**Appendix S1**

**Supplemental Information for:**

**Winter warming rapidly** **increases carbon degradation capacities of fungal communities in tundra soil: potential consequences on** **carbon** **stability**

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**Figure S1.** Rarefaction curves of 28S rRNA gene sequences. C1-C6 are control samples, and W1-W6 are warmed samples.



**Figure S2.** Principal coordinate analyses (PCoA) for **(a)** 28S rRNA genes and **(b)** functional genes of fungal communities. The C1 and C2 samples of control did not produce enough 28S rRNA gene sequences and thus were removed in (a).

**Table S1.** Effects of winter warming on environmental factors.

|  |  |  |  |
| --- | --- | --- | --- |
| Environmental factors | Control | Warmed | *P* |
| Winter soil temperature (°C)  | -5.6a | -3.7 | **< 0.01**b |
| Soil moisture (%) | 47.8 | 52.7 | **0.03** |
| Thaw depth (cm) | 35.3 | 38.4 | **0.03** |
| Labile C pool (LCP, %) | 33.5 | 33.2 | 0.94 |
| Recalcitrant C pool (RCP, %) | 66.5 | 66.8 | 0.94 |
| NH4+-N (ng/g/d) | 49.7 | 37.2 | 0.47 |
| NO3--N (ng/g/d) | 8.4 | 6.2 | 0.59 |
| Net primary productivity (NPP, g m-2)  | 285.5 | 365.0 | 0.08 |
| NPP of deciduous plants (g m-2) | 67.4 | 59.4 | 0.20 |
| NPP of evergreen plants (g m-2) | 51.7 | 52.4 | 0.84 |
| NPP of bryophytes (g m-2) | 19.7 | 22.2 | 0.60 |
| Plant biomass (g m-2) | 552.5 | 620.8 | 0.07 |
| Deciduous plant biomass (g m-2) | 113.7 | 101.3 | 0.30 |
| Evergreen plant biomass (g m-2) | 152.5 | 155.7 | 0.84 |
| Graminoids biomass (g m-2) | 146.7 | 231.0 | **0.05** |
| Bryophytes biomass (g m-2) | 72.4 | 64.5 | 0.19 |
| Lichens biomass (g m-2) | 67.2 | 68.3 | 0.95 |
| Net ecosystem C exchange (NEE, g m-2) | 31.2 | 65.6 | 0.30 |
| Ecosystem respiration (*R*eco, g m-2) | 363.3 | 449.2 | **< 0.01** |
| Winter *R*eco (g m-2) | 62.0 | 126.0 | **< 0.01** |
| Growing season *R*eco (g m-2) | 301.3 | 323.2 | **0.03** |
| Gross primary productivity (GPP, g m-2) | 394.5 | 514.7 | **0.01** |

aThe values are the average of 6 replicates.

b*P*-values were calculated by the two-tailed *t*-test. Bold values represent *P* < 0.05.

**Table S2.** Effects of winter warming on fungal diversity and ecological group abundances.

|  |  |  |  |
| --- | --- | --- | --- |
|  | Control | Warmed | *P* |
| Shannon-Wiener index | 4.46a | 4.70 | 0.34b |
| Richness | 109 | 156 | 0.16 |
| Pielou’s evenness | 0.96 | 0.95 | 0.14 |
| Relative abundance of saprotrophs | 21.05% | 18.70% | 0.72 |
| Relative abundance of plant pathogens | 7.49% | 7.68% | 0.97 |
| Relative abundance of ectomycorrhizal fungi | 4.87% | 0.42% | 0.09 |
| Relative abundance of animal parasites | 0.02% | 0.08% | 0.19 |
| Relative abundance of mycoparasites | 1.44% | 0.03% | 0.25 |
| Relative abundance of mycobionts | 0.12% | 0.08% | 0.72 |

aThe values are the average of 6 replicates.

b*P*-values were calculated by the two-tailed *t*-test.

**Table S3.** Information on C degradation genes detected only in warmed samples.

|  |  |  |  |  |
| --- | --- | --- | --- | --- |
| GenBank ID | Gene product | C Substrate | Fungal species | Normalized signal intensity in GeoChip |
| Control | Warmed |
| 302692112 | Glucose oxidase | Glucose | *Schizophyllum commune* | 0 | 0.71 |
| 302498961 | Glucoamylase | Starch | *Arthroderma benhamiae* | 0 | 0.74 |
| 58267516 | Alpha-amylase | Starch | *Cryptococcus neoformans* | 0 | 0.75 |
| 71020355 | Endochitinase | Chitin | *Ustilago maydis* | 0 | 0.76 |
| 4768909 | Serine protease | Protein | *Metarhizium* sp. | 0 | 0.68 |
| 302899584 | Serine protease | Protein | *Nectria haematococca* | 0 | 0.70 |
| 90265711 | Aspartate protease | Protein | *Pichia* sp. | 0 | 0.70 |
| 302403837 | Metalloprotease | Protein | *Verticillium albo-atrum* | 0 | 0.74 |
| 189207002 | Arabinofuranosidase | Hemicellulose | *Pyrenophora tritici-repentis* | 0 | 0.75 |
| 294991928 | Xylose reductase | Hemicellulose | *Rhodotorula* sp. | 0 | 0.75 |
| 146422009 | Cellobiase | Cellulose | *Meyerozyma guilliermondii* | 0 | 0.67 |
| 309317871 | Exoglucanase | Cellulose | *Puccinia graminis* | 0 | 0.72 |
| 213536803 | Exoglucanase | Cellulose | Unknown | 0 | 0.73 |
| 302404451 | Exoglucanase | Cellulose | *Verticillium albo-atrum* | 0 | 0.70 |
| 49333365 | Exoglucanase | Cellulose | *Volvariella* sp. | 0 | 0.73 |
| 154295968 | Exopolygalacturonase | Pectin | *Botryotinia fuckeliana* | 0 | 0.72 |
| 302410683 | Pectinesterase | Pectin | *Verticillium albo-atrum* | 0 | 0.70 |
| 70986762 | Pectate lyase | Pectin | *Aspergillus fumigatus* | 0 | 0.73 |
| 261203269 | Phospholipase C | Lipid | *Ajellomyces dermatitidis* | 0 | 0.71 |
| 311345586 | Phospholipase D | Lipid | *Arthroderma gypseum* | 0 | 0.70 |
| 296812063 | Phospholipase A2 | Lipid | *Arthroderma otae* | 0 | 0.69 |
| 46116138 | Phospholipase A2 | Lipid | *Gibberella zeae* | 0 | 0.73 |
| 164425151 | Phospholipase D | Lipid | *Neurospora crassa* | 0 | 0.76 |
| 218718280 | Isocitrate lyase | Lipid | *Talaromyces stipitatus* | 0 | 0.83 |
| 218716793 | Vanillin dehydrogenase | Aromatics | *Talaromyces stipitatus* | 0 | 0.71 |
| 39976417 | Glyoxal oxidase | Lignin | *Magnaporthe oryzae* | 0 | 0.71 |
| 238597302 | Phenol oxidase | Lignin | *Moniliophthora perniciosa* | 0 | 0.72 |
| 19848920 | Phenol oxidase | Lignin | *Trametes* sp. | 0 | 0.68 |
| 145245856 | Rhamnogalacturonase | Others | *Aspergillus niger* | 0 | 0.80 |
| 156042197 | Solanesyl-diphosphate synthase | Others | *Sclerotinia sclerotiorum* | 0 | 0.69 |

**Table S4.** Key genes of fMENs of control and warmed samples and fungal species origin.

|  |  |  |  |
| --- | --- | --- | --- |
| GenBank ID | Gene product | Functional process of the gene product | Fungal species origin |
| **Module hubs of control samples** |
| 115397631 | Phenol oxidase | C degradation | *Aspergillus terreus* |
| 237903035 | Phenol oxidase | C degradation | *Uncinocarpus reesii* |
| 21929226 | Manganese peroxidase | C degradation | *Phanerochaete* sp. |
| 88184155 | Endochitinase | C degradation | *Chaetomium globosum* |
| 121719823 | Acetylglucosaminidase | C degradation | *Aspergillus clavatus* |
| 171683305 | Phospholipase D | C degradation | *Podospora anserine* |
| 147225254 | Serine protease | C degradation | *Acremonium* sp. |
| 238582297 | Nitrate reductase | N assimilation | *Moniliophthora perniciosa* |
| 121702879 | Urease | Ammonification | *Aspergillus clavatus* |
| 218723248 | Bifunctional catalase-peroxidase | Fungal virulence | *Talaromyces stipitatus* |
| 238032440 | Calcineurin A | Fungal virulence | *Pichia pastoris* |
| 116505323  | Mycelial catalase | Oxidative stress resistance | *Coprinopsis cinerea* |
| **Connectors of control samples** |
| 32399641 | Phenol oxidase | C degradation | *Lentinus* sp. |
| 46578391  | Phenol oxidase | C degradation | *Trametes* sp. |
| 238582297 | Nitrate reductase | N assimilation | *Moniliophthora perniciosa* |
| **Module hubs of warmed samples** |
| 53791231 | Lignin peroxidase | C degradation | *Trametes* sp. |
| 77681325 | Manganese peroxidase | C degradation | *Trametes* sp. |
| 58176536 | Phenol oxidase | C degradation | *Coriolopsis* sp. |
| 28919715 | Arabinofuranosidase | C degradation | *Neurospora crassa* |
| 169786393 | Pectatelyase | C degradation | *Aspergillus oryzae* |
| 159105229 | Phospholipase A2 | C degradation | *Malassezia globose* |
| 121712381  | Alpha-amylase | C degradation | *Aspergillus clavatus* |
| 115397527 | Glucoamylase | C degradation | *Aspergillus terreus* |
| 189202886 | ATP sulphurylase | Sulphate reduction | *Pyrenophora tritici-repentis* |
| **Connectors of warmed samples** |
| 255942725 | Phospholipase B | C degradation | *Penicillium chrysogenum* |
| 145573242  | Serine protease | C degradation | *Aureobasidium* sp. |
| 7804881 | Endopolygalacturonase | C degradation | *Leptosphaeria* sp. |