**SI Materials and Methods**

**Preparation of bacterial suspensions**

*R. solanacearum* and *Paenibacillus favisporus* Y7 were inoculated in 2 ml of LB (Luria Broth) medium and incubated for 24 h at 30 °C at 180 rpm. The cell density was adjusted to the desired concentration.

*Streptomyces coelicoflavus* F13 was streaked on a plate containing gauze No. 1 medium and incubated at 28 °C for five days. Approximately 5 ml of [sterile](file:///D:\%E6%9C%89%E9%81%93%E8%AF%8D%E5%85%B8\Dict\7.2.0.0703\resultui\dict\?keyword=sterile) [water](file:///D:\%E6%9C%89%E9%81%93%E8%AF%8D%E5%85%B8\Dict\7.2.0.0703\resultui\dict\?keyword=water) was added to the plate to suspend the spores in water, and the resulting suspension was passed through a sterile cotton filter. The spore density was adjusted to the desired concentration.

Table S1. The top 10 hubs of the bacterial networks

|  |  |  |
| --- | --- | --- |
| Genus | Link numbers | |
| CK | KP |
| *Streptomyces* | 532 | 447 |
| *Bacillus* | 267 | 705 |
| *Paenibacillus* | 312 | 267 |
| *Lysobacter* | 309 | 204 |
| *Pseudomonas* | 242 | 232 |
| *Rhizobium* | 196 | 251 |
| *Pedobacter* | 323 | 106 |
| *Chitinophaga* | 302 | 63 |
| *Sphingobium* | 195 | 167 |

Table S2. The positive link numbers between the target hubs (*Streptomyces*, *Paenibacillus* and *Bacillus*) and other nodes as well as the relative abundances of these nodes

|  |  |  |  |  |
| --- | --- | --- | --- | --- |
| Phylum | CK | | KP | |
| Link numbers | Relative abundance (%) | Link numbers | Relative abundance (%) |
| Actinobacteria | 23 | 18.91 | 40 | 13.8 |
| Firmicutes | 9 | 3.09 | 11 | 1.35 |
| Bacteroidetes | 21 | 4.15 | 5 | 0.49 |
| Proteobacteria | 58 | 13.22 | 48 | 5.69 |

Table S3. The negative link numbers between the target hubs (*Streptomyces*, *Paenibacillus* and *Bacillus*) and other nodes as well as the relative abundances of these nodes

|  |  |  |  |  |
| --- | --- | --- | --- | --- |
| Phylum | CK | | KP | |
| Link numbers | Relative abundance (%) | Link numbers | Relative abundance (%) |
| Actinobacteria | 23 | 8.87 | 14 | 11.37 |
| Firmicutes | 5 | 0.52 | 3 | 0.39 |
| Bacteroidetes | 33 | 5.78 | 6 | 0.33 |
| Proteobacteria | 89 | 13.88 | 75 | 7.95 |

Table S4. Distinct genes for the synthesis of antagonistic substances in strains *Paenibacillus favisporus* Y7 and *Streptomyces coelicoflavus* F13

|  |  |  |  |
| --- | --- | --- | --- |
| Strains | KO number | Genes | Functions |
| *Streptomyces coelicoflavus* | K16232 | *gcs* | germicidin synthase |
| K20333 | *toxD* | toxoflavin biosynthesis protein |
| *Paenibacillus favisporus* | K15655 | *srfAB* | surfactin family lipopeptide synthetase B |

Table S5. Soil characteristics

|  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- |
| Available N (mg/kg) | Available P (mg/kg) | Available K (mg/kg) | pH | Total C (%) | Total N (%) |
| 47.25±11.58 | 11.46±2.73 | 90±16.56 | 6.87±0.03 | 0.45±0.08 | 0.09±0.003 |

Table S6. Primers for PCR and QPCR

|  |  |  |  |
| --- | --- | --- | --- |
| Primer | Sequence(5'-3') | Target gene | Reference |
| 27F | AGAGTTTGATCMTGGCTCAGC | 16S rRNA | [1] |
| 1492R | GGTTACCTTGTTACGACTT |
| Eub338 | ACTCCTACGGGAGGCAGCAG | 16S rRNA | [2] |
| Eub518 | ATTACCGCGGCTGCTGG |
| flicF | GAACGCCAAcGGTGCGAACT | *flic* | [3] |
| flicR | GGCGGCCTTCAGGGAGGTC |
| srf1 | GCTTCGTTCACTTCACGGTAGG | *srf* | [4] |
| srf2 | ATGGAGGAAAGACTCGGCTTTT |
| fen1 | TGGATGGTTCCTCCGCTATCTA | *fen* | [4] |
| fen2 | GGTGACGACCGCGCATTTATT |
| itu1 | GCCTCCTGCTCATTGTCCTT | *itu* | [5] |
| itu2 | GACGGCGTATCGTGGAGAAT |
| con2\_67F | TCTGCTGGGATGGGTGAG | con2\_67 | This study |
| con2\_67R | TTCCAAAGTCCGATGCTG |
| con31\_49F | CACCGTCGTGAAGAGCATCG | con31\_49 | This study |
| con31\_49R | TCCCCGCAGGGTCAGGTAG |

Table S7. PCR and qPCR conditions for the different primer pairs used in this study

|  |  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- | --- |
| Primer | Use | Initial denaturing | No. of Cycles | Denaturing | Annealing | Extension | Final extension |
| 27F | PCR | 95°C, 5 min | 35 | 95°C, 30 sec | 60°C, 30 sec | 72°C, 60 sec | 72°C, 5 min |
| 1492R |
| Eub338 | qPCR | 50°C, 2 min 95°C, 2 min | 40 | 95°C, 15 sec | 60°C, 60 sec |  |  |
| Eub518 |
| fliCF | qPCR | 95°C, 10 sec | 40 | 95°C, 5 sec | 60°C, 30 sec |  |  |
| fliCR |
| srf1 | qPCR | 95°C, 10 min | 40 | 95°C, 15 sec | 57°C, 60 sec |  |  |
| srf2 |
| fen1 | qPCR | 95°C, 10 min | 40 | 95°C, 15 sec | 57°C, 60 sec |  |  |
| fen2 |
| itu1 | qPCR | 95°C, 2 min | 40 | 95°C, 15 sec | 60°C, 20 sec |  |  |
| itu2 |
| con2\_67F | qPCR | 95°C, 10 sec | 40 | 95°C, 5 sec | 60°C, 30 sec |  |  |
| con2\_67R |

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Fig. S1. The Shannon index of the KP treatment and the control. Statistical significance was determined based on Student’s t test. \* *P* < 0.05.

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Fig. S2. The relative abundance (%) of bacterial phyla in the control soil and the KP-treated soil at different sampling times.

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Fig. S3. Numbers of culturable Actinobacteria in two other soils amended with KP. HN and HG represented the soil from an open field covered with grass and planted grape for two years in Hebei province of China, respectively. Statistical significance was determined based on Student’s t test. \* *P* < 0.05, \*\* *P* < 0.01, \*\*\* *P* < 0.001.

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Fig. S4. Significant differences in the relative abundance levels of bacterial genera between the KP treatment and the control at 14 days. The largest circles represent the phylum level. The inner circles represent the genus level. The colours of the circles indicate genera enriched in the KP treatment (green) or the control (red). The size of the circle represents the relative abundance of that genus.

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Fig. S5. Significant differences in the relative abundance levels of bacterial genera between the KP treatment and the control at 30 days. The largest circles represent the phylum level. The inner circles represent the genus level. The colours of the circles indicate genera enriched in the KP treatment (green) or the control (red). The size of the circle represents the relative abundance of that genus.

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Fig. S6. Bacterial networks of the control (a) and KP treatment (b). The green and red lines represent negative and positive links, respectively. The node size represents the link numbers of the node.

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Fig. S7. Kernel density for the relative abundances of nodes in the bacterial co-occurrences of CK and KP treatment. The nodes (Actinobacteria and Firmicutes, not including *Streptomyces*, *Paenibacillus* and *Bacillus*) that had positive and negative associations with the target hubs are shown in a and b. The nodes (Proteobacteria and Bacteroidetes) that had positive and negative associations with the target hubs are shown in c and d.

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Fig. S8. A correlational heat map generated using the relative abundances of predicted genes related to the production of antagonistic substances and the hubs (link number >50) belonging to *Streptomyces*, *Paenibacillus* and *Bacillus* based on Pearson correlation distance. The *p*-values were adjusted by the FDR method. \* p.adjust < 0.05, \*\* p.adjust < 0.01, \*\*\* p.adjust < 0.001. The color scale shows the correlation level: red and blue indicate positive and negative associations, respectively.

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Fig. S9. Inhibition levels of *R. solanacearum*, *P. favisporus* Y7 and *S. coelicoflavus* F13 by KP *in vitro*. Statistical significance was determined based on Student’s t test. \* *P* < 0.05, \*\* *P* < 0.01, \*\*\* *P* < 0.001. RS represents *R. solanacearum*.

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Fig. S10. Image showing the inhibitory effects of strains F13 (A) and Y7 (B) on *R. solanacearum* at 24 h *in vitro*. The length of the red line is 1.5 cm.

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Fig. S11. Interactions between *P. favisporus* Y7 and *S. coelicoflavus* F13.

(a) Image showing interactions between F13 and Y7 *in vitro*. The cell density of strain Y7 (b) was stimulated by FBF (fermentation broth from F13) and biomass of strain F13 (c) was stimulated by FBY (fermentation broth from Y7). Error bars indicate one standard deviation from the mean. Different letters among treatments indicate significant differences based on Tukey's test (*P*<0.05).

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Fig. S12. Copy numbers of antagonistic genes in the soil with KP treatment and the control.

a, b and c represent the *srf* (surfactin), *itu* (iturin), and *fen* (fengycin) genes, respectively. Statistical significance was determined based on Student’s t test. \* *P* < 0.05, \*\* *P* < 0.01, \*\*\* *P* < 0.001.

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Fig. S13. Venn diagram for the numbers of reactions of strains F13 and Y7 in the extracellular environment based on genome-scale metabolic models.

C:\Users\hasee\Desktop\共享的氮源的与碳源.tif Fig. S14. The shared carbon and nitrogen sources of strains Y7 and F13 from genome-scale metabolic models.

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Fig. S15. KEGG metabolic pathway of pentose and glucuronate interconversions in *P. favisporus* Y7. The genes related to D-xylose metabolism (*xylA*, *xylB*, *xylD* and *dcxR*) and the production of pectate lyase (*pelC*) are marked with red font.

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Fig. S16. KEGG metabolic pathway of pentose and glucuronate interconversions in *S. coelicoflavus* F13. The genes related to D-xylose metabolism (*xylA*, *xylB*, *xylC* and *xylD*) and the production of pectate lyase (*pelC*) are marked with red font.

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Fig. S17. (a) Copy numbers of *fliC* (*R. solanacearum*) in the sterilized soil. Error bars indicate one standard deviation from the mean. Different letters among treatments indicate significant differences based on Tukey's test (*P*<0.05). Y, F and C represent individual inoculation with strain Y7, strain F13 and the control, respectively. F73, F55 and F37 represent inoculation of strains Y7 and F13 at ratios of 7:3, 5:5 and 3:7, respectively.

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Fig. S18. Copy numbers of *fliC* (a), con31\_49of strain *Streptomyces coelicoflavus* F13 (b), con2\_67of strain *Paenibacillus favisporus* Y7(c) and 16S rRNA (d) between the MK (the soil amended with the microbiome from the KP treatment) and MC (the soil amended with the microbiome from the control) treatments. Statistical significance was determined based on Student’s t test. \* *P* < 0.05, \*\* *P* < 0.01.

**References**

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