Table S1 Differences of bacterial and fungal community compositions between different treatments.

|  |  |  |  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- | --- | --- | --- |
|  | Fertilizer vs. Control | | | Cover crop vs. Control | | | Fertilizer+Cover crop vs. Control | | |
|  | Significant | Increase | Decrease | Significant | Increase | Decrease | Significant | Increase | Decrease |
| **Bacteria** |  |  |  |  |  |  |  |  |  |
| Acidobacteria | 39 | 19 | 20 | 90 | 24 | 66 | 108 | 4 | 104 |
| Actinobacteria | 74 | 27 | 47 | 138 | 78 | 60 | 96 | 69 | 27 |
| Bacteroidetes | 35 | 21 | 14 | 62 | 51 | 11 | 33 | 17 | 16 |
| Chloroflexi | 52 | 19 | 33 | 112 | 53 | 59 | 84 | 11 | 73 |
| Firmicutes | 30 | 20 | 10 | 77 | 68 | 9 | 123 | 114 | 9 |
| Gemmatimonadetes | 45 | 24 | 21 | 84 | 44 | 40 | 49 | 19 | 30 |
| Others | 160 | 71 | 89 | 302 | 189 | 113 | 212 | 49 | 163 |
| Planctomycetes | 120 | 58 | 62 | 196 | 73 | 123 | 218 | 11 | 207 |
| Proteobacteria | 219 | 121 | 98 | 429 | 309 | 120 | 311 | 242 | 69 |
| **Fungi** |  |  |  |  |  |  |  |  |  |
| Ascomycota | 84 | 52 | 32 | 122 | 61 | 61 | 125 | 62 | 63 |
| Basidiomycota | 54 | 36 | 18 | 48 | 17 | 31 | 57 | 24 | 33 |
| Chytridiomycota | 0 | 0 | 0 | 2 | 1 | 1 | 3 | 1 | 2 |
| Glomeromycota | 2 | 2 | 0 | 1 | 1 | 0 | 1 | 1 | 0 |
| Others | 91 | 63 | 28 | 82 | 48 | 34 | 92 | 50 | 42 |
| Zygomycota | 10 | 6 | 4 | 14 | 6 | 8 | 17 | 12 | 5 |

Table S2 Network topological parameters of co-occurrence networks of different sizes of aggregates.

|  |  |  |  |  |
| --- | --- | --- | --- | --- |
|  | Whole soil | Macroaggregate | Microaggregate | Silt+Clay |
| Number of nodes | 938 | 938 | 876 | 786 |
| Fungal nodes | 180 | 215 | 188 | 138 |
| Bacterial nodes | 758 | 723 | 688 | 648 |
| Number of edges | 1635 | 2359 | 1693 | 1427 |
| Fungi-Fungi | 340 | 358 | 645 | 210 |
| Bacteria-Bacteria | 1097 | 1518 | 896 | 1121 |
| Bacteria-Fungi | 198 | 483 | 152 | 96 |
| Clustering coefficient | 0.171 | 0.235 | 0.213 | 0.170 |
| Network diameter | 19 | 12 | 22 | 19 |
| Network density | 0.004 | 0.005 | 0.004 | 0.005 |
| Network heterogeneity | 1.488 | 1.712 | 2.192 | 1.071 |
| Average number of neighbors | 3.484 | 5.028 | 3.865 | 3.631 |
| Network centralization | 0.080 | 0.107 | 0.134 | 0.032 |
| Characteristic path length | 6.953 | 5.103 | 6.742 | 6.622 |
| Connected components | 82 | 64 | 84 | 68 |

Table S3 Abundance, taxonomy and trophic mode (fungi) of OTUs with high degree in the networks of different sized aggregates.

|  |  |  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- | --- | --- |
| Node | Abundance (%) | Degree | Phylum | Class | Order | Family | Genus | Trophic Mode of fungi |
| **Whole soil** | |  |  |  |  |  |  |  |
| OFU-531 | 0.0104 | 78 | Ascomycota | Leotiomycetes | Helotiales | |  | Unclassified |
| OFU-511 | 0.025 | 60 | Zygomycota | Incertae\_sedis\_Zygomycota | | |  | Unclassified |
| OTU-1403 | 0.017 | 46 | Bacteroidetes | |  |  |  |  |
| OFU-593 | 0.0168 | 31 | Basidiomycota | Agaricomycetes | |  |  | Unclassified |
| OFU-282 | 0.0596 | 26 | Chytridiomycota | Blastocladiomycetes | Blastocladiales | Blastocladiaceae | Blastocladiella | Saprotroph |
| OFU-2690 | 0.0314 | 25 | Ascomycota | Saccharomycetes | Saccharomycetales | Incertae\_sedis\_Saccharomycetales | | Saprotroph |
| OTU-935 | 0.0341 | 24 | Bacteroidetes | Sphingobacteriia | Sphingobacteriales | Sphingobacteriaceae | Olivibacter |  |
| OTU-1607 | 0.0114 | 24 | Bacteroidetes | Sphingobacteriia | Sphingobacteriales | Sphingobacteriaceae | Sphingobacterium |  |
| OFU-1672 | 0.011 | 24 |  |  |  |  |  | Unclassified |
| OTU-325 | 0.1068 | 23 | Proteobacteria | Betaproteobacteria | Burkholderiales | Oxalobacteraceae | Massilia |  |
| OTU-776 | 0.0247 | 22 | Bacteroidetes | Sphingobacteriia | Sphingobacteriales | Chitinophagaceae | Niastella |  |
| OFU-204 | 0.0274 | 22 | Basidiomycota | Tremellomycetes | Tremellales | Incertae\_sedis\_Tremellales | Cryptococcus | Pathotroph-Saprotroph-Symbiotroph |
| OTU-460 | 0.0336 | 21 | Bacteroidetes | Sphingobacteriia | Sphingobacteriales | Chitinophagaceae | Flavisolibacter |  |
| OFU-24 | 0.8201 | 20 | Ascomycota | Incertae\_sedis\_Ascomycota | Incertae\_sedis\_Ascomycota | Incertae\_sedis\_Ascomycota | Heydenia | Unclassified |
| OTU-204 | 0.1739 | 20 | Proteobacteria | Gammaproteobacteria | Cellvibrionales | Cellvibrionaceae | Cellvibrio |  |
| **Macroaggregate** | |  |  |  |  |  |  |  |
| OFU-379 | 0.160821 | 105 | Ascomycota | Pezizomycetes | Pezizales | Pezizaceae | Peziza | Saprotroph-Symbiotroph |
| OTU-3034 | 0.093511 | 103 | Proteobacteria | Alphaproteobacteria | Rhodospirillales | Rhodospirillaceae | Defluviicoccus |  |
| OTU-3767 | 0.115446 | 103 | Proteobacteria | Alphaproteobacteria | Rhodospirillales | Rhodospirillaceae | Defluviicoccus |  |
| OTU-4676 | 0.068113 | 103 | Proteobacteria | Deltaproteobacteria | 43F-1404R | |  |  |
| OTU-2666 | 0.113137 | 103 | Proteobacteria | Alphaproteobacteria | Rhodospirillales | Rhodospirillaceae | Defluviicoccus |  |
| OFU-499 | 0.141109 | 49 |  |  |  |  |  | Unclassified |
| OTU-13 | 2.903363 | 29 | Proteobacteria | Alphaproteobacteria | Rhodospirillales | Rhodospirillaceae | Skermanella |  |
| OFU-455 | 0.158974 | 29 | Ascomycota | |  |  |  | Unclassified |
| OTU-3691 | 0.076122 | 29 | Proteobacteria | Deltaproteobacteria | 43F-1404R | |  |  |
| OTU-87 | 0.690422 | 26 | Proteobacteria | Alphaproteobacteria | Rhodospirillales | unidentified\_Rhodospirillales | Candidatus\_Alysiosphaera |  |
| OTU-56 | 1.897124 | 22 | Actinobacteria | Thermoleophilia | Solirubrobacterales | Solirubrobacteraceae | Solirubrobacter |  |
| OTU-10518 | 0.585513 | 22 | Proteobacteria | Gammaproteobacteria | Xanthomonadales | Xanthomonadaceae | |  |
| OFU-9 | 17.58215 | 22 | Ascomycota | Sordariomycetes | Xylariales | Incertae\_sedis\_Xylariales | Monographella | Pathotroph |
| OTU-1475 | 0.090667 | 22 | Planctomycetes | Planctomycetacia | Planctomycetales | Planctomycetaceae | |  |
| OTU-802 | 0.150296 | 21 | Proteobacteria | Gammaproteobacteria | Pseudomonadales | Pseudomonadaceae | Pseudomonas |  |
| OFU-502 | 0.080352 | 20 | Ascomycota | Incertae\_sedis\_Ascomycota | Incertae\_sedis\_Ascomycota | Incertae\_sedis\_Ascomycota | Scolecobasidium | Saprotroph |
| OFU-208 | 0.449176 | 20 | Ascomycota | |  |  |  | Unclassified |
| **Microaggregate** | |  |  |  |  |  |  |  |
| OFU-28 | 3.9814 | 121 | Ascomycota | Pezizomycetes | Pezizales | Pezizaceae | | Saprotroph-Symbiotroph |
| OFU-596 | 0.0164 | 114 | Glomeromycota | |  |  |  | Symbiotroph |
| OFU-706 | 0.0236 | 114 | Ascomycota | Pezizomycetes | Pezizales | Pezizaceae | | Saprotroph-Symbiotroph |
| OFU-1564 | 0.0196 | 114 | Ascomycota | Pezizomycetes | Pezizales | Pezizaceae | Peziza | Saprotroph-Symbiotroph |
| OFU-424 | 0.0638 | 47 | Glomeromycota | |  |  |  | Symbiotroph |
| OFU-338 | 0.0136 | 32 | Basidiomycota | Pucciniomycetes | Pucciniales | Pucciniaceae | Puccinia | Pathotroph |
| OFU-425 | 0.0232 | 29 | Ascomycota | Saccharomycetes | |  |  | Unclassified |
| OFU-577 | 0.014 | 28 | Glomeromycota | |  |  |  | Symbiotroph |
| OFU-441 | 0.0224 | 23 | Ascomycota | Saccharomycetes | |  |  | Unclassified |
| OFU-271 | 0.0614 | 21 | Ascomycota | Saccharomycetes | |  |  | Unclassified |
| OFU-203 | 0.0204 | 20 | Basidiomycota | Agaricomycetes | Boletales |  |  | Unclassified |
| OFU-394 | 0.0166 | 19 | Chytridiomycota | Blastocladiomycetes | Blastocladiales | Blastocladiaceae | Blastocladiella | Saprotroph |
| OFU-131 | 0.0162 | 18 | Ascomycota | Leotiomycetes | Helotiales | Helotiaceae | | Saprotroph-Symbiotroph |
| OFU-1321 | 0.0486 | 16 | Ascomycota | Saccharomycetes | |  |  | Unclassified |
| OTU-717 | 0.0221 | 15 | Verrucomicrobia | Verrucomicrobiae | Verrucomicrobiales | Verrucomicrobiaceae | Roseimicrobium |  |
| OFU-73 | 0.2091 | 14 |  |  |  |  |  | Unclassified |
| **Silt+Clay** | |  |  |  |  |  |  |  |
| OTU-15 | 0.2875 | 29 | Proteobacteria | Alphaproteobacteria | Rhizobiales | Methylobacteriaceae | Microvirga |  |
| OFU-914 | 0.011 | 26 | Glomeromycota | Glomeromycetes | Glomerales | |  | Symbiotroph |
| OTU-552 | 0.0152 | 26 | Bacteroidetes | Bacteroidetes\_vadinHA17 | | |  |  |
| OTU-191 | 0.1345 | 26 | Actinobacteria | unidentified\_Actinobacteria | Frankiales | Geodermatophilaceae | Geodermatophilus |  |
| OTU-2 | 1.8823 | 22 | Actinobacteria | unidentified\_Actinobacteria | Frankiales | Geodermatophilaceae | Blastococcus |  |
| OTU-14625 | 0.3614 | 22 | Proteobacteria | Alphaproteobacteria | Rhizobiales | Methylobacteriaceae | Microvirga |  |
| OFU-395 | 0.0138 | 20 | Ascomycota | Leotiomycetes | |  |  | Unclassified |
| OTU-5205 | 0.2563 | 18 | Proteobacteria | Alphaproteobacteria | Rhodospirillales | Rhodospirillaceae | Skermanella |  |
| OTU-3021 | 0.1961 | 17 | Actinobacteria | unidentified\_Actinobacteria | Propionibacteriales | Nocardioidaceae | Marmoricola |  |
| OFU-407 | 0.0294 | 17 | Ascomycota | Pezizomycetes | |  |  | Unclassified |
| OFU-270 | 0.0538 | 17 | Ascomycota | Dothideomycetes | Pleosporales | Didymosphaeriaceae | Pseudopithomyces | Pathotroph-Saprotroph-Symbiotroph |
| OFU-23 | 3.7377 | 16 | Ascomycota | Pezizomycetes | Pezizales |  |  | Unclassified |
| OFU-420 | 0.0202 | 16 |  |  |  |  |  | Unclassified |
| OTU-10518 | 0.1325 | 16 | Proteobacteria | Gammaproteobacteria | Xanthomonadales | Xanthomonadaceae | |  |
| OTU-546 | 0.0315 | 16 | Chloroflexi | JG30-KF-CM66 | |  |  |  |
| OTU-1529 | 0.0742 | 16 | Actinobacteria | unidentified\_Actinobacteria | Frankiales | Geodermatophilaceae | Modestobacter |  |
| OTU-110 | 0.1525 | 16 | Actinobacteria | unidentified\_Actinobacteria | Propionibacteriales | Nocardioidaceae | Nocardioides |  |

Table S4 Differences of relative abundance of fungi for each trophic mode between different treatments.

|  |  |  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- | --- | --- |
|  | Pathotroph | Pathotroph-Saprotroph | Pathotroph-Saprotroph-Symbiotroph | Pathotroph-Symbiotroph | Saprotroph | Saprotroph-Symbiotroph | Symbiotroph | Unclassified |
| **Whole soil** | |  |  |  |  |  |  |  |
| CK | 4.94+1.89a | 0.89+0.09ab | 20.81+3.85a | 0.48+0.22b | 10.55+1.22a | 16.87+3.71a | 0.45+0.12a | 45.00+2.67a |
| Fertilizer | 2.71+2.05ab | 0.73+0.03b | 6.85+0.45b | 3.71+0.70a | 20.31+8.89a | 15.15+5.43ab | 0.54+0.28a | 49.99+10.20a |
| Cover crop | 2.16+0.86b | 0.78+0.33ab | 20.84+16.74a | 1.9+2.55ab | 11.36+8.98a | 7.44+6.24b | 0.24+0.09a | 55.29+6.09a |
| Fertilizer +Cover crop | 3.25+0.29ab | 1.22+0.51a | 13.79+3.55a | 0.86+0.39ab | 13.75+2.24a | 12.1+1.93ab | 0.34+0.05a | 54.68+6.54a |
| **Macroaggregate** | |  |  |  |  |  |  |  |
| CK | 2.54+1.13a | 10.99+5.23a | 15.1+2.67a | 0.18+0.09b | 9.23+3.26a | 13.4+1.59a | 0.47+0.14b | 48.1+7.52a |
| Fertilizer | 3.41+1.06a | 1.5+0.35b | 22.43+10.97a | 0.21+0.04b | 11.09+2.14a | 11.1+2.61a | 1.64+0.64a | 48.62+10.47a |
| Cover crop | 7.52+10.01a | 0.97+0.22bc | 12.6+7.75ab | 0.68+0.16a | 12.4+4.21a | 13.17+6.60a | 0.59+0.17b | 52.07+5.03a |
| Fertilizer +Cover crop | 2.52+1.20a | 0.49+0.34c | 5.46+1.65b | 3.12+1.96a | 24.03+14.23a | 12.11+6.43a | 0.35+0.17b | 51.92+22.93a |
| **Microaggregate** | |  |  |  |  |  |  |  |
| CK | 1.87+1.32a | 8.55+3.72a | 10.95+6.84ab | 0.24+0.05b | 6.94+1.78b | 28.18+23.86a | 0.67+0.69ab | 42.61+12.21a |
| Fertilizer | 2.58+1.84a | 0.62+0.43b | 13.11+4.52a | 0.22+0.19b | 21.62+17.70a | 10.25+4.53a | 1.38+0.47a | 50.21+8.11a |
| Cover crop | 4.53+1.66a | 0.87+0.31ab | 8.64+2.12ab | 0.36+0.16ab | 9.98+4.15ab | 13.79+7.71a | 0.44+0.23b | 61.39+14.83a |
| Fertilizer +Cover crop | 2.8+0.75a | 0.54+0.23b | 5.46+3.35b | 3.48+1.56a | 18.96+11.94a | 24.74+12.66a | 0.42+0.18ab | 43.59+5.88a |
| **Silt + Clay** | |  |  |  |  |  |  |  |
| CK | 2.53+0.79ab | 7.78+3.43a | 12.94+8.23a | 0.1+0.02d | 7.37+0.51ab | 12.06+3.81b | 0.33+0.04b | 56.88+13.17a |
| Fertilizer | 2.35+0.97b | 0.93+0.39b | 14.74+4.77a | 0.21+0.12c | 6.96+2.84b | 13.53+4.67b | 1.21+0.48a | 60.05+11.62a |
| Cover crop | 4.39+1.63a | 0.91+0.69b | 9.78+2.78a | 0.54+0.04b | 11.14+3.37ab | 23.83+6.73a | 0.33+0.02b | 49.1+6.11ab |
| Fertilizer +Cover crop | 2.86+1.00ab | 0.35+0.14c | 6.74+2.00a | 2.94+0.68a | 14.65+5.61a | 27.95+6.64a | 0.67+0.27a | 43.85+1.19b |

Fig. S1 Bacterial and fungal alpha diversity between different treatments.

Fig. S2 Bacterial and fungal alpha diversity between different sized aggregates. 



Fig. S3 Relationship between OTU abundance and betweenness centrality and degree.



Fig. S4 Differences of betweenness centrality and degree between bacterial and fungal OTUs.



Fig. S5 Differences of relative abundance of fungi for each trophic mode between different treatments.

Fig. S6 Random forest (RF) analysis showed importance (IncMSE% and IncNodePurity) of impact factors for the bacterial NST.