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# Supporting Online Material for

## **Soil bacterial community triggered by organic matter inputs supports a high-yielding pear production**

Li Wang<sup>1</sup>, Xiaomei Ye<sup>1</sup>, Hangwei Hu<sup>2</sup>, Jing Du<sup>1</sup>, Yonglan Xi<sup>1</sup>, Zongzhuan Shen<sup>3</sup>, Jing Lin<sup>4</sup>, Deli  
Chen<sup>2</sup>


### **Affiliations**

<sup>1</sup> Institute of Animal Science, Jiangsu Academy of Agricultural Sciences, Key Laboratory of Crop and Livestock Integrated Farming, Ministry of Agriculture and Rural Affairs, Nanjing 210014, China

<sup>2</sup> Faculty of Veterinary and Agricultural Sciences, University of Melbourne, Melbourne, Victoria 3010, Australia

<sup>3</sup> Jiangsu Provincial Key Lab of Solid Organic Waste Utilization, Jiangsu Collaborative Innovation Center of Solid Organic Wastes, Educational Ministry Engineering Center of Resource-saving fertilizers, The Key Laboratory of Plant Immunity, Nanjing Agricultural University, Nanjing, 210095, China

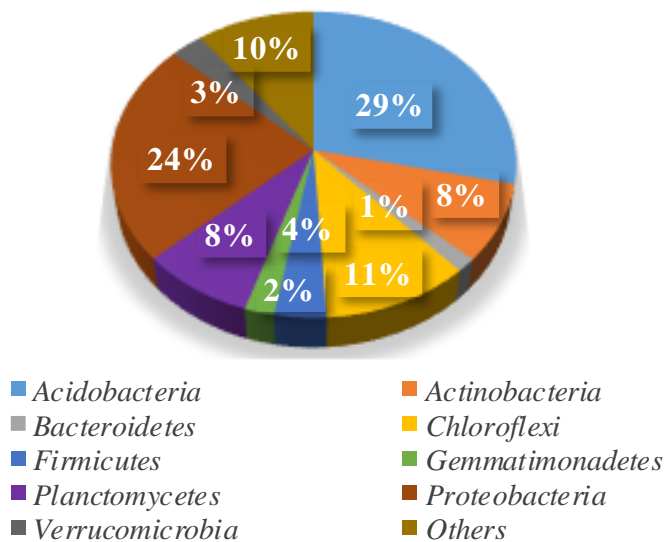
<sup>4</sup> Institute of Pomology, Jiangsu Academy of Agricultural Sciences, Nanjing 210014, China

 Corresponding author: Xiaomei Ye, Institute of Animal Science, Jiangsu Academy of Agricultural Sciences, Key Laboratory of Crop and Livestock Integrated Farming, Ministry of Agriculture and Rural Affairs, Nanjing 210014, China. Zongzhuan Shen, College of Resources and Environmental Sciences, Nanjing Agricultural University, 210095, Nanjing, China. E-mail: shenzongz@njau.edu.cn. Tel: (86)02584395521.

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## Supplemental figures

31 **Fig. S1** Pie chart displaying the average composition of bacterial communities at the phylum level for  
32 all soil samples. Numbers in the pie chart represent the proportion of sequences affiliated to this  
33 phylum to all bacterial sequences.



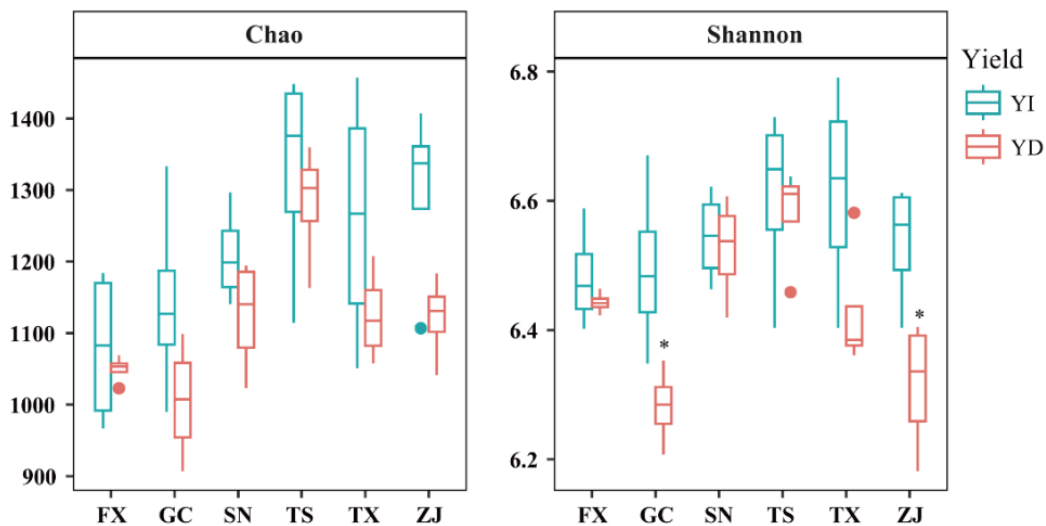
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38 **Fig. S2** Boxplot showing the alpha diversity indices (Chao and Shannon) in yield-invigorating (YI) and  
39 yield-debilitating (YD) orchards of six pair-located orchards.



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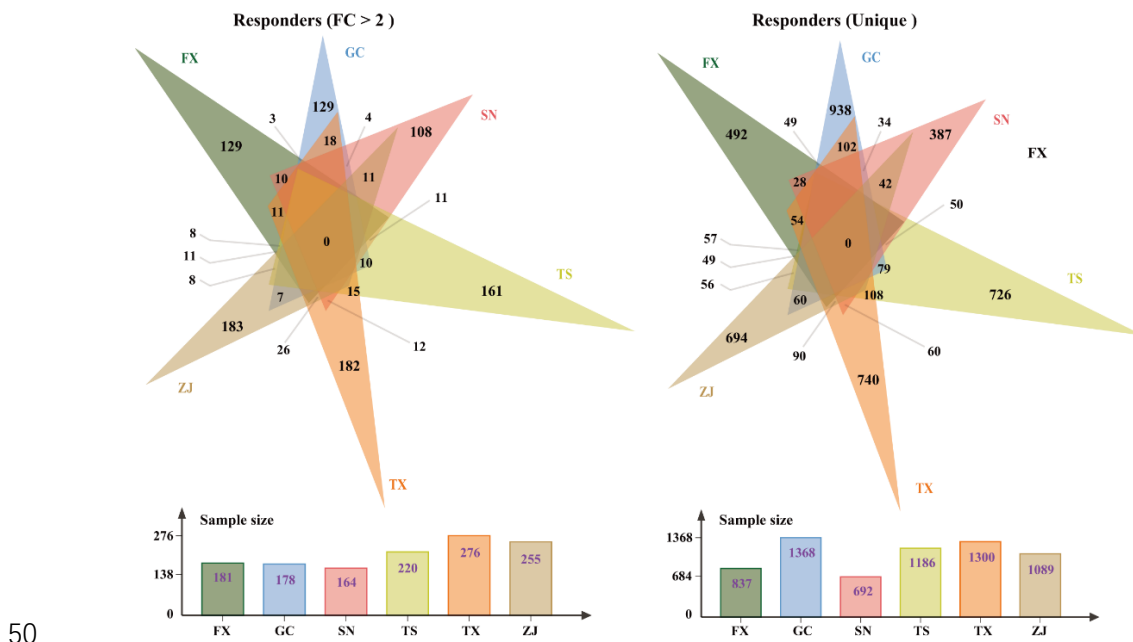
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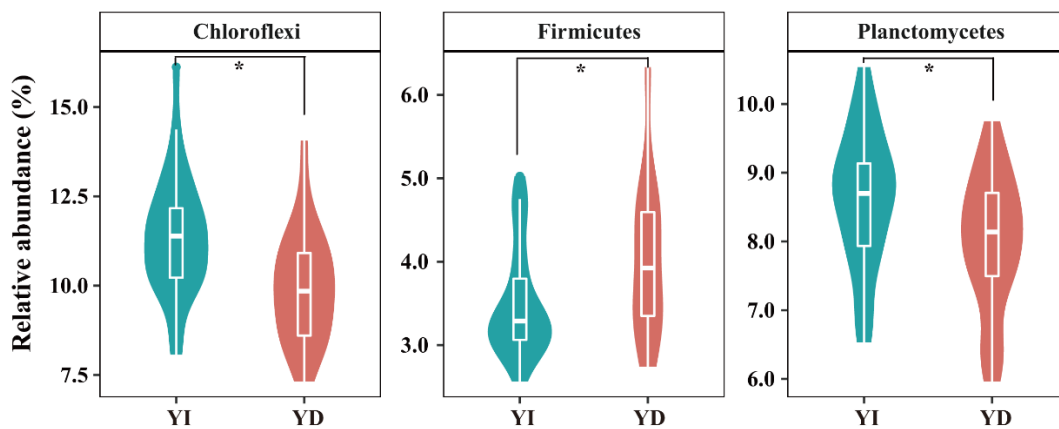
45 **Fig. S3** Venn plot showing the unique and shared bacterial ASVs between yield-invigorating (YI) and  
46 yield-debilitating (YD) orchards for all six sites. Left panel is displaying the “responders”, which the  
47 fold changes (log<sub>2</sub> transformed) of ASVs was larger than 2 in each site in YI soils compared to those in  
48 YD soils. Whereas, the right panel is displaying the “responders”, which the ASVs were unique in YI  
49 soils for each site.



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52 **Fig. S4** Violin plot showing the relative abundance of Chloroflexi, Firmicutes and Planctomycetes in  
53 yield-invigorating (YI) and yield-debilitating (YD) orchards. \* indicates a significant difference  
54 between YI and YD soils based on Wilcoxon tests ( $p < 0.05$ ).



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## Supplemental tables

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59 **Table S1** Field site information of six pair-located orchards. YI and YD represent the orchards were yield-invigorating and yield-debilitating orchards, respectively. The

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relative increase of yield was calculated by as the following equation:  $(YI - YD) / YD \times 100\%$ .

Sample ID	Locations	Administrative division	Soil type	Planting density	Cropping years	Orchard type	Yield (kg/tree)	Relative increase of yield (%)
FX. YI	FX	Fengxian county, Xuzhou city	Sandy soil	3 m × 5 m	3	YI	10.0	49.2
FX. YD					3	YD	6.7	
GC. YI	GC	Gaochun county, Nanjing city	Sandy loam	3 m × 5 m	20	YI	37.5	25.0
GC. YD					20	YD	30.0	
SN. YI	SN	Suining county, Xuzhou city	Sandy soil	1 m × 3 m	4	YI	12.5	25.0
SN. YD					4	YD	10.0	
TS. YI	TS	Tongshan county, Xuzhou city	Sandy soil	3 m × 5 m	4	YI	12.5	25.0
TS. YD					4	YD	10.0	
TX. YI	TX	Taixing county, Taizhou city	Fluvo-aquic soil	3 m × 5 m	6	YI	36.0	28.6
TX. YD					6	YD	28.0	
ZJ. YI	ZJ	Zhangjiagang county, Suzhou city	Loam soil	3 m × 5 m	15	YI	27.5	10.0
ZJ. YD					9	YD	25.0	

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63 **Table S2** Major topological properties of phylogenetic molecular ecological networks of soil bacterial  
 64 communities for yield-invigorating and yield-debilitating orchards.

Network Indexes	YI	YD
Network size	302	235
Total links	448	334
No. of negative interactions	160	105
No. of positive interactions	288	229
Ratio of negative interactions to positive interactions (%)	55.6	45.9
R square of power-law	0.915	0.871
Harmonic geodesic distance (HD)	4.6	4.985
Centralization of betweenness (CB)	0.106	0.154
No. of modules (> 5 nodes)	11	9
Average clustering coefficient (avgCC)	0.152	0.131
Average path distance (GD)	5.494	6.232
Average degree (avgK)	2.967	2.843

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67 **Table S3** The affiliations of keystone nodes identified in the networks constructed by  
 68 yield-invigorating (YI) and yield-debilitating (YD) soils.

Node ID	Network	Phylum	Genus	Function group
ASV26	YI	Acidobacteria	<i>Gp6</i>	Module hubs
ASV296	YI	Acidobacteria	<i>Gp6</i>	
ASV316	YI	Actinobacteria	<i>Gaiella</i>	
ASV6	YD	Acidobacteria	<i>Gp6</i>	
ASV23	YD	Acidobacteria	<i>Gp6</i>	
ASV64	YD	Acidobacteria	<i>Gp17</i>	
ASV66	YD	Acidobacteria	<i>Acanthopleuribacter</i>	
ASV76	YD	Acidobacteria	<i>Gp4</i>	
ASV36	YD	Actinobacteria	<i>Arthrobacter</i>	
ASV126	YD	Proteobacteria	<i>Povalibacter</i>	
ASV256	YI	Actinobacteria	<i>Phycococcus</i>	Connectors
ASV357	YI	Chloroflexi	<i>Longilinea</i>	
ASV115	YI	Others	<i>WPS-1_genera_incertae_sedis</i>	
ASV425	YI	Proteobacteria	<i>Anderseniella</i>	
ASV155	YD	Acidobacteria	<i>Gp6</i>	

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**Table S4** Measured edaphic properties of sampled soils. \* indicates a significant difference between all YI and YD soils based on Wilcoxon tests ( $p < 0.05$ ).

ID	pH	OM* (g/kg)	N (mg/Kg)	AP (mg/Kg)	AK (mg/Kg)	TN (%)	Ca (g/Kg)	Mg (mg/Kg)	Fe (mg/Kg)	Mn (mg/Kg)	Cu (mg/Kg)	Zn (mg/Kg)
FX. YI	6.98±0.02	16.8±2.5	36.8±5.1	16±2	47±4	0.08±0.01	7.5±0.3	194±2	14.4±1.1	3.8±0.6	0.2±0.02	2.5±0.6
FX. YD	6.96±0.05	12.5±1.0	24.4±2.7	19±2	47±3	0.06±0.01	8.6±0.2	196±16	2.1±0.3	3.2±0.3	0.1±0.01	2.1±0.3
GC. YI	5.21±0.11	39.8±7.5	65.1±2.3	188±9	177±21	0.46±0.06	3.7±0.6	628±33	39.6±2.6	36.8±5.0	2.3±0.3	4.9±0.9
GC. YD	5.24±0.09	28.4±1.7	76.6±3.8	96±3	134±20	0.31±0.07	3.2±0.7	265±21	49.2±6.4	49.4±4.3	2.4±0.4	6.1±0.5
SN. YI	6.74±0.05	23.8±3.3	68.4±11.3	126±23	105±13	0.14±0.01	9.4±1.4	493±91	17.2±1.8	4.1±0.2	1.3±0.2	3.5±0.4
SN. YD	6.78±0.05	20.7±3.6	66.5±6.5	167±15	119±17	0.13±0.02	8.5±0.7	454±66	16.7±2.4	4.5±0.5	1.6±0.3	4.0±0.6
TS. YI	6.79±0.01	10.7±0.6	47.1±2.4	84±22	83±15	0.09±0.01	12.3±0.4	286±20	12.5±2.7	5.3±0.5	1.3±0.1	2.7±0.9
TS. YD	7.18±0.32	9.0±1.5	35.5±7.3	12±3	27±4	0.07±0.01	12.8±0.3	386±39	9.9±1.8	3.6±0.2	1.6±0.4	2.2±0.6
TX. YI	6.75±0.07	13.2±1.5	52.0±10.7	210±14	114±33	0.07±0.01	6.4±0.5	474±54	17.9±7.6	4.0±0.9	1.2±0.3	5.0±1.0
TX. YD	6.98±0.21	11.8±0.6	44.4±2.9	82±12	176±19	0.09±0.002	3.9±0.3	399±26	17.8±2.6	2.7±0.7	0.75±0.12	2.8±0.1
ZJ. YI	7.49±0.18	20.7±2.6	49.6±2.2	50±12	36±6	0.11±0.01	6.1±0.1	349±15	16.8±1.2	8.6±0.2	2.8±0.07	1.7±0.2
ZJ. YD	6.92±0.06	17.9±1.8	71.6±8.0	130±22	65±13	0.28±0.03	5.2±0.5	513±46	16.3±0.9	10.1±0.8	2.55±0.21	2.5±0.7
YI (Mean)	6.66±0.72	20.8±10.3	53.2±12.5	112±73	94±50	0.16±0.14	7.6±2.8	404±152	19.7±9.8	10.4±12.3	1.5±0.9	3.4±1.4
YD (Mean)	6.68±0.68	16.7±6.9	53.1±20.5	84±58	95±55	0.16±0.11	7.0±3.4	369±115	18.7±15.2	12.3±17.3	1.5±0.9	3.3±1.5

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77 **Table S5** Correlation coefficients (*R*) and *P* values between selected soil chemical properties in the

78 RDA analysis and bacterial community composition at the ASV level based on Mantel test.

	Mantel test	
	<i>R</i>	<i>P</i>
MN	0.755	0.001
TN	0.580	0.001
OM	0.511	0.001
Ca	0.421	0.001
AP	0.148	0.003
AK	0.379	0.01
N	0.268	0.001
Cu	0.372	0.001

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