|  |  |  |  |
| --- | --- | --- | --- |
| All-factor PERMANOVA test statistics | |  |  |
| Factor | R2 | F | Pr(>F) |
| Substrate | 0.3079 | 19.62 | 0.001 |
| Host species | 0.0751 | 14.37 | 0.001 |
| Site | 0.0864 | 4.13 | 0.001 |
| Substrate x Host species | 0.1057 | 6.74 | 0.001 |
| Substrate x Site | 0.2063 | 3.29 | 0.001 |
| Host species x Site | 0.0551 | 2.63 | 0.002 |
| Substrate x Host species x Site | 0.1216 | 2.32 | 0.001 |
| Residual | 0.0418 |  |  |
| Total | 1 |  |  |
|  |  |  |  |
| Pairwise PERMANOVA comparisons by substrate | | | |
|  | **Endophytes** | **Epiphytes** | **Litter** |
| Epiphytes | 0.0036 | - | - |
| Litter | 0.004 | 0.0015 | - |
| Soil | 0.0015 | 0.0015 | 0.0015 |

**Table 1. PERMANOVA table of substrate, host species, site, and interactions effects on fungal communities.** Included are both the full model comparison and *p*-values from permuted pairwise tests.

|  |  |  |  |  |
| --- | --- | --- | --- | --- |
| Substrate | OTU | FDR | RDP Result with UNITE Database | BLAST Result |
| **Epiphyte** | OTU\_150 | 0.0033 | Ceramothyrium\_carniolicum|SH238238.06FU | *Ceramothyrium* sp. |
|  | OTU\_56 | 0.0033 | Exobasidiomycetes\_sp|SH199847.06FU | Unknown |
|  | OTU\_58 | 0.0033 | Entyloma\_microsporum|SH228434.06FU | Unknown |
|  | OTU\_108 | 0.0033 | Ascomycota\_sp|SH195092.06FU | *Acrodontium* sp. |
|  | OTU\_91 | 0.0033 | Hysterangiales\_sp|SH233926.06FU | Unknown |
| **Endophyte** | OTU\_191 | 0.0033 | Taphrina\_sp|SH235565.06FU | Unknown |
|  | OTU\_48 | 0.0102 | Phyllosticta\_sp|SH198090.06FU | *Phyllosticta* sp. |
|  | OTU\_83 | 0.0116 | Amphisphaeriaceae\_sp|SH210428.06FU | *Seimatosporium* sp. |
|  | OTU\_34 | 0.0219 | Geomyces\_sp\_APA\_2013|SH236520.06FU | Rhytismataceae sp. |
|  | OTU\_683 | 0.0331 | Zygophiala\_wisconsinensis|SH232272.06FU | *Schizothyrium* sp. |
| **Litter** | OTU\_23 | 0.0033 | Glomerella\_tucumanensis|SH229539.06FU | *Colletotrichum* sp. |
|  | OTU\_32 | 0.0033 | Cordana\_solitaria|SH219394.06FU | Xylariales sp. |
|  | OTU\_40 | 0.0033 | Dictyochaeta\_simplex|SH223027.06FU | *Codinaea lambertiae* |
|  | OTU\_52 | 0.0033 | Ascomycota\_sp|SH209179.06FU | *Coleophoma* sp. |
|  | OTU\_112 | 0.0033 | Lophiostoma\_sp|SH215426.06FU | *Amorocoelophoma* sp. |
| **Soil** | OTU\_19 | 0.0033 | Cryptococcus\_podzolicus|SH197001.06FU | *Saitozyma* sp. |
|  | OTU\_41 | 0.0033 | Archaeorhizomyces\_sp|SH197159.06FU | *Archaeorhizomyces* sp. |
|  | OTU\_85 | 0.0033 | Cryptococcus\_terricola|SH215219.06FU | *Solicocozyma terricola* |
|  | OTU\_93 | 0.0033 | Trichoderma\_pubescens|SH222751.06FU | *Trichoderma* sp. |
|  | OTU\_785 | 0.0033 | Pseudogymnoascus\_roseus|SH236509.06FU | *Pseudogymnoascus* sp. |
| **Epiphyte + Endophyte** | OTU\_189 | 0.0033 | Mycosphaerella\_nyssicola|SH216155.06FU | *Ramularia nyssicola* |
| OTU\_479 | 0.0033 | Ascomycota\_sp|SH216151.06FU | *Ramularia* sp. |
|  | OTU\_251 | 0.0073 | Mycosphaerellaceae\_sp|SH216154.06FU | *Ramularia* sp. |
|  | OTU\_3326 | 0.0087 | Mycosphaerellaceae\_sp|SH216163.06FU | *Ramularia* sp. |
|  | OTU\_2 | 0.0116 | Ampelomyces\_quisqualis|SH222882.06FU | Unknown |
| **Epiphyte + Litter** | OTU\_66 | 0.0033 | Tremellales\_sp|SH223473.06FU | *Bulleribasidium* sp. |
| OTU\_68 | 0.0033 | Phoma\_brasiliensis|SH202145.06FU | *Epicoccum* sp. |
|  | OTU\_82 | 0.0033 | Devriesia\_sp|SH195036.06FU | Dothideomycetes sp. |
|  | OTU\_165 | 0.0033 | Dioszegia\_hungarica|SH196970.06FU | *Dioszegia* sp. |
|  | OTU\_226 | 0.0033 | Mycena\_sp\_MLB\_2010a|SH193155.06FU | Unknown |
| **Endophyte + Litter** | OTU\_87 | 0.0330 | Paraconiothyrium\_variabile|SH224124.06FU | *Paraconiothyrium* sp. |
| OTU\_1 | 0.0331 | Colletotrichum\_acerbum|SH233478.06FU | *Colletotrichum* sp. |
|  | OTU\_127 | 0.0353 | Diaporthe\_alleghaniensis|SH214040.06FU | *Diaporthe* sp. |
| **Litter + Soil** | OTU\_380 | 0.0033 | Fungi\_sp|SH207195.06FU | Helotiales sp. |
|  | OTU\_282 | 0.0131 | Stachybotrys\_eucylindrospora|SH227379.06FU | *Striatibotrys* sp. |
|  | OTU\_193 | 0.0197 | Nectriaceae\_sp|SH217311.06FU | *Cylindrocladiella* sp. |
|  | OTU\_121 | 0.0232 | Mycoarthris\_sp|SH209211.06FU | Leotiomycetes sp. |
| **Epiphyte + Endophyte + Litter** | OTU\_4 | 0.0033 | Dothideomycetes\_sp|SH216152.06FU | *Ramularia* sp. |
| OTU\_5 | 0.0033 | Mycosphaerellaceae\_sp|SH216154.06FU | *Ramularia* sp. |
| OTU\_8 | 0.0033 | Davidiella\_tassiana|SH196750.06FU | *Cladosporium* sp. |
|  | OTU\_10 | 0.0033 | Ascomycota\_sp|SH241083.06FU | Didymellaceae sp. |
|  | OTU\_11 | 0.0033 | Alternaria\_eichhorniae|SH224789.06FU | *Alternaria* sp. |

**Table 2. Substrate and cross-substrate indicator OTUs.** Indicator OTUs were determined using the multipatt function in R package “indicspecies”. Substrate groupings with no significant indicator OTUs are not displayed, and only those with a false discovery rate (FDR) < 0.05 are included (maximum of 5 each). Sequence analysis against the UNITE and Fungal RefSeq ITS nucleotide databases determined the closest known taxa.

|  |  |  |  |  |
| --- | --- | --- | --- | --- |
|  | Epiphyte | Endophyte | Litter | Soil |
| Total OTUs | 268 | 202 | 421 | 364 |
| Unique OTUs | 5 (2%) | 2 (1%) | 64 (15%) | 212 (58%) |
| Shared with Epiphytes | - | 180 (89%) | 247 (59%) | 57 (16%) |
| Shared with Endophytes | 180 (67%) | - | 187 (44%) | 43 (12%) |
| Shared with Litter | 247 (92%) | 187 (93%) | - | 145 (40%) |
| Total Shared | 263 (98%) | 200 (99%) | 357 (85%) | 152 (42%) |

**Table 3. Total, unique, and shared OTUs by substrate.** Comparison of the number of OTUs in each of four substrates. Shown are the total number of OTUs, the number of unique OTUs in each substrate and the number of OTUs shared between substrates. Total number of shared OTUs is the number of unique OTUs subtracted from the total number. OTUs were filtered to exclude those with a substrate-weighted abundance of less than 0.01%.

|  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- |
| Shannon Index |  |  |  |  |  |
| Factor | Df | Sum Sq | Mean Sq | F value | Pr(>F) |
| Substrate | 3 | 7.055687768 | 2.351895923 | 7.674778805 | 0.000413258 |
| Host species | 1 | 1.523488881 | 1.523488881 | 4.971495576 | 0.031920704 |
| Site | 4 | 2.463250733 | 0.615812683 | 2.009538808 | 0.113276193 |
| Residuals | 37 | 11.33845696 | 0.306444783 |  |  |
|  | |  |  |  |  |
| Inverse Simpson Index | |  |  |  |  |
| Factor | Df | Sum Sq | Mean Sq | F value | Pr(>F) |
| Substrate | 3 | 670.3535712 | 223.4511904 | 4.731573082 | 0.006820544 |
| Host species | 1 | 230.8735612 | 230.8735612 | 4.888741589 | 0.033292266 |
| Site | 4 | 212.1614829 | 53.04037073 | 1.123128456 | 0.360457341 |
| Residuals | 37 | 1747.345735 | 47.2255604 |  |  |

**Supplementary Table 1. ANOVA tables of substrate, host species, and site effects of within-sample diversity.** Diversity was estimated for Shannon and Inverse Simpson indices using diversity function in vegan.