2=2.57 c	4.99=1.01 b	4.10=1.26 a
	Suc	182=28 a	122=5 a	68.0=19.9 a	2,740=107 a	554=125 a	130=3 ab	229=31 a	124=25 ab	73.7=15.8 a	62.9=7.3 a	30.6=5.6 a	20.6=1.9 b	21.4=1.8 a	5.79=1.52 b	5.14=1.21 a
Mal	180=47 a	118=31 a	70.6=21.1 a	2,284=258 b	410=55 ab	124=2 b	159=5 b	129=12 a	72.5=5.2 a	60.0=4.0 a	32.6=5.0 a	16.8=4.2 b	18.7=2.6 ab	12.1=3.4 a	3.61=0.57 a	
5d	CK	73.5=1.4 c	67.3=2.4 b	32.5=0.4 d	73.5=2.3 c	29.8=0.7 c	126=7 a	76.6=9.4 c	39.7=4.8 c	59.6=3.8 a	50.8=0.6 a	30.9=2.0 bc	21.6=2.6 a	14.9=4.1 ab	8.11=0.98 a	4.33=0.76 a
	Gluc	127=6 b	122=22 a	49.3=13.8 ab	2,321=355 b	104=30 ab	103=29 ab	195=44 ab	169=29 a	60.3=17.0 a	47.6=14.8 ab	42.7=12.7 ab	17.3=2.4 ab	15.5=3.1 a	8.12=1.95 a	4.84=0.71 a
	Fruc	132=9 b	134=24 a	43.7=1.3 c	2,711=94 b	110=4 a	113=39 ab	142=13 b	91.3=1.0 b	51.7=5.5 a	48.2=2.5 a	28.4=2.3 cd	13.6=3.5 bc	17.1=4.5 a	6.78=1.51 a	4.28=1.01 a
	Suc	194=33 a	116=22 a	64.0=4.9 a	2,853=46 a	98.6=4.6 b	109=36 ab	247=9 a	239=81 a	63.7=10.7 a	36.5=5.2 b	42.2=1.1 a	18.9=1.4 a	13.6=2.0 ab	8.32=0.29 a	5.27=1.07 a
Mal	156=38 ab	117=17 a	45.3=10.7 b	2,213=425 b	98.3=2.1 b	104=13 b	130=22 b	171=37 a	70.8=16.8 a	51.9=16.1 ab	25.5=2.1 d	12.3=0.2 c	10.0=1.6 b	7.79=1.98 a	4.28=0.66 a	
9d	CK	85.3=3.0 c	86.8=7.1 b	45.3=3.1 b	93.0=10.7 c	42.5=1.1 d	143=12 b	85.2=10.0 c	54.8=2.8 c	75.7=9.9 bc	60.7=6.7 b	35.5=3.3 b	27.6=5.0 a	18.7=1.2 a	9.82=0.18 b	5.34=0.75 ab
	Gluc	173=38 ab	101=23 b	55.6=11.3 ab	3,133=399 ab	137=36 ab	119=4 a	198=12 b	205=61 ab	71.5=2.8 c	65.0=1.5 c	29.8=1.5 c	30.2=7.7 a	8.04=0.92 d	6.08=1.84 c	3.26=0.92 c
	Fruc	149=8 b	162=18 a	49.9=4.7 ab	3,350=88 a	83.4=15.2 c	167=24 ab	163=36 b	164=30 b	85.0=17.8 ab	84.4=11.2 a	38.5=8.9 bc	23.9=3.4 a	17.2=4.1 ab	8.03=1.54 c	4.31=0.93 bc
	Suc	210=39 a	182=43 a	66.4=13.1 a	2,393=363 b	90.1=19.0 bc	207=42 a	221=44 ab	232=33 a	100=17 ab	107=15 a	50.8=13.6 ab	25.3=6.8 a	13.6=1.4 b	13.6=1.9 a	5.75=0.54 ab
Mal	186=35 ab	186=28 a	62.8=12.5 a	2,894=368 b	165=36 a	164=38 ab	244=14 a	231=39 ab	116=28 a	82.6=16.6 ab	54.9=3.3 a	20.6=3.1 a	10.2=0.6 c	6.19=1.51 c	6.41=0.60 a	
42d	CK	103=3 b	104=12 c	52.6=2.1 b	114=16 c	34.4=2.3 c	169=6 c	90.1=18.0 c	48.7=12.1 b	84.6=1.3 b	71.7=5.4 c	39.2=2.1 d	31.7=2.5 b	14.5=3.9 c	13.8=0.9 c	5.71=0.79 b
	Gluc	277=9 a	249=9 a	153=9 a	1,041=158 b	122=26 ab	300=19 a	329=24 a	216=53 a	193=28 a	189=17 b	94.4=5.0 a	67.7=4.8 a	31.1=7.3 ab	29.6=2.8 b	9.53=2.16 a
	Fruc	257=41 a	227=39 a	153=28 a	1,448=272 ab	104=11 b	285=51 ab	346=79 a	200=43 a	179=40 a	182=37 ab	92.1=19.4 ab	69.4=10.9 a	28.7=2.8 b	34.2=1.6 a	6.54=0.77 b
	Suc	259=29 a	181=5 b	143=29 a	1,460=95 a	100=25 b	259=20 b	265=52 a	177=52 a	177=8 a	196=25 ab	72.2=16.8 bc	63.9=3.7 a	32.1=1.5 ab	26.9=4.0 b	9.68=2.09 a
Mal	265=10 a	234=21 a	142=15 a	1,192=67 b	169=36 a	298=23 ab	192=19 b	208=2 a	171=11 a	221=6 a	65.6=2.7 c	66.3=2.7 a	38.4=5.6 a	31.5=7.7 ab	11.6=2.8 a	

b	Abundance of phylotypes at the phylum/class level ($\times 10^8$ copies g^{-1} dry soil)															
	Alphaprot	Betaprote	Deltaprot	Gammapr	Firmicutes	Acidobact	Actinobact	Bacteroid	Chlorofle	Planctomy	Gemmati	Nitrospi	Cyanobact	Latescibac	Ignavibact	
	eobacteria	obacteria	eobacteria	oteobacte		eria	eria	etes	xi	cetes	monadete	rae	eria	teria	eriae	
	1	2	3	4	5	6	7	8	9	10	11	12	13	14	15	
1d	FON	119=3 b	91.3=4.8 b	51.6=0.7 a	111=6 d	53.2=2.4 d	169=4 a	124=6 c	46.9=3.1 b	91.7=4.4 a	66.2=1.1 b	42.2=2.0 a	31.8=2.6 a	15.8=1.4 c	9.13=1.08 ab	5.03=0.67 a
	FON+Gluc	113=1 c	90.5=21.9 abc	32.6=8.9 b	369=90 bc	2,542=112 b	141=24 bc	167=35 ab	59.0=6.1 a	76.9=2.1 b	68.4=13.0 abc	23.6=3.1 c	29.9=5.5 ab	29.3=6.7 a	11.4=1.6 a	3.66=0.37 b
	FON+Fruc	107=8 c	79.1=5.2 c	39.9=5.1 b	270=29 c	2,410=36 b	145=6 c	151=9 b	46.7=3.1 b	62.0=1.7 c	61.8=1.4 c	29.8=1.2 b	21.9=1.7 c	19.0=2.6 bc	7.90=0.52 b	4.40=0.96 ab
	FON+Suc	82.8=11.4 d	72.5=13.0 c	29.3=6.4 b	358=34 b	2,935=101 a	136=30 abc	87.8=25.0 d	42.7=12.1 ab	47.2=8.3 d	69.8=9.2 abc	19.0=4.6 c	22.4=5.8 bc	17.6=2.2 b	8.31=1.089 b	3.71=0.59 b
	FON+Mal	161=8 a	119=8 a	55.0=6.9 a	559=65 a	2,193=39 c	166=6 ab	204=26 a	48.4=4.5 ab	81.1=6.5 ab	69.7=0.4 a	42.1=5.1 a	34.2=0.2 a	24.7=7.1 ab	9.15=1.07 ab	5.56=0.52 a
3d	FON	82.8=3.2 b	72.5=2.6 b	35.8=2.5 b	85.7=4.9 d	39.6=3.0 d	130=8 a	77.8=5.5 c	50.5=7.9 c	70.9=6.4 a	52.0=1.2 a	30.9=1.4 a	19.9=0.7 b	15.3=1.2 a	7.48=0.12 b	4.74=0.23 a
	FON+Gluc	169=26 a	157=25 a	51.4=10.4 a	2,604=275 ab	418=59 b	151=39 a	152=31 ab	145=16 a	51.4=11.4 bc	62.6=18.2 a	21.1=3.6 b	25.4=1.4 a	14.7=0.6 a	8.00=1.98 ab	3.80=0.99 a
	FON+Fruc	180=23 a	183=40 a	55.1=5.6 a	2,611=166 a	549=65 a	122=24 a	199=29 a	105=23 b	70.5=13.3 bc	54.2=10.8 a	34.5=2.1 a	20.4=2.6 b	12.2=0.9 b	9.93=0.00 a	1.79=0.48 b
	FON+Suc	95.2=17.9 b	57.7=12.2 c	30.0=7.3 b	2,418=7 b	49.2=10.2 ab	73=12 b	138=11 b	63=12 c	45.6=3.3 c	37.2=3.9 b	19.4=2.6 b	14.8=0.5 c	7.45=0.86 c	4.47=1.19 d	1.49=0.40 b
	FON+Mal	154=7 a	145=18 a	52.9=5.0 a	2,268=31 c	259=63 c	133=23 a	140=30 ab	112=14 b	68.1=9.8 ab	55.3=6.6 a	31.9=2.4 a	18.9=2.4 b	11.5=1.0 b	5.74=0.96 cd	4.73=0.48 a
5d	FON	105=5 d	99.4=10.8 c	48.5=1.6 b	108=8 d	43.6=2.0 d	165=4 b	127=4 b	39.0=5.7 c	78.7=2.2 b	54.4=3.4 b	44.3=0.8 b	28.7=1.5 b	15.6=2.3 a	10.2=0.5 b	4.39=0.65 c
	FON+Gluc	293=31 a	253=9 a	83.5=20.0 a	2,992=279 b	257=23 a	234=33 a	287=62 a	211=33 a	126=37 a	103=9 a	53.4=13.5 ab	37.1=5.5 a	18.8=4.5 a	14.9=2.4 a	6.10=1.04 ab
	FON+Fruc	198=32 b	169=21 b	63.9=15.9 ab	3,602=263 a	156=36 b	159=29 b	229=47 a	204=44 a	61.6=5.4 c	62.0=16.0 b	43.3=8.2 b	26.5=0.7 c	14.0=2.7 a	10.4=1.7 b	4.49=1.00 bc
	FON+Suc	247=42 ab	250=27 a	75.3=9.7 a	2,104=271 c	187=48 ab	288=57 a	239=63 a	203=60 ab	101=7 a	112=5 a	63.7=11.9 a	42.6=8.8 a	20.8=5.9 a	15.3=2.6 a	7.78=1.60 a
	FON+Mal	140=3 c	96=6 c	45.3=0.4 c	2,057=565 c	72.6=2.4 c	97.8=20.3 c	119=5 b	123=36 b	46.2=7.5 d	44.2=12.2 b	25.6=0.9 c	11.2=0.9 d	6.25=1.77 b	9.21=2.43 b	2.03=0.22 d
9d	FON	101=11 b	92.0=9.7 b	50.9=4.6 b	95.7=13.8 b	43.5=5.7 d	177=2 b	101=10 c	57=9 b	90.5=6.7 b	71.3=5.0 b	44.0=2.9 b	32.5=1.4 a	22.0=5.0 b	9.25=0.82 b	5.44=0.21 a
	FON+Gluc	191=22 a	164=25 a	55.5=5.2 b	2,339=144 a	96.9=10.5 b	168=30 ab	160=10 ab	276=53 a	83.1=9.0 ab	112=3 a	37.5=8.0 b	25.6=10.4 b	19.8=1.3 b	9.80=2.02 b	5.88=1.04 a
	FON+Fruc	194=53 a	181=42 a	61.7=14.7 ab	2,570=454 a	222=63 a	189=45 ab	187=26 a	231=49 a	118=28 a	121=32 a	50.7=12.3 ab	29.4=2.3 a	26.7=4.4 a	11.8=2.1 ab	5.18=1.47 ab
	FON+Suc	198=43 a	215=61 a	75.2=19.7 ab	2,388=539 a	74.0=0.0 c	222=39 a	216=58 a	289=88 a	67.5=1.4 c	107=13 a	44.0=1.4 b	34.9=9.8 ab	10.1=2.0 c	12.9=0.2 a	7.16=1.69 a
	FON+Mal	211=56 a	217=51 a	74.7=17.3 a	2,653=497 a	97.1=13.6 d	228=59 ab	138=20 b	283=56 a	83.7=6.0 b	122=10 a	60.6=7.8 a	36.7=7.8 a	18.1=5.1 ab	11.0=2.8 ab	3.84=0.60 b
42d	FON	95.3=2.0 c	100=8 c	54.1=3.5 b	90.1=6.4 b	33.1=0.3 c	159=4 c	89.1=9.0 c	48.1=3.1 b	82.5=3.8 b	73.5=1.6 c	39.7=1.9 c	35.5=2.3 c	17.7=1.2 b	13.0=1.8 c	5.92=0.63 b
	FON+Gluc	256=7 b	207=29 ab	134=9 a	1,227=205 a	93.2=19.5 b	288=65 ab	199=24 ab	232=11 a	180=19 a	217=56 ab	71.9=8.6 ab	79.9=22.5 ab	33.9=3.5 a	30.2=4.6 a	9.35=2.09 a
	FON+Fruc	258=4 b	241=6 a	143=8 a	1,230=157 a	128=9 a	296=39 a	226=32 a	242=26 a	210=46 a	191=14 a	78.1=9.9 a	59.8=2.1 b	33.8=6.1 a	27.8=1.2 a	13.4=3.9 a
	FON+Suc	276=12 a	202=11 b	151=15 a	1,092=23 a	117=5 a	276=15 a	206=11 a	225=5 a	191=10 a	212=5 b	63.0=4.2 b	65.2=1.3 a			

Phylum	Abundance of phylotypes at the genus level (x10 ⁸ copies g ⁻¹ dry soil)																					
	Acidobacteria	Actinobacteria			Bacteroidetes	Chloroflexi	Firmicutes				Gemmatimonadetes		Nitrospirae	Proteobacteria								
Class; Order; Family; genus	Acidobacteria; norank; norank; norank	Actinobacteria; Gaiellales; Gaiellales; Gaiella	Actinobacteria; Propionibacteriales; Nocardioidaceae; Marmoricola	Cytophaga; Cytophagales; Cytophagaceae; norank	Anaerolineales; Anaerolineales; Anaerolineaceae; norank	Bacilli; Bacillales; Bacillaceae; Bacillus	Bacilli; Bacillales; Paenibacillaceae; Paenibacillus	Clostridia; Clostridiales; Clostridiaceae; Clostridiaceae_1; Clostridium_m_sensu_stricta_1	Gemmatimonadetes; Gemmatimonadales; Gemmatimonadaceae; norank	Gemmatimonadetes; Gemmatimonadales; norank; norank	Nitrospirae; Nitrospirales; Nitrospiraceae; Nitrospira	Betaproteobacteria; Burkholderiales; Comamonadaceae; Hydrogenophaga	Betaproteobacteria; Nitrosomonadales; Nitrosomonadaceae; norank	Betaproteobacteria; TRAA-20; norank; norank	Deltaproteobacteria; Desulfurellales; Desulfurellaceae; H16	Gammaproteobacteria; Pseudomonadales; Pseudomonadaceae; Azotobacter	Gammaproteobacteria; Pseudomonadales; Pseudomonadaceae; unclassified	Gammaproteobacteria; Pseudomonadales; Pseudomonadaceae; Pseudomonas	Gammaproteobacteria; Xanthomonadales; norank	Gammaproteobacteria; Xanthomonadales; Xanthomonadaceae; Xanthomonas	Gammaproteobacteria; Xanthomonadales; Xanthomonadaceae; Pseudoxanthomonas	
	1	2	3	4	5	6	7	8	9	10	11	12	13	14	15	16	17	18	19	20	21	
1d	CK	125±4 a	15.9±2.4 a	16.4±2.9 b	17.4±1.1 a	41.3±1.1 a	38.7±3.1 c	3.3±0.29 d	1.5±0.35 b	19.1±1.2 a	18.7±0.6 a	33.1±1.8 a	0.4±0.15 d	43.8±2.5 a	18.8±2.9 a	13.6±1.8 a	0.2±0.06 c	0.27±0.08 d	9.4±1.62 d	28.6±2.3 a	20.2±1.7 d	1.6±0.15 c
	Gluc	74.8±4 c	15.3±1.5 a	21.1±1.8 ab	7.0±1.37 d	26.6±5.4 b	225±120 b	40.6±8.3 b	4.9±1.59 a	14.8±1.9 b	11.8±1.6 b	21.2±3.2 b	2.5±0.46 b	37.8±4.7 b	16.4±2.8 a	8.8±1.34 b	31.2±6.2 c	6.87±1.65 c	8.91±3.9 c	22.7±1.3 b	26.9±4.6 bc	5.4±0.91 b
	Fruc	91.8±7.7 b	17.9±5.2 ab	29.1±6.6 ab	11.9±1.4 c	28.6±6.0 b	324±110 a	11.0±2.8 d	1.5±0.50 b	16.0±4.0 ab	7.2±1.3 c	20.5±2.1 b	1.5±0.31 c	29.6±2.2 b	13.0±3.0 ab	6.11±0.25 ab	35.9±8.1 b	8.82±0.90 b	151±13 b	19.4±1.1 c	36.1±5.5 ab	5.4±0.92 b
	Suc	78.9±21.6 bc	8.50±0.45 c	18.3±2.9 b	15.6±2.8 bc	23.3±4.7 b	3425±111 a	36.0±8.5 b	3.35±0.95 a	12.4±0.7 b	8.3±2.6 bc	16.3±3.5 b	3.35±0.32 c	25.5±5.1 b	12.5±0.6 b	11.0±0.93 c	132±10 a	231±2.3 a	210±8 a	17.2±4.1 c	25.3±3.2 c	3.7±0.93 b
Mal	84.0±8.8 bc	10.7±2.3 bc	23.6±7.5 b	20.1±2.4 a	28.1±1.8 b	2365±124 b	144±57 a	5.2±1.02 b	13.9±4.0 ab	11.4±1.1 b	21.2±4.2 b	3.43±1.79 abc	28.9±3.4 b	14.7±2.0 ab	8.55±1.46 b	33.2±7.9 b	61.9±0.6 b	210±65 ab	20.6±1.3 bc	40.7±8.1 a	7.23±0.36 a	
3d	CK	82.0±4.5 a	13.0±1.8 a	11.7±1.6 c	9.7±2.67 b	27.7±4.7 a	46.8±16.0 c	1.17±0.25 d	0.54±0.05 b	16.5±1.8 a	11.9±0.7 a	20.2±0.9 a	0.43±0.12 c	34.0±2.2 a	12.6±3.5 a	7.97±0.18 a	1.62±0.49 b	0.18±0.05 d	6.75±1.19 d	18.4±1.4 a	11.4±0.8 c	0.69±0.15 c
	Gluc	61.4±5.7 c	8.67±1.53 b	30.2±0.2 a	26.6±7.0 a	20.6±0.5 b	1.98±1.1 b	5.2±3.5 c	87.6±13.9 a	10.2±2.6 b	6.5±1.84 b	9.5±1.2±1.2 b	24.2±0.72 b	211±10.9 c	5.3±0.67 b	6.17±0.71 b	17.6±1.09 a	61.5±3.3 ab	202±41 b	11.8±1.6 b	11.6±3.2 a	8.9±5.9 a
	Fruc	60.5±4.8 c	12.9±3.0 ab	29.1±8.3 ab	26.0±4.6 a	16.6±1.6 b	3.05±3.2 c	23.2±4.0 b	1.4±1.53 c	11.4±1.5 b	13.6±3.0 a	25.1±4.3 a	42.7±5.1 a	33.4±10.8 ab	10.8±2.9 a	6.78±1.89 ab	17.6±2.99 a	54.1±3.5 c	182±9 b	20.7±0.1 a	100±10 b	54.0±12.2 ab
	Suc	78.9±21.6 bc	14.5±3.3 ab	21.3±2.1 b	31.0±4.3 a	20.6±5.5 a	2.82±5.9 a	28.5±9.1 a	17.0±24.1 a	13.7±1.7 ab	12.4±2.2 a	19.5±1.8 a	20.8±7.0 b	31.9±4.8 a	11.4±2.9 a	7.17±0.62 b	18.9±4.20 a	73.7±9.9 a	20.9±2.9 a	21.5±2.9 a	15.3±3.0 a	56.6±7.2 ab
Mal	75.7±10.5 b	12.1±2.2 ab	21.2±2.0 b	33.3±3.9 a	28.8±1.8 b	1.87±1.3 b	41.5±8.5 a	8.6±9.1 b	14.7±2.7 ab	12.7±1.2 a	22.2±6.8 a	25.5±10.0 b	32.6±3.0 ab	11.4±3.2 a	6.59±0.66 b	33.2±7.9 b	61.9±0.6 b	33.5±9.9 ab	18.4±5.1 ab	113±27 ab	48.4±7.9 b	
5d	CK	122±7 a	15.9±2.2 a	14.4±2.5 c	15.3±1.1 d	37.9±7.7 a	23.3±1.5 d	2.11±0.50 c	0.73±0.21 d	22.8±1.8 a	17.2±1.1 a	29.9±3.6 a	0.69±0.00 c	45.0±2.3 a	18.7±2.4 a	11.8±0.3 a	0.15±0.07 c	0.10±0.00 c	7.13±0.10 d	26.8±1.0 a	13.1±1.0 b	0.92±0.15 c
	Gluc	67.1±2.1 b	15.8±2.1 a	28.6±5.5 a	42.2±7.0 bc	21.1±5.4 b	35.4±9.5 c	3.6±0.88 b	0.55±0.19 d	14.3±3.5 b	17.9±4.2 ab	17.3±2.3 b	42.2±14.6 ab	37.8±4.4 b	11.8±3.5 b	4.3±0.47 c	16.6±5.86 ab	39.4±9.1 b	10.9±2.0 b	15.3±3.8 c	15.0±13 a	8.8±20.5 a
	Fruc	78.7±23.1 b	7.89±0.82 ab	22.9±3.5 ab	33.1±3.8 b	24.6±1.6 b	101±4.5 a	3.6±0.27 b	2.50±0.27 d	16.4±1.9 b	11.4±1.4 cd	16.4±2.7 b	56.6±16.1 a	33.2±3.4 a	14.9±2.5 ab	8.27±1.36 b	21.9±25.4 a	69.5±5.20 ab	21.8±3.4 a	24.8±4.6 ab	17.8±3.4 a	8.8±7.8 b
	Suc	68.4±17.9 b	8.71±1.24 b	33.4±0.2 a	61.3±2.2 a	27.6±2.6 b	52.6±3.4 b	1.4±1.7 a	10.1±2.7 b	18.8±1.4 b	13.5±2.2 bc	15.9±1.2 b	25.1±2.2 a	26.0±3.1 b	10.8±2.7 b	5.70±1.72 d	17.00±1.28 b	53.9±14.0 ab	34.4±7.8 a	21.3±3.9 c	15.9±2.2 a	100±29 a
Mal	73.3±7.7 b	9.7±1.3 b	16.8±3.5 b	45.9±0.0 b	30.0±1.8 ab	49.2±9.1 bc	5.8±5.2 d	7.3±0.23 b	17.7±4.9 ab	8.5±1.86 d	12.7±1.2 c	45.1±9.8 ab	26.6±1.6 b	7.7±4.70 b	3.31±0.70 d	20.47±8.7 b	59.0±8.0 b	18.6±4.1 a	17.6±3.0 b	18.4±5.1 ab	8.3±12.2 a	
9d	CK	104±8 a	12.5±1.6 ab	11.4±1.2 c	15.9±1.9 d	36.7±5.2 bc	25.8±1.8 c	2.64±0.23 c	0.93±0.16 c	19.3±3.5 bc	15.8±1.1 b	29.1±5.2 a	0.61±0.20 c	43.3±4.0 b	19.8±2.7 a	12.1±1.2 ab	1.86±0.49 c	0.65±0.13 c	8.14±1.16 d	24.9±1.0 b	9.4±4.189 d	1.12±0.34 c
	Gluc	79.2±10.9 b	9.32±0.63 c	30.0±1.6 ab	91.2±24.8 a	31.5±1.3 c	32.3±4.2 b	4.8±0.00 c	3.33±0.94 b	17.8±10.6 c	9.77±1.26 c	22.5±6.9 a	35.5±7.5 a	35.1±0.6 c	6.21±1.88 c	12.65±0.31 a	26.0±5.88 ab	63.5±20.4 ab	190±60 ab	26.6±7.6 b	104±16 b	55.9±7.3 ab
	Fruc	112±19 a	10.1±1.3 bc	21.2±5.6 b	62.1±3.8 b	45.3±10.6 ab	65.2±18.8 a	3.28±0.31 c	2.16±0.61 d	23.9±11.9 b	11.4±1.4 cd	13.8±4.9 b	9.5±2.22 c	23.2±3.4 a	14.9±2.5 ab	9.52±2.70 b	27.1±11.9 a	71.2±12.4 ab	176±31 b	24.8±4.6 ab	8.7±1.1 c	43.8±7.8 b
	Suc	117±36 a	17.4±0.4 a	11.1±1.1 a	30.0±6.0 a	63.1±18.9 a	4.3±1.9 a	2.82±0.26 b	4.4±5.7 a	19.9±5.1 b	29.4±7.9 a	52.6±7.4 a	60.5±12.5 a	16.9±1.3 a	14.5±1.6 a	20.9±2.7 a	33.1±3.5 a	24.9±7.4 a	81.8±5.1 a	27.5±5.8 a	45.2±1.4 a	139±9 a
Mal	114±34 ab	16.2±1.3 ab	24.8±6.6 ab	97.9±7.2 a	53.9±15.2 a	63.4±22.5 a	4.7±4.0 d	8.59±0.95 a	34.8±31.1 a	18.1±0.6 a	21.3±3.2 a	51.3±14.6 ab	62.5±5.1 ab	12.3±2.5 b	6.38±0.31 c	20.27±4.87 ab	59.0±8.0 b	18.8±7.1 b	27.0±1.1 b	92.0±2.1 a	44.9±9.9 b	
42d	CK	83.9±2.6 c	12.2±1.6 b	9.0±2.4 c	9.5±1.2 d	33.9±2.1 d	15.2±0.6 d	1.73±0.49 d	0.85±0.06 c	14.9±10.6 c	15.4±1.4 b	25.9±1.2 d	0.32±0.00 d	45.5±1.3 ab	19.6±2.0 a	12.7±0.7 b	1.05±0.23 c	0.32±0.00 c	7.00±1.09 c	23.6±1.0 b	4.08±0.40 c	2.04±0.08 c
	Gluc	88.5±7.4 c	16.0±0.4 a	26.1±5.3 ab	18.9±1.1 b	44.2±11.2 cd	27.1±4.3 b	3.4±0.32 c	1.30±0.11 d	24.0±0.4 b	16.5±1.3 b	31.2±2.2 c	3.20±0.70 c	56.9±5.1 c	16.8±5.7 b	12.6±0.3 b	27.0±7.3 b	31.9±10.1 b	78.6±7.7 b	36.1±2.9 b	13.9±2.6 b	1.03±0.09 b
	Fruc	110±19 bc	19.6±3.8 a	38.8±8.5 a	37.5±8.7 b	53.3±13.2 bc	21.5±0.9 c	4.2±0.25 b	2.29±0.51 c	35.4±8.5 a	18.6±2.7 ab	43.2±6.8 b	37.2±9.8 b	53.1±17.2 ab	18.3±2.4 a	10.5±0.8 a	19.0±9.7 a	29.2±7.7 b	165±9 a	29.0±5 b	18.6±3.4 ab	8.8±7.2 a
	Suc	126±7 b	20.5±3.7 a	26.6±1.5 ab	41.0±7.6 b	71.8±23.5 a	36.4±3.5 a	4.8±0.93 b	3.38±1.48 b	33.1±8.2 ab	18.2±4.7 ab	48.9±32.8 ab	6.89±0.40 b	77.8±3.5 b	15.0±4.0 a	17.3±2.8 a	74.4±7.7 a	37.8±4.9 a	142±7 a	77.5±2.6 b	17.2±2.7 ab	1.07±0.11 a
Mal	144±6 a	18.3±3.6 a	21.4±1.0 b	63.1±1 a	82.4±35.5 a	44.0±8.0 a	8.5±11.22 a	16.1±2.0 a	31.2±11.5 a	19.2±0.7 a	53.7±12.2 a	19.5±5.4 a	88.0±5.6 a	19.6±3.0 a	16.5±2.6 a	67.8±20 a	25.5±5.5 a	94.3±20.6 b	39.0±1.6 a	32.6±3.5 a	8.23±1.20 a	

Fig. S6 Abundance of bacterial phylotypes at the genus level in Low-FON (a) and High-FON (b) soils. The abundance of the phylotypes was calculated as the relative abundance × the total bacteria abundance (shown in Fig. S2). The length of the bars in each column is proportional to the abundance value of each taxon. Different letters indicate significant differences by Duncan's multiple range test ($P<0.05$). All other designations are the same as those in Table S1.

Taxon No.	0-42d-CK	1d-Sugar	3d-Sugar	5d-Sugar	9d-Sugar	42d-Sugar	0-42d-FON	1d-FON+ Sugar	3d-FON+ Sugar	5d-FON+ Sugar	9d-FON+ Sugar	42d-FON+ Sugar
1	20	25(30.1%)	8(17.0%)	2	21(29.6%)	29 (26.6%)	9	16(25.4%)	15(28.3%)	8(19.5%)	22(25.3%)	15(23.1%)
2	2	1	5	0	1	2	0	4	2	1	3	2
3	0	0	0	0	0	0	0	0	0	1	0	0
4	3	3	3	1	9	8	2	3	4	6	4	1
5	31(33.7%)	12	4	0	7	24	28(40.6%)	8	3	3	20	14
6	0	4	2	1	0	2	0	6	1	1	0	0
7	4	7	2	1	1	1	3	6	1	1	0	3
8	0	0	0	0	0	1	0	2	0	1	0	1
9	5	7	4	3	7	8	5	1	3	4	8	6
10	4	5	2	1	4	5	8	3	4	2	4	5
11	6	6	3	0	3	6	1	3	6	3	8	2
12	0	0	0	0	0	0	0	0	1	0	0	1
13	2	3	3	2	5	4	3	5	2	2	2	2
14	1	2	1	2	1	1	1	1	1	1	0	1
15	7	2	1	0	1	7	3	0	1	0	1	4
16	0	0	4	1	6	2	0	1	4	4	11	5
17	0	0	0	1	0	1	0	1	0	1	1	0
18	1	1	1	2	0	2	0	1	1	0	2	1
19	4	3	1	1	2	4	4	1	0	1	1	1
20	1	1	3	0	2	2	2	1	2	1	0	1
21	1	1	0	0	1	0	0	0	2	0	0	0
Total	92	83	47	18	71	109	69	63	53	41	87	65

	Phylum; Class; Order; Family; Genus
1	Acidobacteria; Acidobacteria; norank_Acidobacteria; norank_Acidobacteria; norank_Acidobacteria
2	Actinobacteria; Actinobacteria; Gaiellales; Gaiellaceae; GaiellaJ4:J22
3	Actinobacteria; Actinobacteria; Propionibacteriales; Nocardiodaceae; Marmoricola
4	Bacteroidetes; Cytophagia; Cytophagales; Cytophagaceae; norank_Cytophagaceae
5	Chloroflexi; Anaerolineae; Anaerolineales; Anaerolineaceae; norank_Anaerolineaceae
6	Firmicutes; Bacilli; Bacillales; Bacillaceae; Bacillus
7	Firmicutes; Bacilli; Bacillales; Paenibacillaceae; Paenibacillus
8	Firmicutes; Clostridia; Clostridiales; Clostridiaceae_1; Clostridium_sensu_stricto_1
9	Gemmatimonadetes; Gemmatimonadetes; Gemmatimonadales; Gemmatimonadaceae; norank_Gemmatimonadaceae
10	Gemmatimonadetes; Gemmatimonadetes; norank_Gemmatimonadetes; norank_Gemmatimonadetes; norank_Gemmatimonadetes
11	Nitrospirae; Nitrospira; norank_Nitrospira; norank_Nitrospira; Nitrospira
12	Proteobacteria; Betaproteobacteria; Burkholderiales; Comamonadaceae; Hydrogenophaga
13	Proteobacteria; Betaproteobacteria; Nitrosomonadales; Nitrosomonadaceae; norank_Nitrosomonadaceae
14	Proteobacteria; Betaproteobacteria; TRA3-20; norank_TRA3-20; norank_TRA3-20
15	Proteobacteria; Deltaproteobacteria; Desulfurellales; Desulfurellaceae; H16
16	Proteobacteria; Gammaproteobacteria; Pseudomonadales; Pseudomonadaceae; Azotobacter
17	Proteobacteria; Gammaproteobacteria; Pseudomonadales; Pseudomonadaceae; unclassified
18	Proteobacteria; Gammaproteobacteria; Pseudomonadales; Pseudomonadaceae; Pseudomonas
19	Proteobacteria; Gammaproteobacteria; Xanthomonadales; norank_Xanthomonadales; norank_Xanthomonadales
20	Proteobacteria; Gammaproteobacteria; Xanthomonadales; Xanthomonadaceae; Lysobacter
21	Proteobacteria; Gammaproteobacteria; Xanthomonadales; Xanthomonadaceae; Pseudoxanthomonas

Fig. S7 Heatmap of connector number. The percentage of Chloroflexi-affiliated OTUs in the total connector was additionally shown in the bracket because they accounted for the largest proportion in the CK and FON treatments, and the percentage of Acidobacteria-affiliated OTUs was also shown in the bracket because they accounted for the largest proportion in almost all sugar-addition treatments (except for at the 5d-Sugar treatment). The designations CK and Sugar indicate that the soil was supplied with water and sugars (i.e., glucose, fructose, sucrose, and maltose), respectively. The designation FON represents the soil inoculated with FON. The samples collected after 0 day (i.e., zero time), 1 day, 3 days, 5 days, 9 days, and 42 days are referred to as 0, 1d, 3d, 5d, 9d, and 42d, respectively.

Network hubs	P_i	Z_i	Relative abundance		Taxonomy (<i>Phylum; Class; Order; Family; Genus</i>)
0-42d-CK					
OTU272	0.71	3.41	0.008%	5	<i>Chloroflexi; Anaerolineae; Anaerolineales; Anaerolineaceae; norank_Anaerolineaceae</i>
OTU1677	0.63	2.69	0.007%	5	<i>Chloroflexi; Anaerolineae; Anaerolineales; Anaerolineaceae; norank_Anaerolineaceae</i>
OTU4724	0.68	2.69	0.005%	5	<i>Chloroflexi; Anaerolineae; Anaerolineales; Anaerolineaceae; norank_Anaerolineaceae</i>
OTU5711	0.76	3.46	0.006%	5	<i>Chloroflexi; Anaerolineae; Anaerolineales; Anaerolineaceae; norank_Anaerolineaceae</i>
OTU6082	0.74	3.07	0.006%	5	<i>Chloroflexi; Anaerolineae; Anaerolineales; Anaerolineaceae; norank_Anaerolineaceae</i>
OTU5709	0.78	2.94	0.006%	9	<i>Gemmatimonadetes; Gemmatimonadetes; Gemmatimonadales; Gemmatimonadaceae; norank_Gemmatimonadaceae</i>
OTU4473	0.80	2.55	0.006%	13	<i>Proteobacteria; Betaproteobacteria; Nitrosomonadales; Nitrosomonadaceae; norank_Nitrosomonadaceae</i>
1d-Sugar					
OTU1074	0.71	2.55	0.052%	1	<i>Acidobacteria; Acidobacteria; norank_Acidobacteria; norank_Acidobacteria; norank_Acidobacteria</i>
OTU5746	0.69	2.55	0.036%	1	<i>Acidobacteria; Acidobacteria; norank_Acidobacteria; norank_Acidobacteria; norank_Acidobacteria</i>
OTU6154	0.73	2.90	0.028%	5	<i>Chloroflexi; Anaerolineae; Anaerolineales; Anaerolineaceae; norank_Anaerolineaceae</i>
OTU4809	0.68	3.04	0.010%	7	<i>Firmicutes; Bacilli; Bacillales; Paenibacillaceae; Paenibacillus</i>
3d-Sugar					
OTU2176	0.65	3.34	0.006%	5	<i>Chloroflexi; Anaerolineae; Anaerolineales; Anaerolineaceae; norank_Anaerolineaceae</i>
5d-Sugar					
None					
9d-Sugar					
OTU243	0.68	3.97	0.006%	5	<i>Chloroflexi; Anaerolineae; Anaerolineales; Anaerolineaceae; norank_Anaerolineaceae</i>
OTU4031	0.66	3.06	0.007%	10	<i>Gemmatimonadetes; Gemmatimonadetes; norank_Gemmatimonadetes; norank_Gemmatimonadetes; norank_Gemmatimonadetes</i>
OTU5552	0.71	3.24	0.005%	19	<i>Proteobacteria; Gammaproteobacteria; Xanthomonadales; norank_Xanthomonadales; norank_Xanthomonadales</i>
42d-Sugar					
OTU3756	0.64	3.09	0.006%	1	<i>Acidobacteria; Acidobacteria; norank_Acidobacteria; norank_Acidobacteria; norank_Acidobacteria</i>
0-42d-FON					
OTU5782	0.68	2.61	0.008%	5	<i>Chloroflexi; Anaerolineae; Anaerolineales; Anaerolineaceae; norank_Anaerolineaceae</i>
OTU6176	0.70	2.90	0.008%	5	<i>Chloroflexi; Anaerolineae; Anaerolineales; Anaerolineaceae; norank_Anaerolineaceae</i>
OTU5507	0.77	2.51	0.006%	9	<i>Gemmatimonadetes; Gemmatimonadetes; Gemmatimonadales; Gemmatimonadaceae; norank_Gemmatimonadaceae</i>
OTU2615	0.73	2.68	0.008%	11	<i>Nitrospirae; Nitrospira; norank_Nitrospira; norank_Nitrospira; Nitrospira</i>
1d-FON+Sugar					
OTU290	0.69	2.52	0.008%	7	<i>Firmicutes; Bacilli; Bacillales; Paenibacillaceae; Paenibacillus</i>
3d-FON+Sugar					
OTU1020	0.63	2.56	0.005%	5	<i>Chloroflexi; Anaerolineae; Anaerolineales; Anaerolineaceae; norank_Anaerolineaceae</i>
OTU1376	0.67	2.73	0.005%	5	<i>Chloroflexi; Anaerolineae; Anaerolineales; Anaerolineaceae; norank_Anaerolineaceae</i>
5d-FON+Sugar					
OTU4753	0.64	2.72	0.010%	2	<i>Actinobacteria; Actinobacteria; Gaiellales; Gaiellaceae; GaiellaJJ4:J22</i>
OTU436	0.64	2.72	0.010%	5	<i>Chloroflexi; Anaerolineae; Anaerolineales; Anaerolineaceae; norank_Anaerolineaceae</i>
9d-FON+Sugar					
OTU928	0.66	2.98	0.006%	1	<i>Acidobacteria; Acidobacteria; norank_Acidobacteria; norank_Acidobacteria; norank_Acidobacteria</i>
OTU6850	0.64	3.47	0.007%	1	<i>Acidobacteria; Acidobacteria; norank_Acidobacteria; norank_Acidobacteria; norank_Acidobacteria</i>
42d-FON+Sugar					
OTU1180	0.67	3.53	0.006%	5	<i>Chloroflexi; Anaerolineae; Anaerolineales; Anaerolineaceae; norank_Anaerolineaceae</i>
OTU4158	0.62	3.07	0.005%	9	<i>Gemmatimonadetes; Gemmatimonadetes; Gemmatimonadales; Gemmatimonadaceae; norank_Gemmatimonadaceae</i>
OTU5429	0.68	2.85	0.006%	20	<i>Proteobacteria; Gammaproteobacteria; Xanthomonadales; Xanthomonadaceae; Lysobacter</i>
			min: 0.005%		
			max: 0.052%		

Fig. S8 Relative abundance, among-module connectivity (P_i), and within module connectivity (Z_i) of network hubs. The designations CK and Sugar represent the soil supplied with water and sugars (i.e., glucose, fructose, sucrose, and maltose), respectively. The designation FON denotes the soil subjected to FON inoculation. The 0, 1d, 3d, 5d, 9d, and 42d indicate samples collected after 0 day (i.e., zero time), 1 day, 3 days, 5 days, 9 days, and 42 days of incubation, respectively. The designations min and max indicate minimum and maximum relative abundance, respectively.

Module hubs	Pi	Zi	Relative abundance	Taxonomy (Phylum; Class; Order; Family; Genus)
0-42d-CK				
OTU1354	0.56	4.16	0.005%	1 Acidobacteria; Acidobacteria; norank_Acidobacteria; norank_Acidobacteria; norank_Acidobacteria
OTU3400	0.58	3.21	0.007%	4 Bacteroidetes; Cytophagia; Cytophagales; Cytophagaceae; norank_Cytophagaceae
OTU3362	0.40	2.83	0.006%	5 Chloroflexi; Anaerolineae; Anaerolineales; Anaerolineaceae; norank_Anaerolineaceae
OTU6736	0.57	3.88	0.006%	13 Proteobacteria; Betaproteobacteria; Nitrosomonadales; Nitrosomonadaceae; norank_Nitrosomonadaceae
1d-Sugar				
OTU3845	0.38	2.76	0.012%	1 Acidobacteria; Acidobacteria; norank_Acidobacteria; norank_Acidobacteria; norank_Acidobacteria
3d-Sugar				
OTU4410	0.47	3.67	0.011%	1 Acidobacteria; Acidobacteria; norank_Acidobacteria; norank_Acidobacteria; norank_Acidobacteria
OTU4497	0.46	2.55	0.005%	1 Acidobacteria; Acidobacteria; norank_Acidobacteria; norank_Acidobacteria; norank_Acidobacteria
OTU4646	0.41	2.55	0.006%	1 Acidobacteria; Acidobacteria; norank_Acidobacteria; norank_Acidobacteria; norank_Acidobacteria
OTU3260	0.59	2.97	0.005%	5 Chloroflexi; Anaerolineae; Anaerolineales; Anaerolineaceae; norank_Anaerolineaceae
OTU4860	0.49	4.19	0.009%	5 Chloroflexi; Anaerolineae; Anaerolineales; Anaerolineaceae; norank_Anaerolineaceae
5d-Sugar				
OTU1062	0.26	2.70	0.010%	1 Acidobacteria; Acidobacteria; norank_Acidobacteria; norank_Acidobacteria; norank_Acidobacteria
OTU5077	0.45	2.80	0.007%	1 Acidobacteria; Acidobacteria; norank_Acidobacteria; norank_Acidobacteria; norank_Acidobacteria
OTU5785	0.35	2.57	0.012%	9 Gemmatimonadetes; Gemmatimonadetes; Gemmatimonadales; Gemmatimonadaceae; norank_Gemmatimonadaceae
OTU6659	0.44	2.68	0.006%	10 Gemmatimonadetes; Gemmatimonadetes; norank_Gemmatimonadetes; norank_Gemmatimonadetes; norank_Gemmatimonadetes
OTU6918	0.43	2.55	0.008%	15 Proteobacteria; Deltaproteobacteria; Desulfurellales; Desulfurellaceae; H116
OTU5755	0.46	3.49	0.011%	20 Proteobacteria; Gammaproteobacteria; Xanthomonadales; Xanthomonadaceae; Lysobacter
9d-Sugar				
OTU6928	0.55	4.03	0.006%	1 Acidobacteria; Acidobacteria; norank_Acidobacteria; norank_Acidobacteria; norank_Acidobacteria
OTU1058	0.52	2.87	0.006%	10 Gemmatimonadetes; Gemmatimonadetes; norank_Gemmatimonadetes; norank_Gemmatimonadetes; norank_Gemmatimonadetes
OTU1181	0.44	2.88	0.005%	10 Gemmatimonadetes; Gemmatimonadetes; norank_Gemmatimonadetes; norank_Gemmatimonadetes; norank_Gemmatimonadetes
OTU331	0.44	3.63	0.006%	19 Proteobacteria; Gammaproteobacteria; Xanthomonadales; norank_Xanthomonadales; norank_Xanthomonadales
OTU1724	0.52	2.53	0.006%	19 Proteobacteria; Gammaproteobacteria; Xanthomonadales; norank_Xanthomonadales; norank_Xanthomonadales
OTU2724	0.28	2.52	0.015%	19 Proteobacteria; Gammaproteobacteria; Xanthomonadales; norank_Xanthomonadales; norank_Xanthomonadales
42d-Sugar				
OTU6280	0.58	3.83	0.006%	4 Bacteroidetes; Cytophagia; Cytophagales; Cytophagaceae; norank_Cytophagaceae
OTU2534	0.54	2.93	0.006%	5 Chloroflexi; Anaerolineae; Anaerolineales; Anaerolineaceae; norank_Anaerolineaceae
OTU6016	0.37	3.00	0.011%	6 Firmicutes; Bacilli; Bacillales; Bacillaceae; Bacillus
OTU2174	0.52	3.00	0.008%	9 Gemmatimonadetes; Gemmatimonadetes; Gemmatimonadales; Gemmatimonadaceae; norank_Gemmatimonadaceae
OTU3086	0.51	3.29	0.006%	9 Gemmatimonadetes; Gemmatimonadetes; Gemmatimonadales; Gemmatimonadaceae; norank_Gemmatimonadaceae
OTU3943	0.35	3.09	0.008%	9 Gemmatimonadetes; Gemmatimonadetes; Gemmatimonadales; Gemmatimonadaceae; norank_Gemmatimonadaceae
OTU2130	0.54	2.80	0.009%	11 Nitrospirae; Nitrospira; norank_Nitrospira; norank_Nitrospira; Nitrospira
OTU4997	0.59	2.63	0.005%	15 Proteobacteria; Deltaproteobacteria; Desulfurellales; Desulfurellaceae; H116
0-42d-FON				
OTU36	0.44	4.43	0.007%	1 Acidobacteria; Acidobacteria; norank_Acidobacteria; norank_Acidobacteria; norank_Acidobacteria
OTU5141	0.50	2.67	0.008%	1 Acidobacteria; Acidobacteria; norank_Acidobacteria; norank_Acidobacteria; norank_Acidobacteria
OTU1088	0.58	3.48	0.006%	5 Chloroflexi; Anaerolineae; Anaerolineales; Anaerolineaceae; norank_Anaerolineaceae
OTU2506	0.48	2.70	0.006%	5 Chloroflexi; Anaerolineae; Anaerolineales; Anaerolineaceae; norank_Anaerolineaceae
OTU3415	0.43	2.90	0.007%	10 Gemmatimonadetes; Gemmatimonadetes; norank_Gemmatimonadetes; norank_Gemmatimonadetes; norank_Gemmatimonadetes
OTU115	0.58	2.58	0.008%	11 Nitrospirae; Nitrospira; norank_Nitrospira; norank_Nitrospira; Nitrospira
1d-FON+Sugar				
OTU2910	0.60	3.04	0.006%	5 Chloroflexi; Anaerolineae; Anaerolineales; Anaerolineaceae; norank_Anaerolineaceae
OTU6448	0.47	2.99	0.006%	5 Chloroflexi; Anaerolineae; Anaerolineales; Anaerolineaceae; norank_Anaerolineaceae
OTU6659	0.47	2.67	0.006%	10 Gemmatimonadetes; Gemmatimonadetes; norank_Gemmatimonadetes; norank_Gemmatimonadetes; norank_Gemmatimonadetes
OTU4667	0.56	3.31	0.010%	20 Proteobacteria; Gammaproteobacteria; Xanthomonadales; Xanthomonadaceae; Lysobacter
3d-FON+Sugar				
OTU6490	0.49	2.86	0.007%	1 Acidobacteria; Acidobacteria; norank_Acidobacteria; norank_Acidobacteria; norank_Acidobacteria
OTU2931	0.53	3.76	0.007%	7 Firmicutes; Bacilli; Bacillales; Paenibacillaceae; Paenibacillus
OTU2487	0.61	2.59	0.008%	9 Gemmatimonadetes; Gemmatimonadetes; Gemmatimonadales; Gemmatimonadaceae; norank_Gemmatimonadaceae
OTU4654	0.58	2.86	0.009%	9 Gemmatimonadetes; Gemmatimonadetes; Gemmatimonadales; Gemmatimonadaceae; norank_Gemmatimonadaceae
OTU4032	0.52	2.86	0.009%	10 Gemmatimonadetes; Gemmatimonadetes; norank_Gemmatimonadetes; norank_Gemmatimonadetes; norank_Gemmatimonadetes
5d-FON+Sugar				
OTU1691	0.39	2.83	0.006%	1 Acidobacteria; Acidobacteria; norank_Acidobacteria; norank_Acidobacteria; norank_Acidobacteria
OTU5778	0.55	3.18	0.011%	1 Acidobacteria; Acidobacteria; norank_Acidobacteria; norank_Acidobacteria; norank_Acidobacteria
OTU6623	0.33	3.66	0.014%	1 Acidobacteria; Acidobacteria; norank_Acidobacteria; norank_Acidobacteria; norank_Acidobacteria
OTU6251	0.52	3.37	0.011%	10 Gemmatimonadetes; Gemmatimonadetes; norank_Gemmatimonadetes; norank_Gemmatimonadetes; norank_Gemmatimonadetes
OTU4661	0.47	3.47	0.008%	15 Proteobacteria; Deltaproteobacteria; Desulfurellales; Desulfurellaceae; H116
9d-FON+Sugar				
OTU2455	0.34	4.41	0.011%	1 Acidobacteria; Acidobacteria; norank_Acidobacteria; norank_Acidobacteria; norank_Acidobacteria
OTU6431	0.41	3.46	0.009%	1 Acidobacteria; Acidobacteria; norank_Acidobacteria; norank_Acidobacteria; norank_Acidobacteria
OTU1802	0.50	2.64	0.014%	2 Actinobacteria; Actinobacteria; Gaiellales; Gaiellaceae; GaiellaJ4;J22
OTU1701	0.28	2.57	0.005%	10 Gemmatimonadetes; Gemmatimonadetes; norank_Gemmatimonadetes; norank_Gemmatimonadetes; norank_Gemmatimonadetes
42d-FON+Sugar				
OTU1324	0.56	3.67	0.008%	1 Acidobacteria; Acidobacteria; norank_Acidobacteria; norank_Acidobacteria; norank_Acidobacteria
OTU2692	0.44	3.23	0.006%	1 Acidobacteria; Acidobacteria; norank_Acidobacteria; norank_Acidobacteria; norank_Acidobacteria
OTU3396	0.33	2.54	0.012%	1 Acidobacteria; Acidobacteria; norank_Acidobacteria; norank_Acidobacteria; norank_Acidobacteria
OTU5061	0.40	3.17	0.006%	1 Acidobacteria; Acidobacteria; norank_Acidobacteria; norank_Acidobacteria; norank_Acidobacteria
OTU3515	0.46	2.60	0.006%	5 Chloroflexi; Anaerolineae; Anaerolineales; Anaerolineaceae; norank_Anaerolineaceae
OTU4719	0.62	2.68	0.007%	5 Chloroflexi; Anaerolineae; Anaerolineales; Anaerolineaceae; norank_Anaerolineaceae
OTU6500	0.50	3.23	0.006%	5 Chloroflexi; Anaerolineae; Anaerolineales; Anaerolineaceae; norank_Anaerolineaceae
OTU290	0.42	3.36	0.006%	7 Firmicutes; Bacilli; Bacillales; Paenibacillaceae; Paenibacillus
OTU4839	0.40	2.68	0.011%	9 Gemmatimonadetes; Gemmatimonadetes; Gemmatimonadales; Gemmatimonadaceae; norank_Gemmatimonadaceae
OTU6172	0.41	2.76	0.006%	9 Gemmatimonadetes; Gemmatimonadetes; Gemmatimonadales; Gemmatimonadaceae; norank_Gemmatimonadaceae
			min: 0.005%	
			max: 0.015%	

Fig. S9 Relative abundance, among-module connectivity (P_i), and within module connectivity (Z_i) of module hubs. The designations CK and Sugar denote the soil with the addition of water and sugars (i.e., glucose, fructose, sucrose, and maltose), respectively. The designation FON represents the soil subjected to FON inoculation. The 0, 1d, 3d, 5d, 9d, and 42d indicate that the samples were collected after 0 day (i.e., zero time), 1 day, 3 days, 5 days, 9 days, and 42 days of incubation, respectively. The designations min and max represent minimum and maximum relative abundance, respectively.

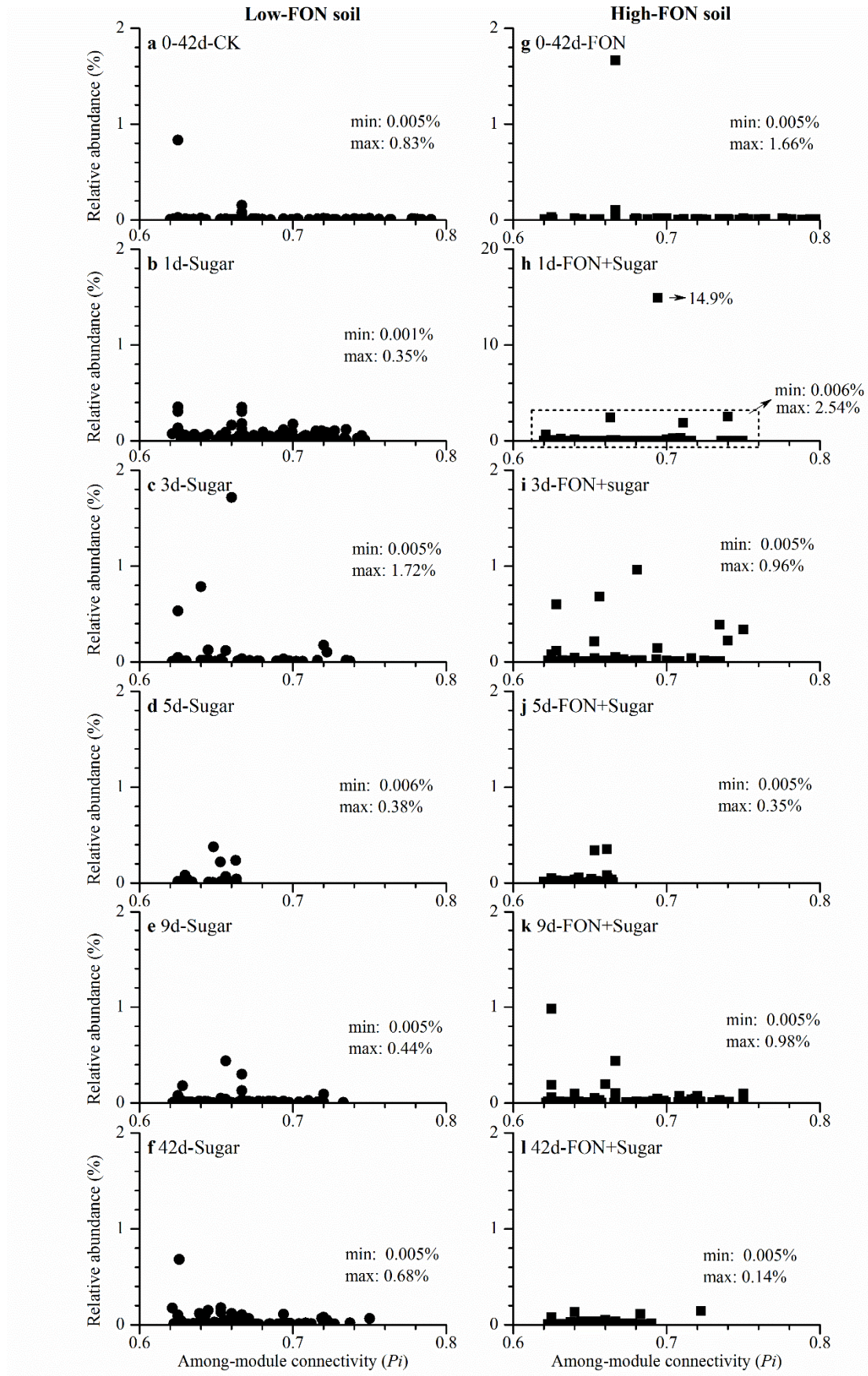


Fig. S10 Relative abundance of connectors in the networks. The minimum and maximum relative abundance are indicated in each panel. In panel h, one OTU had a very high relative abundance

(up to 14.9%) and is indicated by the black arrow. The designations CK and Sugar represent the soil supplied with water and sugars (i.e., glucose, fructose, sucrose, and maltose), respectively. The designation FON represents the soil with FON inoculation. The 0, 1d, 3d, 5d, 9d, and 42d indicate that the samples were collected after 0 day (i.e., zero time), 1 day, 3 days, 5 days, 9 days, and 42 days of microcosm incubation, respectively.