**The** **temporal and spatial response of soil fungal community composition and potential function to wildfire in** **a permafrost region in Canada**

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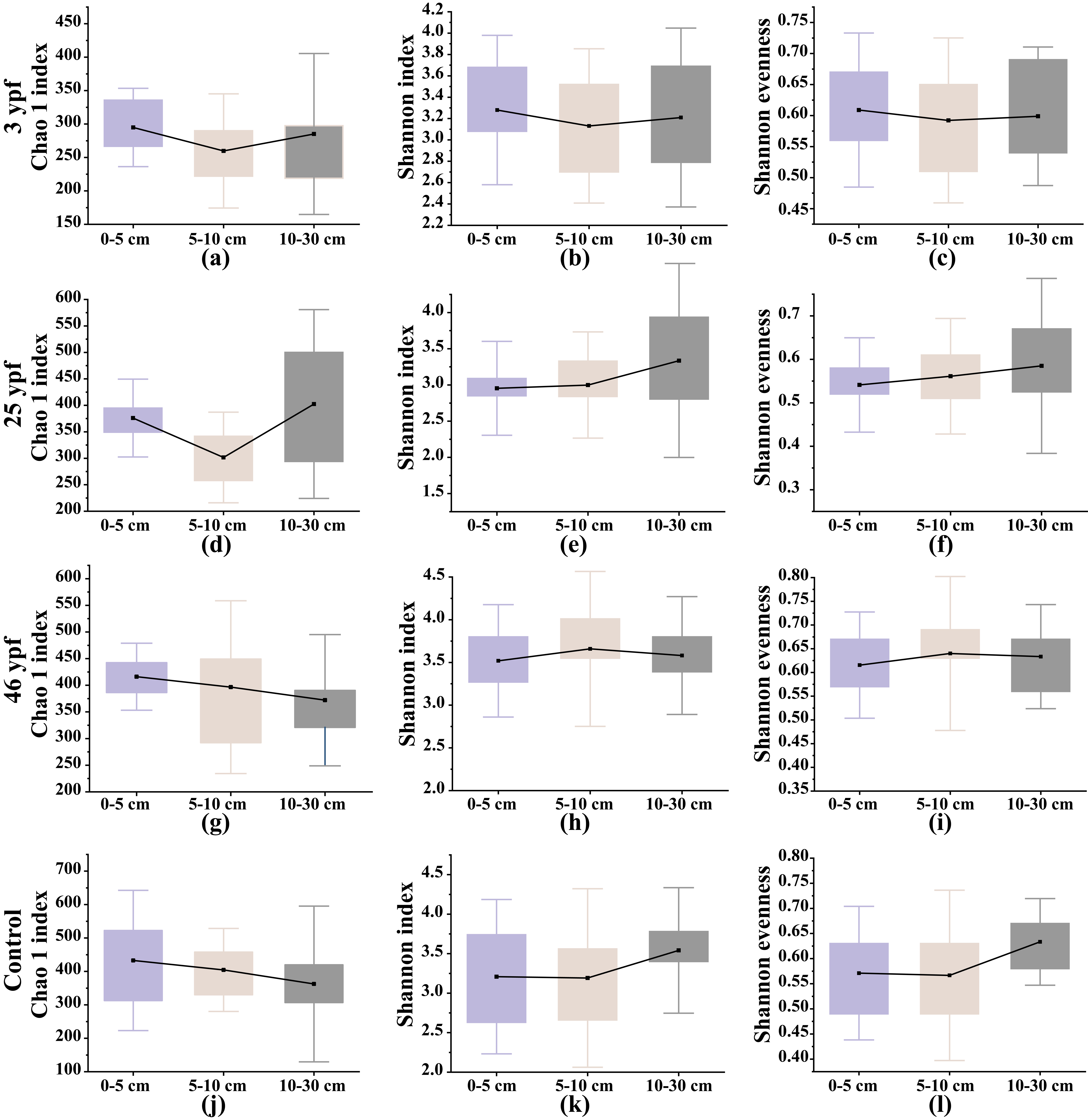
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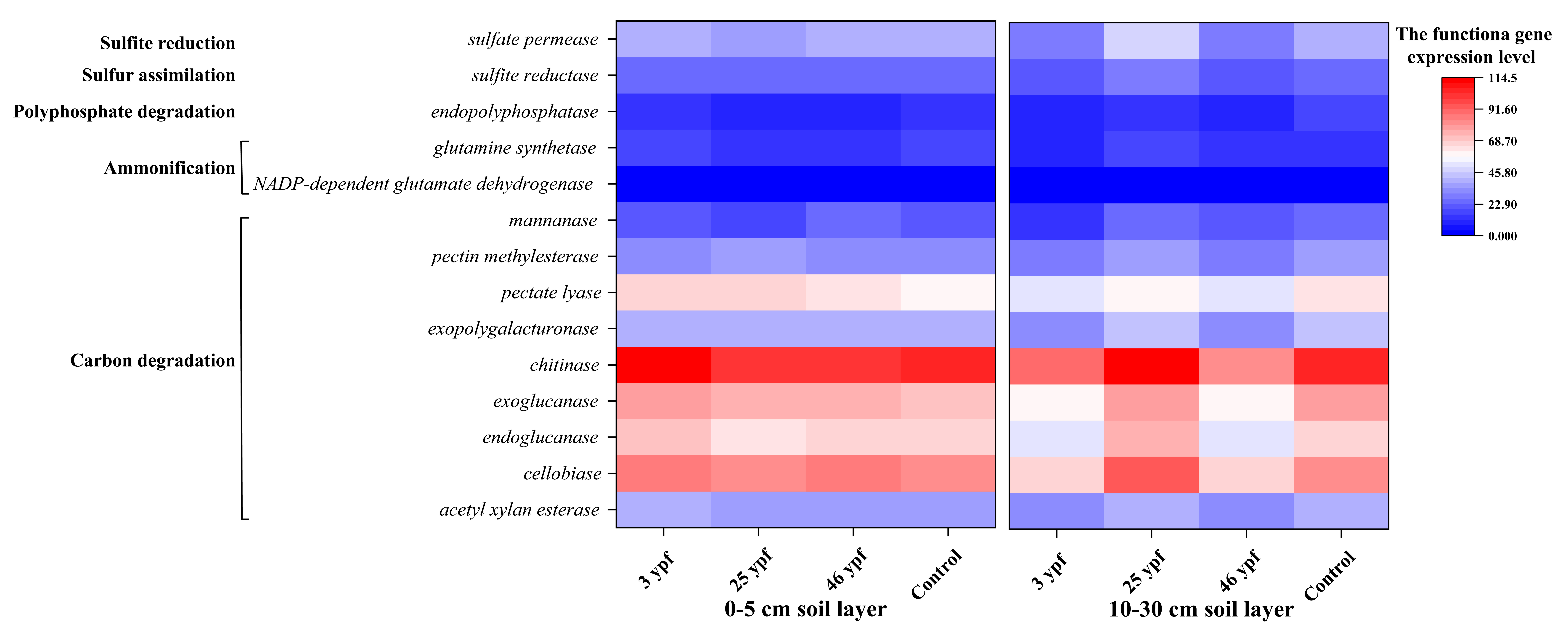
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**Figure S1.** Fungal community richness (a, d, g and j), α-diversity (b, e, h and k), and evenness (c, f. i and l) in different soil layers in the 3 ypf, 25 ypf, 46 ypf and control area. Boxes showing 25–75 percentiles, vertical lines showing the standard deviation (n = 9). Abbreviations: ypf: year-post-fire.



**Figure S2.** The heatmap showing the fungal functional genes differed significantly among the four post-fire chronosequence areas in the two soil layers. Abbreviations: ypf: year-post-fire.

**Table S1.** The mean value (and standard deviations) of abiotic variables and biotic variables across the four post-fire chronosequence areas. Different letters besides the mean values mark the significant differences (*P* < 0.05) in the same soil layer between the four forest areas.

|  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- |
|  | Depth | Fire history | Soil pH | Soil temperature (˚C) | Active layer thickness (cm) | Soil moisture (%) | Soil available C (mg g-1) | Soil available N (mg g-1) | Soil available P (mg g-1) | Soil Type | Coordinates | | | | |
| A line | | B line | | C line |
| Abiotic variable | 5-cm | 3 ypf | 4.54 ± 0.07a | 7.21 (1.67)a | 101 ± 9a | 35.71 (4.18)a | 1.95 ± 0.50a | 0.42 ± 0.12a | 0.15 (0.11)a | Organic | N65°55'398 W137°25'746 | | N65°55'421 W137°25'333 | | N65°55'389 W137°25'660 |
| 25 ypf | 4.81 ± 0.15a | 7.05 (1.24)a | 88 ± 10ab | 37.46 (9.12)a | 1.58 ± 0.32a | 0.29 ± 0.09a | 0.36 (0.35)a | Organic | N66°01'527 W137°14'756 | | N66°01'397 W137°14'956 | | N65°59'005 W137°17'453 |
| 46 ypf | 6.64 ± 0.21b | 8.89 (2.89)a | 49 ± 5b | 52.33 (14.88)b | 5.51 ± 1.40b | 0.26 ± 0.06a | 0.30 (0.25)a | Organic | N68°00'232 W133°28'421 | | N67°59'874 W133°28'260 | | N67°59'942 W133°27'994 |
| Control | 4.77 ± 0.32b | 6.86 (1.36)a | 28 ± 2c | 55.63 (13.41)b | 9.73 ± 3.10c | 0.48 ± 0.14a | 0.29 (0.10)a | Organic | N66°17'823 W136°42'908 | | N65°55'530 W137°25'325 | | N67°57'790 W133°28'280 |
| 10-cm | 3 ypf | 4.70 ± 0.06a | 5.18 (1.58)a | - | 38.62 (6.04)a | 0.30 ± 0.04a | 0.04 ± 0.01a | 0.07 (0.02)a | Mineral | - | - | | - | |
| 25 ypf | 4.81 ± 0.15a | 5.72 (1.89)a | - | 43.17 (10.00)a | 1.03 ± 0.42b | 0.19 ± 0.12a | 0.21 (0.27)a | Organic | - | - | | - | |
| 46 ypf | 6.56 ± 0.14b | 4.87 (1.64)a | - | 45.83 (5.08)a | 0.73 ± 0.12b | 0.15 ± 0.06a | 0.11 (0.09)a | Organic | - | - | | - | |
| Control | 5.00 ± 0.22b | 3.16 (1.90)b | - | 54.36 (17.04)b | 3.62 ± 1.07c | 0.27 ± 0.07b | 0.28 (0.18)a | Organic | - | - | | - | |
| 30-cm | 3 ypf | 5.15 ± 0.14a | 4.01 (1.74)a | - | #80.00 (0) | 0.51 ± 0.12a | 0.05 ± 0.01a | 0.07 (0.03)a | Mineral | - | - | | - | |
| 25 ypf | 5.42 ± 0.11a | 3.64 (2.49)a | - | #80.00 (0) | 0.30 ± 0.05a | 0.05 ± 0.01a | 0.06 (0.03)a | Mineral | - | - | | - | |
| 46 ypf | 7.02 ± 0.12b | 2.80 (1.68)b | - | #80.00 (0) | 0.43 ± 0.02a | 0.02 ± 0.00a | 0.04 (0.01)a | Mineral | - | - | | - | |
| Control | 5.68 ± 0.29b | -0.06 (0.33)b | - | #80.00 (0) | 0.96 ± 0.19b | 0.10 ± 0.01a | 0.09 (0.06)a | Mineral | - | - | | - | |
|  |  |  |  |  |  |  |  |  |  |  |  |  | | | |  |
|  | Depth | Fire history | F:B ratio | Microbial C  (mg g-1) | Microbial N (mg g-1) | Microbial P (mg g-1) | Ground veg. biom. (kg m-2) | Foliage biomass (kg m-2) | Tree biomass (kg m-2) |  |  |  | | | |  |
|  | | | |  |
| Biotic variable | 5-cm | 3 ypf | 0.06 (0.05)a | 3.49 (4.18)a | 0.21 (0.28)bc | 0.089 (0.71)a | 0.45 (0.13)a | 0.0 (0)a | 0.00 (0.00)a |  |  |  | | | |  |
| 25 ypf | 0.09 (0.10)a | 3.01 (2.10)a | 0.26 (0.22)abc | 0.151 (0.15)a | 1.38 (0.38)b | 0.0 (0)a | 0.08 (0.09)a |  |  |  | | | |  |
| 46 ypf | 0.05 (0.06)a | 5.87 (4.47)a | 0.38 (0.31)abc | 0.158 (0.14)a | 1.33 (0.27)b | 682.6 (240)b | 3.77 (1.13)c |  |  |  | | | |  |
| Control | 0.21 (0.18)b | 10.16 (5.67)b | 0.67 (0.28)c | 0.370 (0.25)b | 1.67 (0.65)b | 1265.8 (286)c | 5.21 (0.76)d |  |  |  | | | |  |
| 10-cm | 3 ypf | 0.07 (0.04)a | 0.13 (0.08)a | 0.01 (0.01)a | 0.009 (0.01)a | - | - | 0.00 (0.00)a |  |  |  | | | |  |
| 25 ypf | 0.06 (0.08)a | 3.10 (4.36)a | 0.05 (0.04)abc | 0.069 (0.08)a | - | - | 0.08 (0.44)a |  |  |  | | | |  |
| 46 ypf | 0.09 (0.12)a | 1.32 (0.89)a | 0.11 (0.09)abc | 0.013 (0.02)a | - | - | 2.68 (0.65)b |  |  |  | | | |  |
| Control | 0.21 (0.18)b | 3.38 (1.86)b | 0.42 (0.41)abc | 0.225 (0.23)a | - | - | 5.38 (1.06)d |  |  |  | | | |  |
| 30-cm | 3 ypf | 0.20 (0.13)a | 0.88 (0.96)a | 0.07 (0.10)a | 0.000 (0.00)a | - | - | 0.00 (0.00)a |  |  |  | | | |  |
| 25 ypf | 0.21 (0.15)a | 0.18 (0.09)a | 0.01 (0.01)a | 0.023 (0.03)a | - | - | 0.08 (0.09)a |  |  |  | | | |  |
| 46 ypf | 0.06 (0.03)a | 0.19 (0.10)a | 0.01 (0.01)a | 0.001 (0.00)a | - | - | 3.77 (1.13)c |  |  |  | | | |  |
| Control | 0.42 (0.48)b | 1.36 (1.73)b | 0.13 (0.22)ab | 0.017 (0.03)a | - | - | 5.11 (0.72)d |  |  |  | | | |  |

Note: # indicates soils saturated with water that the moisture reached to the outside range of the detection range. This table is cited from Zhou et al. (Zhou *et al.*, 2020).

**Table S2.** Alpha diversity indices across different post-fire chronosequence areas, consisting of species richness (Chao1 index), diversity (Shannon index), and evenness (Shannon evenness).

|  |  |  |  |  |
| --- | --- | --- | --- | --- |
| Soil depth | Post-fire chronosequence | Chao1 index | Shannon index | Shannon evenness |
| 0 - 5 cm | 3 ypf | 294.87 ± 13.03a | 3.28 ± 0.16a | 0.61 ± 0.03a |
| 25 ypf | 376.00 ± 16.33ab | 2.95 ± 0.14a | 0.54 ± 0.02a |
| 46 ypf | 416.11 ± 13.97b | 3.52 ± 0.15a | 0.62 ± 0.02a |
| Control | 432.90 ± 46.63b | 3.21 ± 0.22a | 0.57 ± 0.03a |
| 5 - 10 cm | 3 ypf | 259.71 ± 18.98a | 3.13 ± 0.16a | 0.59 ± 0.03a |
| 25 ypf | 301.53 ±19.03ab | 3.00 ± 0.16a | 0.56 ± 0.03a |
| 46 ypf | 396.49 ± 36.05bc | 3.66 ± 0.20a | 0.64 ± 0.04a |
| Control | 404.49 ± 27.62c | 3.19 ± 0.25a | 0.57 ± 0.04a |
| 10 - 30 cm | 3 ypf | 285.15 ± 26.75a | 3.21 ± 0.19a | 0.60 ± 0.02a |
| 25 ypf | 402.49 ± 42.01a | 3.34 ± 0.31a | 0.59 ± 0.05a |
| 46 ypf | 372.03 ± 27.37a | 3.58 ± 0.15a | 0.63 ± 0.02a |
| Control | 362.54 ± 51.77a | 3.42 ± 0.20a | 0.61 ± 0.03a |

Data were shown as averages and standard deviations (n = 9). Different letters represent the significant differences (*P* < 0.05) between the analysed post-fire chronosequence areas in each layer. Abbreviations: ypf: year-post-fire.

**Table S3.** The changes of fungal species richness (Chao1) and functional gene diversity with post-fire chronosequence areas based on the linear regression model. Abbreviations: ypf: year-post-fire.

|  |  |  |  |
| --- | --- | --- | --- |
| Richness or gene diversity /soil layer | R2 | Slope ± SE | *P*-value |
| Chao1 / 0-5 cm | 0.305 | 45.42 ±11.76 | < 0.001 |
| Chao1 / 5-10 cm | 0.373 | 52.93 ± 11.77 | < 0.001 |
| Gene diversity / 0-5 cm | 0.478 | −0.04 ± 0.01 | < 0.05 |

**Table S4.** Variation in fungal community structure among the four post-fire chronosequence areas in each soil layer and among the soil layers in each fire chronosequence area by permutational multivariate analysis of variance (PERMANOVA) with adonis test based on Bray-Curtis distance matrices. Abbreviations: ypf: year-post-fire.

|  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- |
| Factor | Main  tests | | Community structure  Soil layer/area | Pair-wise  tests | | |
| F | *P*-value | Soil layer/area | *t* | *P*-value |
| Post-fire chronosequence | 6.655 | 0.001 | 0-5 cm | 3 ypf vs 25 ypf | 1.579 | 0.001 |
| 3 ypf vs 46 ypf | 2.551 | 0.001 |
| 3 ypf vs Control | 1.785 | 0.001 |
| 25 ypf vs 46 ypf | 2.208 | 0.001 |
| 25 ypf vs Control | 1.482 | 0.001 |
| 46 ypf vs Control | 1.937 | 0.001 |
| 5-10 cm | 3 ypf vs 25 ypf | 1.188 | 0.045 |
| 3 ypf vs 46 ypf | 2.029 | 0.001 |
| 3 ypf vs Control | 1.522 | 0.001 |
| 25 ypf vs 46 ypf | 1.911 | 0.001 |
| 25 ypf vs Control | 1.400 | 0.007 |
| 46 ypf vs Control | 1.715 | 0.001 |
| 10-30 cm | 3 ypf vs 25 ypf | 1.634 | 0.001 |
| 3 ypf vs 46 ypf | 2.225 | 0.001 |
| 3 ypf vs Control | 1.491 | 0.002 |
| 25 ypf vs 46 ypf | 1.812 | 0.001 |
| 25 ypf vs Control | 1.298 | 0.003 |
| 46 ypf vs Control | 1.665 | 0.001 |
| Soil depth | 3.342 | 0.001 | 3 ypf area | 0-5 cm vs 5-10 cm | 1.268 | 0.039 |
| 0-5 cm vs 10-30 cm | 1.779 | 0.002 |
| 5-10 cm vs 10-30 cm | 1.170 | 0.056 |
| 25 ypf area | 0-5 cm vs 5-10 cm | 1.143 | 0.117 |
| 0-5 cm vs 10-30 cm | 1.498 | 0.001 |
| 5-10 cm vs 10-30 cm | 1.093 | 0.153 |
| 46 ypf area | 0-5 cm vs 5-10 cm | 1.119 | 0.111 |
| 0-5 cm vs 10-30 cm | 1.837 | 0.001 |
| 5-10 cm vs 10-30 cm | 1.303 | 0.002 |
| Control area | 0-5 cm vs 5-10 cm | 0.878 | 0.806 |
| 0-5 cm vs 10-30 cm | 1.659 | 0.001 |
| 5-10 cm vs 10-30 cm | 1.353 | 0.011 |
| Chronosequence x depth | 1.284 | 0.001 | - | - | - | - |

**Table S5.** Variation in functional gene expression profile among the four post-fire chronosequence areas in each soil layer and among the soil layers in each fire chronosequence area by permutational multivariate analysis of variance (PERMANOVA) with adonis test based on Bray-Curtis distance matrices. Abbreviations: ypf: year-post-fire.

|  |  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- | --- |
| Factor | Main tests | | | Community structure | Pairwise tests | | |
| F | *P*-value | | Soil layer/area | Soil layer/area | *t* | *P*-value |
| Post-fire chronosequnce | 4.158 | | 0.001 | 0-5 cm | 3 ypf vs 25 ypf | 1.442 | 0.194 |
| 3 ypf vs 46 ypf | 2.295 | 0.001 |
| 3 ypf vs Control | 2.122 | 0.001 |
| 25 ypf vs 46 ypf | 1.348 | 0.298 |
| 25 ypf vs Control | 1.351 | 0.302 |
| 46 ypf vs Control | 1.960 | 0.001 |
| 10-30 cm | 3 ypf vs 25 ypf | 2.422 | 0.001 |
| 3 ypf vs 46 ypf | 1.783 | 0.001 |
| 3 ypf vs Control | 2.318 | 0.001 |
| 25 ypf vs 46 ypf | 3.312 | 0.001 |
| 25 ypf vs Control | 2.150 | 0.001 |
| 46 ypf vs Control | 3.168 | 0.001 |
| Soil depth | 3.532 | | 0.006 | 3 ypf area | 0-5 cm vs 5-10 cm | 2.078 | 0.001 |
| 25 ypf area | 0-5 cm vs 5-10 cm | 1.483 | 0.227 |
| 46 ypf area | 0-5 cm vs 5-10 cm | 2.599 | 0.001 |
| Control area | 0-5 cm vs 5-10 cm | 2.242 | 0.001 |
| Chronosequnce x depth | 4.044 | | 0.001 | - | - | - | - |

**Table S6.** Indicator species analysis showing the main indicator taxa (among the top 10 most abundant taxa) at phylum, genus and species level in the four post-fire chronosequence areas in each soil layer. Abbreviations: ypf: year-post-fire.

|  |  |  |  |  |
| --- | --- | --- | --- | --- |
| Soil layer | Area | Main indicator taxa | Indicator value | *P*-value |
| 0-5 cm | 3 ypf | Ascomycota | 0.634 | 0.001 |
| *Calyptrozyma* | 0.979 | 0.013 |
| *Meliniomyces* | 0.749 | 0.003 |
| *Mycena* | 0.736 | 0.048 |
| *Phialocephala* | 0.692 | 0.003 |
| *Exophiala xenobiotica* | 0.971 | 0.001 |
| *Russula suecica* | 0.937 | 0.025 |
| 25 ypf | - | - | - |
| 46 ypf | *Wilcoxina rehmii* | 0.988 | 0.001 |
| control | - | - | - |
| 5-10 cm | 3 ypf | Ascomycota | 0.616 | 0.021 |
| *Calyptrozyma* | 0.994 | 0.001 |
| *Exophiala xenobiotica* | 0.926 | 0.003 |
| 25 ypf | - | - | - |
| 46 ypf | *Wilcoxina rehmii* | 0.963 | 0.001 |
| control | *Meliniomyces* | 0.706 | 0.048 |
| *Meliniomyces variabilis* | 0.847 | 0.006 |
| 10-30 cm | 3 ypf | Ascomycota | 0.59 | 0.029 |
| *Calyptrozyma* | 0.922 | 0.005 |
| *Russula suecica* | 0.938 | 0.046 |
| 25 ypf | - | - | - |
| 46 ypf | *Wilcoxina rehmii* | 0.994 | 0.001 |
| control | *Serendipita* | 0.800 | 0.010 |
| *Oidiodendron maius* | 0.84 | 0.04 |
| *Solicoccozyma terricola* | 0.76 | 0.009 |

**Table S7.** Indicator species analysis showing the main indicator taxa (among the top 10 most abundant taxa) at phylum, genus and species level in the three soil layers in each post-fire chronosequence area. Abbreviations: ypf: year-post-fire.

|  |  |  |  |  |
| --- | --- | --- | --- | --- |
| Area | Soil layer | Main indicator taxa | Indicator value | *P*-value |
| 3 ypf | 0-5 cm | *Meliniomyces* | 0.767 | 0.023 |
| *Oidiodendron maius* | 0.772 | 0.048 |
| 5-10 cm | - | - | - |
| 10-30 cm | - | - | - |
| 25 ypf | 0-5 cm | *Oidiodendron* | 0.900 | 0.016 |
| *Pezoloma* | 0.811 | 0.021 |
| *Oidiodendron maius* | 0.926 | 0.019 |
| *Meliniomyces variabilis* | 0.827 | 0.033 |
| *Pezoloma ericae* | 0.823 | 0.015 |
| 5-10 cm | *Solicoccozyma terricola* | 0.954 | 0.026 |
| 10-30 cm | - | - | - |
| 46 ypf | 0-5 cm | - | - | - |
| 5-10 cm | - | - | - |
| 10-30 cm | *Oidiodendron maius* | 0.846 | 0.033 |
| Control area | 0-5 cm | *Cortinarius* | 0.889 | 0.019 |
| 5-10 cm | *Phialocephala* | 0.771 | 0.028 |
| 10-30 cm | *Exophiala xenobiotica* | 0.993 | 0.002 |
| *Russula suecica* | 0.91 | 0.004 |
| *Solicoccozyma terricola* | 0.905 | 0.003 |

**Table S8.** Contributions of the environmental variables to the variations of fungal communities and functional gene expression profiles using Distance based Linear Model (DistLM) analysis. Explanatory factors that significantly correlated (*P* < 0.05) with variations in the fungal community structures and functional gene expression profiles were highlighted in bold. Abbreviations: ST: soil temperature; TB: tree bomass; GVB: ground vegetation biomass; SM: soil moisture; FB: foliage biomass; MBC, MBN and MBP are microbial biomass C, N and P contents; SAC, SAN and SAP are soil available C, N and P contents; FBR: fungal-to-bacterial ratio.

|  |  |  |  |  |
| --- | --- | --- | --- | --- |
| Community | Variable | F | *P*-value | R2 |
| Fungal community structures | **years** | **3.686** | **0.001** | **0.034** |
| **depths** | **1.458** | **0.039** | **0.014** |
| **pH** | **5.595** | **0.001** | **0.051** |
| ST | 1.373 | 0.060 | 0.013 |
| **TB** | **5.144** | **0.001** | **0.047** |
| **GVB** | **2.531** | **0.001** | **0.024** |
| SM | 1.188 | 0.165 | 0.011 |
| **FB** | **4.148** | **0.001** | **0.038** |
| **MBC** | **1.805** | **0.005** | **0.017** |
| **MBN** | **1.432** | **0.041** | **0.013** |
| **MBP** | **1.499** | **0.021** | **0.014** |
| SAC | 1.376 | 0.062 | 0.013 |
| **SAN** | **2.059** | **0.001** | **0.019** |
| **SAP** | **1.624** | **0.017** | **0.015** |
| FBR | 1.027 | 0.369 | 0.010 |
| Functional gene expression profiles | **years** | **2.027** | **0.047** | **0.084** |
| depths | 1.914 | 0.055 | 0.080 |
| pH | 1.909 | 0.073 | 0.080 |
| ST | 1.165 | 0.272 | 0.050 |
| TB | 1.831 | 0.067 | 0.077 |
| GVB | 1.931 | 0.064 | 0.081 |
| SM | 1.734 | 0.094 | 0.073 |
| FB | 1.700 | 0.082 | 0.072 |
| MBC | 1.438 | 0.154 | 0.061 |
| MBN | 1.449 | 0.164 | 0.062 |
| MBP | 1.164 | 0.246 | 0.050 |
| SAC | 1.377 | 0.144 | 0.059 |
| SAN | 1.588 | 0.119 | 0.067 |
| SAP | 1.900 | 0.054 | 0.079 |
| FBR | 0.763 | 0.600 | 0.034 |