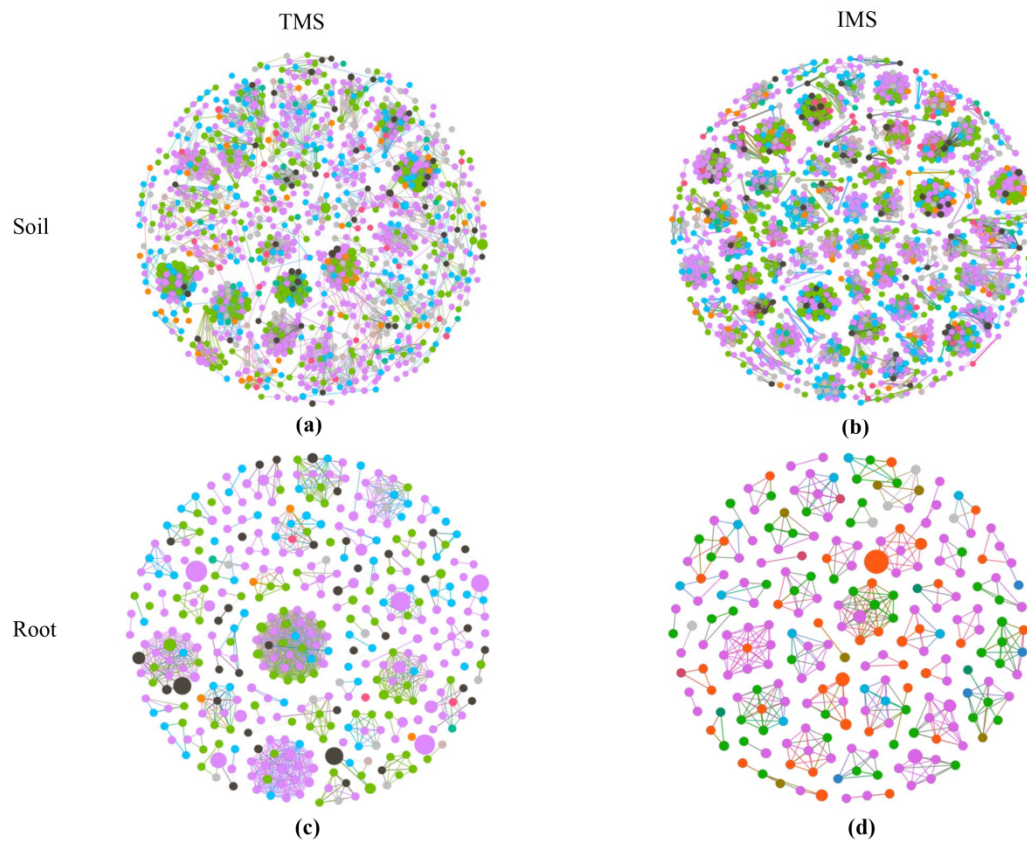


Table S1. Comparative analysis for the relative abundance of dominant bacterial genera in rhizosphere soils and roots of Lei bamboo.

Phylum	Genus	Soil		Root	
		IMS	TMS	IMS	TMS
Acidobacteria	<i>Acidipila</i>	4.02% ± 0.52%a	1.29% ± 0.13%b	5.37% ± 3.01%a	0.08% ± 0.03%b
Acidobacteria	<i>Subgroup_13</i>	5.78% ± 0.68%a	2.48% ± 0.31%b	0.27% ± 0.12%a	0.06% ± 0.06%b
Acidobacteria	<i>Occallatibacter</i>	2.32% ± 0.31%b	5.66% ± 0.50%a	0.16% ± 0.05%a	0.16% ± 0.07%a
Acidobacteria	<i>Subgroup_2</i>	2.05% ± 0.22%b	5.45% ± 0.94%a	0.10% ± 0.07%a	0.14% ± 0.11%a
Acidobacteria	<i>Granulicella</i>	0.91% ± 0.19%a	0.83% ± 0.10%a	2.73% ± 1.47%a	0.69% ± 0.49%b
Actinobacteria	<i>Streptomyces</i>	0.11% ± 0.17%b	0.95% ± 0.53%a	1.19% ± 0.61%a	18.12% ± 13.86%a
Actinobacteria	<i>Mycobacterium</i>	0.54% ± 0.08%b	1.09% ± 0.38%a	2.51% ± 1.00%b	15.17% ± 4.37%a
Actinobacteria	<i>Acidotherrmus</i>	4.07% ± 0.34%a	2.68% ± 0.17%b	5.70% ± 1.98%a	0.82% ± 0.23%b
Actinobacteria	<i>Actinospica</i>	0.38% ± 0.09%b	0.55% ± 0.09%a	3.07% ± 1.43%a	0.16% ± 0.11%b
Firmicutes	<i>Bacillus</i>	0.33% ± 0.15%b	0.58% ± 0.17%a	0.86% ± 0.61%b	3.90% ± 1.21%a
Proteobacteria	<i>Chujaibacter</i>	13.47% ± 2.38%a	1.85% ± 0.15%b	2.03% ± 0.78%a	0.07% ± 0.02%b
Proteobacteria	<i>Burkholderia-Caballeronia-Paraburkholderia</i>	1.00% ± 0.21%b	2.29% ± 0.50%a	2.45% ± 1.47%b	11.66% ± 4.72%a
Proteobacteria	<i>Acidibacter</i>	6.89% ± 0.46%a	3.68% ± 0.32%b	2.89% ± 0.94%a	1.21% ± 0.68%b
Proteobacteria	<i>Acidocella</i>	0.15% ± 0.06%a	0.01% ± 0.01%b	6.31% ± 1.95%a	0.09% ± 0.04%b
Proteobacteria	<i>Acidisoma</i>	0.23% ± 0.08%a	0.11% ± 0.03%b	5.97% ± 0.97%a	0.10% ± 0.04%b
Proteobacteria	<i>Bradyrhizobium</i>	1.05% ± 0.11%b	2.42% ± 0.32%a	0.59% ± 0.19%b	1.72% ± 0.49%a
Proteobacteria	<i>KF-JG30-C25</i>	1.79% ± 0.09%a	1.95% ± 0.16%a	0.15% ± 0.09%a	0.10% ± 0.09%a

Different lowercase letters within rows indicate significant difference ( $p < 0.05$ ).

IMS, intensive management system; TMS, traditional management system.



**Figure S1.** Bacterial networks in bamboo rhizosphere soil (a, b) and root (c, d) collected from intensive management system (IMS) and traditional management system (TMS).