**Lists of tables and figures:**

**Figure A1.** LEfSe analysis results showing bacterial taxa that significantly differed among the different treatments after 16 years (2004 to 2019) of the study by R software using the coin package (v.4.0.3, Vienna, Austria, http://[www.r-project.org](http://www.r-project.org)). Only indicator bacterial taxa with LDA values > 3.5 are shown in the figure. Different colored regions or bars indicate taxa associated with different treatments. The cladogram on the right shows significant differences (*p* < 0.05) in relative abundances of bacterial taxa among the four treatments. The colored circles extending from the inner to outer rings of the cladogram represent phylum, class, order, family, and genus levels, while circle sizes reflect the relative abundances of specific bacterial taxa. Taxa exhibiting significant differences in relative abundances among the treatments are indicated with circles colored in orange, blue, green, or red (corresponding to different treatments), while deep yellow circles correspond to taxa that exhibited similar relative abundances among different treatments. The colored shadows indicate trends for significantly different taxa. Names of significantly enriched taxa are indicated on the right. Only taxa with log LDA scores >3.5 are shown on the cladogram.

**Figure A2**. LEfSe analysis results showing fungal taxa that significantly differed among the different treatments after 16 years (2004 to 2019) of the study by R software using the coin package (v.4.0.3, Vienna, Austria, http://[www.r-project.org](http://www.r-project.org)). Only indicator fungal taxa with LDA values >3.5 are shown in the figure. Different colored regions or bars indicate taxa associated with different treatments. The cladogram on the right shows significant differences (*p* < 0.05) in relative abundances of fungal taxa among the four treatments. The colored circles extending from the inner to outer rings of the cladogram represent phylum, class, order, family, and genus levels, while circle sizes reflect the relative abundances of specific fungal taxa. Taxa exhibiting significant differences in relative abundances among the treatments are indicated with circles colored in orange, blue, green, or red (corresponding to different treatments), while deep yellow circles correspond to taxa that exhibited similar relative abundances among different treatments. The colored shadows indicate trends for significantly different taxa. Names of significantly enriched taxa are indicated on the right. Only taxa with log LDA scores >3.5 are shown on the cladogram.

**Table A1.** Relative abundances of abundant bacterial phyla in soils subjected to different treatments after 16 years (2004 to 2019). The data represent the means ± SD (n=3). Different letters within a column indicate statistically significant differences among the four treatments (the least significant difference, LSD, *p* < 0.05).

|  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- |
| Treatment | Proteobacteria | Actinobacteria | Acidobacteria | Bacteroidetes | Gemmatimonadetes | Chloroflexi |
| CK | 28.55±0.71 c | 32.49±1.79 a  | 14.51±1.00 a  | 7.23±1.54 c | 4.44±1.33 b  | 6.03±0.64 ab  |
| CF | 29.22±1.48 c  | 30.73±2.11 a  | 10.76±0.71 b  | 9.60±0.97 b  | 6.39±0.71 a  | 6.44±0.18 a  |
| M | 35.22±0.98 a  | 24.73±3.14 b  | 13.90±1.97 a  | 10.00±1.10 b  | 6.60±1.03 a  | 4.57±0.35 c  |
| CFM | 32.92±1.57 b  | 24.75±0.59 b  | 11.54±0.14 b  | 12.13±0.64 a | 6.78±0.87 a  | 5.48±0.16 b  |

**Table A2.** Relative abundances of abundant bacterial genera in soils subjected to different treatments after 16 years (2004 to 2019). The data represent the means ± SD (n=3). Different letters within a column indicate statistically significant differences among the four treatments (the least significant difference, LSD, *p* < 0.05).

|  |  |  |  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- | --- | --- | --- |
| Treatment | *Sphingomonas* | *unidentified\_**Acidobacteria* | *Blastococcus* | *Lysobacter* | *Nocardioides* | *Gaiella* | *Pseudarthrobacter* | *Iamia* | *Bryobacter* |
| CK | 4.95±0.56 b | 2.95±0.11 a | 2.27±0.25 a | 0.28±0.03 d | 1.75±0.07 ab | 1.77±0.14 a | 1.48±0.12 a | 0.82±0.05 c | 0.89±0.08 b |
| CF | 4.59±0.21 b | 2.21±0.24 a | 1.59±0.50 b | 0.80±0.04 c | 1.89±0.20 a | 1.31±0.12 b | 1.54±0.26 a | 1.20±0.15 b | 1.18±0.28 ab |
| M | 6.14±0.14 a | 2.88±0.44 a | 1.59±0.51 b | 1.58±0.10 b | 1.36±0.43 b | 1.15±0.11 b | 1.23±0.40 a | 1.35±0.17 ab | 1.32±0.25 a |
| CFM | 5.01±0.26 b | 2.66±0.59 a | 1.56±0.33 b | 2.12±0.15 a | 1.67±0.14 ab | 0.87±0.07 c | 1.13±0.05 a | 1.67±0.23 a | 1.18±0.14 ab |

**Table A3.** Relative abundances of abundant fungal phyla in soils subjected to different treatments after 16 years (2004 to 2019). The data represent the means ± SD (n=3). Different letters within a column indicate statistically significant differences among the four treatments (the least significant difference, LSD, *p* < 0.05).

|  |  |  |  |  |
| --- | --- | --- | --- | --- |
| Treatment | Ascomycota | Mortierellomycota | Basidiomycota | Mucoromycota |
| CK | 77.21±1.65 a | 3.69±1.25 b | 2.34±0.53 b | 3.36±0.75 a |
| CF | 69.09±4.15 bc | 6.16±0.93 ab | 7.48±1.30 a | 0.51±0.27 b |
| M | 72.63±9.06 b | 7.49±3.69 ab | 2.85±0.44 b | 3.32±0.90 a |
| CFM | 61.07±0.60 c | 9.42±1.64 a | 3.57±1.10 b | 2.17±0.25 a |

**Table A4.** Relative abundances (%) of abundant fungal genera in soils subjected to different treatments after 16 years (2004 to 2019). The data represent the means ± SD (n=3). Different letters within a column indicate statistically significant differences among the four treatments (the least significant difference, LSD, *p* < 0.05).

|  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- |
| Treatment | *Mortierella* | *Fusarium* | *Acremonium* | *Alternaria* | *Dactylonectria* | *Rhizopus* |
| CK | 2.68±0.93 b | 4.00±1.78 b | 7.11±2.59 a | 5.67±0.13 a | 3.43±1.36 a | 3.24±0.72 a |
| CF | 4.74±0.71 ab | 8.49±3.03 a | 0.22±0.08 b | 4.10±0.76 b | 0.13±0.06b | 0.27±0.15b |
| M | 6.43±3.72 ab | 3.75±1.31 b | 0.22±0.07 b | 0.67±0.40 c | 0.13±0.10 b | 3.16±0.83 a |
| CFM | 7.89±1.69 a | 3.13±0.40 b | 0.16±0.05 b | 4.77±0.67 ab | 0.12±0.06 b | 0.16±0.07 b |

**Table A5.** Direct and indirect relationships among soil characteristics within the different treatments of this study based on PLS-PM modeling. Path coefficients were calculated after 1,000 bootstraps.

|  |  |  |  |
| --- | --- | --- | --- |
| Relationships | Direct | Indirect | Total |
| Fertilization -> pH | −0.5135 | 0.00000 | −0.5135 |
| Fertilization -> BD | −0.6103 | −0.25620 | −0.8665 |
| Fertilization -> OM | 1.0518 | −0.15204 | 0.8998 |
| Fertilization -> Nutrient | 0.8946 | 0.03749 | 0.9321 |
| Fertilization -> BL | −1.1412 | 1.27655 | 0.1354 |
| Fertilization -> FL | 0.6826 | 0.20322 | 0.8859 |
| Fertilization -> Bact | 0.2100 | −0.15711 | 0.0529 |
| Fertilization -> Fun | 1.5271 | −0.55309 | 0.9740 |
| pH -> BD | 0.4989 | 0.00000 | 0.4989 |
| pH -> OM | −0.5949 | 0.26344 | −0.3314 |
| pH -> Nutrient | 0.4136 | −0.07684 | 0.3367 |
| pH -> BL | 0.2177 | −1.16070 | −0.9430 |
| pH -> FL | 0.3813 | 0.00899 | 0.3903 |
| pH -> Bact | 1.7450 | −1.04413 | 0.7009 |
| pH -> Fun | 0.2382 | −0.39524 | −0.1570 |
| BD -> OM | 0.5280 | 0.00000 | 0.5280 |
| BD -> Nutrient | 0.0845 | 0.18961 | 0.2741 |
| BD -> BL | −1.3433 | 0.29528 | −1.0481 |
| BD -> FL | −0.1227 | 0.10034 | −0.0224 |
| BD -> Bact | −0.4133 | −0.52636 | −0.9397 |
| BD -> Fun | −0.2710 | −0.15585 | −0.4269 |
|  OM -> Nutrient | 0.3591 | 0.00000 | 0.3591 |
| OM -> BL | 0.8706 | −0.21534 | 0.6552 |
| OM -> FL | 0.0541 | 0.09400 | 0.1481 |
| OM -> Bact | 0.4388 | 0.41256 | 0.8514 |
| OM -> Fun | 0.0163 | −0.23778 | −0.2214 |
| Nutrient -> BL | −0.5997 | 0.00000 | −0.5997 |
| Nutrient -> FL | 0.2618 | 0.00000 | 0.2618 |
| Nutrient -> Bact | −0.1157 | −0.41560 | −0.5313 |
| Nutrient -> Fun | −0.6103 | −0.03293 | −0.6432 |
| BL -> Bact | 0.6931 | 0.00000 | 0.6931 |
| FL -> Fun | −0.1258 | 0.00000 | −0.1258 |

Fertilization : Different fertilization treatments, pH: soil pH, BD: soil bulk density, OM: organic matter, nutrient: total nitrogen TN, available nitrogen AN, available phosphorus AP, available potassium AK, BL: bacterial diversity, FL: fungal diversity, Bact: bacterial community, Fun: fungal community.