**Dose-dependent effect of compost amendment on soil bacterial community composition and co-occurrence network patterns in soybean agroecosystem**

**PCR conditions**

The amplification was carried out in a final 25 μL reaction solution including 2.5 μL of 10 × buffer, 1.5 mM of MgCl2, 200 μM of each dNTP, 0.75 μM of each primer, 0.75 U PrimeSTAR HS DNA Polymerase (Takara, Japan), and 1μL of template DNA. The 16S rDNA was amplified with the following conditions: denaturation at 94 °C for 5 min, 30 cycles of denaturation at 94 °C for 40 s, annealing at 56 °C for 1 min, and extension at 72 °C for 1 min, followed by a final extension at 72 °C for 10 min. All PCR products were purified using an agarose gel DNA purification kit (TaKaRa, Japan) and quantified using Nanodrop 2000 (Thermoscientific, USA). Only PCR products with concentration > 10 ngμL-1 and OD 260 / OD 280≈1.8 were used, others were discarded and re-amplified to ensure the Miseq sequencing quality. The final PCR products from all samples were mixed at equimolar concentrations and then subjected to Illumina Miseq platform at Environmental Genome Platform of Chengdu Institute of Biology, Chinese Academy of Sciences.

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| **Table S1.** One way ANOVA examining the effects of compost addition (C) on the abundant phyla of soil bacteria in seedling, flowering and mature stage. | | | | | | | | | |
|  | | Seedling | |  | Flowering | |  | Mature | |
| phylum | | *F* | *P* |  | *F* | *P* |  | *F* | *P* |
| Bacteria | Acidobacteria | 14.14 | 0 |  | 3.57 | 0.051 |  | 2.93 | 0.08 |
| Actinobacteria | 0.27 | 0.9 |  | 9.68 | 0.002 |  | 0.53 | 0.67 |
| Armatimonadetes | 7.89 | 0.004 |  | 3.11 | 0.07 |  | 3.68 | 0.04 |
| Bacteroidetes | 9.59 | 0.002 |  | 2.34 | 0.13 |  | 0.09 | 0.96 |
| Chlamydiae | 0.52 | 0.68 |  | 0.53 | 0.67 |  | 0.50 | 0.69 |
| Chlorobi | 1.71 | 0.22 |  | 0.93 | 0.46 |  | 0.78 | 0.53 |
| Chloroflexi | 1.23 | 0.34 |  | 1.28 | 0.33 |  | 0.36 | 0.78 |
| Cyanobacteria | 1.03 | 0.42 |  | 1.16 | 0.37 |  | 0.39 | 0.77 |
| Elusimicrobia | 3.79 | 0.04 |  | 1.19 | 0.36 |  | 1.15 | 0.37 |
| Fibrobacteres | 5.17 | 0.02 |  | 5.26 | 0.02 |  | 2.34 | 0.13 |
| Firmicutes | 6.38 | 0.009 |  | 0.15 | 0.93 |  | 6.03 | 0.01 |
| Gemmatimonadetes | 3.18 | 0.07 |  | 1.50 | 0.27 |  | 0.19 | 0.90 |
| Nitrospirae | 8.06 | 0.004 |  | 2.1 | 0.16 |  | 0.83 | 0.51 |
| Planctomycetes | 5.31 | 0.02 |  | 0.66 | 0.60 |  | 2.05 | 0.16 |
| Proteobacteria | 0.57 | 0.65 |  | 1.00 | 0.43 |  | 1.37 | 0.3 |
| Verrucomicrobia | 9.35 | 0.002 |  | 2.50 | 0.11 |  | 2.34 | 0.12 |

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| **Table S2.** Kruskal-Willis examining the effects of compost addition (C) on the abundant OTUs of bacteria in seedling, flowering and mature stage. | | | | | | | |
|  | Seedling | | Flowering | | Mature | | Classification |
| Variables | *X*2 | *P* | *X*2 | *P* | *X*2 | *P* |  |
| OTU1 | 10.542 | 0.014 | 4.919 | 0.178 | 1.814 | 0.612 | Proteobacteria|Alphaproteobacteria|Rhizobiales|Bradyrhizobiaceae|Bradyrhizobium |
| OTU2 | 9.61 | 0.022 | 6.945 | 0.074 | 4.386 | 0.223 | Bacteroidetes|Saprospirae|Saprospirales|Chitinophagaceae|Flavisolibacter |
| OTU3 | 11.079 | 0.011 | 6.575 | 0.087 | 4.815 | 0.186 | Acidobacteria|Acidobacteria-6|iii1-15 |
| OTU4 | 11.969 | 0.007 | 5.747 | 0.125 | 5.7 | 0.127 | Proteobacteria|Betaproteobacteria|Ellin6067 |
| OTU5 | 6.401 | 0.094 | 9.087 | 0.028 | 9.364 | 0.025 | Proteobacteria|Betaproteobacteria|Burkholderiales|Oxalobacteraceae|Janthinobacterium |
| OTU6 | 7.037 | 0.071 | 3.872 | 0.276 | 6.702 | 0.082 | Proteobacteria|Alphaproteobacteria|Sphingomonadales|Sphingomonadaceae|Kaistobacter |
| OTU7 | 9.56 | 0.023 | 8.192 | 0.042 | 4.043 | 0.257 | Actinobacteria|Actinobacteria|Actinomycetales|Micrococcaceae|Arthrobacter|psychrolactophilus |
| OTU8 | 9.441 | 0.024 | 1.825 | 0.609 | 4.26 | 0.235 | Proteobacteria|Betaproteobacteria|SC-I-84 |
| OTU9 | 4.482 | 0.214 | 8.372 | 0.039 | 4.457 | 0.216 | Proteobacteria|Betaproteobacteria|Burkholderiales|Comamonadaceae|Variovorax|paradoxus |
| OTU10 | 10.51 | 0.015 | 8.29 | 0.04 | 2.763 | 0.43 | Proteobacteria|Betaproteobacteria|Burkholderiales|Comamonadaceae|Methylibium |
| OTU11 | 10.642 | 0.014 | 2.546 | 0.467 | 4.519 | 0.211 | Proteobacteria|Betaproteobacteria|Burkholderiales|Comamonadaceae|Ramlibacter |
| OTU12 | 5.378 | 0.146 | 8.888 | 0.031 | 1.961 | 0.581 | Actinobacteria|Actinobacteria|Actinomycetales|Nocardioidaceae|Aeromicrobium |
| OTU13 | 1.522 | 0.677 | 7.693 | 0.053 | 3.756 | 0.289 | Bacteroidetes|Flavobacteriia|Flavobacteriales|Flavobacteriaceae|Flavobacterium|succinicans |
| OTU14 | 5.937 | 0.115 | 2.572 | 0.462 | 3.622 | 0.305 | Proteobacteria|Gammaproteobacteria|Xanthomonadales|Xanthomonadaceae |
| OTU15 | 8.67 | 0.034 | 5.227 | 0.156 | 3.501 | 0.321 | Proteobacteria|Gammaproteobacteria|Xanthomonadales|Sinobacteraceae |
| OTU16 | 10.935 | 0.012 | 3.584 | 0.31 | 3.472 | 0.324 | Verrucomicrobia|Spartobacteria|Chthoniobacterales|Chthoniobacteraceae|DA101 |
| OTU17 | 8.5 | 0.037 | 5.961 | 0.114 | 3.921 | 0.27 | Chloroflexi|Ellin6529 |
| OTU18 | 10.508 | 0.015 | 2.854 | 0.415 | 1.541 | 0.673 | Acidobacteria|Solibacteres|Solibacterales|Solibacteraceae|Candidatus|Solibacter |
| OTU19 | 10.245 | 0.017 | 10.321 | 0.016 | 6.492 | 0.09 | Acidobacteria|Chloracidobacteria|RB41 |
| OTU20 | 7.848 | 0.049 | 3.467 | 0.325 | 5.968 | 0.113 | Bacteroidetes|Saprospirae|Saprospirales|Chitinophagaceae |
| OTU21 | 8.4 | 0.038 | 6.169 | 0.104 | 6.997 | 0.072 | Proteobacteria|Alphaproteobacteria|Sphingomonadales|Sphingomonadaceae|Kaistobacter |
| OTU22 | 8.22 | 0.042 | 0.954 | 0.812 | 3.96 | 0.266 | Actinobacteria|Actinobacteria|Actinomycetales|Streptomycetaceae|Streptomyces|mirabilis |
| OTU23 | 8.987 | 0.029 | 7.251 | 0.064 | 3.993 | 0.262 | Verrucomicrobia|Spartobacteria|Chthoniobacterales|Chthoniobacteraceae|DA101 |
| OTU24 | 10.399 | 0.015 | 3.125 | 0.373 | 3.181 | 0.365 | Actinobacteria|Thermoleophilia|Solirubrobacterales |
| OTU25 | 4.447 | 0.217 | 1.402 | 0.705 | 2.99 | 0.393 | Actinobacteria|Actinobacteria|Actinomycetales|Mycobacteriaceae|Mycobacterium |
| OTU26 | 9.675 | 0.022 | 11.389 | 0.01 | 12.882 | 0.005 | Actinobacteria|Actinobacteria|Actinomycetales|Thermomonosporaceae|Actinomadura|vinacea |
| OTU27 | 6.46 | 0.091 | 4.85 | 0.183 | 0.966 | 0.809 | Bacteroidetes|Saprospirae|Saprospirales|Chitinophagaceae |
| OTU28 | 7.056 | 0.07 | 2.301 | 0.512 | 3.982 | 0.263 | Proteobacteria|Alphaproteobacteria|Rhizobiales|Hyphomicrobiaceae|Devosia |
| OTU29 | 2.96 | 0.398 | 0.647 | 0.886 | 1.963 | 0.58 | Actinobacteria|Actinobacteria|Actinomycetales|Micromonosporaceae|Dactylosporangium |
| OTU33 | 7.994 | 0.046 | 4.167 | 0.244 | 5.725 | 0.126 | Actinobacteria|Actinobacteria|Actinomycetales|Nocardioidaceae |
| OTU34 | 1.207 | 0.751 | 8.236 | 0.041 | 1.95 | 0.583 | Actinobacteria|Actinobacteria|Actinomycetales|Micromonosporaceae |
| OTU36 | 9.875 | 0.02 | 10.356 | 0.016 | 9.696 | 0.021 | Actinobacteria|Actinobacteria|Actinomycetales|Streptomycetaceae|Streptomyces |
| OTU37 | 11.622 | 0.009 | 8.182 | 0.042 | 9.066 | 0.028 | Bacteroidetes|Cytophagia|Cytophagales|Cytophagaceae |
| OTU38 | 12.367 | 0.006 | 9.708 | 0.021 | 9.792 | 0.02 | Actinobacteria|Actinobacteria|Actinomycetales|Promicromonosporaceae|Promicromonospora |
| OTU40 | 7.5 | 0.058 | 2.091 | 0.554 | 2.489 | 0.477 | Bacteroidetes|Sphingobacteriia|Sphingobacteriales|Sphingobacteriaceae|Sphingobacterium|multivorum |
| OTU41 | 6.709 | 0.082 | 2.437 | 0.487 | 5.608 | 0.132 | Proteobacteria|Gammaproteobacteria|Xanthomonadales|Xanthomonadaceae|Thermomonas |
| OTU48 | 5.824 | 0.12 | 3.601 | 0.308 | 1.617 | 0.656 | Firmicutes|Bacilli|Bacillales|Bacillaceae|Bacillus|flexus |
| OTU52 | 10.713 | 0.013 | 7.837 | 0.049 | 10.406 | 0.015 | Bacteroidetes|Cytophagia|Cytophagales|Cytophagaceae |
| OTU53 | 0.881 | 0.83 | 7.417 | 0.06 | 0.406 | 0.939 | Proteobacteria|Gammaproteobacteria|Enterobacteriales|Enterobacteriaceae |
| OTU55 | 9.196 | 0.027 | 6.898 | 0.075 | 13.389 | 0.004 | Proteobacteria|Deltaproteobacteria|Myxococcales |
| OTU56 | 6.679 | 0.083 | 0.246 | 0.97 | 0.518 | 0.915 | Proteobacteria|Gammaproteobacteria|Xanthomonadales|Xanthomonadaceae|Stenotrophomonas |
| OTU64 | 8.731 | 0.033 | 7.866 | 0.049 | 10.028 | 0.018 | Proteobacteria|Gammaproteobacteria|Xanthomonadales|Sinobacteraceae|Steroidobacter |
| OTU65 | 13.097 | 0.004 | 9.304 | 0.026 | 11.468 | 0.009 | Proteobacteria|Gammaproteobacteria|Alteromonadales|Alteromonadaceae|Cellvibrio |
| OTU71 | 3.411 | 0.333 | 0.381 | 0.944 | 4.411 | 0.22 | Cyanobacteria|Chloroplast|Streptophyta |
| OTU73 | 11.888 | 0.008 | 9.094 | 0.028 | 3 | 0.392 | Bacteroidetes|Flavobacteriia|Flavobacteriales|Cryomorphaceae|Fluviicola |
| OTU74 | 9.696 | 0.021 | 7.697 | 0.053 | 11.578 | 0.009 | Bacteroidetes|Cytophagia|Cytophagales|Cytophagaceae |
| OTU76 | 12.73 | 0.005 | 8.994 | 0.029 | 11.272 | 0.01 | Proteobacteria|Gammaproteobacteria|Xanthomonadales|Xanthomonadaceae|Luteimonas |
| OTU77 | 10.695 | 0.013 | 3.845 | 0.279 | 5.077 | 0.166 | Bacteroidetes|Sphingobacteriia|Sphingobacteriales|Sphingobacteriaceae|Parapedobacter |
| OTU88 | 9.47 | 0.024 | 8.052 | 0.045 | 9.634 | 0.022 | Chloroflexi|Anaerolineae|CFB-26 |
| OTU125 | 8.452 | 0.038 | 9.68 | 0.021 | 4.775 | 0.189 | Chloroflexi|Anaerolineae|SBR1031|SHA-31 |
| OTU127 | 11.642 | 0.009 | 8.092 | 0.044 | 12.012 | 0.007 | Proteobacteria|Alphaproteobacteria|Rhizobiales|Hyphomicrobiaceae|Devosia |
| OTU132 | 9.158 | 0.027 | 4.868 | 0.182 | 8.744 | 0.033 | Chloroflexi|Chloroflexi|Roseiflexales |
| OTU181 | 9.793 | 0.02 | 5.25 | 0.154 | 7.364 | 0.061 | Bacteroidetes|Flavobacteriia|Flavobacteriales|Flavobacteriaceae|Flavobacterium |
| OTU202 | 2.143 | 0.543 | 2.28 | 0.516 | 10.065 | 0.018 | Proteobacteria|Deltaproteobacteria|Myxococcales |
| OTU205 | 11.987 | 0.007 | 6.566 | 0.087 | 11.323 | 0.01 | Bacteroidetes|Flavobacteriia|Flavobacteriales|Flavobacteriaceae |

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| **Table S3.** The classification at each taxonomic level of the generalists. | | | | | | | | |
| Treatment | Generalist | ID | Phylum | Class | Order | Family | Genus | Speices |
| CK | module hubs | OTU24 | Actinobacteria | Thermoleophilia | Solirubrobacterales |  |  |  |
| CK | module hubs | OTU93 | Acidobacteria | Acidobacteriia | Acidobacteriales | Koribacteraceae |  |  |
| CK | module hubs | OTU209 | Verrucomicrobia | Pedosphaerae | Pedosphaerales | Ellin515 |  |  |
| CK | module hubs | OTU1371 | Planctomycetes | Phycisphaerae | WD2101 |  |  |  |
| CK | connectors | OTU824 | Fibrobacteres | Fibrobacteria | 258ds10 |  |  |  |
| LC | module hubs | OTU59 | Proteobacteria | Deltaproteobacteria | Myxococcales | Myxococcaceae |  |  |
| LC | module hubs | OTU181 | Bacteroidetes | Flavobacteriia | Flavobacteriales | Flavobacteriaceae | Flavobacterium | |
| LC | module hubs | OTU528 | Proteobacteria | Gammaproteobacteria | Alteromonadales | 211ds20 |  |  |
| LC | module hubs | OTU1358 | Chloroflexi | Thermomicrobia |  |  |  |  |
| LC | module hubs | OTU1594 | Proteobacteria | Deltaproteobacteria |  |  |  |  |
| MC | module hubs | OTU32 | Actinobacteria | Actinobacteria | Actinomycetales | Nocardioidaceae | Nocardioides | |
| MC | module hubs | OTU66 | Proteobacteria | Gammaproteobacteria | Xanthomonadales | Sinobacteraceae |  |  |
| MC | module hubs | OTU109 | Proteobacteria | Betaproteobacteria | MND1 |  |  |  |
| MC | module hubs | OTU119 | Actinobacteria | Actinobacteria | Actinomycetales | Microbacteriaceae | Salinibacterium | |
| MC | module hubs | OTU144 | Actinobacteria | Thermoleophilia | Gaiellales | Gaiellaceae |  |  |
| MC | module hubs | OTU211 | Actinobacteria | Thermoleophilia | Gaiellales | Gaiellaceae |  |  |
| MC | module hubs | OTU640 | Bacteroidetes | Cytophagia | Cytophagales | Cytophagaceae | Cytophaga |  |
| MC | module hubs | OTU981 | Actinobacteria | Actinobacteria | Actinomycetales | Thermomonosporaceae | Actinomadura | echinospora |
| MC | module hubs | OTU1005 | AD3 | ABS-6 |  |  |  |  |
| MC | module hubs | OTU1038 | Proteobacteria | Gammaproteobacteria | Legionellales | Coxiellaceae | Aquicella |  |
| MC | module hubs | OTU1094 | Chloroflexi | Thermomicrobia | AKYG1722 |  |  |  |
| MC | module hubs | OTU1193 | Bacteroidetes | Saprospirae | Saprospirales | Chitinophagaceae |  |  |
| MC | module hubs | OTU1233 | Acidobacteria | Acidobacteria-6 | iii1-15 |  |  |  |
| MC | module hubs | OTU1460 | Proteobacteria | Deltaproteobacteria | Myxococcales |  |  |  |
| MC | connectors | OTU284 | Bacteroidetes | Cytophagia | Cytophagales | Cytophagaceae |  |  |
| MC | connectors | OTU317 | Bacteroidetes | Cytophagia | Cytophagales | Cytophagaceae |  |  |
| MC | connectors | OTU1058 | Proteobacteria | Alphaproteobacteria | Sphingomonadales | Sphingomonadaceae | Sphingomonas | |
| MC | connectors | OTU1061 | Actinobacteria | Acidimicrobiia | Acidimicrobiales | C111 |  |  |
| MC | connectors | OTU1182 | Gemmatimonadetes | Gemm-1 |  |  |  |  |
| MC | connectors | OTU1350 | Firmicutes | Bacilli | Bacillales | Paenibacillaceae | Thermobacillus | composti |
| HC | module hubs | OTU28 | Proteobacteria | Alphaproteobacteria | Rhizobiales | Hyphomicrobiaceae | Devosia |  |
| HC | module hubs | OTU50 | Actinobacteria | Thermoleophilia | Solirubrobacterales | Solirubrobacteraceae |  |  |
| HC | module hubs | OTU81 | Bacteroidetes | Saprospirae | Saprospirales | Chitinophagaceae |  |  |
| HC | module hubs | OTU84 | Actinobacteria | Thermoleophilia | Solirubrobacterales |  |  |  |
| HC | module hubs | OTU103 | Actinobacteria | Actinobacteria | Actinomycetales | Nocardioidaceae | Kribbella |  |
| HC | module hubs | OTU173 | Proteobacteria | Alphaproteobacteria | Rhizobiales | Phyllobacteriaceae | Mesorhizobium | |
| HC | module hubs | OTU250 | Proteobacteria | Alphaproteobacteria | Sphingomonadales | Sphingomonadaceae |  |  |
| HC | module hubs | OTU365 | Bacteroidetes | Saprospirae | Saprospirales | Chitinophagaceae |  |  |
| HC | module hubs | OTU497 | Proteobacteria | Alphaproteobacteria | Rhizobiales | Phyllobacteriaceae | Aminobacter | |
| HC | module hubs | OTU676 | Chlorobi |  |  |  |  |  |
| HC | connectors | OTU126 | Proteobacteria | Betaproteobacteria | Burkholderiales | Comamonadaceae |  |  |
| HC | connectors | OTU132 | Chloroflexi | Chloroflexi | Roseiflexales |  |  |  |
| HC | connectors | OTU166 | Proteobacteria | Betaproteobacteria |  |  |  |  |
| HC | connectors | OTU204 | Proteobacteria | Gammaproteobacteria | Alteromonadales | Alteromonadaceae | Cellvibrio |  |
| HC | connectors | OTU484 | Bacteroidetes | Cytophagia | Cytophagales | Cytophagaceae |  |  |
| HC | connectors | OTU493 | Proteobacteria | Betaproteobacteria | MND1 |  |  |  |
| HC | connectors | OTU524 | Bacteroidetes | Flavobacteriia | Flavobacteriales | Flavobacteriaceae | Flavobacterium | gelidilacus |
| HC | connectors | OTU608 | Chloroflexi | Anaerolineae | SBR1031 | A4b |  |  |
| HC | connectors | OTU747 | Proteobacteria | Alphaproteobacteria | Caulobacterales | Caulobacteraceae | Mycoplana | |
| HC | connectors | OTU886 | Bacteroidetes | Flavobacteriia | Flavobacteriales | Flavobacteriaceae | Flavobacterium | |
| HC | connectors | OTU1000 | Proteobacteria | Alphaproteobacteria | Rhodospirillales | Rhodospirillaceae |  |  |
| HC | connectors | OTU1243 | Proteobacteria | Gammaproteobacteria | Oceanospirillales | Halomonadaceae | Halomonas | |
| HC | connectors | OTU25 | Actinobacteria | Actinobacteria | Actinomycetales | Mycobacteriaceae | Mycobacterium | |
| HC | connectors | OTU12 | Actinobacteria | Actinobacteria | Actinomycetales | Nocardioidaceae | Aeromicrobium | |



**Figure. S1.** Zi-Pi plot showing the distribution of soil bacterial OTUs based on their topological roles. Each triangle represents an OTU in CK (yellow), LC (green), MC (red) or HC (blue) network. Abbreviations: CK, control; LC, low level of compost addition; MC, moderate level of compost addition; HC, high level of compost addition.