**Supplementary Materials**

**Table S1.** N and W effects on environmental factors based on linear models.

|  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- |
| Environmental factors | Control | | N*a* | | W | | NW | | N versus control | | W versus control | | N × W  versus control | |
| Average | SD | Average | SD | Average | SD | Average | SD | β*b* | *P* | β | *P* | β | *P* |
| Soil T (℃) | 27.938 | 0.898 | 29.188 | 0.747 | 31.063 | 0.657 | 31.063 | 0.315 | 1.250 | 0.094 | **3.125** | **9.97E-06***c* | -1.250 | 0.094 |
| Water (%) | 20.708 | 1.468 | 22.810 | 1.277 | 20.248 | 1.098 | 20.813 | 1.634 | 2.103 | 0.078 | -0.460 | 0.101 | -1.538 | 0.288 |
| pH | 5.825 | 0.141 | 5.793 | 0.163 | 5.805 | 0.085 | 5.860 | 0.221 | -0.033 | 0.891 | -0.020 | 0.772 | 0.088 | 0.595 |
| Salinity | 0.815 | 0.061 | 0.834 | 0.056 | 0.814 | 0.149 | 0.896 | 0.046 | 0.019 | 0.274 | -0.001 | 0.501 | 0.064 | 0.484 |
| TC (%) | 0.475 | 0.035 | 0.523 | 0.063 | 0.450 | 0.032 | 0.475 | 0.037 | 0.048 | 0.123 | -0.025 | 0.123 | -0.023 | 0.616 |
| TN (%) | 0.048 | 0.005 | 0.050 | 0.000 | 0.048 | 0.005 | 0.048 | 0.005 | 0.002 | 0.574 | 0.000 | 0.574 | -0.002 | 0.574 |
| TC/TN | 9.758 | 1.112 | 9.983 | 0.463 | 9.200 | 0.701 | 10.165 | 0.621 | 0.225 | 0.145 | -0.557 | 0.632 | 0.740 | 0.351 |
| NO2- (μg·g-1) | 0.010 | 0.027 | 0.013 | 0.018 | 0.001 | 0.014 | 0.003 | 0.015 | 0.004 | 0.777 | -0.009 | 0.359 | -0.001 | 0.941 |
| NH4+ (μg·g-1) | 8.825 | 2.304 | 11.527 | 1.528 | 11.705 | 5.799 | 12.756 | 2.358 | 2.700 | 0.295 | 2.880 | 0.253 | -1.650 | 0.638 |
| NO3- (μg·g-1) | 0.911 | 0.054 | 1.051 | 0.272 | 1.008 | 0.051 | 1.057 | 0.217 | 0.143 | 0.305 | 0.100 | 0.565 | -0.095 | 0.602 |
| NH4+/ NO3- | 9.722 | 2.570 | 11.376 | 2.374 | 11.457 | 5.574 | 12.126 | 0.852 | 1.654 | 0.497 | 1.735 | 0.468 | -0.985 | 0.772 |
| P (μg·g-1) | 203.108 | 17.595 | 193.115 | 93.183 | 184.103 | 31.328 | 232.820 | 31.611 | -9.993 | 0.474 | -19.005 | 0.700 | 58.710 | 0.284 |
| AGB (g·m-2 ) | 141.834 | 22.305 | 159.447 | 27.451 | 121.448 | 21.967 | 128.345 | 16.906 | 17.612 | 0.297 | **-20.387** | **0.041** | -10.715 | 0.642 |
| BGB (g·m-2 ) | 64.818 | 9.265 | 72.134 | 11.403 | 56.349 | 9.125 | 59.214 | 7.023 | 7.316 | 0.297 | **-8.469** | **0.041** | -4.451 | 0.642 |
| N2O (mmol·m-2·h-1) | 0.465 | 0.192 | 3.845 | 1.402 | 1.318 | 0.998 | 4.150 | 4.534 | **3.380** | **0.025** | 0.853 | 0.642 | -0.548 | 0.825 |
| CH4 (mmol·m-2·h-1) | 0.303 | 0.319 | 0.098 | 0.188 | 0.860 | 1.017 | 0.278 | 0.362 | -0.205 | 0.193 | 0.558 | 0.221 | -0.378 | 0.521 |
| CO2 (mmol·m-2·h-1) | 1.475 | 0.233 | 1.998 | 0.557 | 1.860 | 0.434 | 1.535 | 0.703 | 0.523 | 0.706 | 0.385 | 0.882 | -0.848 | 0.124 |

*a*Abbreviations: N, nitrogen addition; W, Warming; NW, the dual treatment of N and W; N × W, the interactive effect of N and W; SD, standard deviation; T, temperature; TC, total carbon; TN, total nitrogen; P, phosphorus; AGB, aboveground biomass; BGB, belowground biomass.

*b*All estimated effect sizes (β) are based on environmental factors.

*c*Statistical significance is based on Wald type II F tests. Significant effects (*P* < 0.050) are shown in bold.

**Table S2.** N and W effects on microbial diversity and evenness indices based on linear models.

|  |  |  |  |  |  |  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- |
| Treatment  effects | | Bacteria | | | | | | Fungi | | | | |
| Richness | | Shannon | Simpson | Faith's PD | Pielou's evenness | Richness | Shannon | Simpson | Faith's PD | Pielou's evenness |
| N*a* | β*b* | **1.060** | **1.026** | | **0.995** | **1.011** | **1.017** | -0.33 | 0.489 | 0.241 | 0.453 | 0.621 |
| *t* | **1.997** | **2.025** | | **1.877** | **1.627** | **2.014** | -0.558 | 0.831 | 0.381 | 0.908 | 1.033 |
| *P* | **0.003***c* | **0.002** | | **0.003** | **0.023** | **0.002** | 0.076 | 0.249 | 0.21 | 0.154 | 0.347 |
| W | β | -0.527 | -0.498 | | -0.652 | -0.445 | -0.503 | -0.387 | 0.339 | 0.297 | **-0.005** | 0.467 |
| *t* | -0.992 | -0.982 | | -1.228 | -0.716 | -0.996 | -0.654 | 0.576 | 0.469 | **-0.010** | 0.775 |
| *P* | 0.597 | 0.795 | | 0.458 | 0.495 | 0.803 | 0.06 | 0.142 | 0.254 | **0.015** | 0.204 |
| N × W | β | 0.646 | 0.805 | | 0.727 | 0.272 | 0.823 | -0.963 | **-1.988** | -1.67 | **-1.979** | **-2.076** |
| *t* | 0.861 | 1.124 | | 0.97 | 0.309 | 1.153 | -1.15 | **-2.388** | -1.862 | **-2.806** | **-2.439** |
| *P* | 0.406 | 0.283 | | 0.351 | 0.763 | 0.272 | 0.273 | **0.034** | 0.087 | **0.016** | **0.031** |

*a*Abbreviations: N, nitrogen addition; W, Warming; N × W, the interactive effect of N and W; PD, phylogenetic diversity.

*b*All estimated effect sizes (β) are based on response variables.

*c*Statistical significance is based on Wald type II F tests. Significant effects (*P* < 0.050) are shown in bold.

**Table S3.** N and W effects on abundant bacterial phyla (> 0.1%) and genera (> 0.3%) based on linear models.

|  |  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- | --- |
| Taxonomy | Name | N*a* | | W | | N × W | |
| β*b* | *P* | β | *P* | β | *P* |
| Abundant phyla | Proteobacteria | -0.668 | **0.002***c* | 0.481 | 0.541 | -1.388 | 0.062 |
| Bacteroidetes | 1.127 | 0.205 | 0.296 | 0.768 | -0.898 | 0.392 |
| Acidobacteria | -0.124 | **0.012** | -1.282 | 0.680 | 2.273 | **0.006** |
| Firmicutes | 0.641 | **0.002** | -0.024 | 0.080 | 1.296 | 0.071 |
| Actinobacteria | 0.717 | **0.002** | -0.207 | 0.220 | 1.273 | 0.080 |
| Chloroflexi | -0.233 | 0.601 | -0.132 | 0.479 | 1.026 | 0.345 |
| Planctomycetes | -0.128 | **<0.001** | -0.649 | **0.029** | 2.466 | **<0.001** |
| Chlorobi | 0.776 | 0.540 | 0.066 | 0.483 | -0.892 | 0.412 |
| Verrucomicrobia | 0.000 | **0.016** | -0.688 | 0.383 | 2.032 | **0.016** |
| Cyanobacteria.Chloroplast | -0.068 | 0.877 | -0.102 | 0.925 | 0.311 | 0.784 |
| Chlamydiae | -0.985 | 0.302 | -1.188 | 0.159 | 0.938 | 0.346 |
| Gemmatimonadetes | 0.779 | **0.019** | -0.443 | 0.903 | 0.779 | 0.384 |
| Spirochaetes | 0.208 | 0.649 | 0.830 | 0.489 | -0.908 | 0.406 |
| Armatimonadetes | -0.241 | **0.007** | -1.360 | 0.730 | 2.500 | **0.002** |
| Nitrospira | 0.636 | 0.168 | -0.726 | 0.204 | 0.151 | 0.878 |
| WS3 | 0.725 | **0.041** | -0.682 | 0.425 | 0.618 | 0.507 |
| Synergistetes | -1.024 | 0.369 | -1.058 | 0.336 | 1.118 | 0.283 |
| BRC1 | 0.444 | 0.134 | 0.059 | 0.429 | 0.681 | 0.499 |
| OD1 | 0.664 | 0.608 | -0.640 | **0.033** | -0.861 | 0.351 |
| Abundant genera | Gp1 | -0.975 | 0.089 | -1.56 | 0.928 | 3.065 | **<0.001** |
| Bradyrhizobium | 0.937 | **0.002** | -0.251 | 0.555 | 0.934 | 0.213 |
| Gp3 | 1.321 | **0.002** | -0.834 | **0.027** | 0.009 | 0.989 |
| Conexibacter | 0.595 | **0.002** | -0.04 | 0.074 | 1.354 | 0.059 |
| Gp16 | -0.721 | 0.439 | -0.695 | 0.408 | 2.147 | **0.031** |
| Bacillus | 0.587 | **0.006** | 0.096 | 0.078 | 1.185 | 0.123 |
| Spartobacteria\_genera\_incertae\_sedis | 0.074 | **0.014** | -0.733 | 0.509 | 1.964 | **0.02** |
| Gp7 | 1.238 | **0.005** | -0.272 | 0.702 | 0.234 | 0.772 |
| Phenylobacterium | 0.79 | **0.004** | -0.915 | 0.302 | 1.041 | 0.181 |
| Singulisphaera | -0.063 | **<0.001** | -0.485 | **0.008** | 2.373 | **<0.001** |
| Pseudolabrys | 0.439 | **0.010** | -0.867 | 0.752 | 1.484 | 0.079 |
| Gp6 | 0.126 | **0.009** | -0.977 | 0.975 | 1.976 | **0.017** |
| Aciditerrimonas | -0.269 | 0.096 | -1.428 | 0.324 | 2.014 | **0.030** |
| Burkholderia | 0.088 | **0.008** | -1.433 | 0.223 | 1.989 | **0.013** |
| Ktedonobacter | -0.38 | **0.011** | -0.826 | 0.156 | 2.562 | **0.001** |
| Gemmata | 0.194 | **<0.001** | -0.362 | **0.017** | 2.072 | **0.001** |
| Mycobacterium | 1.058 | **<0.001** | 0.157 | **0.038** | 0.922 | 0.109 |

*a*Abbreviations: N, nitrogen addition; W, Warming; N × W, the interactive effect of N and W.

*b*All estimated effect sizes (β) are based on relative abundances of abundant bacterial phyla (> 0.1%) and genera (> 0.3%). The phyla and genera are listed in the decreasing order of relative abundances.

*c*Statistical significance is based on Wald type II F tests. Significant effects (*P* < 0.050) are shown in bold.

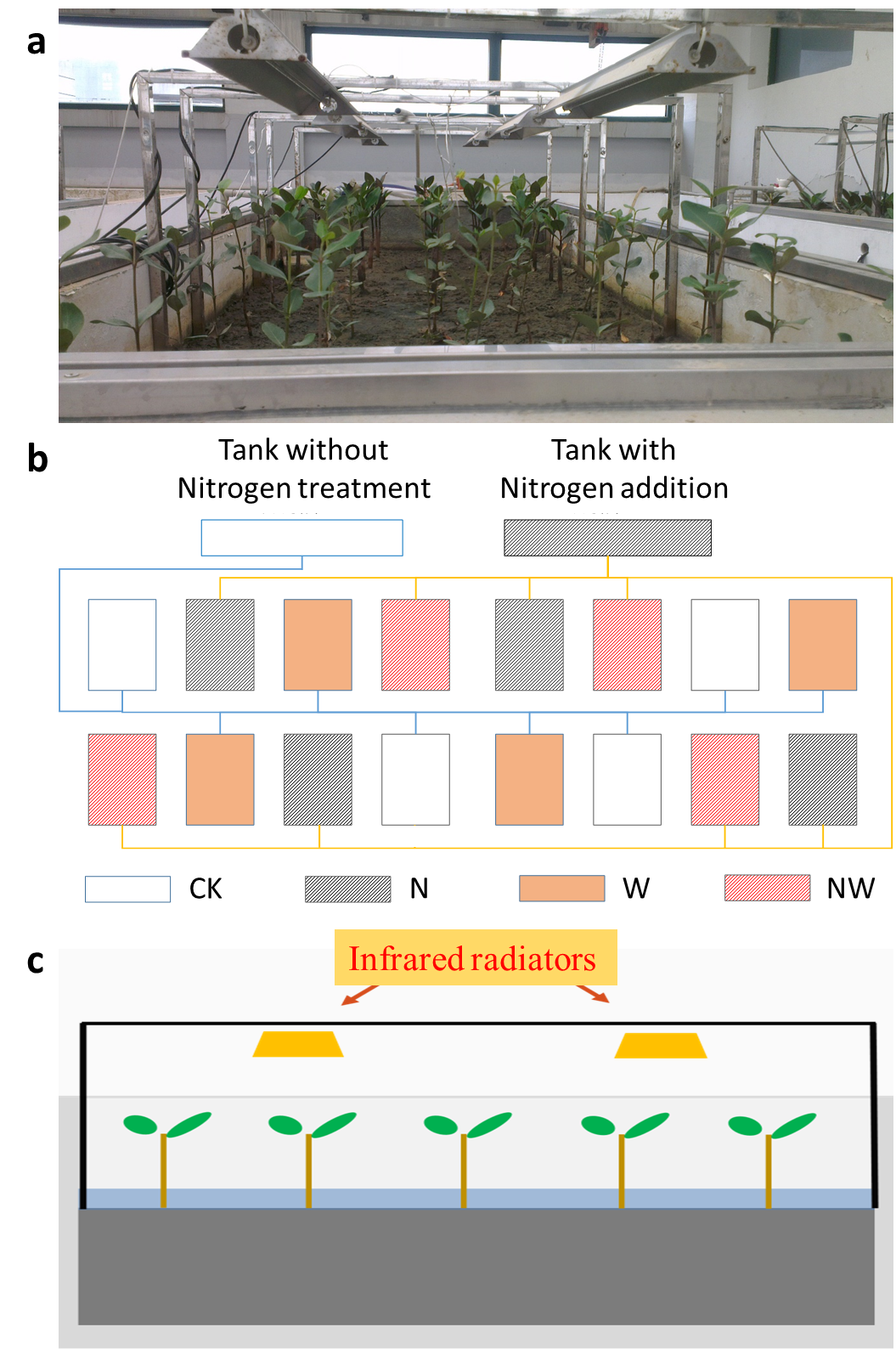
**Table S4.** N and W effects on methanogenic, bacterial nitrifying, and denitrifying genera based on linear models.

|  |  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- | --- |
| Category | Name | N*a* | | W | | N × W | |
| β*b* | *P* | β | *P* | β | *P* |
| Methanogenic genera | Methanoregula | 0.213 | 0.297 | 0.939 | 0.701 | -1.494 | 0.153 |
| Methanocella | -0.261 | 0.675 | -0.365 | 0.547 | 0.052 | 0.963 |
| Methanoculleus | -0.581 | 0.880 | -1.057 | 0.454 | 1.321 | 0.222 |
| Methanospirillum | -0.993 | 0.059 | -0.199 | 0.684 | 0.000 | 1.000 |
| Methanosarcina | -0.513 | 0.728 | -0.642 | 0.564 | 0.642 | 0.564 |
| Methanosaeta | -0.783 | **0.044***c* | 0.261 | 1.000 | -0.522 | 0.584 |
| Methanolinea | 0.327 | 0.272 | 0.763 | 0.822 | -1.743 | 0.090 |
| Methanobacterium | 0.348 | 0.510 | 0.696 | 0.199 | 0.000 | 1.000 |
| Methanocorpusculum | 0.000 | 0.337 | 1.000 | 0.337 | -1.000 | 0.337 |
| Methanosphaera | 0.000 | 0.143 | 1.379 | 0.143 | -1.379 | 0.143 |
| Methanolacinia | 0.000 | 1.000 | -0.732 | 0.183 | 0.000 | 1.000 |
| Methanobrevibacter | 1.000 | 0.337 | 0.000 | 0.337 | -1.000 | 0.337 |
| Methanolobus | 1.000 | 0.337 | 0.000 | 0.337 | -1.000 | 0.337 |
| Methanomicrobium | 1.000 | 0.337 | 0.000 | 0.337 | -1.000 | 0.337 |
| Nitrifying genera | Nitrosospira | 0.715 | 0.441 | -0.328 | 0.232 | -0.621 | 0.552 |
| Nitrospira | 0.641 | 0.181 | -0.733 | 0.181 | 0.092 | 0.926 |
| Nitrosomonas | 0.152 | 0.704 | -0.087 | 0.417 | -0.718 | 0.511 |
| Nitrobacter | 0.648 | **0.015** | -0.259 | 0.542 | 1.037 | 0.234 |
| Nitrosococcus | 0.685 | **0.047** | -0.342 | 1.000 | 0.685 | 0.474 |
| Denitrifying genera | Bradyrhizobium | 0.937 | **0.002** | -0.251 | 0.555 | 0.934 | 0.213 |
| Bacillus | 0.587 | **0.006** | 0.096 | 0.078 | 1.185 | 0.123 |
| Burkholderia | 0.088 | **0.008** | -1.433 | 0.223 | 1.989 | **0.013** |
| Rhodoplanes | 1.525 | **<0.001** | -0.254 | 0.691 | 0.280 | 0.628 |
| Shewanella | 0.028 | 0.323 | 0.003 | 0.346 | 0.977 | 0.348 |
| Rhodobacter | -0.372 | 0.246 | 0.301 | 0.947 | -0.530 | 0.621 |
| Sphingomonas | 0.475 | 0.353 | 0.129 | 0.753 | 0.086 | 0.937 |
| Pseudomonas | 0.176 | 0.329 | -0.527 | 0.754 | 0.717 | 0.508 |
| Paenibacillus | 0.600 | **0.004** | -0.072 | 0.136 | 1.272 | 0.097 |
| Thiobacillus | 0.940 | 0.163 | 0.940 | 0.163 | -0.470 | 0.629 |
| Azoarcus | 0.996 | 0.050 | -0.398 | 0.424 | 0.028 | 0.976 |
| Hyphomicrobium | 0.216 | 0.377 | 0.000 | 0.620 | 0.540 | 0.620 |
| Mesorhizobium | 1.182 | **0.019** | -0.222 | 0.622 | 0.000 | 1.000 |
| Cupriavidus | 0.766 | 0.939 | 0.153 | 0.265 | -1.455 | 0.164 |
| Rhizobium | 1.214 | 0.448 | 0.773 | 0.913 | -1.656 | 0.119 |
| Hydrogenophaga | 0.555 | 0.859 | -0.185 | 0.228 | -0.924 | 0.382 |
| Comamonas | 0.206 | 0.241 | 0.000 | 0.427 | 0.826 | 0.427 |
| Ralstonia | 0.841 | 0.191 | -0.280 | 0.422 | -0.280 | 0.786 |
| Cytophaga | 0.000 | 0.870 | 0.000 | 0.870 | -0.187 | 0.870 |
| Halomonas | 0.235 | 0.211 | 1.412 | 0.211 | -1.647 | 0.089 |
| Massilia | 1.019 | 0.463 | 0.255 | 0.463 | -1.274 | 0.230 |
| Arcobacter | 0.553 | 0.795 | -0.138 | 0.309 | -0.830 | 0.441 |
| Marinobacter | 0.000 | 1.000 | 0.732 | 0.183 | 0.000 | 1.000 |
| Flavobacterium | 0.000 | 0.786 | -0.307 | 0.786 | 0.307 | 0.786 |
| Aeromonas | 1.000 | 0.337 | 0.000 | 0.337 | -1.000 | 0.337 |
| Methylobacterium | 0.830 | 0.232 | -0.415 | 0.232 | -0.415 | 0.682 |
| Thiomicrospira | 0.000 | 0.663 | 1.246 | **0.045** | -0.415 | 0.663 |
| Kocuria | 0.620 | 0.073 | 0.000 | 0.525 | 0.620 | 0.525 |
| Azospirillum | 0.000 | 1.000 | -0.732 | 0.183 | 0.000 | 1.000 |
| Neisseria | 0.000 | 1.000 | 0.732 | 0.183 | 0.000 | 1.000 |
| Thauera | -0.732 | 0.183 | 0.000 | 1.000 | 0.000 | 1.000 |

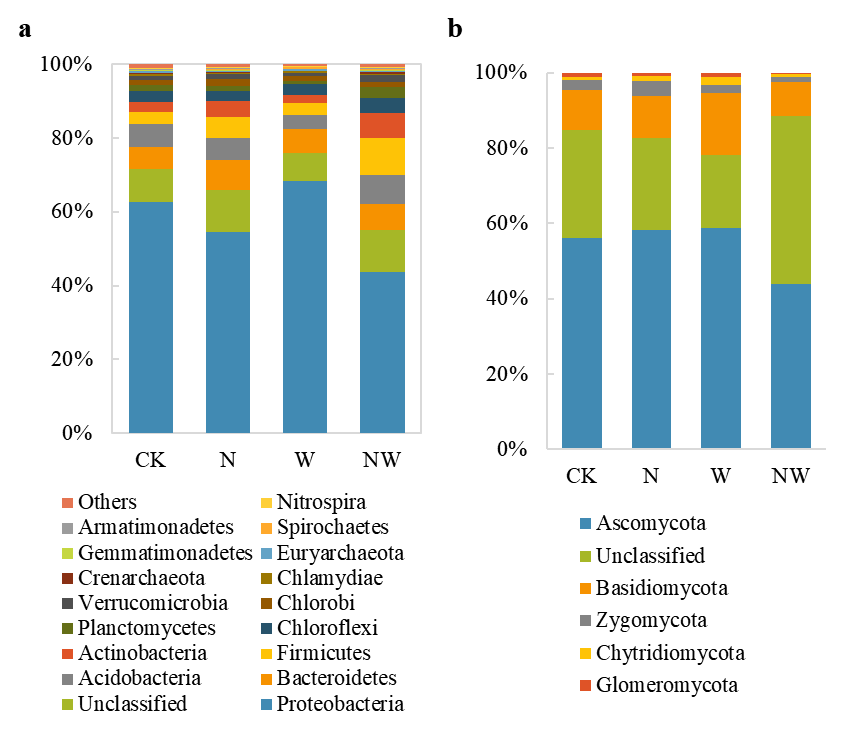
*a*Abbreviations: N, nitrogen addition; W, Warming; N × W, the interactive effect of N and W.

*b*All estimated effect sizes (β) are based on relative abundances of methanogenic, bacterial nitrifying, and denitrifying genera. The genera are listed in the decreasing order of relative abundances.

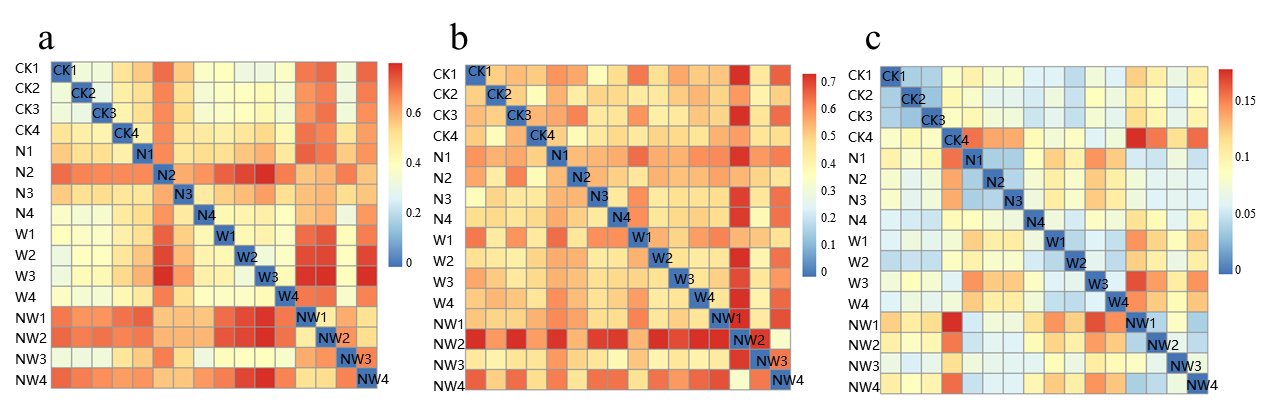
*c*Statistical significance is based on Wald type II F tests. Significant effects (*P* < 0.050) are shown in bold.



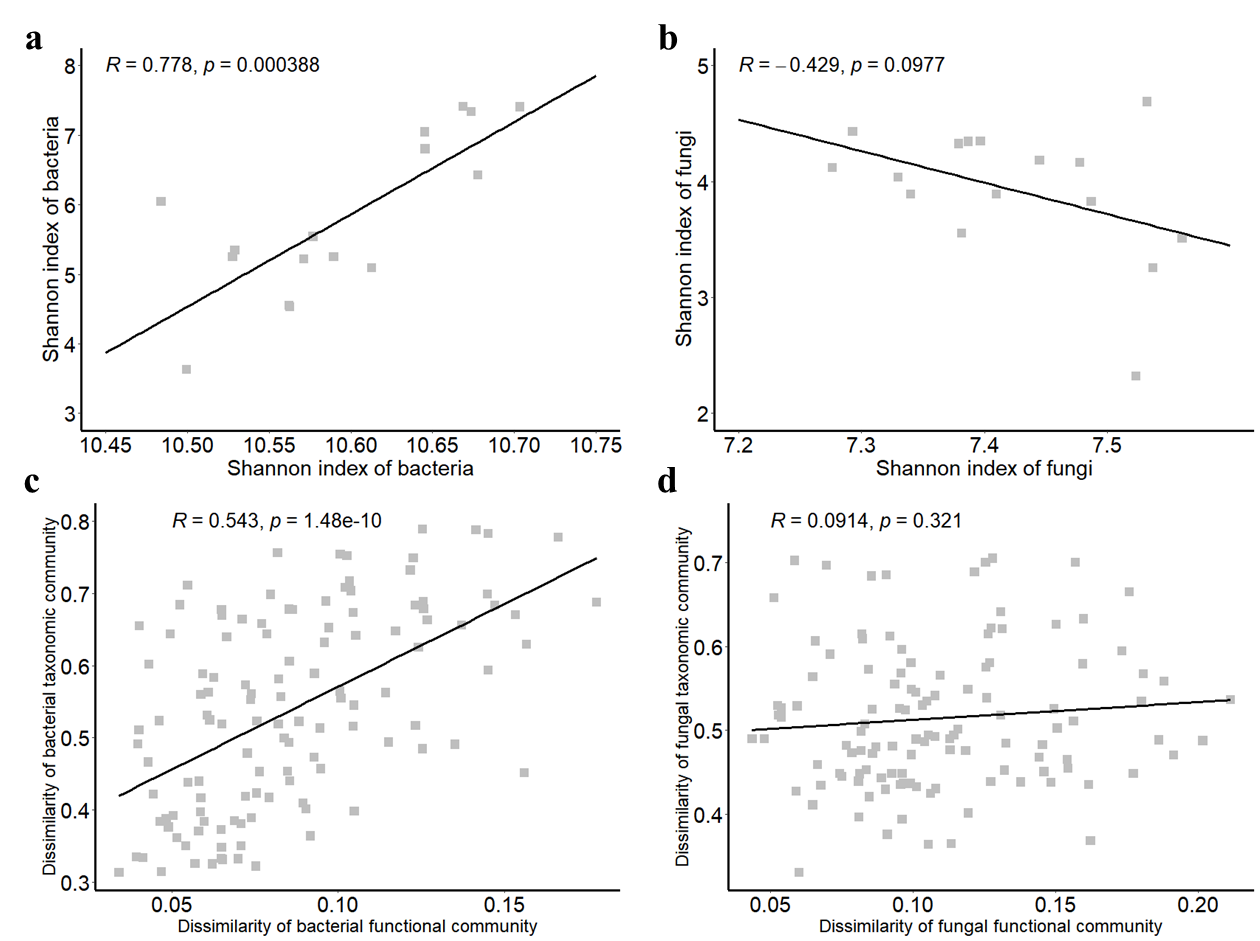
**Fig. S1.** (a) The photo of a laboratory-based plot, (b) A map showing the location distribution of experimental plots, and (c) A scheme showing the setup for the warming treatment. Abbreviations: CK, control; N, nitrogen addition; W, warming; NW, the dual treatment of N and W.



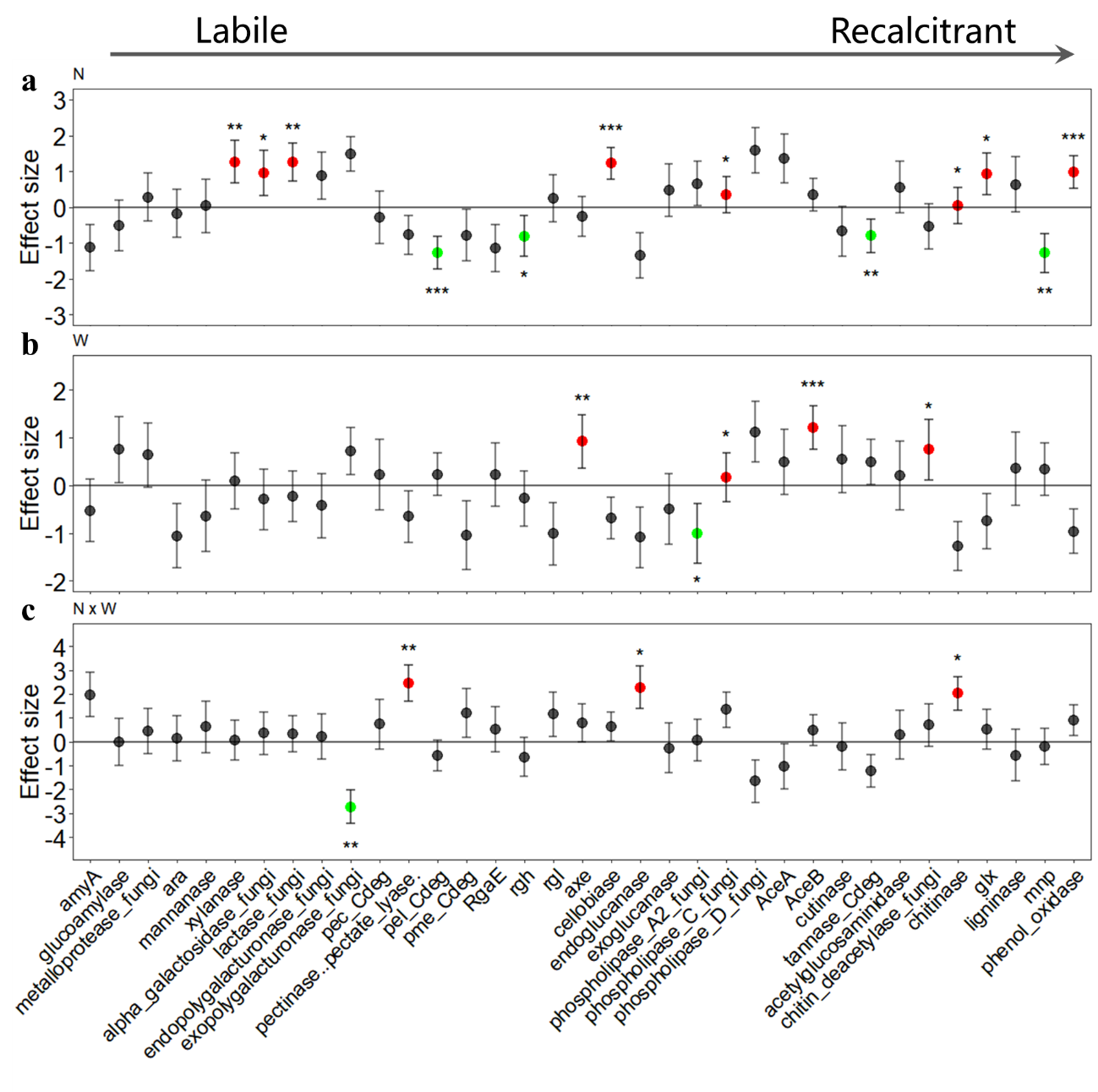
**Fig. S2.** Microbial community composition for **(a)** bacteria and **(b)** fungi.



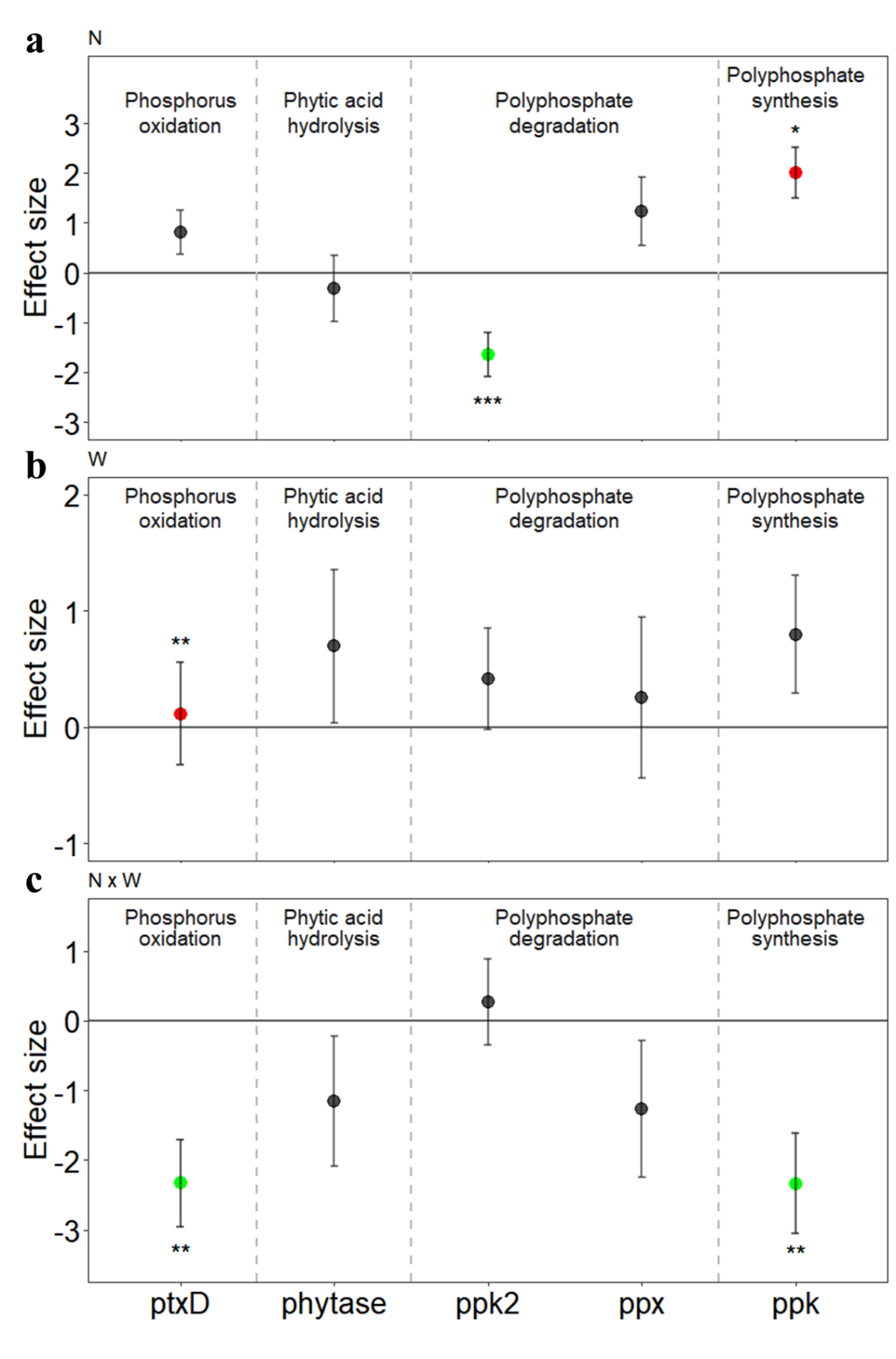
**Fig. S3.** The dissimilarity matrix for **(a)** 16S rRNA gene, **(b)** ITS, and **(c)** GeoChip data. The redder color represents a dissimilarity index close to 1, while the bluer color represents a dissimilarity index close to 0.



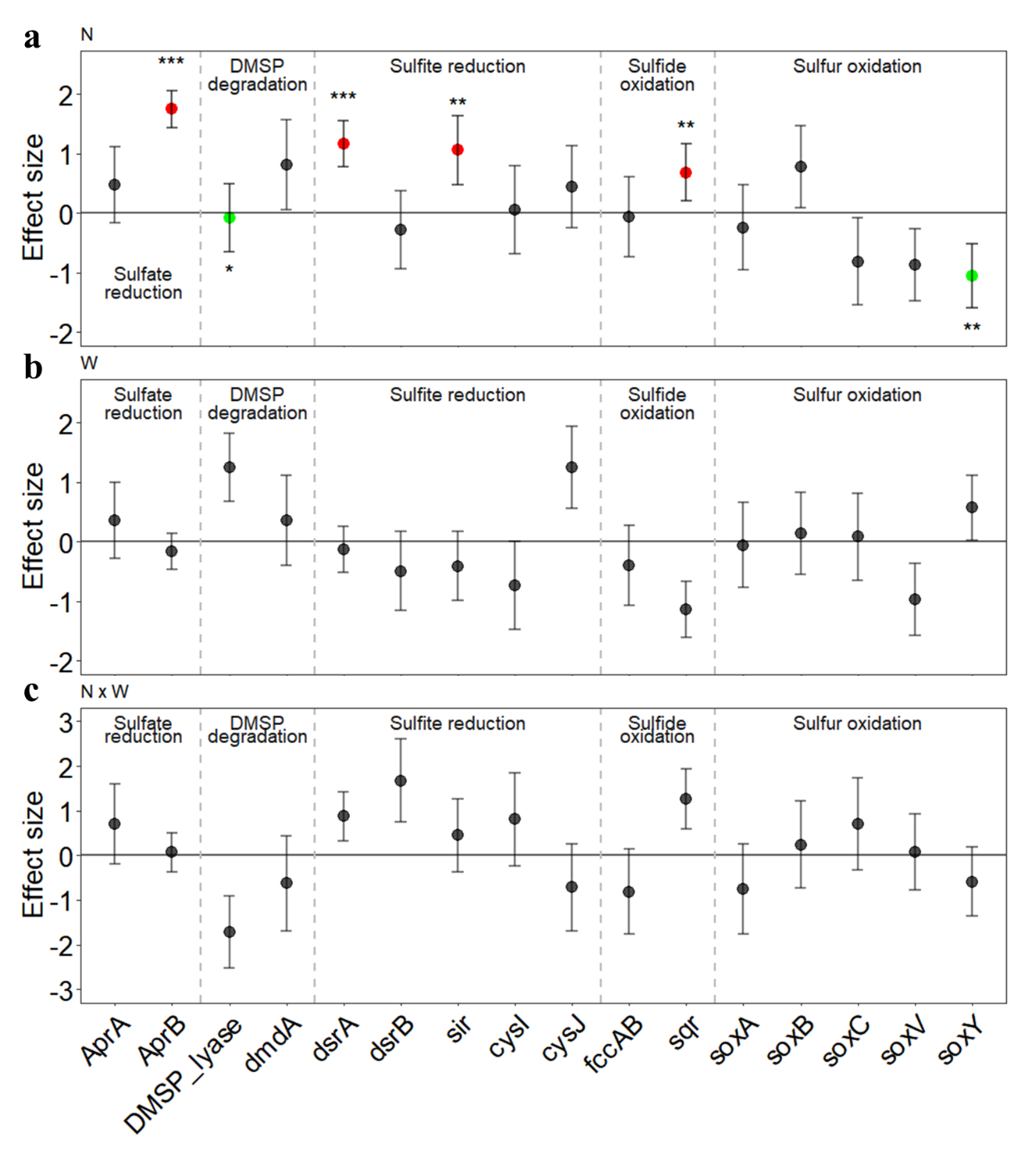
**Fig. S4.** Correlation between **(a)** bacterial taxonomic and functional α-diversities based on Shannon index, **(b)** fungal taxonomic and functional α-diversities based on Shannon index, **(c)** dissimilarity of bacterial taxomomic and functional community composition, and **(d)** dissimilarity of fungal taxomomic and functional community composition.



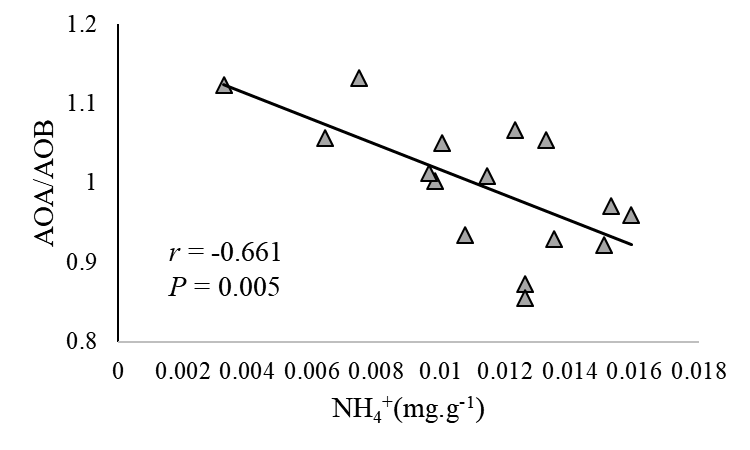
**Fig. S5.** Treatment effects on relative abundances of fungal carbon degradation genes based on linear models. **a**, N: nitrogen addition; **b**, W: warming; **c**, N × W: the interactive of N and W. Red color represents a significant increase in the relative abundance, while green color represents a significant decrease in the relative abundance. Black color represents insignificant changes. The statistical significance is based on F tests. Asterisks represent significant *P*-values: \*, *P* < 0.050; \*\*, *P* < 0.010; \*\*\*, *P* < 0.001. Error bars represent the standard errors of the estimated effect sizes.



**Fig. S6.** Treatment effects on relative abundances of bacterial phosphorus cycling genes based on linear models. **a**, N: nitrogen addition; **b**, W: warming; **c**, N × W: the interactive of N and W. Red color represents a significant increase in the relative abundance, while green color represents a significant decrease in the relative abundance. Black color represents insignificant changes. The statistical significance is based on F tests. Asterisks represent significant *P*-values: \*, *P* < 0.050; \*\*, *P* < 0.010; \*\*\*, *P* < 0.001. Error bars represent the standard errors of the estimated effect sizes.



**Fig. S7.** Treatment effects on relative abundances of bacterial sulfur cycling genes based on linear models. **a**, N: nitrogen addition; **b**, W: warming; **c**, N × W: the interactive of N and W. Red color represents a significant increase in the relative abundance, while green color represents a significant decrease in the relative abundance. Black color represents insignificant changes. The statistical significance is based on F tests. Asterisks represent significant *P*-values: \*, *P* < 0.050; \*\*, *P* < 0.010; \*\*\*, *P* < 0.001. Error bars represent the standard errors of the estimated effect sizes.



**Fig. S8.** Correlation between AOA/AOB and soil ammonium.