

DATA PAPER

Disease epidemics and species interactions: A manipulation of seasonal establishment of fungal diseases in an old field

Rita L. Grunberg¹  | Fletcher W. Halliday¹  | Kayleigh R. O’Keeffe¹ |
Brooklynn N. Joyner¹ | Robert W. Heckman^{1,2}  | Charles E. Mitchell^{1,3} 

¹Department of Biology, University of North Carolina, Chapel Hill, North Carolina, USA

²Department of Integrative Biology, University of Texas at Austin, Austin, Texas, USA

³Environment, Ecology and Energy Program, University of North Carolina, Chapel Hill, North Carolina, USA

Correspondence

Rita L. Grunberg
Email: rita.grunberg@law.duke.edu

Present addresses

Rita L. Grunberg, Wilson Center for Science and Justice at Duke Law, Durham, North Carolina, USA;
Fletcher W. Halliday, Department of Botany and Plant Pathology, Oregon State University, Corvallis, Oregon, USA;
Kayleigh R. O’Keeffe, Department of Biological Sciences, Lehigh University, Bethlehem, Pennsylvania, USA;
Brooklynn N. Joyner, Department of Parks, Recreation & Tourism Management, North Carolina State University, Raleigh, North Carolina, USA; and Robert W. Heckman, US Department of Agriculture Forest Service, Rocky Mountain Research Station, Cedar City, Utah, USA.

Funding information

USDA-NIFA, Grant/Award Number: 2016-67013-25762; Swiss National Science Foundation, Grant/Award Number: PZ00P3_202027; National Science Foundation, Grant/Award Number: DEB-2308472

Handling Editor: Graziella V. DiRenzo

Abstract

Many disease epidemics recur seasonally, and such seasonal epidemics can be shaped by species interactions among parasites, pathogens, or other microbes. Field experiments are a classic approach for understanding species interactions but are rarely used to study seasonal epidemics. Our research objective was to help fill this gap by manipulating the seasonal timing of the establishment of infectious diseases while tracking epidemics and other ecological responses. To do this, we conducted a multiyear field experiment in an old field in the Piedmont of North Carolina, USA, dominated by the grass species tall fescue (*Lolium arundinaceum* (Schreb.) Darbysh). In the field, tall fescue experienced seasonal epidemics of multiple foliar fungal diseases: anthracnose in spring, brown patch in mid-summer, and crown rust in late summer to fall. In a fully randomized design, we applied four fungicide treatments to replicate plots of intact vegetation in specific seasons to manipulate the timing of disease epidemics. One treatment was designed to delay the establishment of anthracnose until mid-summer, and another to delay the establishment of both anthracnose and brown patch until fall. In a third treatment, fungicide was applied year-round, and, in a fourth treatment, fungicide was never applied. The experiment comprised 64 plots, each 2 m × 2 m, surveyed from May 2017 to February 2020. Here, we report a dataset documenting responses in the community structure of both plants and foliar fungi. To track disease prevalence in the host population across seasons and years, this dataset includes monthly leaf-level observations of the disease status of over 100,000 leaves. To quantify transmission and investigate within-host pathogen interactions, we longitudinally surveyed disease status in host individuals of known age at least weekly over two growing seasons. Finally, the dataset includes annual data on infection prevalence of the systemic fungal endophyte *Epichloë coenophiala*, community-level aboveground plant biomass, and plant community cover. These data can be used for meta-analyses, comparisons, and syntheses across systems as ecologists seek to predict and mechanistically understand seasonal disease epidemics. There are no copyrights on the dataset, and we request that users of this dataset cite this paper in all publications resulting from its use.

KEYWORDS

community assembly, disease ecology, Durham, foliar fungal pathogens, longitudinal data, monthly sampling, multiyear experiment, North Carolina, priority effects, seasonal epidemics, tall fescue

CONFLICT OF INTEREST STATEMENT

The authors declare no conflicts of interest.

DATA AVAILABILITY STATEMENT

Data are available as supporting information in Data S1 and are also available on Figshare at <https://doi.org/10.6084/m9.figshare.28057463.v3>.

ORCID

Rita L. Grunberg  <https://orcid.org/0000-0001-9926-4978>
Fletcher W. Halliday  <https://orcid.org/0000-0003-3953-0861>

Robert W. Heckman  <https://orcid.org/0000-0002-2281-3091>

Charles E. Mitchell  <https://orcid.org/0000-0002-1633-1993>

SUPPORTING INFORMATION

Additional supporting information can be found online in the Supporting Information section at the end of this article.

How to cite this article: Grunberg, Rita L., Fletcher W. Halliday, Kayleigh R. O’Keeffe, Brooklynn N. Joyner, Robert W. Heckman, and Charles E. Mitchell. 2025. “Disease Epidemics and Species Interactions: A Manipulation of Seasonal Establishment of Fungal Diseases in an Old Field.” *Ecology* 106(3): e70051. <https://doi.org/10.1002/ecy.70051>

Metadata S1

Disease epidemics and species interactions: A manipulation of seasonal establishment of fungal diseases in an old field

Rita L. Grunberg, Fletcher W. Halliday, Kayleigh R. O’Keeffe, Brooklynn N. Joyner, Robert W. Heckman, and Charles E. Mitchell

Class I. Data Set Descriptors

I.A. Data set identity: Disease epidemics and species interactions: A manipulation of seasonal establishment of fungal diseases in an old field

I.B. Data set identification codes:

Data S1.zip (includes 9 .csv files)

- monthly_disease_survey_171819.csv
- midmonthly_disease_survey_2019.csv
- plot_treatments.csv
- endophyte_prevalence_2019.csv
- plot_biomass_171819.csv
- plot_biomass_sorted_2018.csv
- plant_community_data.csv
- longitudinal_disease_survey_2017.csv
- longitudinal_disease_survey_2018.csv

Metadata S1 (this file)

I.C. Data set description

I.C.1 Originators:

Dr. Fletcher W. Halliday, Dr. Kayleigh R. O’Keeffe, and Dr. Charles E. Mitchell

I.C.2 Abstract:

Many disease epidemics recur seasonally, and such seasonal epidemics can be shaped by species interactions among parasites, pathogens, or other microbes. Field experiments are a classic approach for understanding species interactions, but are rarely used to study seasonal epidemics. Our research objective was to help fill this gap by manipulating the seasonal timing of establishment of infectious diseases while tracking epidemics and other ecological responses. To do this, we conducted a multi-year field experiment in an old field in the Piedmont of North Carolina, USA dominated by the grass species tall fescue (*Lolium arundinaceum* (Schreb). Darbysh). In the field, tall fescue experienced seasonal epidemics of multiple foliar fungal diseases: anthracnose in spring, brown patch in mid-summer, and crown rust in late summer to fall. In a fully randomized design, we applied four fungicide treatments to replicate plots of intact vegetation in specific seasons to manipulate the timing of disease epidemics. One treatment was designed to delay establishment of anthracnose until mid-summer, and another to delay the establishment of both anthracnose and brown patch until fall. In a third treatment, fungicide was applied year-round and, in a fourth treatment, fungicide was never applied. The experiment comprised 64 plots, each 2-m × 2-m, surveyed from May 2017 through February

2020. Here, we report a dataset documenting responses in community structure of both plants and foliar fungi. To track disease prevalence in the host population across seasons and years, this dataset includes monthly leaf-level observations of the disease status of over 100,000 leaves. To quantify transmission and investigate within-host pathogen interactions, we longitudinally surveyed disease status in host individuals of known age at least weekly over two growing seasons. Finally, the dataset includes annual data on infection prevalence of the systemic fungal endophyte *Epichloë coenophiala*, community-level aboveground plant biomass, and plant community cover. These data can be used for meta-analyses, comparisons, and syntheses across systems as ecologists seek to predict and mechanistically understand, seasonal disease epidemics. There are no copyrights on the dataset, and we request that users of this dataset cite this paper in all publications resulting from its use.

I.D. Key words:

Durham, North Carolina, Monthly sampling, Multi-year experiment, Disease ecology, Longitudinal data, Foliar fungal pathogens, Seasonal epidemics, Tall fescue, Priority effects, Community assembly

Class II. Research origin descriptors

II.A. Overall project description:

II.A.1 Identity:

A longitudinal dataset of disease prevalences in a population of tall fescue exposed to different fungicide regimes for three years.

II.A.2 Originators:

The original project aims were developed by Fletcher W. Halliday and Charles E. Mitchell. The experiment was designed by Fletcher W. Halliday and Kayleigh R. O’Keeffe. Disease surveys were conducted by Fletcher W. Halliday, Kayleigh R. O’Keeffe, and Brooklynn N. Joyner. Plant community surveys were conducted by Robert W. Heckman. The project was managed by Brooklynn N. Joyner and Charles E. Mitchell. Data management and cleaning were implemented by Brooklynn N. Joyner and Rita L. Grunberg. Visualizations, statistics, and synthesis of research data was conducted by Rita L. Grunberg.

II.A.3 Period of study:

Data collection occurred from May 2017 to February 2020. During this period, we conducted a monthly disease prevalence survey every 30 days. In addition, we conducted weekly longitudinal disease surveys on individually tracked tall fescue tillers in 2017 and 2018, and annual plant community surveys at the end of the growing season in 2017, 2018, and 2019.

II.A.4 Objectives:

The goal of this project was to assess the role of historical contingency in disease epidemics within a population of tall fescue. Results of a previous study in this system suggested a strong role for historical contingency in seasonal disease epidemics, in particular that epidemics of brown patch, which start in summer, may be suppressed by a priority effect of anthracnose epidemics, which start in spring and can persist through summer (Halliday et al., 2017). To test this and other potential historical contingencies, we manipulated tall fescue's history of exposure to disease using fungicide treatments that varied in duration throughout the growing season. In our system, the start of many disease epidemics were consistent across years, so fungicide treatments were started at approximately the same month each year to delay the start of certain epidemics (Halliday et al., 2017). In addition to disease data, we assayed plant diversity, plant biomass, and the presence of a mutualist endophyte of tall fescue, *Epichloë coenophiala*, in response to the fungicide treatments. These data provide information on various foliar fungal disease epidemics in tall fescue and their responses to different fungicide treatment regimens over three years. Importantly, we also provide longitudinal infection data on tracked host individuals (i.e., tall fescue tillers) along with population-level disease prevalence.

II.A.5 Abstract:

Many disease epidemics recur seasonally, and such seasonal epidemics can be shaped by species interactions among parasites, pathogens, or other microbes. Field experiments are a classic approach for understanding species interactions, but are rarely used to study seasonal epidemics. Our research objective was to help fill this gap by manipulating the seasonal timing of establishment of infectious diseases while tracking epidemics and other ecological responses. To do this, we conducted a multi-year field experiment in an old field in the Piedmont of North Carolina, USA dominated by the grass species tall fescue (*Lolium arundinaceum* (Schreb.) Darbysh). In the field, tall fescue experienced seasonal epidemics of multiple foliar fungal diseases: anthracnose in spring, brown patch in mid-summer, and crown rust in late summer to fall. In a fully randomized design, we applied four fungicide treatments to replicate plots of intact vegetation in specific seasons to manipulate the timing of disease epidemics. One treatment was designed to delay establishment of anthracnose until mid-summer, and another to delay the establishment of both anthracnose and brown patch until fall. In a third treatment, fungicide was applied year-round and, in a fourth treatment, fungicide was never applied. The experiment comprised 64 plots, each 2-m × 2-m, surveyed from May 2017 through February 2020. Here, we report a dataset documenting responses in community structure of both plants and foliar fungi. To track disease prevalence in the host population across seasons and years, this dataset includes monthly leaf-level observations of the disease status of over 100,000 leaves. To quantify transmission and investigate within-host pathogen interactions, we longitudinally surveyed disease status in host individuals of known age at least weekly over two growing seasons. Finally, the dataset includes annual data on infection prevalence of the systemic fungal endophyte *Epichloë coenophiala*, community-level aboveground plant biomass, and plant

community cover. These data can be used for meta-analyses, comparisons, and syntheses across systems as ecologists seek to predict and mechanistically understand, seasonal disease epidemics. There are no copyrights on the dataset, and we request that users of this dataset cite this paper in all publications resulting from its use.

II.A.6 Sources of funding:

This work was supported by the NSF-USDA joint program in Ecology and Evolution of Infectious Diseases (USDA-NIFA AFRI grant 2016-67013-25762). F. Halliday was supported by the Ambizione grant (PZ00P3_202027) from the Swiss National Science Foundation. R. Heckman was supported in part by the USDA Forest Service, Rocky Mountain Research Station. The findings and conclusions in this publication are those of the author and should not be construed to represent any official USDA or U.S. Government determination or policy.

II.B. Specific subproject description

II.B.1 Site description

II.B.1.a Site type: old-field grassland

II.B.1.b Geography: Widener Farm in the Duke Forest Teaching and Research Laboratory in Orange Co., North Carolina, USA (Figure 1). Latitude and longitude of experimental plots: 36 00.5370, -79 01.0841



Figure 1. Photograph of the field site with experimental plots established throughout (delineated by the white poles). Plant community surveys were conducted within an established subplot of the plot (delineated by the blue poles). Photograph taken by Brooklynn. N. Joyner.

II.B.1.c Habitat: North Carolina Piedmont old field grassland dominated by tall fescue and other perennial herbaceous plants.

II.B.1.d Geology, landform: Tilled for row crops from the mid-1950s until 1996.

II.B.1.e Watersheds, hydrology: NA

II.B.1.f Site history: This research site was originally used to grow row crops until 1996 and is now mowed annually in the summer to maintain herbaceous plant dominance.

II.B.1.g Climate: Average of 1,221 mm of annual precipitation. Detailed historic climate data for this site is available through Duke Forest Research and Teaching Lab.

II.B.2 Experimental or sampling design

II.B.2.a. Design characteristics: There are 4 fungicide application treatments that coincide with the start of the focal pathogen epidemics (Table 1, below).

Table 1. Summary of the four treatments, their timing of fungicide application, and goal of the treatment.

Treatment	Fungicide exposure	Goal
Control	Never sprayed with fungicide	Ambient disease; expose population to anthracnose first
7-month	January to July, the beginning of the brown patch epidemic	Expose the host population to anthracnose and brown patch simultaneously
9- month	January to September, the beginning of the crown rust epidemic	Expose the host population to anthracnose, brown patch, and crown rust simultaneously
Always sprayed	Year-round spraying of fungicide	Exclude disease from population

In total, there are 64 plots and each treatment is replicated in 16 plots; fungicide treatments were randomly assigned to plots (i.e., no spatial blocking). We used the non-systemic fungicide Dithane75DF Rainshield, (75% mancozeb, Dow AgroSciences, Indianapolis, Indiana, USA), applied with a backpack sprayer at the recommended rate (20 g fungicide/1 gal of water). The volume sprayed was adjusted throughout the growing season to ensure all leaves were covered with the fungicide.

These fungicide treatments were designed to manipulate the order of arrival of three foliar fungal parasites using a topical fungicide application that excluded pathogens from a plot until specific epidemics began (Table 1); this occurs roughly at two points in time – first, during July when both anthracnose and brown patch epidemics are occurring, and second, during September when crown rust epidemics start and all three pathogen epidemics overlap in the host population. The time for ceasing fungicide application in a treatment to manipulate exposure was based on data from Halliday *et al.* (2017).

DISEASE DATA: From this experiment, we collected various types of infection data:

(1) **monthly prevalence** surveys for all plots (file name: monthly_disease_survey_171819),

- **PREVALENCE DATA, MONTHLY:** Approximately every 30 days a prevalence survey was conducted in all 64 plots of the experiment. Within each plot, 20 random resident tillers (i.e., individual grass shoots) were visually inspected for disease symptoms. Data range from May 2017 to February 2020. In a few cases, this “monthly” survey cycle of approximately 30 days led to a calendar month with no survey (e.g., November 2019) because surveys were conducted immediately before and after that month. There was no December 2017 prevalence survey.

(2) **mid-monthly** surveys in 2019 (file name: midmonthly_disease_survey_2019), and

- **PREVALENCE DATA, MIDMONTHLY:** In the fall of 2019, three “mid-monthly” surveys were conducted at a smaller scale to get a better resolution of ongoing pathogen epidemics. Our aim was to document a more precise arrival of brown patch and crown rust. Every ~15 days we conducted an additional prevalence survey of 10 random tillers per plot. These mid-monthly surveys were conducted in August, October, and November 2019.

(3) **longitudinal** surveys on tracked plants (file name: longitudinal_disease_survey_2017, longitudinal_disease_survey_2018).

- **LONGITUDINAL DATA:** In 2017, sentinel outplants were deployed into resident vegetation throughout the plots for surveying on a weekly basis. They were deployed in 3 waves, or cohorts, to coincide with the arrival of the *Rhizoctonia* and *Puccinia* epidemics following Halliday *et al.* (2017). One tiller (i.e., individual grass shoot) on each outplant was surveyed weekly for fungal and herbivory damage; every leaf on the tiller was surveyed until the leaf naturally senesced. Thus, we have longitudinal infection data for each leaf on a marked tiller. Surveys began in July 2017 and ended November 2017. After the last survey, the tiller of the plant was collected to be tested for *Epichloë coenophiala* presence and the aboveground biomass was collected. The seed for the outplants was standard cultivar KY-31 provided by Rebecca McCulley at the University of Kentucky (received in May 2017). In 2018, we marked resident tillers (i.e., individual grass shoots) and conducted disease surveys on a weekly basis.

When surveys detected a brown patch lesion, that tiller was harvested to build a culture collection of *Rhizoctonia solani* (for a separate project on *Rhizoctonia* population genetics). Otherwise, each leaf on each tiller was tracked until it died or until the season's final survey.

ENDOPHYTE DATA: Along with disease prevalence data, we collected data on the prevalence of the mutualistic, vertically transmitted, systemic fungal endophyte, *Epichloë coenophiala*, in 2019. Ten tillers were collected from each of the 64 plots during the first week of November in 2019 (Nov 4-8th); prevalence was estimated as the proportion of tillers that tested positive for *Epichloë*.

PLANT COMMUNITY DATA: Towards the end of each growing season (October or November), we conducted plant community surveys in each plot. The cover of all plant species plus litter and bare ground was visually estimated within a 0.75-m $\times$ 0.75-m permanent quadrat in each plot. Plant community surveys were conducted on 9 November 2017, 10 October 2018, and 10 October 2019 by R. Heckman.

PLANT BIOMASS DATA: At the end of the growing season, total above-ground biomass was collected from each plot. Methodology for obtaining biomass samples differed each year (see section II.B.3.a).

II.B.2.b. Permanent plots: There are 64 plots arranged in a 4 $\times$ 16 array. These plots are 2-m $\times$ 2-m and each plot is separated by 1 m with a 2-m mowed buffer surrounding the entire experimental area (Figure 2, below).

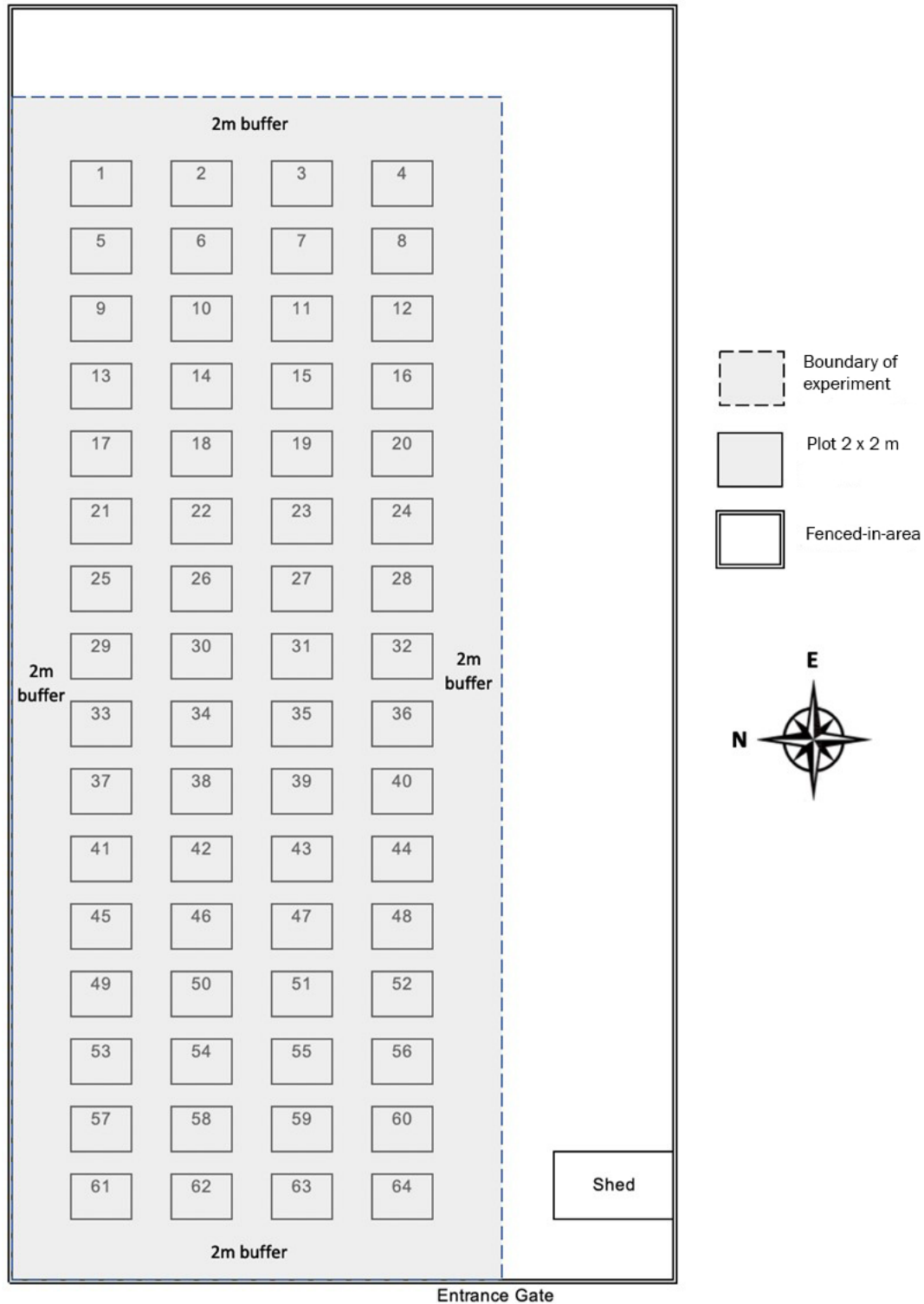


Figure 2. Map of the 64 experimental plots and their spatial arrangement. Plots are labeled 1–64, which correspond to their plot ID in data files.

II.B.2.c. Data collection period, frequency, etc.: The frequency of data collection varied per each aim of the project (described below in section II.B.3.a). The core dataset consists of a monthly disease survey for three years.

II. B.3 Research methods

II.B.3.a Field/laboratory:

For disease surveys (i.e., all Disease Data in section 2.a), disease symptoms were visually assessed on each living leaf within a tiller (i.e., individual grass shoot). A leaf was considered living until 90% of its tissue senesced. Leaves were identified relative to each other, where the outermost leaf (leaf ID = 1) is the oldest and the innermost leaf is the youngest (leaf ID = greatest numeric value) (Figure 3). Beginning with the oldest leaf, we recorded pathogen and herbivory damage present in the living part of the leaf. Lesions or damages in senesced tissue were not recorded.

Plot-level disease surveys (Prevalence all treatments, Disease Data) included randomly sampling 20 tillers per plot (Figure 4).

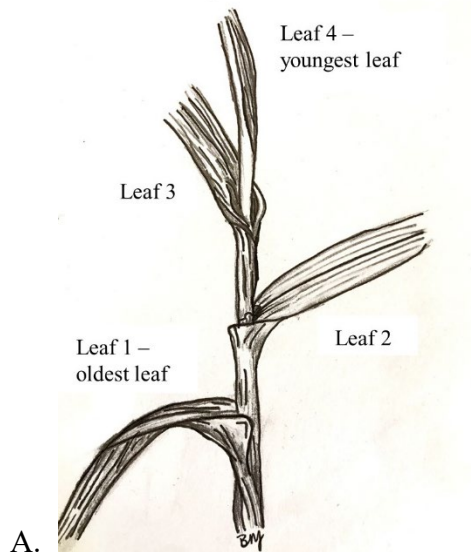


Figure 3. Diagram showing leaf ID within a tiller. The oldest is leaf 1 and the youngest is leaf 4. Drawn by Brooklynn N. Joyner.

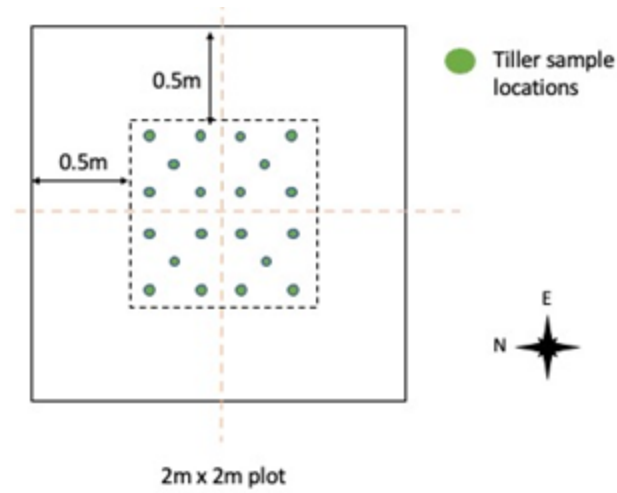


Figure 4. Diagram for systematic random sampling of tillers within experimental plots.

Marked tillers for the longitudinal disease data were tagged using a plastic band placed just below the oldest living leaf on the tiller – all leaves above the band were living and all leaves below the band were senesced. All leaves on the tiller were surveyed for disease as per the monthly disease surveys. If the tiller died, we recorded a putative cause of death (e.g., disease, rodent, drought) and selected a new tiller to survey. For resident tillers selected in plots (2018 longitudinal data), we located an existing tiller that is closest in proximity, in any direction, to the tiller that died. We removed the band from the dead tiller and placed it below the oldest living leaf on the new tiller. A new Tiller ID was assigned. For outplants growing in pots (2017 longitudinal data), we randomly picked another tiller in the pot for tracking, here we removed the plastic ID band from the dead tiller and placed it below the oldest living leaf on the new tiller. Because the fescue plant was in a pot, we knew that all the tillers were from the same individual, so we assigned a new tiller ID, but not a new plant ID.

Epichloë coenophiala infection status (i.e., Endophyte data in section 2.a) was assayed using an immunoblot assay (Agrinostics Ltd. Co, Watkinsville, GA, USA) following directions by the manufacturer. To assess infection, tillers were harvested from the field, put on ice, and stored in -20 °C freezer until processed in the lab. A 1.6 to 3.2-mm-thick cross-section taken from about 3.2 mm from the base of the stored tiller was used in the immunoblot assay.

For the plant community data (Plant community data in section 2.a), we measured the absolute cover of every plant species independently from each other since plants may overlap spatially. Thus, total cover within a plot can exceed 100% in plots.

The method of collecting biomass (Biomass data in section 2.a) differed between years. Specifically, we varied the area of the harvested sample and whether or not biomass was sorted into different functional groups or left unsorted. In 2017, a 0.75-m × 0.75-m (total area 0.5625 m²) subplot was created in the southeast corner of each plot. For estimating biomass, all the

vegetation rooted within the subplot was harvested, oven-dried, and weighed together. In 2018, two 0.10-m² rectangular “strips” were harvested for biomass, resulting in a total of 0.20 m² of harvested area per plot. Biomass from each strip was sorted, oven-dried, and weighed as one of the following categories: fescue, non-fescue monocots, woody dicots, non-woody dicots, dead material of any kind. In 2019, two 0.10-m² rectangular strips were harvested for biomass, but their placement was rotated 90° from the 2018 locations. Biomass was harvested, oven-dried, and weighed together. Biomass was not sorted/categorized in 2017 and 2019. Raw biomass values were converted into units of g per m² by dividing the raw biomass (in g) by the area sampled that year (0.5625 m² in 2017 and 0.2 m² in 2018 and 2019).

II.B.3.b Instrumentation: N/A

II.B.3.c Taxonomy and systematics: Fungal diseases were identified using Smiley *et al.* 2005 Compendium of Turfgrass Diseases, Third Edition: <https://doi.org/10.1094/9780890546154> References for taxonomic keys, identification, and location of voucher specimens, etc.

II.B.3.d Permit history: This experiment was approved by Duke Forest under research registration number: R1617-434.

II.B.4 Project personnel: Principal investigators of project: Fletcher Halliday, Kayleigh O’Keeffe, and Charles E. Mitchell. Primary funding source principal investigators: Iganizio Carbone, Corbin Jones, James Umbanhowar, and Charles E. Mitchell; Technicians: Anita Simha, Matthew Carey, Julie Long, Storm Crews, Charles Muirhead, Julia Knorr, Ryan Cook; Supervisors: Brooklynn N. Joyner; Students: Fletcher Halliday, Kayleigh O’Keeffe, Anita Simha, Brandon Wheeler, Jordan Link, Claire Thefaine, Safiyyah Motaib; Postdoctoral researchers: Rita Grunberg, Fletcher Halliday, Robert Heckman; Secondary funding source investigators: Fletcher Halliday, Robert Heckman

Class III. Data set status and accessibility

III.A Status

III.A.1 Latest update: 07-Oct-2024

III.A.2 Latest archive date: 07-Oct-2024

III.A.3 Metadata status: Latest update was upon submission 07-Oct-2024

III.A.4 Data verification: Completed 07-Oct-2024

III.B Accessibility

III.B.1 Storage location and medium: These data are available as supporting information to the Ecology data paper (in Data S1) and are also available on Figshare at <https://doi.org/10.6084/m9.figshare.28057463.v3>.

III.B.2 Contact person: Dr. Charles E. Mitchell, University of North Carolina at Chapel Hill Department of Biology, mitchell@bio.unc.edu

III.B.3 Copyright restrictions: None

III.B.4 Proprietary restrictions: Please cite this data-paper when using its data in publications. We request that researchers inform us of how they are using this data.

III.B.5 Costs: None.

Class IV. Data structural descriptors

The data set includes 9 files that are in DataS1.zip. The zip folder contains:

1. [monthly_disease_survey_171819.csv] the monthly disease surveys for 2017, 2018, 2019 in the 64 experimental plots
2. [midmonthly_disease_survey_2019.csv] the midmonthly disease survey for 2019
3. [plot_treatments.csv] contains information on the plot location and fungicide application
4. [endophyte_prevalence_2019.csv] prevalence of the endophyte, *Epichloë coenophiala*, in 2019
5. [plot_biomass_171819.csv] total plot biomass for 2017, 2018, 2019
6. [plot_biomass_sorted_2018.csv] plant community biomass in 2018. This includes the sorted biomass data
7. [plant_community_data.csv] updated version of the plant species absolute cover data from 64 plots for 2017, 2018, 2019.
8. [longitudinal_disease_survey_2017.csv] longitudinal disease data on outplants in 2017
9. [longitudinal_disease_survey_2018.csv] longitudinal disease data on resident plants in 2018.

IV.A Data set file

Identity: monthly_disease_survey_171819.csv

Size: 20 columns and 116,693 records, including header row, 10,583 KB.

Format and storage mode: Comma-separated values (.csv)

Header information: See column descriptions in section B.

Alphanumeric attributes: Mixed.

Special characters/fields: Missing information was classified as “NA” in each cell.

Identity: midmonthly_disease_survey_2019.csv

Size: 20 columns and 6,401 records, including header row, 460 KB.

Format and storage mode: Comma-separated values (.csv)

Header information: See column descriptions in section B.

Alphanumeric attributes: Mixed.

Special characters/fields: Missing information was classified as “NA” in each cell.

Identity: plot_treatments.csv

Size: 4 columns and 65 records, including header row, 2 KB.

Format and storage mode: Comma-separated values (.csv)

Header information: See column descriptions in section B.

Alphanumeric attributes: Mixed.

Special characters/fields: Missing information was classified as “NA” in each cell.

Identity: endophyte_prevalence_2019.csv

Size: 12 columns and 64 records, including header row, 3 KB.

Format and storage mode: Comma-separated values (.csv)

Header information: See column descriptions in section B.

Alphanumeric attributes: Mixed.

Special characters/fields: Missing information was classified as “NA” in each cell.

Identity: plot_biomass_171819.csv

Size: 3 columns and 193 records, including header row, 5 KB.

Format and storage mode: Comma-separated values (.csv)

Header information: See column descriptions in section B.

Alphanumeric attributes: Mixed.

Special characters/fields: Missing information was classified as “NA” in each cell.

Identity: plot_biomass_sorted_2018.csv

Size: 7 columns and 65 records, including header row, 4 KB.

Format and storage mode: Comma-separated values (.csv)

Header information: See column descriptions in section B.

Alphanumeric attributes: Mixed.

Special characters/fields: Missing information was classified as “NA” in each cell.

Identity: plant_community_data.csv

Size: 46 columns and 193 records, including header row, 22 KB.

Format and storage mode: Comma-separated values (.csv)

Header information: See column descriptions in section B.

Alphanumeric attributes: Mixed.

Special characters/fields: Missing information was classified as “NA” in each cell.

Identity: longitudinal_disease_survey_2017.csv

Size: 17 columns and 35,957 records, including header row, 2,597KB.

Format and storage mode: Comma-separated values (.csv)

Header information: See column descriptions in section B.

Alphanumeric attributes: Mixed.

Special characters/fields: Missing information was classified as “NA” in each cell.

Identity: longitudinal_disease_survey_2018.csv

Size: 22 columns and 46,054 records, including header row, 3,327 KB.

Format and storage mode: Comma-separated values (.csv)

Header information: See column descriptions in section B.

Alphanumeric attributes: Mixed.

Special characters/fields: Missing information was classified as “NA” in each cell.

IV.B Variable information

Table 2. List of column headers and definitions for monthly_disease_survey_171819.csv and midmonth_disease_survey_2019.csv

Variable identity	Variable definition	Units of measurement
month	Approximate month of disease survey, note that surveys occurred approx. every 30 days.	month, character
year	year of disease survey	year, numeric
plot	unique experimental plot ID, 1-64	ID, character
survey_date	Exact date of survey	month-day-year
fungicide	Duration of fungicide exposure treatments (see table 1 for more info on treatments)	character
plant	numeric order of plants surveyed (1-20 per plot, these do not refer to a unique ID, as plants were randomly sampled in the population; see Figure 4 for example)	numeric
leaf	number of leaf surveyed, 1 is the oldest	numeric
damage	Describes if there is damage on the leaf, either due to disease or herbivory	D: damaged, ND: no damage, S: senesced between surveys
anthracnose	anthracnose symptoms, caused chiefly by <i>Colletotrichum cereale</i>	presence (1) or absence (0)
crown_rust	crown rust symptoms, caused by <i>Puccinia coronata</i>	presence (1) or absence (0)
brown_patch	brown patch symptoms, caused by <i>Rhizoctonia solani</i>	presence (1) or absence (0)
smut	leaf smut symptoms	presence (1) or absence (0)
gl	grey leaf spot symptoms	presence (1) or absence (0)
rrust	red rust symptoms, caused by <i>Puccinia graminis</i>	presence (1) or absence (0)

sclerotinia	sclerotinia symptoms	presence (1) or absence (0)
tml	Tiny Mystery Lesion. Symptom of an unknown fungal pathogen.	presence (1) or absence (0)
scrape	scraping damage; most scaping damage appeared to be from mollusks and beetles	presence (1) or absence (0)
mining	leaf mining	presence (1) or absence (0)
mech	mechanical damage, including damage from mowing	presence (1) or absence (0)
chlo	presence of chlorosis	presence (1) or absence (0)

Table 3. List of column headers and definitions for plot_treatments.csv

Variable identity	Variable definition	Units of measurement
plot	unique experimental plot ID, plotID_1-64. Refer to plot map (Figure 2).	ID, character
row	row ID within the experimental area	Row ID, numeric
column	column ID within the experimental area	Column ID, numeric
fungicide	duration of fungicide exposure	treatment, character

Table 4. List of column headers and definitions for epichloe_prevalence.csv

Variable identity	Variable definition	Units of measurement
plot	unique experimental plot ID, plotID_1-64	ID, character
tiller_a	Tiller A <i>Epichloë</i> infection status	presence (1) or absence (0)
tiller_b	Tiller B <i>Epichloë</i> infection status	presence (1) or absence (0)
tiller_c	Tiller C <i>Epichloë</i> infection status	presence (1) or absence (0)
tiller_d	Tiller D <i>Epichloë</i> infection status	presence (1) or absence (0)
tiller_e	Tiller E <i>Epichloë</i> infection status	presence (1) or absence (0)
tiller_f	Tiller F <i>Epichloë</i> infection status	presence (1) or absence (0)
tiller_g	Tiller G <i>Epichloë</i> infection status	presence (1) or absence (0)
tiller_h	Tiller H <i>Epichloë</i> infection status	presence (1) or absence (0)
tiller_i	Tiller I <i>Epichloë</i> infection status	presence (1) or absence (0)

tiller_j	Tiller J <i>Epichloë</i> infection status	presence (1) or absence (0)
epichloe_prevalence	overall plot level prevalence of <i>Epichloë</i>	Percentage of plants infected with <i>Epichloë</i>

Table 5. List of column headers and definitions for plot_biomass_171819.csv

Variable identity	Variable definition	Units of measurement
plot	unique experimental plot ID, plotID_1-64	ID, character
year	year biomass sample was measured	year, numeric
total_biomass	estimated plot biomass per square meter	g dried above-ground biomass per m ²

Table 6. List of column headers and definitions for plot_biomass_sorted2018.csv

Variable identity	Variable definition	Units of measurement
plot	unique experimental plot ID, plotID_1-64	ID, character
year	year biomass sample was measured	year, numeric
dead	leaf litter in plot	g per m ²
fescue	fescue biomass in plot	g per m ²
monocots	non-fescue monocot biomass in plot	g per m ²
dicots	non-woody dicot biomass in plot	g per m ²
woody	woody biomass in plot	g per m ²

Table 7. List of column headers and definitions for plant_community_data.csv

Variable identity	Variable definition	Units of measurement
plot	unique experimental plot ID, plotID_1-64	ID, character
year	year plant community sampled	year, numeric
Acalypha.sp.	cover of unique plant species in plot	absolute cover, percentage
Allium.vineale	cover of unique plant species in plot	absolute cover, percentage
Andropogon.virginicus	cover of unique plant species in plot	absolute cover, percentage
Anthoxanthum.odoratum	cover of unique plant species in plot	absolute cover, percentage
Apocynum.cannabinum	cover of unique plant species in plot	absolute cover, percentage
Celtis.laevigata	cover of unique plant species in plot	absolute cover, percentage

Conyza.canadensis	cover of unique plant species in plot	absolute cover, percentage
Cynodon.dactylon	cover of unique plant species in plot	absolute cover, percentage
Daucus.carota	cover of unique plant species in plot	absolute cover, percentage
Desmodium.sp.	cover of unique plant species in plot	absolute cover, percentage
Digitaria.sanguinalis	cover of unique plant species in plot	absolute cover, percentage
Eragrostis.capillaris	cover of unique plant species in plot	absolute cover, percentage
Fraxinus.sp.	cover of unique plant species in plot	absolute cover, percentage
Holcus.lanatus	cover of unique plant species in plot	absolute cover, percentage
Houstonia.sp.	cover of unique plant species in plot	absolute cover, percentage
Ipomoea.sp.	cover of unique plant species in plot	absolute cover, percentage
Juncus.sp.	cover of unique plant species in plot	absolute cover, percentage
Juniperus.virginiana	cover of unique plant species in plot	absolute cover, percentage
Lespedeza.cuneata	cover of unique plant species in plot	absolute cover, percentage
Litter	cover of unique plant species in plot	absolute cover, percentage
Lolium.arundinaceum	cover of unique plant species (tall fescue) in plot	absolute cover, percentage
Lonicera.japonica	cover of unique plant species in plot	absolute cover, percentage
Oxalis.dillenii	cover of unique plant species in plot	absolute cover, percentage
Parthenocissus.quinquefolia	cover of unique plant species in plot	absolute cover, percentage
Paspalum.dilatatum	cover of unique plant species in plot	absolute cover, percentage
Paspalum.notatum	cover of unique plant species in plot	absolute cover, percentage
Pinus.taeda	cover of unique plant species in plot	absolute cover, percentage
Plantago.aristata	cover of unique plant species in plot	absolute cover, percentage
Plantago.lanceolata	cover of unique plant species in plot	absolute cover, percentage
Poa.pratensis	cover of unique plant species in plot	absolute cover, percentage
Ranunculus.sp.	cover of unique plant species in plot	absolute cover, percentage
Rosa.multiflora	cover of unique plant species in plot	absolute cover, percentage
Rubus.argutus	cover of unique plant species in plot	absolute cover, percentage
Setaria.parviflora	cover of unique plant species in plot	absolute cover, percentage
Solanum.carolinense	cover of unique plant species in plot	absolute cover, percentage
Sorghum.halepense	cover of unique plant species in plot	absolute cover, percentage
Steinchisma.hians	cover of unique plant species in plot	absolute cover, percentage
Toxicodendron.radicans	cover of unique plant species in plot	absolute cover, percentage
Tridens.flavus	cover of unique plant species in plot	absolute cover, percentage
Tripsacum.dactyloides	cover of unique plant species in plot	absolute cover, percentage
Unknown Asteraceae 1	cover of unique plant species in plot	absolute cover, percentage
Unknown Fabaceae 1	cover of unique plant species in plot	absolute cover, percentage
Verbesina.occidentalis	cover of unique plant species in plot	absolute cover, percentage
Vitis.sp.	cover of unique plant species in plot	absolute cover, percentage

--	--	--

Table 8. List of column headers and definitions for longitudinal_disease_survey_2017.csv

Variable identity	Variable definition	Units of measurement
outplant	ID number for outplants in the 2017 survey	Identifier, character
tiller_number	The number of the tiller sampled in a given outplant. As tillers senesced and a new tiller of the plant is tracked, it is assigned a new tiller ID of 2, 3, and so on. Use outplant + tiller_number as unique identifier, as many outplants will have data from multiple tillers.	Identifier, character
plot	unique experimental plot ID, plotID_1-64. Refer to plot map (Figure 2).	Identifier, character
plotloc2017	Location of surveyed tiller in plot.	Identifier, character
survey_date	date of survey	month-date-year
popgen	Identified if tiller was harvested for <i>Rhizoctonia</i> population genetics project	Yes = harvested, No = not harvested
leaf	Leaf ID	Numeric, leaf number corresponds to order within tiller
damage	Describes if there is damage on the leaf, either due to disease or herbivory	D: damaged, ND: no damage, S: senesced between surveys
anthracnose	anthracnose symptoms, caused chiefly by <i>Colletotrichum cereale</i>	presence (1) or absence (0)
crown_rust	crown rust symptoms, caused by <i>Puccinia coronata</i>	presence (1) or absence (0)
brown_patch	brown patch symptoms, caused by <i>Rhizoctonia solani</i>	presence (1) or absence (0)

mech	mechanical damage, including mowing	presence (1) or absence (0)
gls	grey leaf spot symptoms	presence (1) or absence (0)
rrust	red rust symptoms, caused by <i>Puccinia graminis</i>	presence (1) or absence (0)
unk1	fungal lesion not identified, just identified as something that didn't look like any of the other pathogens in our study. Unfortunately, there is no description or photo.	presence (1) or absence (0)
chew	evidence of chewing herbivory	presence (1) or absence (0)
scrape	scraping damage; most scaping damage appeared to be from mollusks and beetles	presence (1) or absence (0)

Table 9. List of column headers and definitions for longitudinal_disease_survey_2018.csv

Variable identity	Variable definition	Units of measurement
plot	unique experimental plot ID, plotID_1-64. Refer to plot map (Figure 2).	Identifier, character
plotloc2018	Location of surveyed tiller in plot.	Identifier, character
tiller	Tiller ID. IDs for resident plants begin as tillers 1 - 1152. Once a tiller has died and is replaced with a new tiller, an ID beginning in the 3000s is assigned. "new tiller" ID's range from 3000-3059, with #s 3016 & 3017 unintentionally being skipped. Combine PlotLoc and ID data for unique tiller IDs.	Identifier, character
survey_date	date of survey	month-day-year
popgen	Identified if tiller was harvested for <i>Rhizoctonia</i> population genetics project	yes = used for pop gen; no = not used for pop gen
leaf	Leaf ID	numeric
damage	Describes if there is damage on the leaf, either due to disease or herbivory	D: damaged, ND: no damage, S: senesced between surveys
chew	evidence of chewing herbivory	presence (1) or absence (0)
scrape	scraping damage; most scaping damage appeared to be from mollusks and beetles	presence (1) or absence (0)

mech	mechanical damage, including damage from mowing	presence (1) or absence (0)
anthracnose	anthracnose symptoms, caused by <i>Colletotrichum cereale</i>	presence (1) or absence (0)
crown_rust	crown rust symptoms, caused by <i>Puccinia coronata</i>	presence (1) or absence (0)
brown_patch	brown patch symptoms, caused by <i>Rhizoctonia solani</i>	presence (1) or absence (0)
chlo	presence of chlorosis	presence (1) or absence (0)
lw	Leaf Wetting damage, could be associated with fungal or bacterial infections	presence (1) or absence (0)
smut	Stripe Smut fungus	presence (1) or absence (0)
gls	grey leaf spot symptoms	presence (1) or absence (0)
sclerotinia	sclerotinia symptoms	presence (1) or absence (0)
rrust	red rust symptoms, caused by <i>Puccinia graminis</i>	presence (1) or absence (0)
os	Orange Spot damage. An orange spot/lesion that was differentiated from Chlorosis and anthracnose. Identified separately until the Plant Disease and Insect Clinic at NCSU clarified that it was not caused by a pathogen and is most likely some type of chlorosis from stress or leaf senescence.	presence (1) or absence (0)
tml	Tiny Mystery Lesion. Symptom of an unknown fungal pathogen.	presence (1) or absence (0)
P-side	Pesticide residue present on leaves	presence (1) or absence (0)

IV.B.1 Variable identity: see tables 2-9

IV.B.2 Variable definition: see tables 2-9

IV.B.3 Units of measurement: see tables 2-9

IV.B.4 Data type

IV.B.4.a Storage type: Mixed.

IV.B.4.b. List and definition of variable codes: See variable information tables 2-9.

IV.B.4.c. Range for numeric values:

- Plant species cover ranges from zero to one hundred for absolute cover (plant_community_data.csv)
- Plant community biomass data ranges from 302.667 grams to 2319.000 grams (plot_biomass_171819.csv)
- Sorted plant community biomass data ranges from 0.00 grams to 990.700 grams (plot_biomass_sorted2018.csv)

IV.B.4.d. Missing value codes: NA indicates missing data

IV.B.4.e. Precision: Balance precision for biomass data

IV.B.5 Data format

IV.B.5.a Fixed, variable length

IV.B.5.b Columns: Start column, end column

IV.B.5.c Number of decimal places: The only decimal data are the biomass data (plot_biomass_171819.csv and plot_biomass_sorted2018.csv). Owing to a communication error, biomass values in 2019 were recorded as integers, so no decimals are reported in those data. All other biomass data are reported to two decimal places. Note that final decimals of zero may not appear when opening the data in some software packages.

IV.C. Data anomalies: NA

Class V. Supplemental descriptors

V.A. Data acquisition

V.A.1. Data forms or acquisition methods: Data collections methods are described in section Class II.B.3

V.A.2. Location of completed data forms: Scanned data sheets are stored within a local repository and hard copies are stored within the Mitchell Lab at the University of North Carolina at Chapel Hill. Please contact Dr. Charles Mitchell for access.

V.A.3. Data entry verification procedures: All datasets were manually checked under the supervision of Brooklynn Joyner. Manual checks were performed on any missing, duplicate, and errors in data entry. A hard copy of field data was checked against our computer copy when errors were found and any changes to the data were documented in the Mitchell Lab repository.

V.B. Quality assurance/quality control procedures: Distributions of the raw data were visualized to check for outliers and summary data descriptions (e.g., means, maxima, minima)

were also quantified. Outliers were not removed from the dataset, but were visually inspected to determine if they were erroneous. We did not identify any erroneous outliers.

V.C. Related materials: Associated photographs of *Epichloë* immunoblot assays (for endophyte prevalence data) and scanned versions of the raw data are stored in Mitchell Lab repository and are available upon request.

V.D. Computer programs and data-processing algorithms: N/A

V.E. Archiving

V.E.1. Archival procedures: All datasets are archived on FigShare (Grunberg et al. 2024) at <https://doi.org/10.6084/m9.figshare.28057463.v2>

V.E.2 Redundant archival sites: The dataset was also archived in the Mitchell Lab local repository in .CSV format.

V.F. Publications and results:

V.F.1. Disease decreases variation in host community structure in an old-field grassland
<https://doi.org/10.1101/2022.08.15.503989>

V.G. History of data set usage

V.G.1. Data request history: None.

V.G.2. Data set update history: None.

V.G.3. Review history: The data has been reviewed by Brooklynn Joyner and Rita Grunberg.

V.G.4. Questions and comments from secondary users: None.

Literature Citations

Grunberg, Rita, Fletcher W. Halliday, Kayleigh R. O'Keeffe, Brooklynn N. Joyner, Robert W. Heckman, and Charles E. Mitchell. 2024. "Data: Disease Epidemics and Species Interactions: A Manipulation of Seasonal Establishment of Fungal Diseases in an Old Field". figshare. doi:10.6084/m9.figshare.28057463.v3.

Halliday, F.W., Umbanhowar, J. & Mitchell, C.E. (2017). Interactions among symbionts operate across scales to influence parasite epidemics. *Ecol. Lett.*, 20, 1285–1294.

Smiley, R.W., Dernoeden, P.H. & Clarke, B.B. (2005). *Compendium of Turfgrass Diseases, Third Edition. Compend. Turfgrass Dis. Third Ed.* American Phytopathological Society.