

1 Supporting Online Material for

2 **Soil bacterial community triggered by organic matter inputs**

3 **associates with a high-yielding pear production**

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Supplemental figures

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

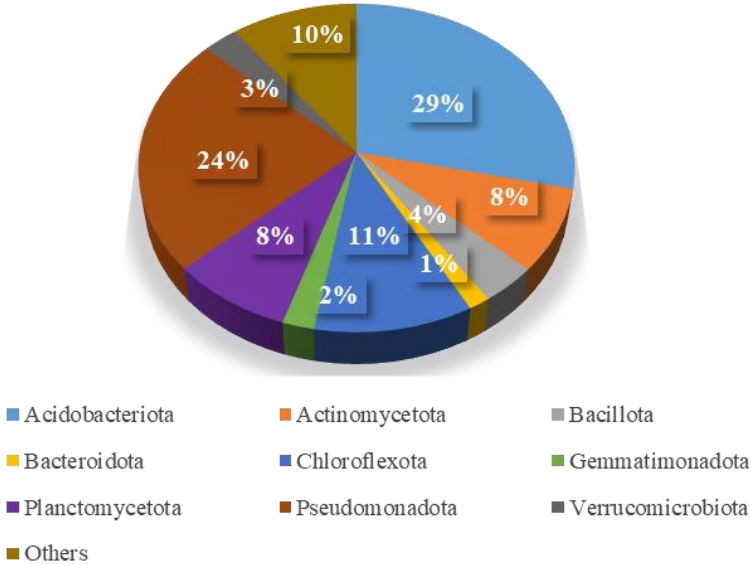
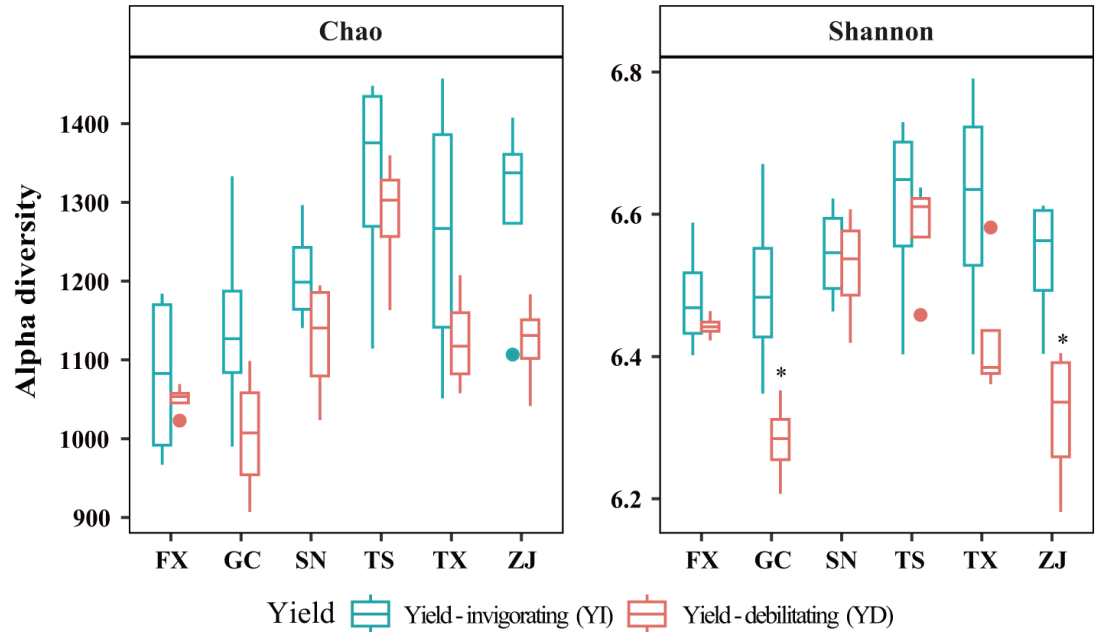
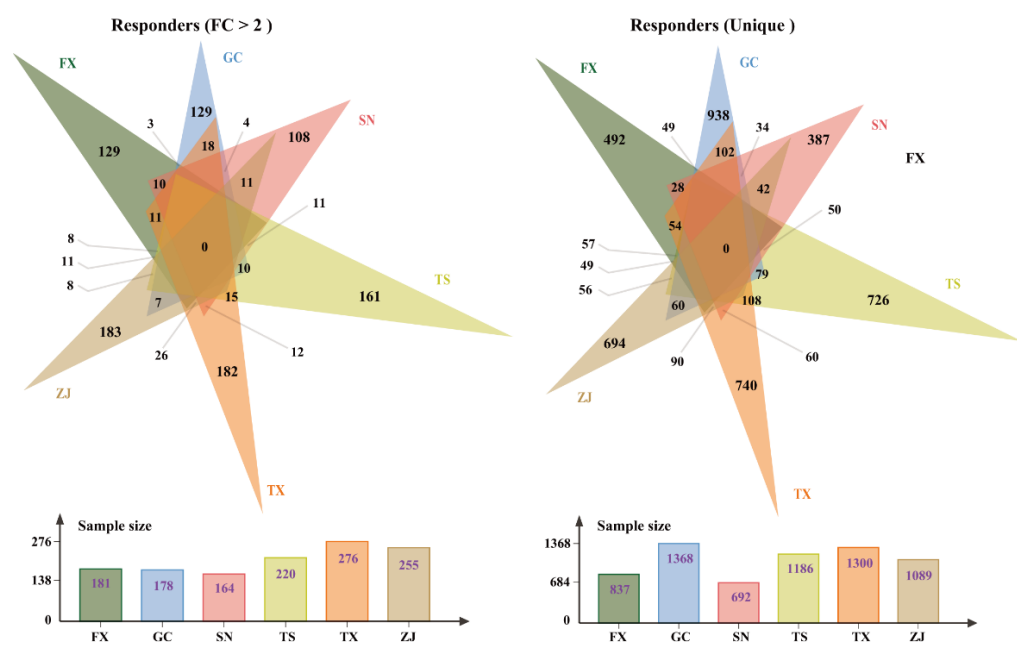


Fig. S2 Boxplot showing the alpha diversity indices (Chao and Shannon) in yield-invigorating (YI) and yield-debilitating (YD) orchards of six pair-located orchards.



41 **Fig. S3** Venn plot showing the unique and shared bacterial ASVs between yield-invigorating (YI) and
 42 yield-debilitating (YD) orchards for all six sites. Left panel is displaying the “responders”, which the
 43 fold changes (log2 transformed) of ASVs was larger than 2 in each site in YI soils compared to those in
 44 YD soils. Whereas, the right panel is displaying the “responders”, which the ASVs were unique in YI
 45 soils for each site.



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 49 **Fig. S4** Violin plot showing the relative abundance of Bacteroidota, Chloroflexota and Planctomycetota
 50 in yield-invigorating (YI) and yield-debilitating (YD) orchards. * indicates a significant difference
 51 between YI and YD soils based on Wilcoxon tests ($p < 0.05$).

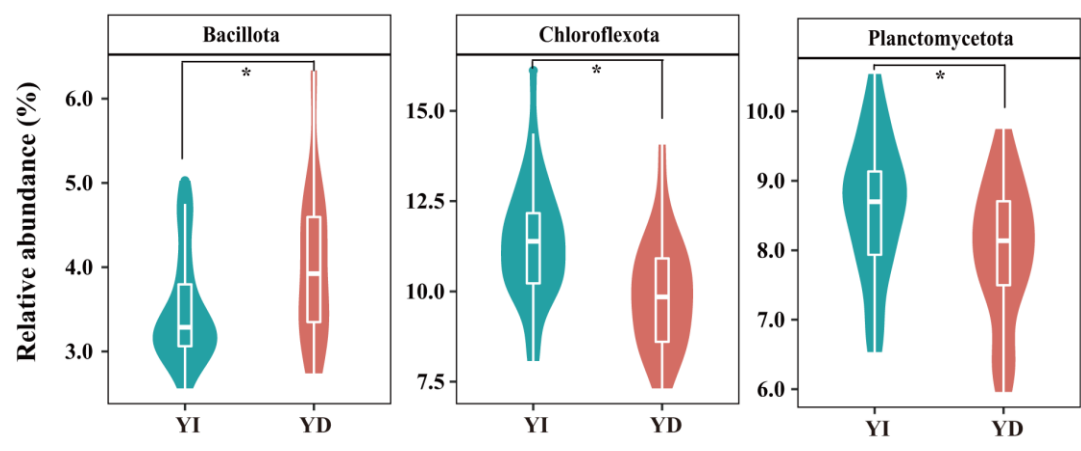


Fig. S5 Genus-level taxonomic analysis of bacterial sequences obtained from yield-invigorating (YI) and yield-debilitating (YD) orchards using the STAMP software. Cyan bars represent the YI soils and pink bars represent the YD soils.

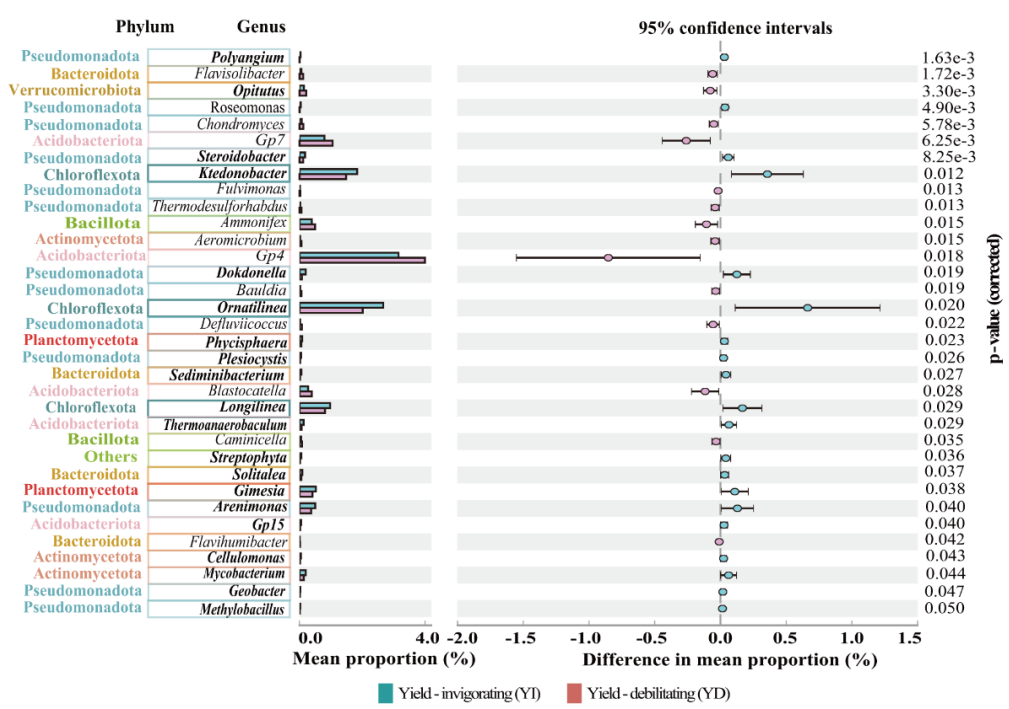
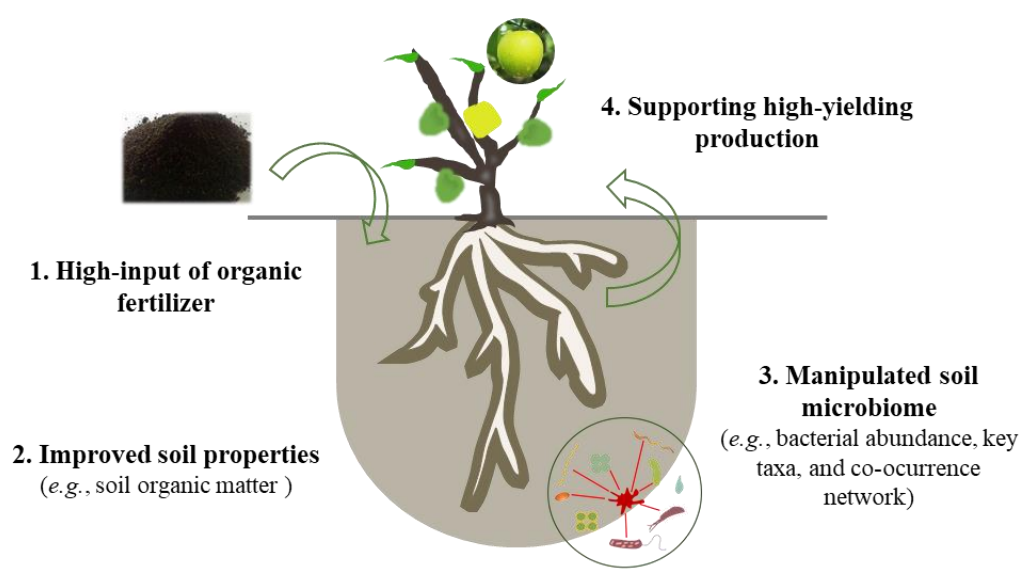


Fig. S6 Conceptual model illustrating the biotic and abiotic factors in affecting the crop production.



Supplemental tables

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 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	

Table S2 Fertilization information for each orchard sampled in this study. YI and YD represent the orchards were yield-invigorating and yield-debilitating orchards, respectively.

Sample ID	location	N (kg/tree)	P ₂ O ₅ (kg/tree)	K ₂ O (kg/tree)	Organic matter (kg/tree)
FX. YI	FX	0.80	0.80	1.00	50
FX. YD		0.80	0.80	1.00	25
GC. YI	GC	0.40	0.40	0.80	27.5
GC. YD		0.40	0.40	0.80	15
SN. YI	SN	0.45	0.45	0.45	35
SN. YD		0.45	0.45	0.45	20
TS. YI	TS	0.75	0.75	0.75	35
TS. YD		0.75	0.75	0.75	15
TX. YI	TX	0.45	0.60	0.45	50
TX. YD		0.45	0.60	0.45	25
ZJ. YI	ZJG	0.55	0.55	0.55	30
ZJ. YD		0.55	0.55	0.55	15

Notes: The amounts of N, P₂O₅, K₂O displaying here are the total amounts of fertilizer applied into each orchard per season. The chemical fertilizers applied in each orchard are urea, superphosphate, potassium chloride, and compound fertilizer based on the farmer option. The type of organic matter applied for each orchard are also different. For yield-invigorating and yield-debilitating orchards in FX, SN, TS, TX, and ZJ, organic fertilizer was pig manure bought from local organic fertilizer companies. Meanwhile, for yield-invigorating and yield-debilitating orchards in GC, organic fertilizer was the mixture of chicken manure and rape seed cake.

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81 **Table S3** 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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85 **Table S4** Major topological properties of phylogenetic molecular ecological networks of soil bacterial
 86 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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89 **Table S5** The affiliations of keystone nodes identified in the networks constructed by yield-invigorating (YI) and yield-debilitating (YD) soils.

Node ID	Network	Phylum	Genus	Function group
ASV26	YI	Acidobacteriota	<i>Gp6</i>	Module hubs
ASV296	YI	Acidobacteriota	<i>Gp6</i>	
ASV316	YI	Acidobacteriota	<i>Gaiella</i>	
ASV6	YD	Acidobacteriota	<i>Gp6</i>	
ASV23	YD	Acidobacteriota	<i>Gp6</i>	
ASV64	YD	Acidobacteriota	<i>Gp17</i>	
ASV66	YD	Acidobacteriota	<i>Acanthopleuribacter</i>	
ASV76	YD	Acidobacteriota	<i>Gp4</i>	
ASV36	YD	Actinomycetota	<i>Arthrobacter</i>	
ASV126	YD	Pseudomonadota	<i>Povalibacter</i>	Connectors
ASV256	YI	Actinomycetota Chloroflexota	<i>Phycococcus</i>	
ASV357	YI		<i>Longilinea</i>	
ASV115	YI	Others	<i>WPS-I_genera_incertae_sedis</i>	
ASV425	YI	Pseudomonadota	<i>Andersenella</i>	
ASV155	YD	Acidobacteriota	<i>Gp6</i>	

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92 **Table S6** Correlation coefficients (*R*) and *P* values between selected soil chemical properties in the

93 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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