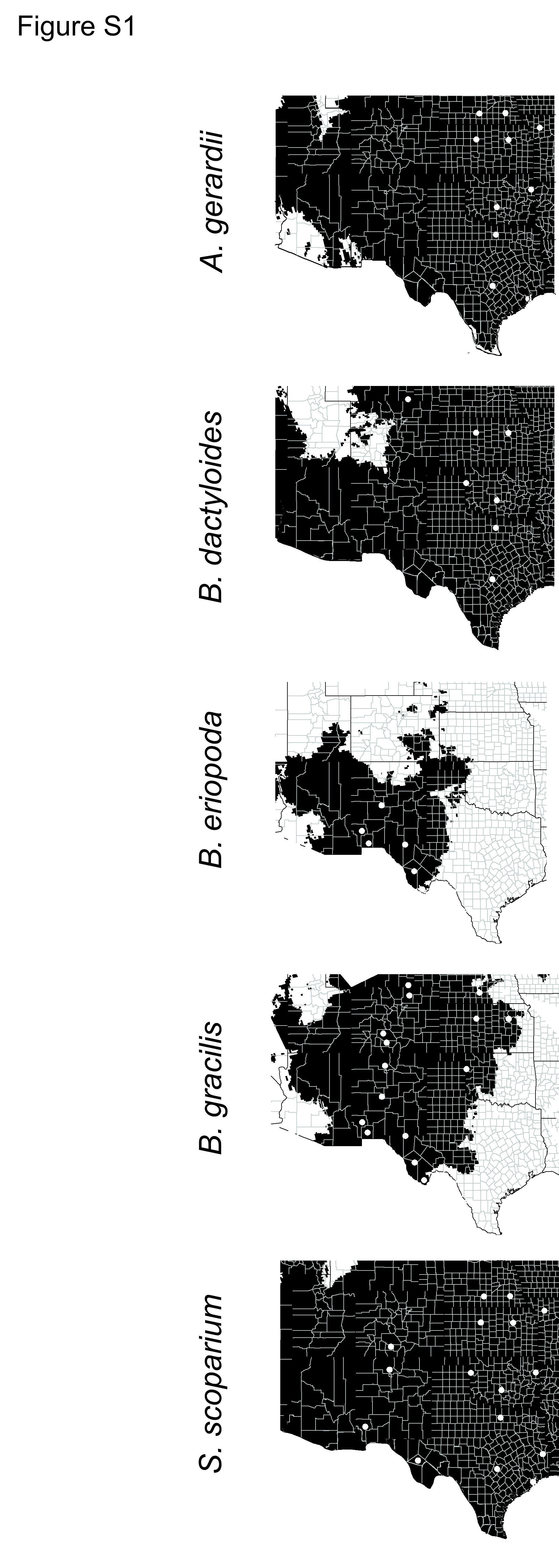
**Supplementary Material**

**Table S1**. List of grass species and sites sampled across three replicate latitudinal gradients (E= East, M = Middle, W=West) across the North American plains. Coordinates are given in decimal degrees, and elevation is in meters. Bin indicates the categorical bin for latitude used in analysis (N=North, NM=North-Middle, SM=South-Middle, S=South). Date indicates the month/day on which samples were collected during the year 2015. Plants were not grazed by cattle at the time of sampling, and sites lacked cattle during sampling excepting CAD and DMT. Sampling dates were timed to match phenologies among sites based on 30-year normal growing degree days (mean = 2656°C ± 351 *s.d.*).

| Plant species | Site | Grassland | Gradient | Latitude | Longitude | Elevation | Bin | Date |
| --- | --- | --- | --- | --- | --- | --- | --- | --- |
| *Andropogon gerardii* | UHC | tallgrass | E | 29.39087 | -95.03443 | -20 | S | 2015-06-29 |
|  | NWP | tallgrass | E | 36.04170 | -94.81370 | 250 | NC | 2015-07-17 |
|  | KNZ | tallgrass | E | 39.07450 | -96.60360 | 860 | N | 2015-08-03 |
|  | ONF | tallgrass | E | 39.80954 | -94.13184 | 208 | SC | 2015-07-18 |
|  | SCP | tallgrass | E | 40.69482 | -96.85447 | 406 | N | 2015-08-07 |
|  | LBJ | mixed grass | M | 30.18470 | -97.86750 | 250 | S | 2015-07-01 |
|  | CAD | mixed grass | M | 33.30787 | -97.60542 | 339 | SC | 2015-07-06 |
|  | KAE | tallgrass | M | 34.97790 | -97.52280 | 335 | SC | 2015-07-16 |
|  | HAR | mixed grass | M | 39.08780 | -99.15590 | 613 | N | 2015-08-05 |
|  | LAR | tallgrass | M | 40.66462 | -98.90630 | 632 | N | 2015-08-09 |
| *Bouteloua dactyloides* | KNZ | tallgrass | E | 39.07450 | -96.60360 | 860 | N | 2015-08-03 |
|  | LBJ | mixed grass | M | 30.18331 | -97.87680 | 231 | S | 2015-07-02 |
|  | CAD | mixed grass | M | 33.30862 | -97.60532 | 335 | SC | 2015-07-05 |
|  | KAE | tallgrass | M | 34.98053 | -97.52155 | 335 | SC | 2015-07-16 |
|  | HAR | mixed grass | M | 39.08780 | -99.15590 | 613 | N | 2015-08-05 |
|  | FCP | mixed grass | M | 36.02350 | -99.94390 | 635 | NC | 2015-07-20 |
|  | HPG | shortgrass | W | 41.12200 | -104.53130 | 1930 | N | 2015-08-24 |
| *Bouteloua eriopoda* | BNP | desert | W | 29.23005 | -103.37832 | 1201 | S | 2015-07-15 |
|  | DMT | desert | W | 30.34736 | -104.04668 | 1494 | S | 2015-07-16 |
|  | GMT | desert | W | 31.95908 | -104.76002 | 1551 | S | 2015-07-14 |
|  | FMT | desert | W | 32.03624 | -107.64451 | 1434 | SC | 2015-08-29 |
|  | GNF | desert | W | 32.79587 | -108.18346 | 1881 | SC | 2015-08-29 |
|  | SEV | desert | W | 34.34214 | -106.62261 | 1645 | SC | 2015-08-23 |
|  | CNF | shortgrass | W | 36.23189 | -106.37604 | 1864 | NC | 2015-09-5 |
| *Bouteloua gracilis* | KNZ | tallgrass | E | 39.07450 | -96.60360 | 860 | N | 2015-08-03 |
|  | SCP | tallgrass | E | 40.69234 | -96.85299 | 406 | N | 2015-08-07 |
|  | CAD | mixed grass | M | 33.30870 | -97.60635 | 351 | SC | 2015-07-06 |
|  | HAR | mixed grass | M | 39.08780 | -99.15590 | 613 | N | 2015-08-05 |
|  | LAR | tallgrass | M | 40.66462 | -98.90630 | 632 | N | 2015-08-09 |
| *Bouteloua gracilis* (cont.) | FCP | mixed grass | M | 36.02350 | -99.94390 | 635 | NC | 2015-07-20 |
|  | BNP | desert | W | 29.27425 | -103.28608 | 1705 | S | 2015-07-15 |
|  | DMT | desert | W | 30.34758 | -104.03952 | 1466 | S | 2015-07-16 |
|  | GMT | desert | W | 31.95908 | -104.76002 | 1551 | S | 2015-07-14 |
|  | FMT | desert | W | 32.16806 | -107.75105 | 1311 | SC | 2015-08-30 |
|  | GNF | desert | W | 32.79587 | -108.18346 | 1881 | SC | 2015-08-29 |
|  | SEV | desert | W | 34.34214 | -106.62261 | 1645 | SC | 2015-08-23 |
|  | CNF | shortgrass | W | 36.23189 | -106.37604 | 1864 | NC | 2015-09-05 |
|  | BLM | shortgrass | W | 37.62755 | -106.25329 | 2388 | NC | 2015-09-04 |
|  | RNF | shortgrass | W | 38.18820 | -106.51498 | 2747 | NC | 2015-09-04 |
|  | CPR | shortgrass | W | 40.50100 | -104.45450 | 1640 | N | 2015-08-23 |
|  | HPG | shortgrass | W | 41.12200 | -104.53130 | 1930 | N | 2015-08-24 |
| *Schizachyrium scoparium* | UHC | tallgrass | E | 29.39087 | -95.03443 | -20 | S | 2015-06-29 |
|  | SFA | tallgrass | E | 31.09185 | -94.26535 | 75 | S | 2015-07-04 |
|  | NWP | tallgrass | E | 36.04170 | -94.81370 | 250 | NC | 2015-07-17 |
|  | KNZ | tallgrass | E | 39.07450 | -96.60360 | 860 | N | 2015-08-03 |
|  | ONF | tallgrass | E | 39.80954 | -94.13184 | 208 | SC | 2015-07-18 |
|  | SCP | tallgrass | E | 40.69234 | -96.85299 | 406 | N | 2015-08-07 |
|  | LBJ | mixed grass | M | 30.18225 | -97.87452 | 250 | S | 2015-07-01 |
|  | CAD | mixed grass | M | 33.30787 | -97.60542 | 339 | SC | 2015-07-06 |
|  | KAE | tallgrass | M | 34.97790 | -97.52280 | 335 | SC | 2015-07-16 |
|  | HAR | mixed grass | M | 39.08780 | -99.15590 | 613 | N | 2015-08-05 |
|  | LAR | tallgrass | M | 40.66462 | -98.90630 | 632 | N | 2015-08-09 |
|  | FCP | mixed grass | M | 36.02350 | -99.94390 | 635 | NC | 2015-07-20 |
|  | DMT | desert | W | 30.69382 | -104.12415 | 1824 | S | 2015-07-17 |
|  | GNF | desert | W | 32.74914 | -108.28760 | 1825 | SC | 2015-08-30 |
|  | CNF | shortgrass | W | 36.22032 | -106.37158 | 1834 | NC | 2015-09-05 |
|  | BLM | shortgrass | W | 37.61693 | -106.26240 | 2374 | NC | 2015-09-04 |
|  |  |  |  |  |  |  |  |  |

**Figure S1.** Range maps for five foundation grass species: *Andropogon gerardii*, *Bouteloua dactyloides*, *B. eriopoda*, *B. gracilis*, and *Schizachyrium scoparium*. Note that for all species but *B. eriopoda*, southern records approached the southern species range limits, and typically indicate accessions from high elevation sites. For *B. eriopoda*, our sampling effort exceeded its northern, rather than southern, range limit. Map distribution data from BIEN (Enquist BJ, Condit R, Peet RK, Schildhauer M, Thiers BM. (2016) Cyberinfrastructure for an integrated botanical information network to investigate the ecological impacts of global climate change on plant biodiversity. PeerJ Preprints 4:e2615v2 https://doi.org/10.7287/peerj.preprints.2615v2).

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**Appendix S1. Fungal cultures: Detailed methods and results.**

***Fungal*** ***cultures***. We isolated fungi from surface-sterilized roots within 48 h of field collection. Roots were surface sterilized in 70% ethanol for 1 min, 1% sodium hypochlorite for 1 minute, then rinsed with sterile water three times. In a biosafety cabinet, we cut each root section into 2-3 mm fragments using sterile technique. We randomly chose six fragments from each individual, then inserted each fragment into the center of a unique cell in a 48-well tissue culture plate (Fisher Scientific, Walham, MA) filled with malt extract agar (MEA) plus antibiotics (streptomycin and tetracycline, 50 mg/L). Plates were sealed with parafilm then incubated at room temperature. For negative controls, we pressed surface-sterilized roots against MEA plates to ensure no fungal growth from root surfaces. Plates were checked daily, and unique morphotypes were transferred into 50 mm petri dishes of the same media to create pure cultures.

From these pure cultures, we archived representatives in sterile cryovials filled with 1 ml sterile water. We extracted genomic DNA from each pure culture using the Wizard genomic DNA purification kit (Promega, Madison, WI). We used PCR to amplify the Internal Transcribed Spacer (ITS) region using primers ITS1F (Gardes and Bruns 1993) and ITS4 (White et al. 1990) and the large subunit (LSU) region using primers LR0R and LR3 (Vilgalys and Hester 1990). PCR reactions contained 12.5 μl of PCR master mix (Promega, Madison, WI), 3 μl of 1% bovine serum albumin (BSA), 1 μl of each primer (5μM), 6.5 μl of nuclease-free water, and 1 μl of DNA. Water was used for negative controls. PCR reactions were run at 95°C for 5 min; 35 cycles of 94°C for 30 s, annealing at 50°C for 30 s, and extension at 72°C for 45 s; and a final extension at 72°C for 7 min. We checked PCR products using gel electrophoresis (1.2 % agarose in Tris-acetate-EDTA buffer). Samples were sequenced using the forward primer at Beckman Coulter Genomics (Danvers, MA). We successfully sequenced 1,033 isolates, then trimmed and edited them in Sequencher (Gene Codes, Ann Arbor, MI). Identifications were made with Basic Local Alignment Search Tool (BLAST) (Altschul et al. 1997) and UNITE (Kõljalg et al. 2013). We deposited sequences under GenBank numbers MK809076-MK809103 for SSU, MK809104-MK809135 for LSU, MK808044-MK809075 for ITS. Other data files, and data curation, analysis and graphics scripts are available through the Environmental Data Initiative (Rudgers et al. 2021).

***Results. Comparison of Illumina- versus Culture-based methods.*** The majority of Illumina sequences belonged to phylum Ascomycota (70%) with 28% Basidiomycota. Ascomycota comprised 96% of sequenced isolates, and Basidiomycota were 4%, and culture-based datasets were similar in composition. Arbuscular mycorrhizal fungi were infrequent (<2% Glomeromycota) among Illumina sequences and absent in culture. The Illumina dataset had rare basal fungi (Chytridiomycota – 0.03%, Rozellomycota – 0.01%, and former Zygomycota – 0.51%). Taxa were unevenly represented between the Illumina and culture datasets. Within Basidiomycota, Agaricales (16% of all sequences, 3% of cultures) and Auriculariales (2% Illumina, 0% cultures) were most common. Among taxa with genus-level assignments, *Fusarium* was abundant(1% of all Illumina sequences, 27% of cultures), as well as *Marasmius* (3.2% Illumina, 1% cultures), *Periconia* (2.2% Illumina, 13% cultures), and *Moniliophthora* (2.1% Illumina, 1% cultures). Many taxa lacked generic assignments: unclassified Pleosporales were 18% of all Illumina sequences, unclassified ascomycetes were 4.8%, and unclassified Nectriaceae were 4.3%.

Root-associated fungal communities of foundation grasses were dominated by Ascomycota (70%) with <30% of sequences assigned to Basidiomycota and <2% to Glomeromycota, and no Glomeromycota in culture due to their obligate host-associations. These compositional profiles were similar to prior studies on grasses (Mandyam and Jumpponen 2005, Porras-Alfaro and Bayman 2011), but represent a more holistic survey in the breadth of both plant species and latitudes examined. Use of the ITS2 region likely biased our dataset against detection and taxonomic resolution of arbuscular mycorrhizal fungi (Glomeromycota), which is improved by targeting the small subunit rRNA (SSU rRNA) gene (Opik et al. 2010). However, recent comparisons suggest our approach was unlikely to alter the relative importance of environmental correlates of fungal communities and may only produce slightly different Glomeromycota composition than the SSU (Berruti et al. 2017, Lekberg et al. 2018).

**Appendix S2. Detailed methods for root microscopy.**

We selected roots by the presence of root hairs and lack of obvious pathogenic lesions or physical damage, then placed them into 1.5 ml tubes filled with 1M KOH for clearing. We incubated tubes at 65ºC for up to 1 h or at room temperature overnight, with incubation time determined by pilot tests. Roots were stained with ~1 ml of 1% HCl containing lactophenol cotton blue (1:50 v/v) before incubating at room temperature for ~30 min. Stained roots were stored in acidified glycerol (1% HCl – 99% glycerol) at 5ºC until microscopy (within 7 mo). We captured five digital images for each stained root section (~200X magnification) at random distances from the root edge (Olympus BX53F microscope, DP80 Dual CCD Color and Monochrome Camera, Olympus Corporation of the Americas, Center Valley, PA).

**Appendix S3. Detailed methods for next-generation sequencing.**

We generated amplicons in duplicate 50 µl PCR reactions containing 2 ng DNA template, 200 µM dNTPs, 1 µM each primer, 10 µl of 5x Phusion Green HF Buffer with 1.5 mM MgCl2, 1 unit (0.5 µl) of Phusion Green Hot Start II High-Fidelity DNA polymerase (ThermoFisher Scientific, Pittsburgh, PA), and 22.5 µl of sterile molecular grade water. Cycles had an initial 30 s denaturing at 98ºC, followed by 35 cycles of denaturing at 98ºC for 10 s, annealing at 56ºC for 10 s, extension at 72ºC for 60 s, and a final extension at 72ºC for 5 min. To remove residual nucleotides and primers, duplicate PCR amplicons were combined and cleaned using AgenCourt AMPure XP (Beckman-Coulter, Indianapolis, IN) using the 96-well magnetic SPRIplate according to manufacturer protocol, except for a 1:1 bead solution to amplicon ratio. MID-incorporated, cleaned amplicons were quantified using Invitrogen’s Quant-iT dsDNA Assay Kit (ThermoFisher Scientific Pittsburgh, PA) and pooled at 300 ng of amplicon DNA per sample. The pools were AMPure XP cleaned again to remove residual primers. Illumina-specific primers and adapters were added using NEBNext® DNA MasterMix (New England Biolabs Inc., Ipswich, MA) at the Integrated Genomics Facility at Kansas State University (Manhattan, KS). Libraries were paired-end sequenced (MiSeq Reagent Kit v3; Illumina, San Diego, CA) with 2 × 300 cycles in a combined run.

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**Table S2**. Means for analysis of dispersion and centroids for nonmetric multidimensional scaling (NMDS) analysis of fungal composition among latitudes. Within each grass species, significant differences among latitude categories are shown by differed letters.

|  |  |  |  |  |  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- |
| **Dispersion** | | | | | **Composition** | | | | | | |
| Latitude | *N* | mean | *s.e.* |  | Axis 1 | *s.d.* | Axis 2 | *s.d.* | Axis 3 | *s.d.* |  |
| *A. gerardii* | | | | | | | | | | | |
| N | 44 | 63.92 | 0.43 | a | -0.52 | 0.39 | 0.06 | 0.74 | -0.01 | 0.70 | ab |
| NM | 11 | 43.10 | 1.95 | b | 0.30 | 0.13 | -0.05 | 0.12 | 0.43 | 0.23 | a |
| SM | 33 | 61.59 | 0.97 | c | 0.45 | 0.40 | -0.02 | 0.77 | -0.01 | 0.53 | ab |
| S | 21 | 30.16 | 1.90 | d | 0.22 | 0.08 | -0.07 | 0.05 | -0.20 | 0.07 | b |
| *B. dactyloides* | | | | | | | | | | | |
| N | 31 | 59.17 | 1.28 | a | -0.45 | 0.37 | 0.18 | 0.54 | 0.11 | 0.51 | a |
| NM | 12 | 58.92 | 2.44 | a | 0.05 | 0.46 | -0.40 | 0.71 | -0.16 | 0.64 | b |
| SM | 24 | 61.71 | 1.22 | a | 0.33 | 0.65 | -0.05 | 0.78 | 0.08 | 0.49 | abc |
| S | 12 | 35.53 | 3.26 | b | 0.44 | 0.20 | 0.03 | 0.19 | -0.28 | 0.13 | c |
| *B. eriopoda* | | | | | | | | | | | |
| NM | 11 | 39.79 | 3.54 | a | -0.58 | 0.27 | 0.25 | 0.41 | 0.28 | 0.07 | a |
| SM | 32 | 61.28 | 0.82 | b | 0.08 | 0.63 | -0.10 | 0.67 | -0.42 | 0.55 | a |
| S | 35 | 55.32 | 1.28 | c | 0.11 | 0.56 | 0.01 | 0.59 | 0.30 | 0.28 | a |
| *B. gracilis* | | | | | | | | | | | |
| N | 65 | 63.24 | 0.57 | a | -0.33 | 0.48 | -0.42 | 0.75 | 0.07 | 0.61 | a |
| NM | 46 | 50.08 | 1.63 | b | 0.06 | 0.30 | 0.20 | 0.25 | 0.15 | 0.46 | b |
| SM | 42 | 60.81 | 0.95 | c | 0.20 | 0.68 | 0.30 | 0.63 | -0.23 | 0.46 | ac |
| S | 33 | 53.45 | 1.90 | b | 0.32 | 0.51 | 0.17 | 0.39 | -0.05 | 0.37 | bc |
| *S. scoparium* | | | | | | | | | | | |
| N | 44 | 64.25 | 0.35 | a | -0.30 | 0.45 | -0.35 | 0.83 | 0.13 | 0.55 | a |
| NM | 44 | 58.90 | 1.14 | b | 0.05 | 0.51 | 0.36 | 0.39 | -0.07 | 0.36 | ab |
| SM | 42 | 64.27 | 0.59 | a | -0.01 | 0.84 | -0.08 | 0.38 | -0.04 | 0.61 | ab |
| S | 42 | 55.40 | 2.03 | b | 0.27 | 0.45 | 0.07 | 0.41 | -0.02 | 0.55 | b |
|  |  |  |  |  |  |  |  |  |  |  |  |

**Table S3**. Results from indicator species analysis to identify which fungal taxa were most responsible for divergence of root-associated fungi among five grass species. OTU ID is the unique identifier in the rarified Illumina dataset, Culture ID is the unique identifier from the Sanger-sequenced culture dataset [*NA* indicates taxa not present in culture, \* indicates taxa that were also indicators of latitudinal gradients]. Indicator is the Dufrene-Legendre value for each plant species; larger values signal stronger indicators of the species’ unique fungal community. *P* values are given for each indicator. *N* is the total number of samples in which each OTU was observed out of a total of 624 samples. Proportion is the proportional abundance of the taxon in the rarified Illumina dataset for each plant species.

|  |  |  |  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- | --- | --- | --- |
| Grass species | OTU ID | Culture ID | Indicator | *P* | *N* | Proportion | Fungal Species | Order | Phylum |
| *A. gerardii* | Otu00031 | DS740 | 0.40 | 0.001 | 419 | 0.67 | *Fusarium chlamydosporum* species complex 4-b | Hypocreales | Ascomycota |
|  | Otu00002 | DS26 | 0.39 | 0.001 | 487 | 0.78 | *Fusarium incarnatum-equiseti* species complex 16 | Hypocreales | Ascomycota |
|  | Otu00235 | *NA* | 0.38 | 0.001 | 123 | 0.20 | *Mortierella* sp. | Mortierellales | Zygomycota |
|  | Otu00233 | *NA* | 0.37 | 0.001 | 152 | 0.24 | Montagnulaceae unclassified | Pleosporales | Ascomycota |
|  | Otu00021 | DS292 | 0.36 | 0.001 | 391 | 0.63 | *Microdochium* sp. | Xylariales | Ascomycota |
| *B. dactyloides* | Otu00011\* | *NA* | 0.43 | 0.001 | 142 | 0.23 | unclassified | Sordariales | Ascomycota |
|  | Otu00490 | *NA* | 0.31 | 0.001 | 153 | 0.25 | Glomeromycota unclassified | unclassified | Glomeromycota |
|  | Otu00040 | *NA* | 0.30 | 0.001 | 312 | 0.50 | Pleosporales unclassified | Pleosporales | Ascomycota |
|  | Otu00176 | DS510 | 0.28 | 0.003 | 196 | 0.31 | *Gaeumannomyces incrustans* | Magnoporthales | Ascomycota |
|  | Otu00219 | *NA* | 0.28 | 0.001 | 190 | 0.30 | Glomeromycota unclassified | unclassified | Glomeromycota |
| *B. eriopoda* | Otu00240 | *NA* | 0.55 | 0.001 | 128 | 0.21 | *Chaetomium* sp. | Sordariales | Ascomycota |
|  | Otu00015 | DS573 | 0.54 | 0.001 | 454 | 0.73 | *Curvularia spicifera* | Pleosporales | Ascomycota |
|  | Otu00012\* | DS1223 | 0.50 | 0.001 | 204 | 0.33 | Marasmiaceae *incertae sedis 2* | Agaricales | Basidiomycota |
|  | Otu00466 | *NA* | 0.44 | 0.001 | 113 | 0.18 | *Glomus* sp. SOV | Glomerales | Glomeromycota |
|  | Otu00073 | DS233 | 0.33 | 0.001 | 276 | 0.44 | Sordariales *incertae sedis* | Sordariales | Ascomycota |
| *B. gracilis* | Otu00001\* | DS1084 | 0.31 | 0.001 | 557 | 0.89 | *Darksidea alpha* | Pleosporales | Ascomycota |
|  | Otu00269 | *NA* | 0.23 | 0.001 | 160 | 0.26 | *Aureobasidium pullulans* | Dothideales | Ascomycota |
|  | Otu00065 | DS860 | 0.22 | 0.036 | 266 | 0.43 | *Paraconiothyrium* sp. 2 | Pleosporales | Ascomycota |
|  | Otu00067 | DS795 | 0.19 | 0.038 | 267 | 0.43 | *Fusarium incarnatum-equiseti* species complex 16 | Hypocreales | Ascomycota |
|  | Otu00962 | DS211 | 0.18 | 0.001 | 208 | 0.33 | *Darksidea* sp. 4 | Pleosporales | Ascomycota |
| *S. scoparium* | Otu00079 | *NA* | 0.32 | 0.001 | 203 | 0.33 | *Xylaria* sp. | Xylariales | Ascomycota |
|  | Otu00048 | *NA* | 0.29 | 0.002 | 222 | 0.36 | Pleosporales unclassified | Pleosporales | Ascomycota |
|  | Otu00033 | DS1590 | 0.29 | 0.001 | 239 | 0.38 | Hypocreales *incertae sedis* 2 | Hypocreales | Ascomycota |
|  | Otu00060 | DS147 | 0.28 | 0.001 | 279 | 0.45 | Sordariales incertae sedis 5 | Sordariales | Ascomycota |
|  | Otu00597 | DS994 | 0.24 | 0.043 | 131 | 0.21 | *Biappendiculispora japonica* | Pleosporales | Ascomycota |

**Table S4**. Results from linear regression and indicator species analysis to identify the fungal taxa most responsible for latitudinal gradients in composition for each grass species. OTU ID is the unique identifier in the rarified Illumina dataset, Culture ID is the unique identifier from the Sanger-sequenced culture dataset [*NA* indicates taxa not present in culture]. *β* is the slope with standard error (*s.e.*) of the proportional abundance of each OTU within a grass species regressed on latitude, and *P* values test the hypothesis that slope = 0. SIMPER is the percentage contribution of each fungal taxon to divergence among latitude bins of N = North or S = South (SIMPER, Primer v. 6.1.10; Clarke & Gorley, 2009).

| Grass species | OTU ID | Culture ID | *β* | *s.e.* | *P* | Latitude | SIMPER | Fungal Species | | Order | Phylum |
| --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- |
| *B. eriopoda* | 00019 | *NA* | 1.22 | 0.33 | 0.0004 | N | 6.6 | unclassified | Pleosporales | | Ascomycota |
| *B. dactyloides* | 00032 | *NA* | 0.70 | 0.25 | 0.0060 | N | 7.2 | unclassified | Pleosporales | | Ascomycota |
| *S. scoparium* | 00001 | DS1084 | 0.37 | 0.18 | 0.0366 | N | 10.1 | *Darksidea alpha* | Pleosporales | | Ascomycota |
| *S. scoparium* | 00082 | *NA* | 0.36 | 0.12 | 0.0025 | N | 2.3 | *Mycena adonis* | Agaricales | | Basidiomycota |
| *S. scoparium* | 00043 | DS980 | 0.34 | 0.12 | 0.0056 | N | 7.3 | *Lachnum* sp. 3 | Helotiales | | Ascomycota |
| *A. gerardii* | 00034 | *NA* | 0.33 | 0.15 | 0.0300 | N | 5.0 | unclassified | Pleosporales | | Ascomycota |
| *S. scoparium* | 00029 | *NA* | 0.31 | 0.08 | 0.0002 | N | 3.3 | unclassified | unclassified | | Ascomycota |
| *B. dactyloides* | 00064 | *NA* | 0.30 | 0.10 | 0.0039 | N | 1.0 | unclassified | Pleosporales | | Ascomycota |
| *B. gracilis* | 00039 | *NA* | 0.29 | 0.11 | 0.0058 | N | 3.5 | unclassified | unclassified | | Ascomycota |
| *A. gerardii* | 00013 | DS959 | 0.24 | 0.11 | 0.0332 | N | 1.2 | *Anthostomella* sp. | Xylariales | | Ascomycota |
| *A. gerardii* | 00046 | DS1170 | 0.24 | 0.06 | 0.0001 | N | 7.8 | *Alternaria* sp. | Pleosporales | | Ascomycota |
| *A. gerardii* | 00043 | DS980 | 0.23 | 0.08 | 0.0047 | N | 2.8 | *Lachnum* sp. 3 | Helotiales | | Ascomycota |
| *B. dactyloides* | 00019 | *NA* | 0.22 | 0.10 | 0.0250 | N | 0.7 | unclassified | Pleosporales | | Ascomycota |
| *S. scoparium* | 00017 | DS1001 | 0.20 | 0.09 | 0.0240 | N | 3.9 | *Lachnum* sp. 1 | Helotiales | | Ascomycota |
| *B. gracilis* | 00011 | *NA* | 0.20 | 0.09 | 0.0283 | N | 1.8 | unclassified | Sordariales | | Ascomycota |
| *B. gracilis* | 00032 | *NA* | 0.18 | 0.05 | 0.0008 | N | 2.9 | unclassified | Pleosporales | | Ascomycota |
| *B. gracilis* | 00044 | DS1136 | 0.18 | 0.08 | 0.0272 | N | 0.6 | *Gelasinospora saitoi* | Sordariales | | Ascomycota |
| *B. gracilis* | 00057 | *NA* | 0.17 | 0.05 | 0.0004 | N | 1.3 | unclassified | unclassified | | Ascomycota |
| *B. dactyloides* | 00011 | *NA* | -2.22 | 0.34 | 0.0000 | S | 38.4 | unclassified | Sordariales | | Ascomycota |
| *B. eriopoda* | 00062 | *NA* | -1.81 | 0.52 | 0.0008 | S | 3.9 | *Moniliophthora* sp. | Agaricales | | Basidiomycota |
| *B. eriopoda* | 00008 | DS250 | -0.97 | 0.35 | 0.0072 | S | 10.3 | *Paraconiothyrium brasiliense* | Pleosporales | | Ascomycota |
| *B. gracilis* | 00001 | DS1084 | -0.70 | 0.26 | 0.0075 | S | 52.6 | *Darksidea alpha* | Pleosporales | | Ascomycota |
| *B. gracilis* | 00008 | DS250 | -0.67 | 0.11 | 0.0000 | S | 13.5 | *Paraconiothyrium brasiliense* | Pleosporales | | Ascomycota |
| *A. gerardii* | 00006 | DS100 | -0.66 | 0.07 | 0.0000 | S | 12.0 | *Periconia macrospinosa* | Pleosporales | | Ascomycota |
| *A. gerardii* | 00005 | DS10 | -0.63 | 0.08 | 0.0000 | S | 14.8 | *Fusarium chlamydosporum species complex* 4-b | Hypocreales | | Ascomycota |
| *S. scoparium* | 00006 | DS100 | -0.48 | 0.07 | 0.0000 | S | 16.9 | *Periconia macrospinosa* | Pleosporales | | Ascomycota |
| *A. gerardii* | 00009 | DS1129 | -0.45 | 0.10 | 0.0000 | S | 8.4 | *Trichoderma gamsii* | Hypocreales | | Ascomycota |
| *S. scoparium* | 00005 | DS10 | -0.43 | 0.06 | 0.0000 | S | 12.5 | *Fusarium chlamydosporum species complex* 4-b | Hypocreales | | Ascomycota |
| *B. dactyloides* | 00140 | *NA* | -0.43 | 0.10 | 0.0000 | S | 2.9 | unclassified | Hypocreales | | Ascomycota |
| *A. gerardii* | 00035 | DS130 | -0.35 | 0.15 | 0.0221 | S | 3.2 | *Marasmius curreyi* | Agaricales | | Basidiomycota |
| *B. gracilis* | 00024 | DS212 | -0.31 | 0.10 | 0.0023 | S | 0.7 | *Monosporascus* sp. 1 | Sordariales | | Ascomycota |
| *S. scoparium* | 00125 | *NA* | -0.28 | 0.09 | 0.0037 | S | 0.8 | *Campanella* sp. | Agaricales | | Basidiomycota |
| *S. scoparium* | 00009 | DS1129 | -0.26 | 0.05 | 0.0000 | S | 10.8 | *Trichoderma gamsii* | Hypocreales | | Ascomycota |
| *A. gerardii* | 00023 | DS850 | -0.24 | 0.05 | 0.0000 | S | 4.2 | *Talaromyces pinophilus* | Eurotiales | | Ascomycota |
| *B. gracilis* | 00005 | DS10 | -0.23 | 0.06 | 0.0003 | S | 8.1 | *Fusarium chlamydosporum species complex* 4-b | Hypocreales | | Ascomycota |
| *S. scoparium* | 00045 | DS135 | -0.23 | 0.07 | 0.0007 | S | 1.0 | *Marasmiaceae incertae sedis* 1 | Agaricales | | Basidiomycota |
|  |  |  |  |  |  |  |  |  |  | |  |