**Supplementary Materials**

**Table S1** Amplification primers used in this study

|  |  |  |
| --- | --- | --- |
| **Target genus** | **Primers** | **Sequence (5'-3')** |
| Bacteria 16S rDNA | 520F | AYTGGGYDTAAAGNG |
| 802R | TACNVGGGTATCTAATCC |
| Fungal ITS | FocSc-1 | CAGGGGATGTATGAGGAGGCTAGGCTA |
| FocSc-2 | GTGACAGCGTCGTCTAGTTCCTTGGAG |
| ITS5F | GGAAGTAAAAGTCGTAACAAGG |
| ITS2 | GCTGCGTTCTTCATCGATGC |

F and R represent the forward and reverse primers, respectively.

**Table S2** Soil properties in this study

|  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- |
| **Treatments** | **Organic matter (g·kg**−1**)** | **Available phosphorus (mg·kg**−1**)** | **Available potassium (mg·kg**−1**)** | **Available nitrogen （mg·kg**−1**)** | **pH** |
| Cf | 24.76±1.94a | 43.72±4.90c | 641.56±13.21a | 194.25±29.51a | 6.28±0.10a |
| Bm | 22.13±2.52a | 121.03±16.63a | 414.69±62.71b | 198.20±18.61a | 5.59±0.05c |
| Pr | 20.84±2.27a | 71.05±4.19b | 148.43±12.58c | 45.49±3.76b | 6.11±0.06b |
| Cn | 5.70±3.04b | 143.06±67.18b | 28.56±0.93a | 45.00±3.49ab | 7.56±0.06a |
| Bb | 9.06±1.11a | 196.34±14.97a | 25.92±1.43b | 47.25±7.35ab | 7.51±0.06a |
| Pp | 6.21±1.58b | 184.26±11.57ab | 22.26±0.73c | 49.82±5.85a | 7.58±0.08a |



**Fig. S1** The number of *Fusarium oxysporum* in rotation (A) and residue (B) treatment across all samples from six replicates. The treatment abbreviations are defined in Fig. 1.

**Table S3** Bacterial and fungal community richness and diversity in the treatment and control

|  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- |
|  |  | Samples | Community richncess | | Community diversity | |
|  |  | Chao1 | ACE | Shannon | Invsimpson |
| Rotation | Bacteria | CBf | 5607.38±160.91a | 5652.06±141.25b | 6.90±0.04b | 291.42±28.40c |
| BBm | 5599.46±113.88a | 5680.21±98.89ab | 6.96±0.03b | 365.09±24.82b |
| PBr | 5599.46±113.88a | 5680.21±98.89ab | 6.96±0.03b | 365.09±24.82b |
| **CRf** | **5316.38±153.45b** | **5438.51±105.60c** | **6.12±0.07d** | **51.68±3.75e** |
| **BRm** | **5150.60±134.08c** | **5296.82±127.34c** | **5.91±0.03e** | **75.76±4.16d** |
| **PRr** | **5289.96±143.47bc** | **5370.47±177.93c** | **6.25±0.09c** | **49.98±6.71e** |
| Fungi | CBf | 1347.73±74.32bc | 1348.38±65.36a | 4.99±0.03a | 61.72±2.88a |
| BBm | 1420.73±47.90ab | 1405.47±41.83a | 4.92±0.04b | 47.30±2.22b |
| PBr | 1378.33±62.86abc | 1376.18±56.47a | 4.34±0.02c | 20.76±0.34c |
| **CBf** | **1327.96±65.20c** | **1348.16±88.52a** | **3.89±0.02e** | **17.63±0.34d** |
| **BRm** | **1183.06±64.09d** | **1223.33±117.53b** | **3.99±0.08d** | **20.89±1.90c** |
| **PRr** | **1428.41±52.19a** | **1438.66±49.32a** | **3.81±0.08f** | **13.57±0.78e** |
| Residue | Bacteria | CBn | 5958.58±147.87a | 6054.71±121.66a | 7.04±0.02b | 305.61±11.38b |
| BBb | 6096.80±89.88a | 6156.87±53.30a | 7.14±0.05a | 292.23±44.74b |
| PBp | 5981.80±92.15a | 6079.70±51.56a | 7.19±0.02a | 395.73±17.91a |
| **CRn** | **4759.93±132.88c** | **4875.62±101.13c** | **5.67±0.05d** | **71.31±2.7d** |
| **BRb** | **5224.85±84.84b** | **5307.80±80.27b** | **6.35±0.05c** | **136.15±11.74c** |
| **PRp** | **4662.83±216.33c** | **4798.12±189.73c** | **5.66±0.09d** | **59.62±5.03d** |
| Fungi | CBn | 1468.25±88.66a | 1463.74±76.23a | 4.87±0.04a | 50.27±2.17a |
| BBb | 1378.73±36.01b | 1391.00±50.76b | 4.22±0.10b | 24.33±2.48b |
| PBp | 1398.30±24.56b | 1391.75±35.53b | 4.87±0.07a | 47.11±7.36a |
| **CRn** | **1180.86±21.61c** | **1193.66±20.88d** | **3.82±0.08c** | **18.32±1.53c** |
| **BRb** | **1208.25±48.45c** | **1236.61±42.77cd** | **4.15±0.05b** | **24.93±1.95b** |
| **PRp** | **1220.39±29.86c** | **1252.99±38.52c** | **4.20±0.02b** | **26.41±0.70b** |

**Table S4** Permutational multivariate analysis of variance (PERMANOVA) for principal coordinate analysis (PCoA)

|  |  |  |  |  |  |  |  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- |
|  | **Rotation** | | | | | |  | **Residue** | | | | | |
|  | Bacteria | | | Fungi | | |  | Bacteria | | | Fungi | | |
|  | **F.Model** | **Pr (>F)** | **Sig** | **F.Model** | **Pr (>F)** | **Sig** |  | **F.Model** | **Pr (>F)** | **Sig** | **F.Model** | **Pr (>F)** | **Sig** |
| CBf-BBm | 65.83 | 0.002 | \*\* | 130.43 | 0.002 | \*\* | CBn-BBb | 19.63 | 0.002 | \*\* | 110.20 | 0.005 | \*\* |
| CBf-PBr | 72.80 | 0.001 | \*\*\* | 279.88 | 0.003 | \*\* | CBn-PBp | 15.48 | 0.003 | \*\* | 24.00 | 0.003 | \*\* |
| CBf-CRf | 130.72 | 0.004 | \*\* | 371.64 | 0.001 | \*\*\* | CBn-CRn | 123.28 | 0.003 | \*\* | 232.83 | 0.004 | \*\* |
| CBf-BRm | 160.60 | 0.004 | \*\* | 334.15 | 0.001 | \*\*\* | CBn-BRb | 96.45 | 0.002 | \*\* | 218.10 | 0.002 | \*\* |
| CBf-PRr | 130.25 | 0.003 | \*\* | 290.16 | 0.003 | \*\* | CBn-PRp | 142.07 | 0.003 | \*\* | 302.71 | 0.003 | \*\* |
| BBm-PBr | 21.77 | 0.003 | \*\* | 138.15 | 0.005 | \*\* | BBb-PBp | 9.27 | 0.003 | \*\* | 33.72 | 0.003 | \*\* |
| BBm-CRf | 102.95 | 0.003 | \*\* | 314.67 | 0.004 | \*\* | BBb-CRn | 101.49 | 0.005 | \*\* | 307.73 | 0.002 | \*\* |
| BBm-BRm | 129.51 | 0.003 | \*\* | 268.04 | 0.002 | \*\* | BBb-BRb | 70.53 | 0.003 | \*\* | 174.83 | 0.001 | \*\*\* |
| BBm-PRr | 104.01 | 0.002 | \*\* | 292.22 | 0.001 | \*\*\* | BBb-PRp | 111.31 | 0.001 | \*\*\* | 327.72 | 0.002 | \*\* |
| PBr-CRf | 97.69 | 0.001 | \*\*\* | 458.41 | 0.004 | \*\* | PBp-CRn | 115.35 | 0.007 | \*\* | 104.33 | 0.002 | \*\* |
| PBr-BRm | 109.45 | 0.003 | \*\* | 474.32 | 0.006 | \*\* | PBp-BRb | 81.64 | 0.004 | \*\* | 79.40 | 0.007 | \*\* |
| PBr-PRr | 100.56 | 0.003 | \*\* | 443.03 | 0.002 | \*\* | PBp-PRp | 126.91 | 0.005 | \*\* | 93.53 | 0.001 | \*\*\* |
| CRf-BRm | 87.27 | 0.002 | \*\* | 582.15 | 0.003 | \*\* | CRn-BRb | 38.51 | 0.003 | \*\* | 109.44 | 0.002 | \*\* |
| CRf-PRr | 11.35 | 0.002 | \*\* | 61.30 | 0.003 | \*\* | CRn-PRp | 31.15 | 0.001 | \*\*\* | 172.62 | 0.002 | \*\* |
| BRm-PRr | 108.45 | 0.004 | \*\* | 485.67 | 0.003 | \*\* | BRb-PRp | 45.30 | 0.004 | \*\* | 166.16 | 0.001 | \*\*\* |

**Table S5** Bacteria and fungal phylum level with Fusarium relative abundance [correlation](javascript:;) in the rotation and residue addition treatments

|  |  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- | --- |
|  | **Phylum level** | **pearson's rank correlation coefficient** | **spearman's rank correlation coefficient** |  | **Phylum level** | **pearson's rank correlation coefficient** | **spearman's rank correlation coefficient** |
|  | **Rotation** | | |  | **Residue** | | |
| **Bacteria** | *Proteobacteria* | -0.232 | -0.112 |  | *Proteobacteria* | -0.040 | -0.269 |
|  | *Bacteroidetes* | 0.248 | 0.159 |  | *Acidobacteria* | -0.098 | 0.072 |
|  | *Acidobacteria* | 0.390\* | 0.241 |  | *Bacteroidetes* | 0.086 | -0.072 |
|  | ***Firmicutes*** | **-0.515\*\*** | **-0.474\*\*** |  | *Firmicutes* | 0.318 | -0.174 |
|  | *Verrucomicrobia* | 0.291 | 0.166 |  | *Gemmatimonadetes* | -0.094 | -0.028 |
|  | *Cyanobacteria/Chloroplast* | 0.109 | 0.069 |  | *Actinobacteria* | 0.252 | 0.527\*\* |
|  | *Chloroflexi* | 0.289 | 0.190 |  | *Verrucomicrobia* | 0.221 | 0.468\*\* |
|  | *Gemmatimonadetes* | 0.118 | 0.05 |  | *Chloroflexi* | -0.167 | -0.107 |
|  | *Actinobacteria* | 0.149 | 0.069 |  | *Planctomycetes* | -0.168 | -0.105 |
|  | *Planctomycetes* | 0.334\* | 0.238 |  | *Cyanobacteria/Chloroplast* | 0.340\* | 0.513\*\* |
|  | *Thaumarchaeota* | 0.360\* | 0.128 |  | ***Thaumarchaeota*** | **-.482\*\*** | **-.403\*** |
|  | *Armatimonadetes* | 0.532\*\* | 0.346\* |  | *candidate division WPS-1* | -0.210 | -0.148 |
|  | *candidate division WPS-1* | 0.407\* | 0.241 |  | *Euryarchaeota* | 0.199 | 0.680\*\* |
|  | *Nitrospirae* | 0.196 | 0.305 |  | *Armatimonadetes* | -0.016 | 0.123 |
|  | *Parcubacteria* | 0.114 | 0.234 |  | *Woesearchaeota* | 0.070 | 0.479\*\* |
|  | *Latescibacteria* | 0.324 | 0.198 |  | *Parcubacteria* | -0.072 | 0.016 |
|  | *Synergistetes* | 0.350\* | 0.242 |  | *Nitrospirae* | -0.401\* | -0.311 |
|  | *Ignavibacteriae* | 0.288 | 0.126 |  | *candidate division WPS-2* | 0.366\* | 0.621\*\* |
|  | *Aquificae* | 0.298 | 0.122 |  | *Aquificae* | -0.214 | 0.097 |
|  | *Woesearchaeota* | 0.420\* | 0.314 |  | *Fibrobacteres* | 0.308 | 0.542\*\* |
|  | *Others* | 0.280 | 0.052 |  | *Others* | -0.261 | -0.101 |
| **Fungi** | *Ascomycota* | 0.225 | 0.092 |  | ***Ascomycota*** | **-0.608\*\*** | **-0.603\*\*** |
|  | *Basidiomycota* | 0.026 | -0.069 |  | *Basidiomycota* | 0.845\*\* | 0.659\*\* |
|  | *Chytridiomycota* | -0.310 | -0.202 |  | *Chytridiomycota* | 0.061 | 0.473\*\* |
|  | *Fungi\_unidentified* | -0.284 | 0.007 |  | *Fungi\_unidentified* | -0.121 | -0.083 |
|  | *Glomeromycota* | -0.164 | 0.010 |  | *Glomeromycota* | 0.121 | 0.315 |
|  | *Microsporidia* | -0.207 | -0.117 |  | *Microsporidia* | -0.173 | -0.198 |
|  | *Zygomycota* | 0.033 | 0.132 |  | *Zygomycota* | 0.184 | 0.194 |

**Table S6** Bacteria and fungi top 30 in the rotation

|  |  |  |  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- | --- | --- | --- |
|  | | Rotation | | | | | | *F value* | *p valve* |
| Bulk soil | | | Rhizosphere soil | | |
| CBf | BBm | PBr | CRf | BRm | PRr |
| Bacteria | ***Burkholderia*** | **0.41±0.04d** | **0.56±0.06d** | **0.59±0.05d** | **14.83±0.9b** | **4.09±0.24c** | **17.31±1.24a** | **892.486** | **0** |
| *Gemmatimonas* | 9.56±0.7b | 12.18±1.6a | 6.82±0.76c | 3.13±0.39d | 1.99±0.08e | 3.5±0.07d | 155.455 | 0 |
| *Bacillus* | 0.6±0.03d | 0.66±0.02d | 0.98±0.07d | 8.81±0.57b | 9.29±0.58a | 2.32±0.14c | 903.754 | 0 |
| *Gp3* | 1.12±0.07d | 4.11±0.47a | 3.23±0.31b | 1.75±0.17c | 1.04±0.09d | 1.83±0.1c | 149.561 | 0 |
| *Subdivision3\_genera\_incertae\_sedis* | 1.99±0.15c | 2.84±0.21b | 4.7±0.7a | 1.08±0.18d | 1.09±0.09d | 1.24±0.11d | 117.744 | 0 |
| *Gp1* | 0.82±0.03d | 2.97±0.29b | 3.85±0.22a | 1.05±0.18c | 1.14±0.11c | 1.11±0.09c | 318.248 | 0 |
| *Rhizobium* | 0.36±0.02d | 0.34±0.03d | 0.39±0.03d | 2.4±0.16b | 5.9±0.27a | 1.54±0.08c | 1547.579 | 0 |
| *Gp6* | 2.78±0.29a | 3.01±0.42a | 2.24±0.27b | 1.11±0.11c | 0.46±0.05d | 1.14±0.12c | 108.343 | 0 |
| *Nitrososphaera* | 3.18±0.96a | 2.12±0.46b | 1.06±0.53c | 1.22±0.3c | 0.19±0.03d | 1.33±0.27c | 24.078 | 0 |
| ***Sphingosinicella*** | **0.96±0.12b** | **1.54±0.3a** | **0.76±0.1c** | **1.5±0.12a** | **0.78±0.06bc** | **1.44±0.09a** | **34.389** | **0** |
| *Sphingomonas* | 1.52±0.16a | 1.1±0.22b | 0.63±0.08c | 1.46±0.08a | 0.73±0.03c | 1.53±0.06a | 63.9 | 0 |
| *Ohtaekwangia* | 3.63±0.69a | 0.56±0.04bc | 0.76±0.08bc | 0.47±0.03c | 0.9±0.08b | 0.52±0.07c | 110.278 | 0 |
| *Gp7* | 2.53±0.2a | 1.47±0.17b | 1.56±0.15b | 0.28±0.03c | 0.32±0.03c | 0.29±0.02c | 332.472 | 0 |
| ***Pseudomonas*** | **0.44±0.03d** | **0.33±0.02e** | **0.42±0.05d** | **1.14±0.1c** | **1.51±0.09b** | **2.24±0.09a** | **734.736** | **0** |
| *Gaiella* | 0.73±0.03c | 1.55±0.09b | 1.67±0.17a | 0.55±0.02d | 0.45±0.03e | 0.68±0.05c | 232.897 | 0 |
| *Ramlibacter* | 0.38±0.04e | 0.67±0.04d | 0.78±0.11c | 0.98±0.08b | 1.66±0.14a | 1.08±0.08b | 144.801 | 0 |
| *WPS-1\_genera\_incertae\_sedis* | 0.55±0.1d | 1.51±0.32a | 1.21±0.23b | 0.98±0.21bc | 0.41±0.07d | 0.86±0.21c | 23.141 | 0 |
| *Pseudolabrys* | 0.85±0.06b | 1.18±0.11a | 0.93±0.13b | 0.9±0.09b | 0.53±0.04c | 0.95±0.07b | 34.533 | 0 |
| *Flavisolibacter* | 0.51±0.06d | 1.49±0.1a | 0.63±0.04c | 1.03±0.09b | 0.65±0.07c | 0.95±0.05b | 144.745 | 0 |
| *Sphingobium* | 0.4±0.02e | 0.41±0.03e | 0.64±0.07c | 0.91±0.06b | 2.38±0.14a | 0.52±0.02d | 706.026 | 0 |
| *Massilia* | 0.09±0.02d | 0.12±0.01d | 0.13±0.02d | 1.6±0.14b | 1.28±0.12c | 1.85±0.12a | 488.285 | 0 |
| *Opitutus* | 0.66±0.09c | 0.88±0.2b | 1.44±0.06a | 0.66±0.11c | 0.66±0.06c | 0.66±0.04c | 51.638 | 0 |
| *Candidatus Koribacter* | 0.7±0.05c | 1.44±0.12b | 1.64±0.09a | 0.38±0.05d | 0.39±0.02d | 0.38±0.06d | 374.989 | 0 |
| *Zhizhongheella* | 0.92±0.09c | 1.28±0.07b | 1.51±0.21a | 0.42±0.03d | 0.4±0.03d | 0.41±0.04d | 138.149 | 0 |
| *Georgfuchsia* | 0.15±0.02e | 0.16±0.02e | 0.25±0.03d | 0.54±0.03b | 3.38±0.17a | 0.42±0.04c | 1668.911 | 0 |
| *Limnobacter* | 1.27±0.14a | 1.36±0.11a | 1.12±0.17b | 0.31±0.02c | 0.24±0.03c | 0.31±0.02c | 173.519 | 0 |
| *Bradyrhizobium* | 0.9±0.15b | 1.02±0.1a | 0.77±0.09c | 0.58±0.06d | 0.42±0.05e | 0.67±0.03cd | 34.297 | 0 |
| *Streptacidiphilus* | 0.13±0.02e | 0.31±0.02d | 0.57±0.07c | 0.77±0.06b | 2.02±0.23a | 0.45±0.04c | 261.47 | 0 |
| *Conexibacter* | 0.69±0.04c | 1.2±0.16b | 1.44±0.18a | 0.28±0.06d | 0.25±0.02d | 0.34±0.03d | 148.902 | 0 |
| *Aridibacter* | 1.99±0.19a | 1.01±0.13b | 0.55±0.08c | 0.23±0.04d | 0.17±0.03d | 0.22±0.02d | 283.112 | 0 |
| Fungi | ***Penicillium*** | **3.18±0.24f** | **10.37±0.58d** | **30.72±0.37a** | **25.47±0.9b** | **6.51±0.3e** | **15.46±0.91c** | **1883.824** | **0** |
| ***Talaromyces*** | **0.45±0.07d** | **0.57±0.04d** | **1.53±0.06c** | **13.93±0.52b** | **0.82±0.06d** | **20.25±0.65a** | **3772.971** | **0** |
| ***Fusarium*** | **2.81±0.23c** | **4.42±0.28b** | **4.49±0.21b** | **2.37±0.11d** | **7.68±0.49a** | **1.42±0.33e** | **335.457** | **0** |
| *Mortierella* | 0.85±0.05c | 8.04±0.28b | 11.00±0.30a | 0.21±0.03d | 0.21±0.03d | 0.19±0.02d | 4705.191 | 0 |
| *Chaetomium* | 7.68±0.55a | 1.86±0.1b | 0.66±0.06d | 1.08±0.06c | 0.37±0.03e | 1.95±0.17b | 758.942 | 0 |
| *Campylocarpon* | 0.17±0.03c | 0.18±0.01c | 0.21±0.02c | 3.99±0.18b | 0.16±0.02c | 6.23±0.67a | 526.652 | 0 |
| *Haematonectria* | 2.33±0.13b | 2.97±0.37a | 1.81±0.07c | 0.7±0.04d | 1.84±0.08c | 0.72±0.08d | 169.358 | 0 |
| *Aspergillus* | 0.63±0.15f | 0.77±0.05e | 3.14±0.07a | 1.31±0.02c | 2.02±0.13b | 0.94±0.02d | 681.922 | 0 |
| *Derxomyces* | 0.72±0.09c | 1.16±0.18b | 0.3±0.05d | 0.56±0.06c | 1.63±0.08a | 0.74±0.29c | 59.154 | 0 |
| *Trichoderma* | 1.45±0.11a | 1.29±0.23b | 0.92±0.07c | 0.2±0.02d | 0.85±0.11c | 0.21±0.02d | 122.606 | 0 |
| *Spizellomyces* | 3.52±0.23a | 0.65±0.06b | 0.08±0.02d | 0.23±0.03c | 0.09±0.01d | 0.18±0.04cd | 1084.35 | 0 |
| *Kurtzmanomyces* | 1.13±0.06b | 2.65±0.32a | 0.42±0.13c | 0.02±0d | 0.29±0.07c | 0.02±0d | 297.31 | 0 |
| *Dermatocarpon* | 1.56±0.11a | 0.9±0.1b | 0.61±0.1c | 0.22±0.03e | 0.13±0.02e | 0.44±0.16d | 175.068 | 0 |
| *Elaphocordyceps* | 0.33±0.03c | 0.36±0.05c | 0.81±0.09b | 0.37±0.04c | 1.4±0.1a | 0.3±0.03c | 293.846 | 0 |
| *Hyphodiscus* | 0.22±0.02c | 0.27±0.03c | 0.26±0.04c | 0.83±0.11b | 1.74±0.17a | 0.22±0.04c | 297.354 | 0 |
| *Ophiostoma* | 0.5±0.07bc | 0.8±0.09a | 0.56±0.05b | 0.32±0.03d | 0.49±0.09bc | 0.47±0.03c | 34.57 | 0 |
| *Paraglomus* | 0.08±0.04b | 0.05±0.01b | 2.31±0.16a | 0.02±0b | 0.04±0.01b | 0.04±0.01b | 1101.656 | 0 |
| *Purpureocillium* | 0.37±0.09b | 0.77±0.04a | 0.77±0.11a | 0.19±0.02c | 0.17±0.02c | 0.14±0.02c | 144.932 | 0 |
| *Acremonium* | 0.39±0.1b | 0.69±0.12a | 0.38±0.03b | 0.12±0.01d | 0.3±0.03c | 0.12±0.02d | 58.866 | 0 |
| *Phialosimplex* | 1.6±0.23a | 0.02±0.01b | 0.03±0.01b | 0.06±0.01b | 0.01±0.01b | 0.08±0.02b | 266.822 | 0 |
| *Xylomyces* | 0.2±0.05d | 0.23±0.05cd | 0.39±0.05a | 0.26±0.01c | 0.33±0.04b | 0.38±0.04a | 21.608 | 0 |
| *Candida* | 0.45±0.03b | 0.82±0.08a | 0.29±0.03c | 0.02±0e | 0.13±0.03d | 0.02±0e | 410.034 | 0 |
| *Cantharellus* | 0.09±0.03d | 0.16±0.04c | 0.1±0.02d | 0.33±0.04b | 0.93±0.08a | 0.08±0.01d | 329.552 | 0 |
| *Microdiplodia* | 0.03±0.02c | 0.02±0.01c | 0.03±0.01c | 0.61±0.04b | 0.03±0.01c | 0.91±0.09a | 556.045 | 0 |
| *Pseudallescheria* | 1.08±0.12a | 0.21±0.07b | 0.08±0.01c | 0.05±0.01c | 0.05±0.01c | 0.08±0.01c | 312.125 | 0 |
| *Colletotrichum* | 0.07±0.02d | 0.18±0.04b | 0.12±0.02c | 0.06±0.01d | 0.85±0.05a | 0.06±0.01d | 664.066 | 0 |
| *Myrothecium* | 0.05±0.02e | 0.06±0.01e | 0.12±0.02d | 0.22±0.02c | 0.62±0.05a | 0.27±0.03b | 355.664 | 0 |
| *Podospora* | 1.02±0.13a | 0.14±0.06b | 0.05±0.01c | 0.02±0c | 0.02±0c | 0.03±0.01c | 284.431 | 0 |
| *Sporothrix* | 0.79±0.09a | 0.06±0.01c | 0.24±0.03b | 0.02±0.01c | 0.03±0.01c | 0.01±0.01c | 375.293 | 0 |
| *Ophiocordyceps* | 0.41±0.05a | 0.1±0.03de | 0.08±0.02e | 0.16±0.01c | 0.21±0.02b | 0.13±0.03cd | 88.915 | 0 |

**Table S7** Bacteria and fungi top 30 in the residue

|  |  |  |  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- | --- | --- | --- |
|  |  | Residue | | | | | | *F value* | *p valve* |
| Bulk soil | | | Rhizosphere soil | | |
| CBn | BBb | PBp | CRn | BRb | PRp |
| Bacteria | ***Pseudomonas*** | **2.77±0.21c** | **0.96±0.13e** | **1.62±0.2d** | **6.02±0.3b** | **2.53±0.12c** | **8.95±0.69a** | **501.235** | **0** |
| ***Gemmatimonas*** | **4.14±0.28b** | **4.04±0.94b** | **5.38±0.38a** | **1.03±0.11d** | **2.04±0.07c** | **1.35±0.08d** | **99.325** | **0** |
| *Gp4* | 2.6±0.32b | 4.32±1.37a | 4.01±0.49a | 0.93±0.15c | 2.65±0.42b | 1.2±0.23c | 28.053 | 0 |
| *Sphingobium* | 0.36±0.03d | 0.38±0.05d | 0.35±0.03d | 5.85±0.61a | 5.12±0.58b | 3.24±0.19c | 313.224 | 0 |
| *Azohydromonas* | 1.38±0.18d | 0.94±0.17e | 1.3±0.13d | 1.76±0.17c | 4.08±0.37a | 2.66±0.16b | 181.881 | 0 |
| *Gp6* | 2.5±0.25c | 3.68±0.75a | 3.13±0.68b | 0.61±0.09d | 1.01±0.15d | 0.66±0.09d | 57.324 | 0 |
| *Nitrososphaera* | 2.05±0.67c | 5±1.18a | 2.94±0.57b | 0.24±0.07d | 0.21±0.03d | 0.22±0.09d | 63.269 | 0 |
| *Bacillus* | 0.16±0.01d | 0.17±0.02d | 0.17±0.01d | 3.02±0.28b | 0.87±0.03c | 5.99±0.31a | 1143.859 | 0 |
| *Subdivision3\_genera\_incertae\_sedis* | 2.03±0.31bc | 2.44±0.39a | 2.17±0.12ab | 0.83±0.09d | 1.79±0.18c | 0.84±0.11d | 54.112 | 0 |
| *Georgfuchsia* | 0.9±0.08d | 0.44±0.07e | 0.35±0.02e | 3.11±0.18a | 2.41±0.15c | 2.88±0.13b | 691.169 | 0 |
| *Rhizobium* | 0.11±0.01d | 0.13±0.01d | 0.13±0.02d | 4±0.12a | 2.58±0.12b | 1.97±0.11c | 2258.315 | 0 |
| *Thauera* | 0.09±0.01e | 0.11±0.02de | 0.19±0.02d | 2.77±0.11b | 1.14±0.06c | 3.75±0.15a | 2202.346 | 0 |
| *Spartobacteria\_genera\_incertae\_sedis* | 1.4±0.29c | 2.15±0.16a | 1.79±0.22b | 0.64±0.11e | 1.12±0.23d | 0.77±0.21e | 46.58 | 0 |
| *Pseudoduganella* | 0.19±0.02d | 0.15±0.02d | 0.18±0.02d | 4.64±0.14a | 1.69±0.08b | 0.66±0.02c | 4105.211 | 0 |
| *Flavisolibacter* | 0.86±0.03d | 1.11±0.15c | 1.4±0.14b | 0.85±0.11d | 1.73±0.13a | 1.43±0.07b | 58.426 | 0 |
| *Klebsiella* | 0.12±0.02d | 0.11±0.02d | 0.1±0.02d | 3.94±0.16a | 0.86±0.06c | 2.04±0.18b | 1397.574 | 0 |
| *Opitutus* | 2.39±0.09a | 1.04±0.19c | 1.4±0.12b | 0.5±0.03de | 0.61±0.07d | 0.39±0.06e | 291.48 | 0 |
| *Gp3* | 1.25±0.11b | 1.55±0.23a | 1.33±0.12b | 0.53±0.05d | 1.02±0.06c | 0.59±0.05d | 69.252 | 0 |
| *GpXIII* | 1.93±0.36b | 2.4±0.52a | 1.68±0.31b | 0.05±0.01c | 0.13±0.02c | 0.06±0.01c | 85.471 | 0 |
| *Sphingomonas* | 0.73±0.08d | 0.78±0.07d | 0.9±0.07c | 1.07±0.03b | 1.61±0.16a | 1.12±0.07b | 76.264 | 0 |
| *Chitinophaga* | 0.43±0.05f | 0.83±0.14d | 0.58±0.06e | 1.37±0.14b | 1.17±0.14c | 1.59±0.13a | 90.289 | 0 |
| *Terrimonas* | 0.5±0.03e | 1.32±0.22b | 0.98±0.1c | 0.68±0.05d | 1.54±0.19a | 0.85±0.07c | 54.985 | 0 |
| *Novosphingobium* | 0.16±0.03d | 0.17±0.03d | 0.14±0.02d | 3.33±0.08a | 1.17±0.05b | 0.74±0.04c | 4830.116 | 0 |
| *Azonexus* | 1.97±0.13a | 0.59±0.08d | 1.21±0.14b | 0.42±0.06e | 0.76±0.04c | 0.65±0.04cd | 230.009 | 0 |
| *Anaeromyxobacter* | 1.6±0.06a | 0.9±0.14c | 1.44±0.11b | 0.33±0.06e | 0.79±0.05d | 0.34±0.02e | 240.659 | 0 |
| *Povalibacter* | 0.42±0.01e | 0.68±0.07cd | 0.6±0.07d | 0.7±0.04 | 2.01±0.16a | 0.92±0.05b | 315.957 | 0 |
| *Ohtaekwangia* | 1.62±0.13a | 0.63±0.1cd | 1.29±0.13b | 0.55±0.12d | 0.75±0.16c | 0.41±0.08e | 90.152 | 0 |
| *Heliimonas* | 0.22±0.03d | 0.15±0.02d | 0.21±0.03d | 1.22±0.19c | 1.47±0.19b | 1.82±0.18a | 185.339 | 0 |
| *Neorhizobium* | 0.1±0.01d | 0.08±0.01d | 0.11±0.01d | 1.83±0.07a | 1.2±0.04c | 1.53±0.08b | 1804.869 | 0 |
| *Falsibacillus* | 0.17±0.02d | 0.24±0.02d | 0.2±0.02d | 1.39±0.16b | 0.99±0.06c | 1.71±0.14a | 319.516 | 0 |
| Fungi | ***Fusarium*** | **3.29±0.19b** | **6.91±0.95a** | **3.95±2.64b** | **3.37±0.3b** | **6.47±0.41a** | **3.02±0.14b** | **13.081** | **0** |
| ***Elaphocordyceps*** | **0.11±0.03c** | **0.06±0.02c** | **0.26±0.06c** | **1.45±0.23b** | **1.69±0.18b** | **12.17±0.46a** | **2650.663** | **0** |
| ***Aspergillus*** | **3.88±0.46a** | **2.28±0.36c** | **3.16±0.59b** | **1.22±0.14d** | **0.77±0.06e** | **2.05±0.1c** | **67.602** | **0** |
| *Chaetomium* | 1.47±0.12b | 3.04±0.39a | 3.41±0.75a | 0.27±0.03d | 0.94±0.06c | 0.84±0.03c | 79.457 | 0 |
| *Trichoderma* | 0.27±0.03c | 5.12±0.38a | 0.32±0.05c | 0.13±0.02c | 1.88±0.16b | 0.15±0.02c | 816.623 | 0 |
| *Acremonium* | 1.15±0.13b | 2.87±0.34a | 0.86±0.22c | 0.93±0.1bc | 1.12±0.09b | 0.3±0.04d | 136.127 | 0 |
| *Blastobotrys* | 0.03±0.01d | 1.55±0.55c | 0.03±0.02d | 0±0d | 1.93±0.15b | 3.04±0.41a | 119.022 | 0 |
| *Penicillium* | 1.27±0.11b | 0.77±0.13d | 1.05±0.14c | 0.67±0.28d | 0.84±0.06d | 1.48±0.07a | 26.303 | 0 |
| *Dermatocarpon* | 2.21±0.16a | 0.85±0.13bc | 0.81±0.33cd | 0.41±0.04e | 1.04±0.12b | 0.63±0.02d | 87.472 | 0 |
| *Mortierella* | 1.3±0.06b | 0.66±0.05c | 1.53±0.13a | 0.26±0.07d | 1.26±0.1b | 0.21±0.03d | 291.911 | 0 |
| *Cantharellus* | 0.02±0.01b | 0.69±0.22b | 3.38±3.22a | 0.01±0b | 0.01±0b | 0.01±0b | 6.263 | 0 |
| *Hyphodiscus* | 0.16±0.03d | 0.06±0.02d | 0.11±0.03d | 1.39±0.21a | 1.24±0.12b | 1.08±0.06c | 227.21 | 0 |
| *Mycosphaerella* | 0.01±0.01d | 0.01±0d | 0.01±0.01d | 0.32±0.05c | 0.42±0.05b | 2.68±0.14a | 1540.775 | 0 |
| *Stachybotrys* | 0.45±0.1bc | 0.47±0.07bc | 0.73±0.13a | 0.32±0.03d | 0.52±0.04b | 0.39±0.04cd | 19.905 | 0 |
| *Ophiocordyceps* | 0.26±0.04cd | 0.08±0.03d | 0.52±0.41b | 1.3±0.06a | 0.15±0.02cd | 0.36±0.03bc | 41.431 | 0 |
| *Colletotrichum* | 0.52±0.08b | 0.43±0.07c | 0.46±0.07bc | 0.34±0.03d | 0.26±0.02e | 0.67±0.04a | 38.518 | 0 |
| *Cladorrhinum* | 0.24±0.03c | 0.42±0.07b | 1.43±0.3a | 0.03±0.01d | 0.08±0.03cd | 0.23±0.03c | 96.877 | 0 |
| *Derxomyces* | 0.14±0.03d | 0.07±0.03e | 0.05±0.04e | 0.74±0.06b | 0.23±0.04c | 0.84±0.12a | 187.247 | 0 |
| *Scutellinia* | 1.04±0.09a | 0.06±0.01c | 0.67±0.09b | 0.01±0.01c | 0±0c | 0±0c | 452.447 | 0 |
| *Purpureocillium* | 0.46±0.09a | 0.34±0.05b | 0.45±0.08a | 0.13±0.02c | 0.17±0.04c | 0.19±0.02c | 40.465 | 0 |
| *Bionectria* | 0.28±0.08b | 0.9±0.09a | 0.24±0.07bc | 0.04±0.01d | 0.19±0.06c | 0.04±0.02d | 160.202 | 0 |
| *Corynespora* | 0.09±0.02c | 0.02±0.01d | 0.28±0.07b | 0.03±0.01d | 0.03±0.01d | 0.96±0.1a | 335.527 | 0 |
| *Talaromyces* | 0.04±0.03c | 0.37±0.09a | 0.03±0.02c | 0.18±0.13b | 0.37±0.04a | 0.37±0.02a | 34.655 | 0 |
| *Podospora* | 0.54±0.07a | 0.17±0.02c | 0.47±0.12b | 0.05±0.01d | 0.05±0.01d | 0.07±0.01d | 88.221 | 0 |
| *Myrothecium* | 0.03±0.01b | 0.06±0.02b | 0.03±0.01b | 0.06±0.03b | 0.07±0.01b | 1±0.1a | 478.706 | 0 |
| *Ophiostoma* | 0.35±0.02a | 0.28±0.07b | 0.27±0.05b | 0.05±0.01d | 0.1±0.02c | 0.07±0.01cd | 70.616 | 0 |
| *Microdochium* | 0.09±0.02d | 0.05±0.02e | 0.22±0.03b | 0.12±0.02c | 0.14±0.03c | 0.46±0.03a | 191.8 | 0 |
| *Kurtzmanomyces* | 0.61±0.19a | 0.18±0.1b | 0.2±0.11b | 0.03±0.01c | 0.03±0.01c | 0.01±0c | 33.07 | 0 |
| *Phoma* | 0.24±0.07a | 0.14±0.02cd | 0.19±0.05ab | 0.13±0.02cd | 0.12±0.02d | 0.17±0.02bc | 7.918 | 0 |
| *Funneliformis* | 0.39±0.09a | 0.07±0.02c | 0.3±0.17b | 0.07±0.02c | 0.05±0.01c | 0.03±0.01c | 22.279 | 0 |



**Fig. S2** LDA scores (≥5) calculated for bacterial and fungal community composition differences at the top genus level between the difference treatments soils in the rotation (A and C) and the residue amendment (B and D), respectively. The treatments abbreviations were defined in Fig. 1.

**Table S8** Pearson and spearman’s rank correlation coefficient between the abundant bacterial and fungal genus with the *Fusarium* **abundance**

|  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- |
|  | Rotation | pearson's rank correlation coefficient | spearman's rank correlation coefficient | Residue | pearson's rank correlation coefficient | spearman's rank correlation coefficient |
| Bacteria genus | ***Burkholderia*** | **-0.558\*\*** | **-0.443\*\*** | ***Pseudomonas*** | **-0.524\*\*** | **-0.440\*\*** |
| *Gemmatimonas* | NS | -0.028 | *Gemmatimonas* | NS | NS |
| *Bacillus* | 0.364\* | NS | *Gp4* | 0.387\* | NS |
| *Gp3* | NS | NS | *Sphingobium* | NS | NS |
| *Subdivision3\_genera\_incertae\_sedis* | NS | NS | *Azohydromonas* | NS | NS |
| *Gp1* | NS | 0.403\* | *Gp6* | 0.355\* | NS |
| *Rhizobium* | 0.626\*\* | NS | *Nitrososphaera* | 0.360\* | NS |
| *Gp6* | NS | NS | *Bacillus* | -0.424\*\* | NS |
| ***Nitrososphaera*** | **-0.482\*\*** | **-0.403\*** | *Subdivision3\_genera\_incertae\_sedis* | 0.453\*\* | NS |
| ***Sphingosinicella*** | **-0.539\*\*** | **-0.529\*\*** | *Georgfuchsia* | NS | NS |
| ***Sphingomonas*** | **-0.778\*\*** | **-0.757\*\*** | *Rhizobium* | NS | NS |
| *Ohtaekwangia* | NS | 0.481\*\* | *Thauera* | -0.388\* | NS |
| *Gp7* | NS | 0.365\* | *Spartobacteria\_genera\_incertae\_sedis* | 0.426\*\* | NS |
| *Pseudomonas* | NS | -0.363\* | *Pseudoduganella* | NS | NS |
| *Gaiella* | NS | NS | *Flavisolibacter* | NS | NS |
| *Ramlibacter* | 0.548\*\* | NS | *Klebsiella* | -0.358\* | NS |
| *WPS-1\_genera\_incertae\_sedis* | NS | NS | *Opitutus* | NS | NS |
| *Pseudolabrys* | -0.515\*\* | NS | *Gp3* | 0.488\*\* | NS |
| *Flavisolibacter* | NS | NS | *GpXIII* | NS | NS |
| *Sphingobium* | 0.775\*\* | NS | *Sphingomonas* | NS | NS |
| *Massilia* | NS | -0.445\*\* | *Chitinophaga* | NS | NS |
| *Opitutus* | NS | NS | *Terrimonas* | 0.703\*\* | 0.502\*\* |
| *Candidatus Koribacter* | NS | 0.341\* | *Novosphingobium* | NS | NS |
| *Zhizhongheella* | NS | NS | *Azonexus* | NS | NS |
| *Georgfuchsia* | 0.790\*\* | NS | *Anaeromyxobacter* | NS | NS |
| *Limnobacter* | NS | NS | *Povalibacter* | 0.425\*\* | NS |
| *Bradyrhizobium* | NS | NS | *Ohtaekwangia* | NS | NS |
| *Streptacidiphilus* | 0.756\*\* | NS | *Heliimonas* | NS | NS |
| *Conexibacter* | NS | NS | *Neorhizobium* | NS | NS |
| *Aridibacter* | NS | NS | *Falsibacillus* | NS | NS |
| Fungal genus | *Penicillium* | NS | NS | *Fusarium* | 1.000\*\* | 1.000\*\* |
| ***Talaromyces*** | **-0.687\*\*** | **-0.530\*\*** | *Elaphocordyceps* | -0.333\* | NS |
| *Fusarium* | 1.000\*\* | 1.000\*\* | ***Aspergillus*** | **-0.378\*** | **-0.354\*** |
| *Mortierella* | NS | 0.415\* | *Chaetomium* | NS | NS |
| ***Chaetomium*** | **-0.380\*** | **-0.581\*\*** | *Trichoderma* | 0.743\*\* | 0.581\*\* |
| ***Campylocarpon*** | **-0.694\*\*** | **-0.675\*\*** | *Acremonium* | 0.601\*\* | 0.602\*\* |
| *Haematonectria* | 0.445\*\* | 0.537\*\* | *Blastobotrys* | NS | NS |
| *Aspergillus* | 0.486\*\* | 0.380\* | ***Penicillium*** | **-0.453\*\*** | **-0.540\*\*** |
| *Derxomyces* | 0.662\*\* | 0.385\* | *Dermatocarpon* | NS | NS |
| *Trichoderma* | 0.373\* | 0.467\*\* | *Mortierella* | NS | NS |
| *Spizellomyces* | NS | -0.371\* | *Cantharellus* | 0.336\* | NS |
| *Kurtzmanomyces* | NS | 0.496\*\* | *Hyphodiscus* | NS | NS |
| *Dermatocarpon* | NS | NS | *Mycosphaerella* | NS | NS |
| *Elaphocordyceps* | 0.899\*\* | 0.776\*\* | *Stachybotrys* | NS | NS |
| *Hyphodiscus* | 0.706\*\* | 0.446\*\* | *Ophiocordyceps* | NS | -0.544\*\* |
| *Ophiostoma* | NS | 0.483\*\* | ***Colletotrichum*** | **-0.516\*\*** | **-0.541\*\*** |
| *Paraglomus* | NS | 0.410\* | *Cladorrhinum* | NS | NS |
| *Purpureocillium* | NS | 0.353\* | *Derxomyces* | -0.426\*\* | NS |
| *Acremonium* | 0.356\* | 0.567\*\* | *Scutellinia* | -0.351\* | NS |
| *Phialosimplex* | NS | -0.753\*\* | *Purpureocillium* | NS | NS |
| *Xylomyces* | NS | NS | *Bionectria* | 0.573\*\* | 0.402\* |
| *Candida* | NS | 0.493\*\* | ***Corynespora*** | **-0.401\*** | **-0.608\*\*** |
| *Cantharellus* | 0.772\*\* | 0.482\*\* | *Talaromyces* | 0.468\*\* | 0.399\* |
| ***Microdiplodia*** | **-0.691\*\*** | **-0.700\*\*** | *Podospora* | NS | NS |
| *Pseudallescheria* | NS | NS | *Myrothecium* | NS | NS |
| *Colletotrichum* | 0.895\*\* | 0.886\*\* | *Ophiostoma* | NS | NS |
| *Myrothecium* | 0.600\*\* | NS | ***Microdochium*** | **-0.393\*** | **-0.503\*\*** |
| *Podospora* | NS | NS | *Kurtzmanomyces* | NS | NS |
| *Sporothrix* | NS | 0.421\* | ***Phoma*** | **-0.369\*** | **-0.406\*** |
| *Ophiocordyceps* | NS | NS | *Funneliformis* | NS | NS |

NS = not significant, \* and \*\* represent significance at *P* < 0.05 and 0.01, respectively.

**Table S9** Topological properties of the empirical molecular ecological networks of microbial communities in treatments

|  |  |  |  |  |  |  |  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- |
| **Network metrics** | **Treatments** | | | | | | | | | | | | |
| **Rotation** | | | | | |  | **Residue** | | | | | |
| Bulk soil | | | Rhizosphere soil | | |  | Bulk soil | | | Rhizosphere soil | | |
| CBf | BBm | PBr | CRf | BRm | PRr |  | CBn | BBb | PBp | CRn | BRb | PRp |
| **Empirical networks** |  |  |  |  |  |  |  |  |  |  |  |  |  |
| Number of nodes | 226.00 | 258.00 | 195.00 | 157.00 | 160.00 | 211.00 |  | 251.00 | 84.00 | 224.00 | 147.00 | 155.00 | 142.00 |
| Number of edges | 221.00 | 383.00 | 347.00 | 132.00 | 245.00 | 374.00 |  | 404.00 | 201.00 | 573.00 | 252.00 | 153.00 | 134.00 |
| Number of positive correlations | 110.00 | 193.00 | 164.00 | 92.00 | 145.00 | 196.00 |  | 210.00 | 146.00 | 326.00 | 158.00 | 89.00 | 82.00 |
| Number of negative correlations | 111.00 | 190.00 | 183.00 | 40.00 | 100.00 | 178.00 |  | 194.00 | 55.00 | 247.00 | 94.00 | 64.00 | 52.00 |
| Ratio of positive to negative correlations | 0.99 | 1.02 | 0.90 | 2.30 | 1.45 | 1.10 |  | 1.08 | 2.65 | 1.32 | 1.68 | 1.39 | 1.58 |
| Average connectivity (avgK) | 1.96 | 2.97 | 3.56 | 1.68 | 3.06 | 3.55 |  | 3.22 | 4.79 | 5.12 | 3.43 | 1.97 | 1.89 |
| Average path distance (GD) | 6.51 | 8.44 | 5.67 | 3.12 | 5.25 | 7.83 |  | 8.29 | 2.67 | 4.46 | 4.65 | 3.08 | 2.97 |
| Average clustering coefficient (avgCC) | 0.21 | 0.34 | 0.30 | 0.14 | 0.27 | 0.32 |  | 0.31 | 0.37 | 0.30 | 0.38 | 0.21 | 0.20 |
| Graph density | 0.01 | 0.01 | 0.02 | 0.01 | 0.02 | 0.02 |  | 0.01 | 0.06 | 0.02 | 0.02 | 0.01 | 0.01 |
| Number of modules | 53.00 | 35.00 | 36.00 | 39.00 | 34.00 | 23.00 |  | 35.00 | 19.00 | 38.00 | 22.00 | 33.00 | 34.00 |
| Modularity | 0.91 | 0.85 | 0.78 | 0.94 | 0.79 | 0.82 |  | 0.82 | 0.44 | 0.53 | 0.78 | 0.92 | 0.91 |
| **Random networks** |  |  |  |  |  |  |  |  |  |  |  |  |  |
| GD ± SD | 7.782±0.584 | 5.021±0.100 | 3.943±0.080 | 7.345±1.544 | 4.085±0.109 | 4.173±0.072 |  | 4.564±0.094 | 2.872±0.073 | 3.289±0.061 | 3.906±0.099 | 7.640±0.687 | 7.737±1.019 |
| avgCC ± SD | 0.006±0.004 | 0.011±0.005 | 0.024±0.006 | 0.012±0.004 | 0.024±0.009 | 0.020±0.007 |  | 0.016±0.007 | 0.121±0.015 | 0.089±0.012 | 0.032±0.010 | 0.008±0.005 | 0.009±0.007 |
| Modularity±SD | 0.821±0.010 | 0.620±0.007 | 0.520±0.010 | 0.889±0.010 | 0.567±0.013 | 0.534±0.008 |  | 0.580±0.008 | 0.348±0.012 | 0.373±0.006 | 0.524±0.011 | 0.805±0.011 | 0.821±0.013 |

**Table S10** Linear models (LM) for the relationships of physicochemical indicators with disease incidence and the relative importance of each indicators in the crop rotation and residue amendment system. *P* was results of ANOVAs.

|  |  |  |  |  |  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- |
| Crop rotation | df | F | *P* | r | Relative importance | Residue amendment | df | F | *P* | r | Relative importance |
| OM | 1 | 8.94 | 0.011 | 3.88 | 22.22% | OM | 1 | 53.09 | 0.000 | -2.41 | 6.28% |
| AP | 1 | 17.84 | 0.001 | -2.21 | 7.28% | AP | 1 | 89.40 | 0.000 | 6.01 | 16.37% |
| AK | 1 | 19.45 | 0.001 | 3.55 | 36.45% | AK | 1 | 223.59 | 0.000 | 3.62 | 28.88% |
| AN | 1 | 4.29 | 0.061 | -1.52 | 7.16% | AN | 1 | 7.69 | 0.016 | 2.77 | 45.10% |
| pH | 1 | 2.30 | 0.155 | -1.52 | 8.37% | Residuals | 13 |  |  |  |  |
| Residuals | 12 |  |  |  |  |  |  |  |  |  |  |
|  |  |  |  |  |  |  |  |  |  |  |  |
| **Model summary: R2 = 0.738, AIC = 106.76, p < 0.001** | | | | |  | **Model summary: R2 = 0.956, AIC = 64.44, p < 0.001** | | | | |  |
| Proportion of variance explained by model: 81.49% | | | | |  | Proportion of variance explained by model: 96.64% | | | | |  |



**Fig. S3** *Zi-Pi* value of the empirical molecular ecological networks of microbial communities in treatments