**Supplementary Materials**

**Table S1. ANOVA outputs for fungal biomass**. Fungal biomass (nmol PLFA g-1 dry soil) and arbuscular mycorrhizal fungal biomass (nmol NLFA g-1 dry soil) were based on phospholipid fatty acid (PLFA) and neutral lipid fatty acid (NLFA) analysis. The degrees of freedom for each factor is 1 and the total degrees of freedom for each model is 19.

|  |  |  |  |
| --- | --- | --- | --- |
|  | **Sum of Sq** | ***F-*value** | ***P*-value** |
| **Fungal biomass (organic)** |  |  |  |
| (Intercept) | 15181.5 | 30.9429 | 4.29E-05 |
| Heated | 120.6 | 0.2457 | 0.6268 |
| Nitrogen | 58.8 | 0.1199 | 0.7336 |
| Heated × Nitrogen | 275.6 | 0.5617 | 0.4645 |
| **Fungal biomass (mineral)** |  |  |
| (Intercept) | 524.42 | 16.1668 | 0.0009879 |
| Heated | 46.46 | 1.4324 | 0.248804 |
| Nitrogen | 6.13 | 0.1891 | 0.6694642 |
| Heated × Nitrogen | 0.3 | 0.0093 | 0.9242527 |
| **AMF biomass (organic)** |  |  |
| (Intercept) | 365320 | 19.4436 | 0.0004385 |
| Heated | 8916 | 0.4745 | 0.5007821 |
| Nitrogen | 909 | 0.0484 | 0.8287299 |
| Heated × Nitrogen | 4836 | 0.2574 | 0.6188281 |
| **AMF biomass (mineral)** |  |  |
| (Intercept) | 16260.1 | 8.2962 | 0.01088 |
| Heated | 211 | 0.1077 | 0.74706 |
| Nitrogen | 1115.8 | 0.5693 | 0.4615 |
| Heated × Nitrogen | 861.5 | 0.4395 | 0.51678 |

**Table S2. Permutational analysis of variance (PERMANOVA) table summarizing changes in fungal community composition across the treatments**.Significant differences (*P* ≤ 0.05) are bolded.The degrees of freedom for each factor is 1 and the total degrees of freedom for each model is 19. Abbreviations: AMF = arbuscular mycorrhizal fungi; EMF = ectomycorrhizal fungi, Sap = saprotrophic fungi; Paths = pathotrophic fungi; Sq = squares.

|  |  |  |  |  |
| --- | --- | --- | --- | --- |
|  | **Sums of Sq.** | **F-value** | **R2** | **P-value** |
| **Total fungi (organic)** |  |  |  |  |
| Heating (H) | 0.56 | 1.45 | 0.07 | **0.028** |
| Nitrogen (N) | 0.5 | 1.28 | 0.06 | 0.08 |
| H x N | 0.46 | 1.18 | 0.06 | 0.16 |
| **Total fungi (mineral)** |  |  |  |  |
| Heating | 0.5 | 1.28 | 0.7 | 0.19 |
| Nitrogen | 0.26 | 0.67 | 0.04 | 0.84 |
| H x N | 0.26 | 0.64 | 0.03 | 0.87 |
| **AMF (organic)** |  |  |  |  |
| Heating | 0.33 | 2.32 | 0.12 | **0.026** |
| Nitrogen | 0.16 | 1.16 | 0.06 | 0.30 |
| H x N | 0.22 | 1.53 | 0.08 | 0.15 |
| **AMF (mineral)** |  |  |  |  |
| Heating | 0.23 | 1.19 | 0.07 | 0.28 |
| Nitrogen | 0.26 | 1.31 | 0.08 | 0.21 |
| H x N | 0.24 | 1.22 | 0.07 | 0.27 |
| **EMF (organic)** |  |  |  |  |
| Heating | 0.58 | 1.42 | 0.07 | **0.047** |
| Nitrogen | 0.53 | 1.31 | 0.07 | 0.11 |
| H x N | 0.43 | 1.05 | 0.05 | 0.42 |
| **EMF (mineral)** |  |  |  |  |
| Heating | 0.50 | 1.23 | 0.07 | 0.24 |
| Nitrogen | 0.28 | 0.66 | 0.04 | 0.8 |
| H x N | 0.26 | 0.64 | 0.3 | 0.83 |
| **Sap (organic)** |  |  |  |  |
| Heating | 0.61 | 1.85 | 0.09 | **0.01** |
| Nitrogen | 0.42 | 1.25 | 0.06 | 0.143 |
| H x N | 0.53 | 1.6 | 0.08 | **0.019** |
| **Sap (mineral)** |  |  |  |  |
| Heating | 0.52 | 1.4 | 0.07 | **0.04** |
| Nitrogen | 0.39 | 1.05 | 0.05 | 0.38 |
| H x N | 0.37 | 0.99 | 0.05 | 0.47 |
| **Paths (organic)** |  |  |  |  |
| Heating | 0.34 | 0.93 | 0.05 | 0.6 |
| Nitrogen | 0.34 | 0.92 | 0.05 | 0.58 |
| H x N | 0.48 | 1.31 | 0.07 | 0.14 |
| **Paths (mineral)** |  |  |  |  |
| Heating | 0.31 | 0.77 | 0.04 | 0.8 |
| Nitrogen | 0.48 | 1.11 | 0.06 | 0.29 |
| H x N | 0.53 | 1.31 | 0.07 | 0.12 |

**Table S3.** **ANOVA summary tables outlining fungal alpha diversity (richness and diversity) responses to the treatments.** Significant values are in bold (*P* ≤ 0.05). The degrees of freedom for each factor is 1 and the total degrees of freedom for each model is 19. Abbreviations: AMF = arbuscular mycorrhizal fungi; EMF = ectomycorrhizal fungi, Sap = saprotrophic fungi; Paths = pathotrophic fungi; Sq = squares.

|  |  |  |  |  |
| --- | --- | --- | --- | --- |
|  |  | **Sum of Sq** | ***F*-value** | ***P*-value** |
| *Richness* | **Total fungi (organic)** |  |  |  |
|  | Heated | 774 | 0.7 | 0.42 |
|  | Nitrogen | 2890 | 2.58 | 0.13 |
|  | Heated × N | 994 | 0.89 | 0.36 |
| *Shannon* | Heated | 1.64 | 4.97 | **0.04** |
|  | Nitrogen | 2 | 6.06 | **0.025** |
|  | Heated × N | 1.3 | 3.94 | 0.06 |
| *Richness* | **Total fungi (mineral)** |  |  |  |
|  | Heated | 1369 | 2.7 | 0.12 |
|  | Nitrogen | 32 | 0.06 | 0.80 |
|  | Heated × N | 708 | 1.39 | 0.25 |
| *Shannon* | Heated | 0.002 | 0.007 | 0.93 |
|  | Nitrogen | 0.000 | 0.0001 | 0.99 |
|  | Heated × N | 0.03 | 0.09 | 0.77 |
| *Richness* | **AMF (organic)** |  |  |  |
|  | Heated | 18 | 0.28 | 0.59 |
|  | Nitrogen | 72.2 | 1.13 | 0.29 |
|  | Heated × N | 11.1 | 0.17 | 0.68 |
| *Shannon* | Heated | 1.15 | 7.77 | **0.009** |
|  | Nitrogen | 0.1 | 0.64 | 0.43 |
|  | Heated × N | 0.36 | 2.4 | 0.13 |
| *Richness* | **AMF (mineral)** |  |  |  |
|  | Heated | 0.1 | 0.002 | 0.96 |
|  | Nitrogen | 32.1 | 0.80 | 0.38 |
|  | Heated × N | 56.6 | 1.41 | 0.24 |
| *Shannon* | Heated | 0.54 | 3.51 | 0.07 |
|  | Nitrogen | 0.01 | 0.08 | 0.78 |
|  | Heated × N | 0.008 | 0.05 | 0.82 |
| *Richness* | **EMF (organic)** |  |  |  |
|  | Heated | 193.6 | 4.55 | **0.048** |
|  | Nitrogen | 62.5 | 1.47 | 0.24 |
|  | Heated × N | 105.8 | 2.49 | 0.13 |
| *Shannon* | Heated | 1.74 | 12.16 | **0.003** |
|  | Nitrogen | 1.32 | 9.22 | **0.008** |
|  | Heated × N | 1.53 | 10.67 | **0.005** |
| *Richness* | **EMF (mineral)** |  |  |  |
|  | Heated | 1.6 | 0.06 | 0.82 |
|  | Nitrogen | 0.0 | 0.03 | 0.86 |
|  | Heated × N | 7.2 | 0.25 | 0.62 |
| *Shannon* | Heated | 0.006 | 0.02 | 0.89 |
|  | Nitrogen | 0.000 | 0.00 | 1 |
|  | Heated × N | 0.000 | 0.0001 | 0.99 |
| *Richness* | **Sap (organic)** |  |  |  |
|  | Heated | 52.9 | 0.64 | 0.44 |
|  | Nitrogen | 160 | 1.93 | 0.18 |
|  | Heated × N | 64.8 | 0.78 | 0.39 |
| *Shannon* | Heated | 0.03 | 0.21 | 0.65 |
|  | Nitrogen | 0.06 | 0.42 | 0.53 |
|  | Heated × N | 0.04 | 0.3 | 0.59 |
| *Richness* | **Sap (mineral)** |  |  |  |
|  | Heated | 240 | 5.7 | **0.03** |
|  | Nitrogen | 19.6 | 0.47 | 0.5 |
|  | Heated × N | 19.6 | 5.35 | **0.03** |
| *Shannon* | Heated | 1.52 | 4.37 | 0.053 |
|  | Nitrogen | 0.57 | 1.65 | 0.22 |
|  | Heated × N | 0.66 | 1.89 | 0.19 |
| *Richness* | **Paths (organic)** |  |  |  |
|  | Heated (H) | 4.9 | 0.56 | 0.47 |
|  | Heated | 57.6 | 6.6 | **0.02** |
|  | Nitrogen | 0.2 | 0.03 | 0.88 |
| *Shannon* | Heated × N | 0.07 | 0.3 | 0.6 |
|  | Heated | 0.76 | 3 | 0.1 |
|  | Nitrogen | 0.1 | 0.4 | 0.54 |
| *Richness* | **Paths (mineral)** |  |  |  |
|  | Heated | 12.1 | 2.06 | 0.17 |
|  | Nitrogen | 0.4 | 0.07 | 0.8 |
|  | Heated × N | 24.2 | 4.1 | 0.06 |
| *Shannon* | Heated | 0.93 | 5.58 | **0.03** |
|  | Nitrogen | 0.25 | 1.46 | 0.24 |
|  | Heated × N | 2.15 | 12.82 | **0.002** |

**Table S4.** **ANOVA output summarizing treatment effects on fungal community evenness in the organic horizon for general fungi, ectomycorrhizal fungi (EMF), and arbuscular mycorrhizal fungi (AMF).** The degrees of freedom for each factor is 1 and the total degrees of freedom for each model is 19. Significant values are in bold (*P* ≤ 0.05).

|  |  |  |  |
| --- | --- | --- | --- |
|  | **Sum of Sq** | ***F*-value** | ***P*-value** |
| **Fungi (organic)** |  |  |  |
| (Intercept) | 2.21506 | 214.0164 | 1.11E-10 |
| Heated | 0.0563 | 5.4392 | **0.03308** |
| Nitrogen | 0.05782 | 5.586 | **0.03109** |
| Heated × N | 0.0411 | 3.9707 | 0.06364 |
|  |  |  |  |
| **EMF (organic)** |  |  |  |
| (Intercept) | 1.88318 | 148.3006 | 1.66E-09 |
| Heated | 0.10022 | 7.8921 | **0.012597** |
| Nitrogen | 0.09841 | 7.7496 | **0.013277** |
| Heated × N | 0.11118 | 8.7555 | **0.009236** |
|  |  |  |  |
| **AMF (organic)** |  |  |  |
| (Intercept) | 2.99064 | 387.38 | 2.20E-16 |
| Heated | 0.07323 | 9.485 | **0.004016** |
| Nitrogen | 0.00259 | 0.336 | 0.565877 |
| Heated × N | 0.0204 | 2.642 | 0.113045 |

**Table S5.** **ANOVA outputs summarizing treatment effects on the relative abundances of ectomycorrhizal fungi (EMF), saprotrophs, and pathotrophs** . The degrees of freedom for each factor is 1 and the total degrees of freedom for each model is 19.

|  |  |  |  |
| --- | --- | --- | --- |
|  | **Sum of Sq** | ***F*-value** | ***P*-value** |
| **EMF (organic)** |  |  |  |
| (Intercept) | 2.54504 | 89.2864 | 6.01E-08 |
| Heated | 0.02687 | 0.9428 | 0.346 |
| Nitrogen | 0.00345 | 0.1209 | 0.7326 |
| Heated × N | 0.00789 | 0.2766 | 0.6061 |
| **Saprotrophs (organic)** |  |  |  |
| (Intercept) | 0.033207 | 22.5844 | 0.0002164 |
| Heated | 0.0001 | 0.068 | 0.7976654 |
| Nitrogen | 0.000414 | 0.2818 | 0.602823 |
| Heated × N | 0.000951 | 0.647 | 0.4329903 |
| **Pathotrophs (organic)** |  |  |  |
| (Intercept) | 0.0005 | 4.4022 | 0.05213 |
| Heated | 0.00019583 | 1.7242 | 0.20768 |
| Nitrogen | 0.00000119 | 0.0105 | 0.91978 |
| Heated × N | 0.00023387 | 2.059 | 0.17056 |
| **EMF (mineral)** |  |  |  |
| (Intercept) | 2.80647 | 89.2431 | 6.03E-08 |
| Heated | 0.03121 | 0.9923 | 0.334 |
| Nitrogen | 0.00822 | 0.2615 | 0.6161 |
| Heated × N | 0.01086 | 0.3454 | 0.5649 |
| **Saprotrophs (mineral)** |  |  |  |
| (Intercept) | 0.031633 | 2.0888 | 0.1677 |
| Heated | 0.023584 | 1.5573 | 0.23 |
| Nitrogen | 0.000036 | 0.0024 | 0.9617 |
| Heated × N | 0.019549 | 1.2908 | 0.2726 |
| **Pathotrophs (mineral)** |  |  |  |
| (Intercept) | 0.00011653 | 3.4236 | 0.08283 |
| Heated | 0.00006107 | 1.7943 | 0.19912 |
| Nitrogen | 0.00002233 | 0.656 | 0.42986 |
| Heated × N | 0.00004639 | 1.3629 | 0.26013 |

**Table S6. The results of similarity percentage analysis showing OTUs significantly contributing to the dissimilarity between treatment versus control plots**. For a link to the taxonomy of the most influential OTUs (Top 10) see Table S6.

|  |  |  |  |
| --- | --- | --- | --- |
| **Treatment** | **OTU** | **Simper value** | **P-value** |
| Heated | OTU113 | 0.084804596 | 0.018 |
| Heated | OTU130 | 0.016609195 | 0.001 |
| Heated | OTU18 | 0.016149425 | 0.018 |
| Heated | OTU352 | 0.005114942 | 0.003 |
| Heated | OTU143 | 0.005068965 | 0.018 |
| Heated | OTU171 | 0.004770115 | 0.034 |
| Heated | OTU11 | 0.00316092 | 0.046 |
| Heated | OTU14 | 0.002747126 | 0.003 |
| Heated | OTU1565 | 0.002413793 | 0.01 |
| Heated | OTU174 | 0.002356322 | 0.034 |
| Heated | OTU639 | 0.001954023 | 0.017 |
| Heated | OTU13 | 0.001712644 | 0.032 |
| Heated | OTU247 | 0.001252874 | 0.014 |
| Heated | OTU43 | 0.001149425 | 0.011 |
| Heated | OTU189 | 0.000804598 | 0.014 |
| Heated | OTU250 | 0.000712644 | 0.04 |
| Heated | OTU273 | 0.000678161 | 0.041 |
| Heated | OTU373 | 0.000632184 | 0.028 |
| Heated | OTU42 | 0.000586207 | 0.011 |
| Heated | OTU255 | 0.000574713 | 0.019 |
| Heated | OTU437 | 0.000528736 | 0.028 |
| Heated | OTU272 | 0.00045977 | 0.002 |
| Heated | OTU405 | 0.000448276 | 0.046 |
| Heated | OTU550 | 0.000402299 | 0.019 |
| Heated | OTU27 | 0.000344828 | 0.005 |
| Heated | OTU370 | 0.000344828 | 0.008 |
| Heated | OTU452 | 0.000344828 | 0.019 |
| Heated | OTU181 | 0.000287356 | 0.015 |
| Heated | OTU80 | 0.000229885 | 0.034 |
| Heated | OTU162 | 0.000229885 | 0.036 |
| Heated | OTU382 | 0.000172414 | 0.044 |
| Heated x N | OTU185 | 0.02991954 | 0.015 |
| Heated x N | OTU18 | 0.016149425 | 0.019 |
| Heated x N | OTU130 | 0.015862069 | 0.001 |
| Heated x N | OTU143 | 0.00491954 | 0.026 |
| Heated x N | OTU171 | 0.004873563 | 0.029 |
| Heated x N | OTU11 | 0.003218391 | 0.037 |
| Heated x N | OTU234 | 0.002816092 | 0.004 |
| Heated x N | OTU376 | 0.002655172 | 0.007 |
| Heated x N | OTU14 | 0.002574713 | 0.007 |
| Heated x N | OTU174 | 0.00245977 | 0.016 |
| Heated x N | OTU1565 | 0.002356322 | 0.023 |
| Heated x N | OTU269 | 0.002356322 | 0.025 |
| Heated x N | OTU639 | 0.001954023 | 0.022 |
| Heated x N | OTU225 | 0.001896552 | 0.002 |
| Heated x N | OTU23 | 0.001735632 | 0.048 |
| Heated x N | OTU803 | 0.001724138 | 0.024 |
| Heated x N | OTU13 | 0.001678161 | 0.04 |
| Heated x N | OTU212 | 0.00137931 | 0.004 |
| Heated x N | OTU289 | 0.001264368 | 0.002 |
| Heated x N | OTU247 | 0.001264368 | 0.012 |
| Heated x N | OTU161 | 0.001229885 | 0.029 |
| Heated x N | OTU43 | 0.001137931 | 0.022 |
| Heated x N | OTU64 | 0.000747126 | 0.033 |
| Heated x N | OTU6 | 0.000747126 | 0.008 |
| Heated x N | OTU1855 | 0.000632184 | 0.021 |
| Heated x N | OTU373 | 0.00062069 | 0.031 |
| Heated x N | OTU272 | 0.00045977 | 0.002 |
| Heated x N | OTU405 | 0.000448276 | 0.043 |
| Heated x N | OTU148 | 0.000448276 | 0.019 |
| Heated x N | OTU370 | 0.000402299 | 0.001 |
| Heated x N | OTU71 | 0.000402299 | 0.041 |
| Heated x N | OTU27 | 0.000344828 | 0.004 |
| Heated x N | OTU452 | 0.000344828 | 0.018 |
| Heated x N | OTU181 | 0.000287356 | 0.009 |
| Heated x N | OTU336 | 0.000287356 | 0.024 |
| Heated x N | OTU343 | 0.000229885 | 0.041 |
| Heated x N | OTU286 | 0.000229885 | 0.04 |
| Heated x N | OTU162 | 0.000229885 | 0.038 |
| Heated x N | OTU26 | 0.000172414 | 0.049 |
| Heated x N | OTU382 | 0.000172414 | 0.049 |
| Nitrogen | OTU50 | 0.115022986 | 0.013 |
| Nitrogen | OTU18 | 0.016149425 | 0.022 |
| Nitrogen | OTU130 | 0.015517241 | 0.006 |
| Nitrogen | OTU143 | 0.005172414 | 0.018 |
| Nitrogen | OTU171 | 0.004735632 | 0.042 |
| Nitrogen | OTU174 | 0.002425287 | 0.017 |
| Nitrogen | OTU539 | 0.002425287 | 0.048 |
| Nitrogen | OTU14 | 0.002402299 | 0.021 |
| Nitrogen | OTU1565 | 0.002367816 | 0.021 |
| Nitrogen | OTU639 | 0.001954023 | 0.018 |
| Nitrogen | OTU247 | 0.001241379 | 0.017 |
| Nitrogen | OTU161 | 0.001195402 | 0.041 |
| Nitrogen | OTU43 | 0.001149425 | 0.017 |
| Nitrogen | OTU373 | 0.000632184 | 0.021 |
| Nitrogen | OTU405 | 0.00045977 | 0.023 |
| Nitrogen | OTU272 | 0.00045977 | 0.002 |
| Nitrogen | OTU370 | 0.000402299 | 0.003 |
| Nitrogen | OTU71 | 0.000402299 | 0.046 |
| Nitrogen | OTU452 | 0.000344828 | 0.018 |
| Nitrogen | OTU27 | 0.000287356 | 0.012 |
| Nitrogen | OTU80 | 0.000229885 | 0.037 |
| Nitrogen | OTU1413 | 0.000229885 | 0.034 |
| Nitrogen | OTU162 | 0.000218391 | 0.047 |
| Nitrogen | OTU26 | 0.000172414 | 0.041 |

**Table S7. The main taxa driving changes in community composition in the treatment plots.** Summaries of the relative abundances of the top ten OTUs with taxonomic assignments driving dissimilarity in community composition between treatment versus control plots identified via similarity percentage analysis (see Table S5 for complete list of OTUs).

|  |  |  |  |  |
| --- | --- | --- | --- | --- |
| **OTU** | **Taxonomy** | **Control** | **Heated** | **Ratio (Trt-Control)** |
| OTU113 | *Russula laurocerasi*  | 0.00137931 | 0.169885058 | 0.168505747 |
| OTU1223 | *Russula sp. 1223* | 0.00045977 | 0.043793104 | 0.043333333 |
| OTU130 | *Amanita fulva*  | 0.033333333 | 0.000114943 | -0.033218391 |
| OTU18 | *Eurotiales sp. 18* | 0.032298851 | 0 | -0.032298851 |
| OTU352 | *Mortierella gemmifera*  | 0 | 0.010229885 | 0.010229885 |
| OTU143 | *Herpotrichiellaceae sp. 143* | 0.010344828 | 0.001034483 | -0.009310345 |
| OTU171 | *Cortinarus sp. 171* | 0.00954023 | 0 | -0.00954023 |
| OTU11 | *Saccharomycetales sp. 11* | 0.006321839 | 0 | -0.006321839 |
| OTU14 | *Mortierella pulchella*  | 0.005632184 | 0.000229885 | -0.005402299 |
| OTU1565 | *Cortinarius sp. 1565* | 0.004827586 | 0 | -0.004827586 |
|  |  | Control | Heated x N | Ratio (Trt-Control) |
| OTU185 | *Boletus rubropunctus*  | 0.00045977 | 0.060114942 | 0.059655172 |
| OTU18 | *Eurotiales sp. 18* | 0.032298851 | 0 | -0.032298851 |
| OTU130 | *Amanita fulva*  | 0.033333333 | 0.001609195 | -0.031724138 |
| OTU143 | *Herpotrichiellaceae sp. 143* | 0.010344828 | 0.002528736 | -0.007816092 |
| OTU171 | *Cortinarus sp. 171* | 0.00954023 | 0.003563218 | -0.005977011 |
| OTU11 | *Saccharomycetales sp. 11* | 0.006321839 | 0.003333333 | -0.002988506 |
| OTU234 | *Cladophialophora sp 234* | 0 | 0.005632184 | 0.005632184 |
| OTU376 | *Herpotrichiellaceae sp. 376* | 0.000344828 | 0.005517241 | 0.005172414 |
| OTU14 | *Mortierella pulchella*  | 0.005632184 | 0.000804598 | -0.004827586 |
| OTU1565 | *Cortinarius sp. 1565* | 0.004827586 | 0.000574713 | -0.004252874 |
|  |  | Control | Nitrogen | Ratio (Trt-Control) |
| OTU50 | *Russula subsulphurea*  | 0.022873563 | 0.234942529 | 0.212068965 |
| OTU18 | *Eurotiales sp. 18* | 0.032298851 | 0 | -0.032298851 |
| OTU130 | *Amanita fulva*  | 0.033333333 | 0.004597701 | -0.028735632 |
| OTU143 | *Herpotrichiellaceae sp. 143* | 0.010344828 | 0 | -0.010344828 |
| OTU171 | *Cortinarus sp. 171* | 0.00954023 | 0.000114943 | -0.009425287 |
| OTU14 | *Mortierella pulchella*  | 0.005632184 | 0.00137931 | -0.004252874 |
| OTU1565 | *Cortinarius sp. 1565* | 0.004827586 | 0.000229885 | -0.004597701 |
| OTU639 | *Clitocybe subditopoda*  | 0.003908046 | 0 | -0.003908046 |
| OTU247 | *Trechispora sp. 247* | 0.002528736 | 0.000229885 | -0.002298851 |
| OTU161 | *Chaetothyriales sp. 161* | 0.002528736 | 0.000689655 | -0.00183908 |

**Table S8. ANOVA output summarizing treatment effects on fungal functional gene relative abundances**. Only functional genes where significant effects were identified are displayed. Significant effects are in bold (*P* ≤ 0.05).

|  |  |  |  |
| --- | --- | --- | --- |
|  | **Sum of Sq** | ***F*-value** | ***P*-value** |
| **Cellobiohydrolase** |  |  |  |
| (Intercept) | 1.94E-07 | 20.4265 | 0.0004071 |
| Heated | 1.06E-10 | 0.0112 | 0.9172974 |
| Nitrogen | 5.49E-08 | 5.7731 | **0.0296662** |
| Heated × N | 2.39E-08 | 2.5129 | 0.1337699 |
|  |  |  |  |
| **Total hydrolytic enzymes** |  |  |  |
| (Intercept) | 6.85E-07 | 9.8716 | 0.006717 |
| Heated | 3.12E-07 | 4.4982 | **0.05101** |
| Nitrogen | 4.62E-08 | 0.6651 | 0.42754 |
| Heated × N | 1.11E-08 | 0.16 | 0.69483 |
|  |  |  |  |
| **Manganese peroxidase** |  |  |  |
| (Intercept) | 2.66E-06 | 20.7564 | 0.0003787 |
| Heated | 1.05E-06 | 8.1941 | **0.0118617** |
| Nitrogen | 6.12E-08 | 0.4776 | 0.5000715 |
| Heated × N | 1.84E-07 | 1.4344 | 0.2496317 |

**Table S9.** **Correlations between soil organic matter composition and soil fungal characteristics and soil organic carbon.** Statistics show the correlation and P-values determined from vector fitting using the *envfit* function. Due to autocorrelation among the vectors, we could not include all potential predictor variables and therefore selected the most ecologically relevant variables.

|  |  |  |
| --- | --- | --- |
|  | ***r2*** | ***P*-value** |
| Total soil organic carbon | 0.7246 | 0.001 |
| Fungal hydrolytic enzyme genes | 0.4566 | 0.009 |
| Negative co-occurrence probability | 0.2964 | 0.051 |
| Saprotrophic composition (NMDS1) | 0.2862 | 0.063 |
| Fungal cellobiohydrolase enzyme genes | 0.2633 | 0.083 |
| EMF composition (NMDS1) | 0.2437 | 0.087 |
| Fungal manganese peroxidase genes | 0.2648 | 0.092 |
| Fungal composition (NMDS1) | 0.1168 | 0.366 |
| EMF Shannon diversity | 0.0466 | 0.701 |
| Saprotrophic Shannon diversity | 0.0266 | 0.817 |
| Fungal Shannon diversity | 0.0074 | 0.953 |

**Table S10.** **. The main AMF taxa driving changes in community composition in the treatment plots.** The results of similarity percentage analysis showing arbuscular mycorrhizal fungal OTUs significantly contributing to the dissimilarity between treatment versus control plots. The virtual taxon (VT) number is also shown where a significant alignment was made.

|  |  |  |  |  |
| --- | --- | --- | --- | --- |
| **Taxonomy** | **species** | **Treatment** | **Average** | ***P-*value** |
| *Glomus sp 3* | OTU3 | C vs. Heated | 0.13976661 | 0.042 |
| *Glomus sp 2* | OTU2 | C vs. Heated | 0.05486551 | 0.025 |
| *Glomus sp 15* | OTU15 | C vs. Heated | 0.04620253 | 0.001 |
| *Glomus sp VT00149* | OTU21 | C vs. Heated | 0.0160087 | 0.04 |
| *Glomus sp. 49* | OTU49 | C vs. Heated | 0.00428797 | 0.048 |
| *Glomus VT00194* | OTU37 | C vs. Heated | 0.00261076 | 0.049 |
| *Unknown* | OTU63 | C vs. Heated | 0.00245253 | 0.026 |
| *Glomus sp. 65* | OTU65 | C vs. Heated | 0.00173259 | 0.008 |
| *Glomus sp. 93* | OTU93 | C vs. Heated | 0.00145174 | 0.041 |
| *Unknown sp. 106* | OTU106 | C vs. Heated | 0.00094146 | 0.027 |
| *Glomus VT00149 iso 2* | OTU108 | C vs. Heated | 0.00079114 | 0.011 |
| *Glomus VT00194 iso 3* | OTU88 | C vs. Heated | 0.00057358 | 0.016 |
| *Archaeospora sp VT00009* | OTU94 | C vs. Heated | 0.00053797 | 0.044 |
| *Glomus sp 61* | OTU61 | C vs. Heated | 0.00023734 | 0.045 |
| *Glomus sp 2* | OTU2 | C. vs. HN | 0.05934039 | 0.015 |
| *Glomus sp. 49* | OTU49 | C. vs. HN | 0.00456388 | 0.047 |
| *Glomus VT00219* | OTU51 | C. vs. HN | 0.0033129 | 0.038 |
| *Acaulospora VT00024* | OTU28 | C. vs. HN | 0.00276899 | 0.045 |
| *Glomus sp. 65* | OTU65 | C. vs. HN | 0.00170589 | 0.05 |
| *Archaeospora VT00004* | OTU14 | C. vs. HN | 0.00165645 | 0.009 |
| *Glomus sp 93* | OTU93 | C. vs. HN | 0.00158228 | 0.031 |
| *Paraglomus sp 58* | OTU58 | C. vs. HN | 0.00078619 | 0.007 |
| *Glomus VT00151* | OTU33 | C. vs. HN | 0.00069225 | 0.01 |
| *Glomus VT00194 iso 3* | OTU88 | C. vs. HN | 0.00057358 | 0.044 |
| *Glomus sp 2* | OTU2 | C vs. N | 0.05566456 | 0.017 |
| *Glomus sp 23* | OTU23 | C vs. N | 0.04084652 | 0.032 |
| *Scutellospora sp. 48* | OTU48 | C vs. N | 0.0141693 | 0.033 |
| *Glomus VT00194* | OTU37 | C vs. N | 0.00262658 | 0.044 |
| *Glomus sp. 65* | OTU65 | C vs. N | 0.00173259 | 0.008 |
| *Glomus sp. 93* | OTU93 | C vs. N | 0.00142801 | 0.048 |
| *Glomus sp. 92* | OTU92 | C vs. N | 0.00116297 | 0.037 |
| *Unknown sp. 106* | OTU106 | C vs. N | 0.00096915 | 0.008 |
| *Glomus VT00360* | OTU96 | C vs. N | 0.00093354 | 0.028 |
| *Glomus VT00194 iso 3* | OTU88 | C vs. N | 0.00057358 | 0.02 |

**Figure S1. The relative abundance of ectomycorrhizal fungi (EMF) across the treatments.** There were no significant differences across the treatment plots. The dashed line shows the median relative abundance of EMF across all samples (median = 70%).



**Figure S2. The relative abundance of fungal cellobiohydrolase genes across the treatments**. Significant differences are indicated using different lower-case letters (*P ≤* 0.05).



**Figure S3.** **The correlation between suberin- and cutin-derived compound concentrations and fungal negative co-occurrence probability.** Different color points show the treatment effects. Blue, orange, green, and pink points show the control, heated, N addition, and heated × N addition plots, respectively.



**Figure S4.** **The relative abundance of AMF taxa identified via similarity percentage analysis contributing significantly to variation between treatment and control plot AMF community compositions.** Values shown the mean (n = 5) and error bars are the standard error.

