

<sup>1</sup> Increasing prevalence of plant-fungal symbiosis across two  
<sup>2</sup> centuries of environmental change

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## Abstract

Species' distributions and abundances are shifting in response to ongoing global climate change. Mutualistic microbial symbionts can provide hosts with protection from environmental stress that may promote resilience under environmental change, however this change may also disrupt species interactions and lead to declines in hosts and/or symbionts. Symbionts preserved within natural history specimens offer a unique opportunity to quantify changes in microbial symbiosis across broad temporal and spatial scales. We asked how the prevalence of seed-transmitted fungal symbionts of grasses (*Epichloë* endophytes) has changed over time in response to climate change, and how these changes vary across host species' distributions. Specifically, we examined 2,346 herbarium specimens of three grass host species (*Agrostis hyemalis*, *Agrostis perennans*, *Elymus virginicus*) collected over the past two centuries (1824 – 2019) for the presence or absence of *Epichloë* symbiosis. Analysis of an approximate Bayesian spatially-varying coefficients model revealed that endophytes increased in prevalence over the last two centuries from ca. 25% to ca. 75% prevalence, on average, across three host species. Changes in seasonal climate drivers were associated with increasing endophyte prevalence. Notably, increasing precipitation during the peak growing season for *Agrostis* species and decreasing precipitation for *E. virginicus* were associated with increasing endophyte prevalence. Changes in the variability of precipitation and temperature during off-peak seasons were also important predictors of increasing endophyte prevalence. Our model performed favorably in an out-of-sample predictive test with contemporary survey data from across 63 populations, a rare extra step in collections-based research. However, there was greater local-scale variability in endophyte prevalence in contemporary data compared to model predictions, suggesting new directions that could improve predictive accuracy. Our results provide novel evidence for a cryptic biological response to climate change that may contribute to the resilience of host-microbe symbiosis through fitness benefits to symbiotic hosts.

## Introduction

38 Understanding how biotic interactions are altered by global change is a major goal of basic and  
39 applied ecological research (Blois et al., 2013; Gilman et al., 2010). Documented responses to envi-  
40 ronmental change, such as shifts in species' distributions (Aitken et al., 2008) and phenology (Piao  
41 et al., 2019), are typically blind to concurrent changes in associated biotic interactions. Empirically  
42 evaluating these biotic changes – whether interacting species shift in tandem with their partners  
43 or not (HilleRisLambers et al., 2013) – is crucial to predicting the reorganization of Earth's biodi-  
44 versity under global change. Such evaluations have been limited because few datasets on species  
45 interactions extend over sufficiently long time scales of contemporary climate change (Poisot et al.,  
46 2021).

47 Natural history specimens, which were originally collected to document and preserve taxonomic  
48 diversity, present a unique opportunity to explore long-term changes in biodiversity and ecological  
49 interactions across broad spatial and temporal scales (Davis, 2023; Meineke et al., 2018). Natural  
50 history collections, built and maintained by the efforts of thousands of scientists, are invaluable  
51 time machines, primarily comprised of physical specimens of organisms along with information  
52 about the time and place of their collection. These specimens often preserve physical legacies  
53 of ecological processes and species' interactions from dynamically changing environments across  
54 time and space (Lendemer et al., 2020). For example, previous researchers have examined the  
55 flowers, pollen grains, and leaves of specimens within plant collections (herbaria) to document shifts  
56 in reproductive phenology (Berg et al., 2019; Park et al., 2019; Willis et al., 2017), pollination  
57 (Duan et al., 2019; Pauw and Hawkins, 2011), and herbivory (Meineke et al., 2019) related to  
58 anthropogenic climate change. Herbarium specimens have also been used to identify the origins  
59 and population genomics of plant diseases such as *Phytophthora*, the Irish potato famine pathogen  
60 (Ristaino et al., 2001; Ristaino, 2002; Yoshida et al., 2013), and have been proposed as vehicles  
61 to track other emerging plant pathogens (Bradshaw et al., 2021; Ristaino, 2020). However, few  
62 previous studies have leveraged biological collections to examine climate change-related shifts in a

63 particularly common type of interaction: mutualistic microbial symbiosis.

64 Microbial symbionts are common to all macroscopic organisms and can have important effects  
65 on their hosts' survival, growth and reproduction (McFall-Ngai et al., 2013; Rodriguez et al., 2009).  
66 Many microbial symbionts act as mutualists, engaging in reciprocally beneficial interactions with  
67 their hosts in ways that can ameliorate environmental stress. For example, bacterial symbionts of  
68 insects, such as *Wolbachia*, can improve their hosts' thermal tolerance (Reno et al., 2019; Truitt  
69 et al., 2019), and arbuscular mycorrhizal fungi, documented in 70-90% of families of land plants  
70 (Parniske, 2008), allow their hosts to persist through drought conditions by improving water and  
71 nutrient uptake (Cheng et al., 2021). On the other hand, changes in the mean and variance of  
72 environmental conditions may disrupt microbial mutualisms by changing the costs and benefits  
73 of the interaction for each partner in ways that can cause the interaction to deteriorate (Aslan  
74 et al., 2013; Fowler et al., 2024). Coral bleaching (the loss of symbiotic algae) due to temperature  
75 stress (Sully et al., 2019) is perhaps the best known example, but this phenomenon is not unique  
76 to corals. Lichens exposed to elevated temperatures experienced loss of photosynthetic function  
77 along with changes in the composition of their algal symbiont community (Meyer et al., 2022).  
78 How commonly and under what conditions microbial mutualisms deteriorate or strengthen under  
79 climate change remain unanswered questions (Frederickson, 2017). Previous work suggests that  
80 these alternative responses may depend on the intimacy and specialization of the interaction as well  
81 as the physiological tolerances of the mutualist partners (Rafferty et al., 2015; Toby Kiers et al.,  
82 2010; Warren and Bradford, 2014).

83 Understanding how microbial symbioses are affected by climate change is additionally compli-  
84 cated by spatial heterogeneity in the direction and magnitude of environmental change (IPCC, 2021).  
85 Beneficial symbionts are likely able to shield their hosts from environmental stress in locations that  
86 experience a small degree of change, but symbionts in locations that experience changes of large  
87 magnitude may be pushed beyond their physiological limits (Webster et al., 2008). Additionally,  
88 symbionts are often unevenly distributed across their host's distribution. Facultative symbionts  
89 may be absent from portions of the host range (Afkhami et al., 2014), and hosts may engage with

90 a diversity of partners (different symbiont species or locally-adapted strains) across environments  
91 (Fowler et al., 2023; Fraude et al., 2008; Rolshausen et al., 2018). Identifying broader spatial trends  
92 in symbiont prevalence is therefore an important step in developing predictions for where to expect  
93 changes in the symbiosis in future climates.

94 *Epichloë* fungal endophytes are specialized symbionts of cool-season grasses, estimated from  
95 surveys to associate with ~ 20 – 30% of species across the diverse Poaceae family (Leuchtmann,  
96 1992). Within the cool-season grass subfamily (Pooideae), it has been estimated that between 17%  
97 to 40% of sampled species act as *Epichloë* hosts (Card et al., 2014; Iannone et al., 2011). They  
98 are predominantly transmitted vertically from maternal plants to offspring through seeds. Vertical  
99 transmission creates a feedback between the fitness of host and symbiont (Douglas, 1998; Fine,  
100 1975; Rudgers et al., 2009). Over time, endophytes that act as mutualists should rise in prevalence  
101 within a host population, particularly under environmental conditions that elicit protective benefits  
102 (Donald et al., 2021). *Epichloë* are known to improve their hosts' drought tolerance (Decunta et al.,  
103 2021) and protect their hosts against herbivores (Ambrose et al., 2014; Crawford et al., 2010) and  
104 pathogens (Tian et al., 2017; Xia et al., 2018) likely through the production of a suite of biologically  
105 active molecules, including diverse alkaloids, proteins, and other secondary metabolites. The fitness  
106 feedback induced by vertical transmission leads to the prediction that endophyte prevalence should  
107 be high in populations where these fitness benefits are most important. Previous survey studies  
108 of contemporary populations have documented large-scale spatial patterns in endophyte prevalence  
109 structured by environmental gradients (Afkhami, 2012; Bazely et al., 2007; Granath et al., 2007;  
110 Sneck et al., 2017). We predicted that endophyte prevalence should track temporal changes in  
111 environmental drivers (i.e. drought) that elicit strong fitness benefits.

112 Early research on *Epichloë* used herbarium specimens to describe the broad taxonomic diversity  
113 of grass host species that harbor these symbionts (White and Cole, 1985), establishing that endo-  
114 phyte symbiosis could be identified in plant tissue from as early as 1851. However, no subsequent  
115 studies, to our knowledge, have used the vast resources of biological collections to quantitatively  
116 assess spatio-temporal trends in endophyte prevalence and their environmental correlates. Grasses

117 are commonly collected and identified based on the presence of their reproductive structures, mean-  
118 ing that preserved specimens typically contain seeds, conveniently preserving the seed-transmitted  
119 fungi along with their host plants on herbarium sheets. This creates the opportunity to leverage  
120 the unique spatio-temporal sampling of herbarium collections to examine the response of this sym-  
121 biosis to historical climate change. However, the predictive ability derived from historical analyses  
122 is rarely tested against contemporary data (Lee et al., 2024). Critically evaluating whether insights  
123 from historical reconstruction are predictive of variation across contemporary populations is a cru-  
124 cial step for the field to move from reading signatures of the past to forecasting ecological dynamics  
125 into the future.

126 In this study, we assessed the long-term responses of *Epichloë* endophyte symbiosis to climate  
127 change through the use of herbarium specimens of three North American host grass species (*Agrostis*  
128 *hyemalis*, *Agrostis perennans*, and *Elymus virginicus*). We first addressed questions describing  
129 spatial and temporal trends in endophyte prevalence: (i) How has endophyte prevalence changed  
130 over the past two centuries? and (ii) How spatially variable are temporal trends in endophyte  
131 prevalence across eastern North America? We then addressed how climate change may be driving  
132 trends in endophyte prevalence by asking: (iii) What is the relationship between temporal trends  
133 in endophyte prevalence and associated changes in climate drivers? We predicted that overall  
134 endophyte prevalence would increase over time in tandem with climate change, and that localized  
135 hotspots of endophyte change would correspond spatially to hotspots of climate warming and drying.  
136 Finally, we evaluated (iv) how our model, built on data from historic specimens, performed in an out-  
137 of-sample test using data on endophyte prevalence from contemporary surveys of host populations.  
138 To answer these questions we examined a total of 2,346 historic specimens collected across eastern  
139 North America between 1824 and 2019, and evaluated model performance against contemporary  
140 surveys comprising 1,442 individuals from 63 populations surveyed between 2013 and 2020.

141

## Methods

142

### *Focal species*

143 Our surveys focused on three native North American grasses: *Agrostis hyemalis*, *Agrostis perennans*,  
144 and *Elymus virginicus* that host *Epichloë* symbionts. These cool-season grass species have broad  
145 distributions covering much the eastern United States (Fig. 1) and are commonly represented in  
146 natural history collections. Cool-season grasses grow during the cooler temperatures of spring and  
147 autumn due to their reliance on *C*<sub>3</sub> photosynthesis. *A. hyemalis* is a small short-lived perennial  
148 species that germinates in autumn to late winter winter and typically flowers between March and  
149 July (most common collection month: May). *A. perennans* is of similar stature but is longer lived  
150 than *Agrostis hyemalis* and flowers in late summer and early autumn (most common collection  
151 month: September). *A. perennans* is more sparsely distributed, tending to be found in shadier and  
152 moister habitats, while *A. hyemalis* is commonly found in open and recently disturbed habitats.  
153 Both *Agrostis* species are recorded from throughout the Eastern US, but *A. perennans* has a slightly  
154 more northern distribution, whereas *A. hyemalis* is found rarely as far north as Canada and is listed  
155 as a rare plant in Minnesota. *E. virginicus* is a larger and longer-lived species that is more broadly  
156 distributed than the *Agrostis* species. It begins flowering as early as March or April but continues  
157 throughout the summer (most common collection month: July).

158 Both *Agrostis* species host *Epichloë amarillans* (Craven et al., 2001; Leuchtmann et al., 2014),  
159 and *Elymus virginicus* typically hosts *Epichloë elymi* (Clay and Schardl, 2002). The fungal sym-  
160 bionts primarily reproduce asexually and are passed from maternal plant to offspring by vertical  
161 transmission through seeds. These symbionts are also capable of horizontal transmission between  
162 hosts via the production of external reproductive structures, including sexual spore-bearing stro-  
163 mata that grow over host inflorescences (known as 'choke disease') and epiphyllous conidia on leaf  
164 surfaces that produce asexual spores (Tadych et al., 2014). Evidence suggests that production of  
165 horizontal transmission structures by *Epichloë* occurs at low levels, and may be influenced by en-

166 vironmental and genotypic factors (Brem and Leuchtmann, 1999; Meijer and Leuchtmann, 2000;  
167 Tintjer et al., 2008). In line with this, monitoring of long-term plots of *A. perennans* and *E. virginicus*  
168 showed no production of stromata on *A. perennans* and on only less than 1% of *E. virginicus*  
169 plants over 14 years (Fowler et al., 2024). A similar low frequency of stromata formation (only  
170 0.37% of recorded inflorescences) was observed for *A. hyemalis* in a separate field experiment (Don-  
171 ald et al., 2021). Some host species have shown the capacity to partner with multiple symbiont  
172 species or strains, and in some cases multiple symbiont lineages can co-exist within a host popu-  
173 lation (Mc Cargo et al., 2014). However, surveys have typically found limited *Epichloë* genotypic  
174 diversity within host populations (Treindl et al., 2023). Across host populations, concentrations of  
175 biologically-active biomolecules and the genes associated with their production vary substantially  
176 (Schardl et al., 2012). In this analysis, we focus on the presence/absence of *Epichloë* symbionts,  
177 and we discuss potential implications of symbiont genotypic diversity in the Discussion.

178 *Herbarium surveys*

179 We visited nine herbaria between 2019 and 2022 (see Table A1 for a summary of specimens included  
180 from each collection). With permission from herbarium staff, we acquired seed samples from 1135  
181 *A. hyemalis* specimens collected between 1824 and 2019, 357 *A. perennans* specimens collected  
182 between 1863 and 2017, and 854 *E. virginicus* specimens collected between 1839 and 2019 (Fig. 1,  
183 Fig. 2A, Fig. A1). We chose our focal species in part because they are commonly represented in  
184 herbarium collections and produce many seeds, meaning that small samples would not diminish the  
185 value of specimens for future studies. We collected 5-10 seeds per specimen after examining the  
186 herbarium sheet under a dissecting microscope to ensure that we collected mature seeds, not florets  
187 or unfilled seeds, fit for our purpose of identifying fungal endophytes with microscopy. We excluded  
188 specimens for which information about the collection location and date were unavailable.

189 Each specimen was assigned geographic coordinates based on collection information recorded on  
190 the herbarium sheet using the geocoding functionality of the *ggmap* R package (Kahle and Wickham,  
191 2019). Many specimens had digitized collection information readily available, but for those that

192 did not, we transcribed information printed on the herbarium sheet. The identity of each specimen  
193 collector was gathered as part of the sample's metadata. Collections were geo-referenced to the  
194 nearest county centroid, or nearest municipality when that information was available. For fifteen  
195 of the oldest specimens, only information at the state level was available, and so we used the state  
196 centroid. The median pairwise distance between georeferenced coordinate points was 841 km. The  
197 median longitudinal width of the bounding boxes generated to geocode municipality, county, or  
198 state centroids was 44.7 km. Among those specimens geo-referenced at the state level, the largest  
199 bounding box, spanning the state of Texas, was 1233 km wide. The smallest bounding boxes were  
200 less than 1 km across for small municipalities (while this suggests high precision, we note that some  
201 specimens were collected in natural habitat nearby to small municipalities not encompassed by these  
202 bounding boxes).

203 Our visits focused on herbaria with historic strengths in grass collections (e.g. Texas A&M,  
204 Missouri Botanic Garden) and other herbaria in the Southern Great Plains region of the United  
205 States. While these nine herbaria garnered specimens that span the focal species' ranges, our dataset  
206 unevenly samples across the study region (Fig. 1). Texas, Oklahoma, Louisiana, and Missouri are  
207 the most represented states. Uneven sampling was most pronounced for *A. perennans*, which has  
208 much of its range in the northeastern US. We explore the potential influence of spatial bias in  
209 sampling on our results through a simulation analysis (Appendix A - Supporting Methods).

210 After collecting seed samples, we quantified the presence or absence of *Epichloë* fungal hyphae  
211 in each specimen using microscopy. We first softened seeds with a 10% NaOH solution, then stained  
212 the seeds with aniline blue-lactic acid stain and squashed them under a microscope cover slip. We  
213 examined the squashed seeds for the presence of fungal hyphae at 200-400X magnification (Bacon  
214 and White, 2018). On average we scored 4.7 intact seeds per specimen of *A. hyemalis*, 4.2 seeds  
215 per specimen of *A. perennans*, and 3.8 seeds per specimen of *E. virginicus*; we scored 10,342 seeds  
216 in total. Due to imperfect vertical transmission, the production of symbiont-free offspring from  
217 symbiotic hosts (Afkhami and Rudgers, 2008), it is possible that symbiotic host-plants produce a  
218 mixture of symbiotic and non-symbiotic seeds. We therefore designated a specimen as endophyte-

219 symbiotic if *Epichloë* hyphae were observed in one or more of its seeds, or non-symbiotic if *Epichloë*  
220 hyphae were observed in none of its seeds. To capture uncertainty in the endophyte identification  
221 process, we recorded both a "liberal" and a "conservative" endophyte score for each plant specimen.  
222 When we confidently identified endophytes within a specimen's seeds, we assigned matching liberal  
223 and conservative scores. When we identified potential endophytes with unusual morphology, low  
224 uptake of stain, or a small amount of fungal hyphae across the scored seeds, we recorded a positive  
225 identification for the liberal score and a negative identification for the conservative score. We  
226 recorded the identity of each scorer as part of the data collection process. 89% of scored plants  
227 had matching liberal and conservative scores, reflecting high confidence in endophyte status. The  
228 following analyses used the liberal status, however repeating all analyses with the conservative status  
229 yielded qualitatively similar results (Fig. A8).

230 *Modeling spatial and temporal changes in endophyte prevalence*

231 We assessed spatial and temporal changes in endophyte prevalence across each host distribution,  
232 quantifying the "global" temporal trends averaged across space, and then examining spatial hetero-  
233 geneity in the direction and magnitude of endophyte change (hotspots and coldspots) across the spa-  
234 tial extent of each host's distribution. To account for the spatial non-independence of geo-referenced  
235 occurrences, we used an approximate Bayesian method, Integrated Nested Laplace Approximation  
236 (INLA), to construct spatio-temporal models of endophyte prevalence. INLA provides a computa-  
237 tionally efficient method of ascertaining parameter posterior distributions for certain models that  
238 can be formulated as latent Gaussian Models (Rue et al., 2009). Many common statistical models,  
239 including structured and unstructured mixed-effects models, can be represented as latent Gaussian  
240 Models. We incorporated spatial heterogeneity into this analysis using spatially-structured intercept  
241 and slope parameters implemented as stochastic partial differential equations (SPDE) to approxi-  
242 mate a continuous spatial Gaussian process. This SPDE approach is a flexible method of smoothing  
243 across space while explicitly accounting for spatial dependence between data-points (Bakka et al.,  
244 2018; Lindgren et al., 2011). Fitting models with structured spatial effects is possible with MCMC

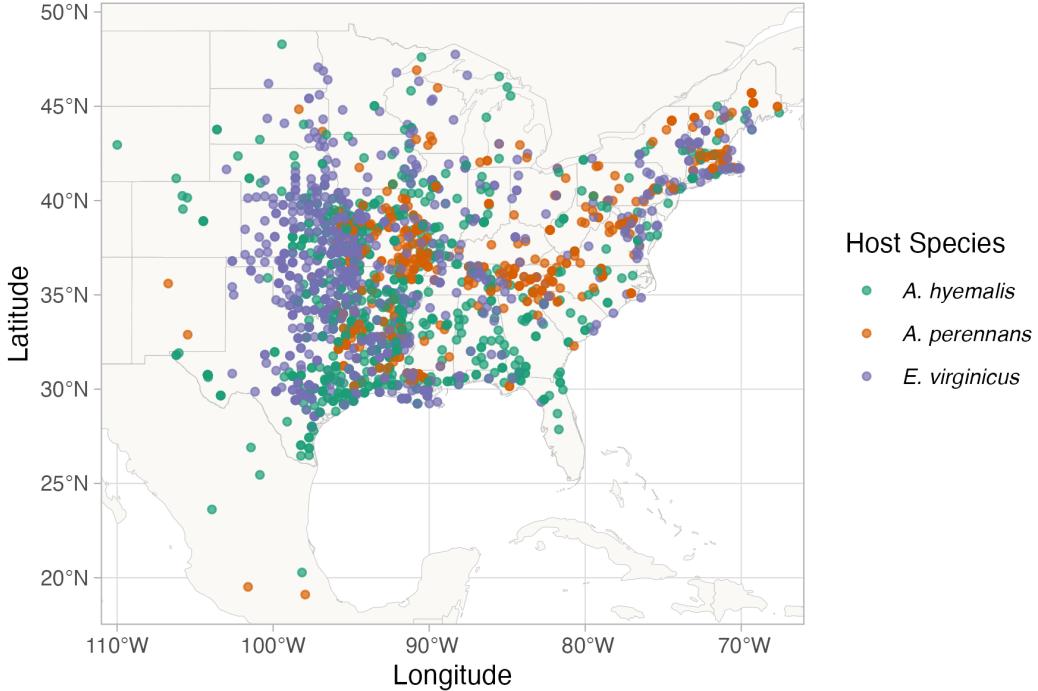


Figure 1: Collection locations of herbarium specimens sampled for *Epichloë* endophytes.

Specimens span eastern North America from nine herbaria, and are colored by host species (*A. hyemalis*: green, *A. perennans*: orange, *E. virginicus*: purple). Map lines delineate study areas and do not necessarily depict accepted national boundaries.

245 sampling but can require long computation times, making INLA an effective alternative. This ap-  
 246 proach has been used to model spatial patterns in flowering phenology (Willems et al., 2022), the  
 247 abundance of birds (Meehan et al., 2019) and butterflies (Crossley et al., 2022), the distribution of  
 248 temperate trees (Engel et al., 2022) as well as the population dynamics of endangered amphibians  
 249 (Knapp et al., 2016) and other ecological processes (Beguin et al., 2012).

250 We estimated global and spatially-varying trends in endophyte prevalence using a joint-likelihood  
 251 model. For each host species  $h$ , endophyte presence/absence of the  $i^{th}$  specimen ( $P_{h,i}$ ) was modeled  
 252 as a Bernoulli response variable with expected probability of endophyte occurrence  $\hat{P}_{h,i}$ . We modeled  
 253  $\hat{P}_{h,i}$  as a linear function of collection year, with intercept  $A_h$  and slope  $T_h$  defining the global  
 254 temporal trend in endophyte prevalence specific to each host species as well as with spatially-

255 varying intercepts  $\alpha_{h,l_i}$  and slopes  $\tau_{h,l_i}$  associated with location ( $l_i$ , the unique latitude-longitude  
 256 combination of the  $i$ th observation). The joint-model structure allowed us to “borrow information”  
 257 across species in the estimation of shared variance terms for the spatially-dependent random effect  
 258  $\delta_{l_i}$ , intended to account for residual spatial variation, and  $\chi_{c_i}$  and  $\omega_{s_i}$ , the i.i.d.-random effects  
 259 indexed for each collector identity ( $c_i$ ) and scorer identity ( $s_i$ ) of the  $i^{th}$  specimen.

$$\text{logit}(\hat{P}_{h,i}) = A_h + T_h * \text{year}_i + \alpha_{h,l_i} + \tau_{h,l_i} * \text{year}_i + \delta_{l_i} + \chi_{c_i} + \omega_{s_i} \quad (1)$$

260 By including random effects for collectors and scorers, we accounted for “nuisance” variance that  
 261 may bias predictions for changes in endophyte prevalence. Previous work suggests that behavior of  
 262 historical botanists may introduce biases into ecological inferences made from historic collections  
 263 (Kozlov et al., 2020). Prolific collectors who contribute thousands of specimens may be more or  
 264 less likely to collect certain species, or specimens with certain traits (Daru et al., 2018). Similarly,  
 265 the process of scoring seeds for hyphae involved multiple researchers (or "scorers") who, even with  
 266 standardized training, may vary in their likelihood of positively identifying *Epichloë*.

267 We performed model fitting using the *inlabru* R package (Bachl et al., 2019). Global intercept  
 268 and slope parameters,  $A$  and  $T$ , were given vague priors. Collector and scorer random effects,  $\chi$  and  
 269  $\omega$  respectively, were centered at 0 with precision parameters assigned penalized complexity (PC) pri-  
 270 ors with parameter values  $U_{PC} = 1$  and  $a_{PC} = 0.01$  (Simpson et al., 2017). Each spatially-structured  
 271 parameter depended on a covariance matrix according to the proximity of each pair of collection  
 272 locations (Bakka et al., 2018; Lindgren et al., 2011). The covariance matrix was approximated using  
 273 a Matérn covariance function, with each data point assigned a location according to the nodes of  
 274 a mesh of non-overlapping triangles encompassing the study area (Fig. A2). Matérn covariance  
 275 functions are widely used in spatially explicit statistical modeling because of their mathematical  
 276 tractability and flexibility. This covariance structure relies on the assumption that the underlying  
 277 process is stationary and isotropic, such that spatial autocorrelation between data points depends  
 278 only on their relative positions (Bakka et al., 2018).

279 Implementing spatially-structured parameters in INLA with this SPDE approach is useful par-

ticularly because space is treated as a continuous variable, allowing the model to make efficient use of the data and generate predictions across the entire study region. The SPDE approach is flexible enough that it can capture smooth trends across space that are informed by the data rather than by spatial regions chosen *a priori* by researchers. However this flexibility also invites the risk of overfitting, as with other non-linear modeling approaches (Lapeyrolerie and Boettiger, 2023; Ramaniandra et al., 2023; Ward et al., 2014). Priors for the Matérn covariance function, termed “range” and “variance”, define how proximity effects decay with distance. The choice of priors for these types of spatial models is an area of active research (Bakka et al., 2018; Simpson et al., 2017), but another advantage of the INLA approach is that its computational efficiency allows for prior sensitivity analyses. Results presented in the main text reflect a prior range of 342 kilometers (i.e. a 50% probability of estimating a range less than 342 kilometers). We tested a range of values (from 68 kilometers to 1714 kilometers) and meshes (presented in the Supporting Methods – *Mesh and Prior Sensitivity Analysis*), finding that while the magnitude and uncertainty of effects varied, model results were qualitatively similar, i.e. the same direction of effects across space. We assessed model fit with visual posterior predictive checks (Fig. A3) and measurements of AUC (Figs. A4-A5) (Gelman and Hill, 2006). Through results and discussion that follow, we refer to the model described in this section as the “endophyte prevalence model”.

### 297 *Modeling distributions of host species*

298 The herbarium records did not encompass the entirety of each host species’ range. Therefore, we  
299 used additional data sources to model the geographic distribution of each host species, with two  
300 goals: (1) generate realistic maps on which we could project the predictions of the INLA model,  
301 and (2) use the geographic distributions to test for relationships between climate change drivers and  
302 trends in endophyte prevalence. We followed the ODMAP (overview, data, model, assessment,  
303 prediction) protocol (Crossley et al., 2022) (see Supporting Methods). In short, we used presence-  
304 only observations of each host species from Global Biodiversity Information Facility (GBIF) between  
305 1990 to 2020 (713 occurrence records for *A. hyemalis* (GBIF.Org, 2025a), 656 occurrence records

306 for *A. perennans* (GBIF.Org, 2025b), and 2338 occurrence records for *E. virginicus* (GBIF.Org,  
307 2025c)). We fit maximum entropy (MaxEnt) models using the maxent function in the R package  
308 *dismo* (Hijmans et al., 2017) using the following seasonal climate predictors (1990-2020 climate  
309 normals): mean and standard deviation of spring, summer, and autumn temperature, and mean  
310 and standard deviation of spring, summer, and autumn cumulative precipitation.

311 We generated 10,000 pseudo-absences as background points, and split the occurrence data into  
312 75% for model training and 25% for model testing. The performance of models was evaluated with  
313 AUC (Jiménez-Valverde, 2012). We found AUC values of 0.862, 0.838, 0.821 respectively for *Agrostis*  
314 *hyemalis*, *Agrostis perennans*, and *Elymus virginicus* indicating good model fit to data. We used  
315 the training sensitivity (true positive rate) and specificity (true negative rate) to set a threshold for  
316 transforming the continuous predicted probabilities into binary presence - absence host distribution  
317 maps on which we projected INLA predictions of endophyte prevalence (Liu et al., 2005).

318 *Assessing the role of climate drivers*

319 We assessed how the magnitude of climate change may have driven changes in endophyte prevalence  
320 by assessing correlations between changes in climate and changes in endophyte prevalence predicted  
321 from our spatial model at evenly spaced pixels across the study area.

322 We first downloaded monthly temperature and precipitation rasters from the PRISM climate  
323 group (Daly and Bryant, 2013) covering the time period between 1895 and 2020 using the *prism*  
324 R package (Hart and Bell, 2015). PRISM provides reconstructions of historic climate variables  
325 across the United States by spatially interpolating weather station data (Di Luzio et al., 2008).  
326 Because the magnitude of observed climate change differs across seasons, and because different  
327 growing seasons is a key feature of the biology of our focal host species, we calculated 30-year  
328 climate normals for seasonal mean temperature and cumulative precipitation for the recent (1990  
329 to 2020) and historic (1895 to 1925) periods. We used three four-month seasons within the year  
330 (Spring: January, February, March, April; Summer: May, June, July, August; Autumn: September,  
331 October, November, December). This division of seasons allowed us to quantify differences in

the primary climate change drivers, temperature and precipitation, associated with the two “cool” seasons, when we expected our focal species to be most active (*A. hyemalis* flowering phenology: spring; *E. virginicus*: spring and summer; *A. perennans*: autumn). In addition to mean climate conditions, environmental variability itself can influence population dynamics (Tuljapurkar, 1982) and changes in variability are a key prediction of climate change models (IPCC, 2021; Stocker et al., 2013). Therefore, we calculated the standard deviation for each annual and seasonal climate driver across each 30-year period. We then took the difference between recent and historic periods for the mean and standard deviation for each climate driver (Figs. A13-A15). All together, we assessed twelve potential climate drivers: the mean and standard deviation of spring, summer, and autumn temperature, as well as the mean and standard deviation of spring, summer, and autumn cumulative precipitation (the same climate covariates used in the MaxEnt models).

We then evaluated whether areas that have experienced the greatest changes in endophyte prevalence (hotspots of endophyte change) are associated with high degrees of change in climate (hotspots of climate change). To do so, we modeled the fitted, spatially-varying slopes of endophyte change through time ( $\tau_{h,l}$ ) as a linear function of environmental covariates, with a Gaussian error distribution for a set of pixels across each host distribution. The continuous SPDE approach taken from our endophyte prevalence model allows us to generate predictions of temporal trends in prevalence at arbitrarily many pixels across each host distribution. Balancing computation time with resolution, we generated predicted trends for 546, 645, and 753 pixels across each host distribution for *A. perennans*, *A. hyemalis*, and *E. virginicus* respectively (pixel dimensions: *A. perennans* = 65 km x 36 km; *A. hyemalis* = 61km x 45 km; *E. virginicus* = 62 km x 40 km ). Fitting regressions to many pixels across the study region risks artificially inflating confidence in our results due to large sample sizes, and so we performed this analysis using only a random subsample of 250 pixels across the study region; other sizes of subsample yielded similar results. Data from each host species were analyzed separately. Throughout the results and discussion that follow, we refer to this analysis as the “*post hoc* climate regression analysis”.

358        *Validating model performance with in-sample and out-of-sample tests*

359    We evaluated the predictive ability of the endophyte prevalence model using both in-sample training  
360    data from the herbarium surveys, and with out-of-sample test data, an important but rarely used  
361    strategy in ecological studies (Lee et al., 2024; Tredennick et al., 2021). We generated out-of-  
362    sample test data from contemporary surveys of endophyte prevalence in natural populations of *A.*  
363    *hyemalis* and *E. virginicus* in Texas and the southern US. Surveys of *E. virginicus* were conducted  
364    in 2013 as described in Sneck et al. (2017), and surveys of *A. hyemalis* took place between 2015  
365    and 2020. Population surveys of *A. hyemalis* were initially designed to cover longitudinal variation  
366    in endophyte prevalence towards its range edge, while surveys of *E. virginicus* were designed to  
367    cover latitudinal variation. In total, we visited 43 populations of *A. hyemalis* and 20 populations  
368    of *E. virginicus* across the south-central US, with emphasis on Texas and neighboring states (Fig  
369    A12). number of plants sampled per population: 22.9); note that this sampling design provided  
370    greater local depth of information than the herbarium records, where only one plant was sampled at  
371    each locality. We quantified the endophyte status of each individual with microscopy as described  
372    for the herbarium surveys (with 5-10 seeds scored per individual), and calculated the prevalence  
373    of endophytes within the population (proportion of plants that were endophyte-symbiotic). For  
374    each population, we compared the observed fraction of endophyte-symbiotic hosts to the predicted  
375    probability of endophyte occurrence  $\hat{P}$  derived from the model for that location and year. The  
376    contemporary survey period (2013-2020) is at the most recent edge of the time period encompassed  
377    by the historical specimens used for model fitting.

378        **Results**

379        *How has endophyte prevalence changed over time?*

380    Across more than 2300 herbarium specimens dating back to 1824, we found that prevalence of  
381    *Epichloë* endophytes increased over the last two centuries for all three grass host species (Fig. 2).

382 On average, endophytes of *A. perennans* and *E. virginicus* increased from ~ 40 % to 70% prevalence  
383 across the study region, and *A. hyemalis* increased from ~ 25% to over 50% prevalence. Our model  
384 indicates high confidence that overall temporal trends are positive across species (99% probability  
385 of a positive overall year slope in *A. hyemalis*, 92% probability of a positive overall year slope in *A.*  
386 *perennans*, and 91% probability of a positive overall year slope in *E. virginicus*) (Fig. A6).

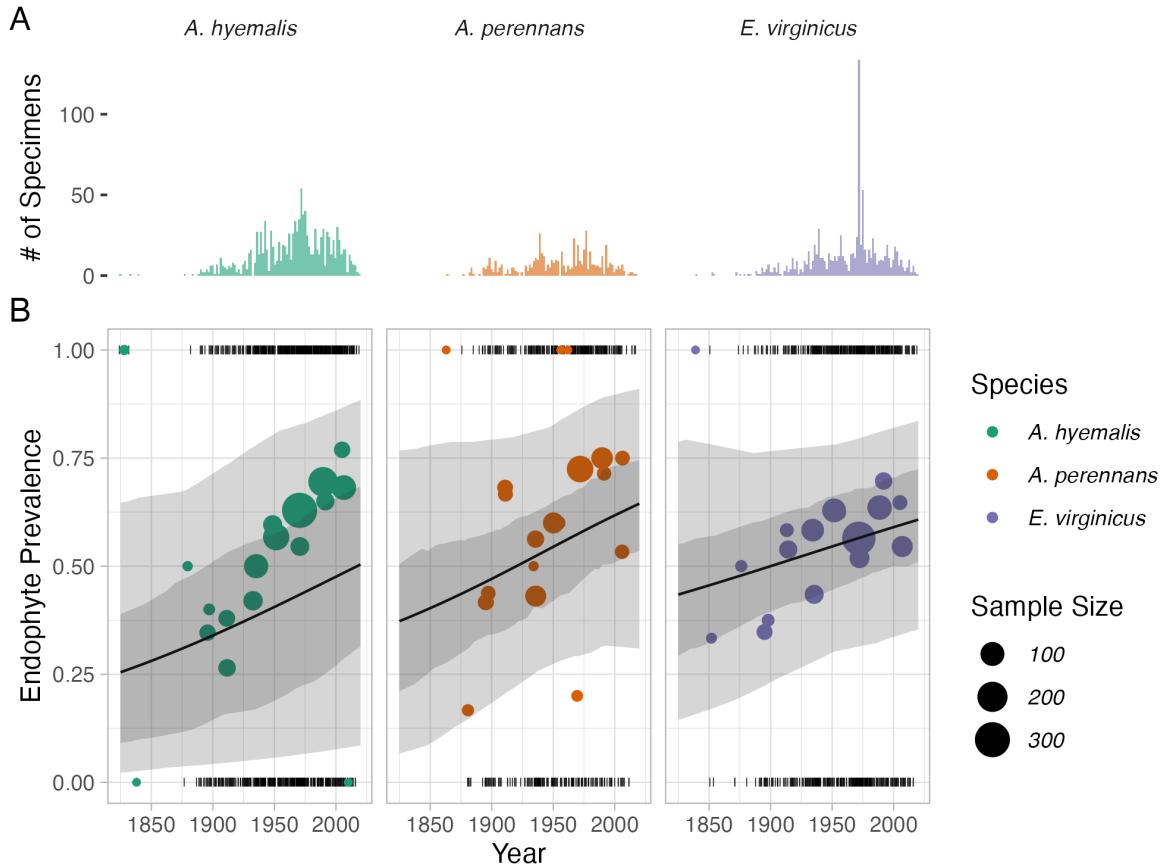


Figure 2: **Temporal trends in endophyte prevalence.** (A) Histograms show the frequency of scored specimens through time for each host species. (B) Lines show mean endophyte prevalence predicted by the endophyte prevalence model over the study period along with the 50% and 95% CI bands incorporating parameter uncertainty and variation associated with collector and scorer random effects. Colored points are binned means of the observed endophyte presence/absence data (black dashes). Colors represent each host species (*A. hyemalis*: green, *A. perennans*: orange, *E. virginicus*: purple) and point size represents the number of specimens.

387 The model appears to under-predict the observed increase in endophyte prevalence relative to  
 388 the data, particularly for *A. hyemalis* (Fig. 2B), but the model is accounting for random effects  
 389 and spatial non-independence that are not readily seen in the figure. We found no evidence that  
 390 collector biases influenced our results. Collector random effects were consistently small (Fig. A9),

391 and models fit with and without this random effect provide qualitatively similar results. The identity  
392 of individual scorers, the researchers who identified endophyte status microscopically, did contribute  
393 to observed patterns in endophyte prevalence. For example, 3 of the 25 scorers were significantly  
394 more likely than average to assign positive endophyte status, as indicated by 95% credible intervals  
395 greater than zero, while 4 of the 25 had 95% credible intervals below zero (Fig. A10).

396 *How spatially variable are temporal trends in endophyte prevalence?*

397 While there was an overall increase in endophyte prevalence, our model revealed hotspots and  
398 coldspots of change across the host species' ranges, which are mapped in Fig. 3 across geographic  
399 ranges predicted by MaxEnt species distribution models. In some regions, posterior mean estimates  
400 of spatially varying temporal trends indicate that *A. hyemalis* and *A. perennans* experienced in-  
401 creases in prevalence by as much as 2% per year over the study period. Posterior estimates of  
402 uncertainty in spatially varying slopes indicate that these hotspots of change may have experienced  
403 increases of up to 5% per year while declines in prevalence may be as great as -4% per year for  
404 the *Agrostis* species. (Fig. A7) In contrast, *E. virginicus* experienced increases up to around 1%  
405 per year, with uncertainty ranging between 3.5% increases and 2.5% decreases (Fig. A7) Taken  
406 together, both *Agrostis* species show areas of both strong increasing and declining prevalence, while  
407 *E. virginicus* had an overall weaker and geographically more homogeneous increase in endophyte  
408 prevalence. Notably, endophytes are predicted to have increased most strongly towards the western  
409 range edge of *A. hyemalis* (Fig. 3A) and across the northeastern US for *A. perennans* (Fig. 3B).  
410 Broad increases in prevalence on average, along with increases towards range edges that had low  
411 historic prevalence result in range expansions of the symbiosis for both *Agrostis* species (Fig. 4).  
412 Increases in prevalence were strongest in regions with low historic prevalence for the *Agrostis* species  
413 (Fig. A11 A-B), but for *E. virginicus* trends did not differ according to historic prevalence (A11  
414 C).

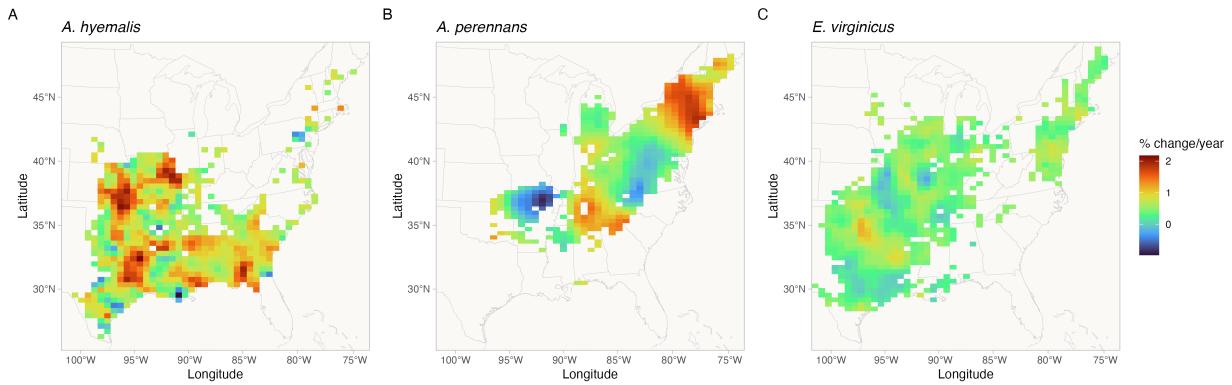


Figure 3: Predicted posterior mean of spatially-varying slopes representing change in endophyte prevalence for each host species ((A)*A. hyemalis*; (B)*A. perennans*; (C)*E. virginicus*). Spatially-varying trends are estimated from the endophyte prevalence model. Color indicates the relative change in predicted endophyte prevalence. Map lines delineate study areas and do not necessarily depict accepted national boundaries.

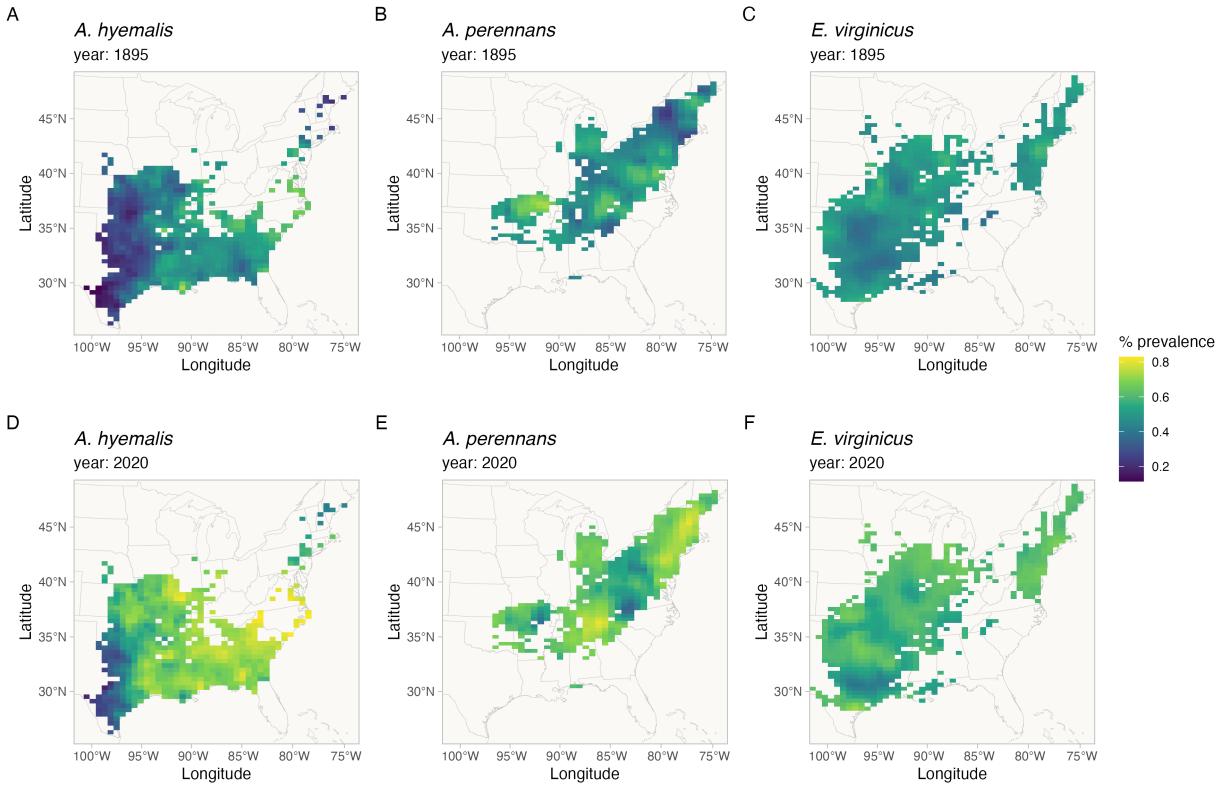


Figure 4: Predicted endophyte prevalence for each host species in 1895 and 2020. Predictions of prevalence come from the endophyte prevalence model. Color indicates the posterior mean endophyte prevalence for (A, D) *A. hyemalis*, (B, E) *A. perennans*, and (C, F) *E. virginicus*. Map lines delineate study areas and do not necessarily depict accepted national boundaries.

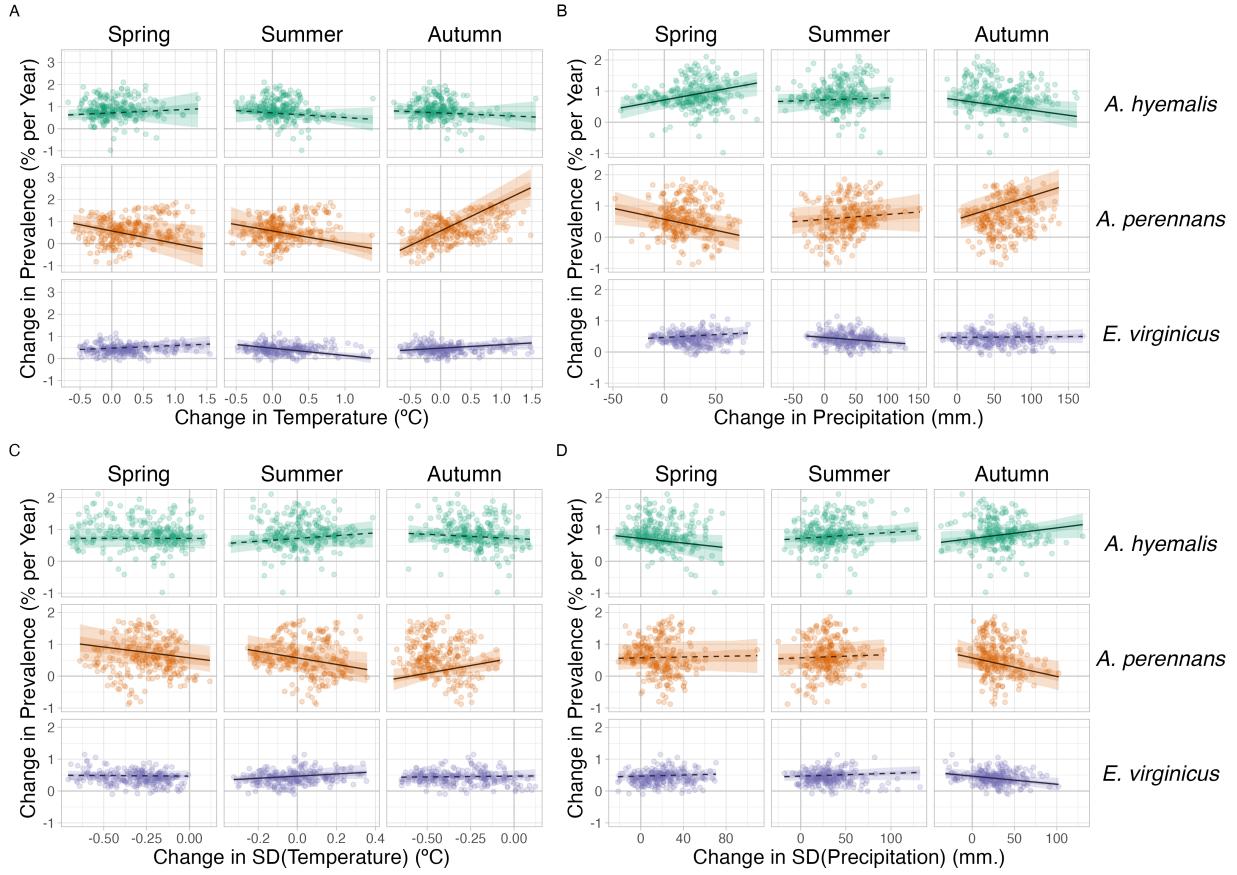
415     *What is the relationship between variation in temporal trends in endophyte  
416     prevalence and changes in climate drivers?*

417     We found that trends in endophyte prevalence were strongly associated with one or more seasonal  
418     climate change drivers (Fig. 5). For the majority of the study region, the climate has become  
419     wetter (an average increase in annual precipitation of 60 mm) with relatively minimal temperature  
420     warming (an average increase in annual temperature of 0.02 °C) over the last century (Fig. A13-  
421     A15), a consequence of regional variation in global climate change (IPCC, 2021). Within the

422 region, climate changes were spatially variable; certain locations experienced increases in annual  
423 precipitation as large as 375 mm or decreases up to 54 mm across the last century, while annual  
424 temperature changes ranged from warming as great as 1.4 °C to cooling by 0.46 °C.

425 Spatially variable climate trends were predictive of trends in endophyte prevalence. For exam-  
426 ple, among the tested climate drivers, strong increases in endophyte prevalence for *A. perennans*  
427 were most strongly associated with increasing autumn precipitation and with increasing mean and  
428 variability in autumn temperature (greater than 97% posterior probabilities of positive slopes). For  
429 this species, each 1 °C increase in autumn temperature was associated with a 1.07 % greater increase  
430 per year in endophyte prevalence (Fig. 5A) and a 100 mm increase in precipitation was associated  
431 with a 0.8% greater increase per year in endophyte prevalence (Fig. 5B). This result aligns with  
432 the species' autumn active growing season, however other seasonal climate drivers were also posi-  
433 tively associated with increasing endophyte prevalence in this host species. In particular, we found  
434 cooler and drier springs and cooler summers to be associated with increasing endophyte prevalence  
435 (greater than 99% posterior probabilities of negative slopes), though these slopes were generally of  
436 smaller magnitude than those for autumn climate drivers. Changes in endophyte prevalence across  
437 the ranges of *A. hyemalis* and *E. virginicus* were less strongly driven by changes in climate. Like  
438 *A. perennans*, climate during peak growing season (spring for *A. perennans* and summer for *E. vir-*  
439 *ginicus*) emerged most commonly as drivers of changes in endophyte prevalence. Across the tested  
440 climate drivers, increases in mean spring precipitation were the strongest predictor of increasing  
441 trends in endophyte prevalence for *A. hyemalis* (Fig. 5B) (greater than 99% posterior probability  
442 of a positive slope). For this species, an increase of 100 mm in spring precipitation was associated  
443 with 0.6% per year stronger increases in endophyte prevalence relative to regions with no change in  
444 precipitation. The next greatest slopes were those associated with variability in spring precipitation  
445 (greater than 96% posterior probability of a negative slope), as well as in the mean and variabil-  
446 ity of autumn climate (greater than 98% probability of negative and positive slopes, respectively).  
447 Changes in endophyte prevalence in *E. virginicus* were not strongly associated with changes in most  
448 climate drivers, but regions with reduced variability in autumn precipitation (Fig. 5B) and with

449 cooler and more variable summer temperatures (Fig. 5A,C) experienced the largest increases in  
450 endophyte prevalence. Our analysis indicated relatively high confidence that these climate drivers  
451 influence endophyte prevalence shifts in *E. virginicus* (greater than 99% posterior probability of ei-  
452 ther negative or positive slopes respectively), however they translate, for example, to less than a  
453 0.4% decrease in endophyte prevalence per year for each  $1^{\circ}C$  of summer warming over the century.  
454 Repeating this analysis using all pixels across each species' distribution were qualitatively similar  
455 to these results.



**Figure 5: Relationships between predicted trends in endophyte prevalence and changes in seasonal climate drivers.** Lines show marginal predicted relationship between spatially-varying trends in endophyte prevalence and changes in mean and variability of climate ((A): mean temperature, (B): cumulative precipitation, (C): standard deviation in temperature, (D): standard deviation in precipitation) estimated from the *post hoc* climate regression analysis. Confidence bands represent the 50 and 95% CI, colored by host species (*A. hyemalis*: green, *A. perennans*: orange, *E. virginicus*: purple). Slopes with greater than 95% posterior probability of being either positive or negative are represented as solid lines while those that have less than 95% probability are dashed. Points are the values of pre-computed SVC trends and climate drivers at 250 randomly sampled pixels across each host's distribution used in model fitting for the *post hoc* climate regression analysis.

456      *Evaluation of model performance on an out-of-sample test*

457      Tests of the endophyte prevalence model's predictive performance, as quantified by AUC and by  
458      visual posterior predictive checks, indicated good predictive ability. Model performance was similar  
459      between historic herbarium specimens used as training data and the out-of-sample test data from  
460      contemporary surveys (AUC = 0.79 and 0.77 respectively; Fig. A5-A4). The model successfully  
461      captured broad regional trends in endophyte prevalence seen in the contemporary survey data,  
462      such as decline endophyte prevalence in *A. hyemalis* towards western longitudes (Fig. 6A) and an  
463      increase towards northern latitudes (Fig. 6B). It is noteable that model predictions for endophyte  
464      prevalence exhibited relatively little local geographic variation, whereas the out-of-sample survey  
465      data were highly variable with populations spanning 0% to 100% endophyte-symbiotic plants (Fig.  
466      6C), indicating population-to-population variation not captured in the endophyte prevalence model.

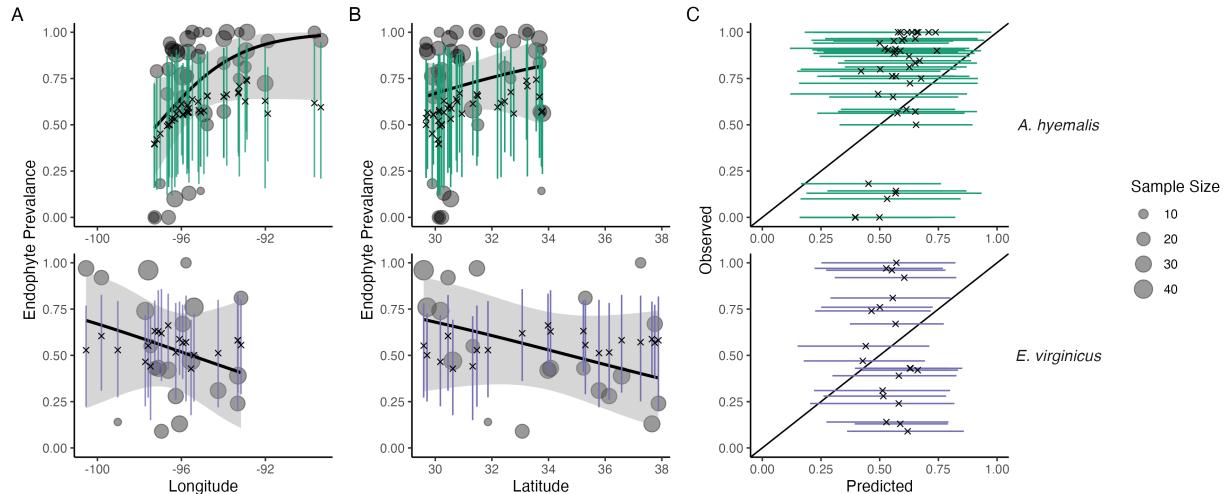


Figure 6: **Predictive performance for contemporary test data.** (A) The endophyte prevalence model, trained on historic herbarium collection data, performed modestly at predicting prevalence in contemporary population surveys. The model captured regional trends across (A) longitude and (B) latitude. Crosses indicate predicted mean prevalence along with the 95% CI (colored lines: *A. hyemalis*: green, orange, *E. virginicus*: purple) from the herbarium model. Contemporary prevalence is represented by grey points (point size reflects sample size) along with trend lines from generalized linear models (black line and shaded 95% confidence interval). (C) Comparison of contemporary observed population prevalence vs. predicted endophyte prevalence shows that contemporary test data had more variance between populations than in model predictions.

## Discussion

Our examination of historic plant specimens revealed previously hidden shifts in microbial symbiosis over the last two centuries. For the three grass host species we examined, there have been strong increases in prevalence of *Epichloë* endophyte symbiosis. We interpret increases in prevalence of *Epichloë*, which are predominantly vertically transmitted, as adaptive changes that improve the fitness of their hosts under increasing environmental stress. This interpretation is in line with theory predicting that positive fitness feedback caused by vertical transmission leads beneficial symbionts

474 to rise in prevalence within a population (Donald et al., 2021; Fine, 1975). We further found that  
475 trends in endophyte prevalence often varied across the host distribution in association with changes  
476 in climate drivers, consistent with the hypothesis that increases in endophyte prevalence are driven  
477 by context-dependent benefits to hosts that confer resilience under environmental change. Taken  
478 together, our results suggest an overall strengthening of host-symbiont mutualism over the last two  
479 centuries.

480 *Responses of host-microbe symbioses to climate change*

481 Differences across host species underscore that while all of these  $C_3$  grasses share similar broad-scale  
482 distributions, each engages in unique biotic interactions and has unique responses to environmental  
483 drivers. We identified hotspots of change for *A. perennans*, which was the species whose endophyte  
484 prevalence was most responsive to changes in climate drivers (Fig. 5). Predicted declines of 0.9%  
485 per year in the southern portion of its range and predicted increases of up to 2% per year in the  
486 north suggest a potential poleward range shift of endophyte-symbiotic plants (Fig. 3B); whether  
487 the overall host distribution is shifting in parallel is an exciting next question.

488 Based on previous work demonstrating that endophytes can shield their hosts from drought  
489 stress (reviewed in Decunta et al. (2021)), we generally predicted that drought conditions would be  
490 a driver of increasing endophyte prevalence. In contrast to this expectation, increasing prevalence  
491 for *A. perennans* was associated with both increasing autumn temperature and precipitation (Fig.  
492 5). To our knowledge, the response of the symbiosis in *A. perennans* to drought has not been  
493 examined experimentally, but in a greenhouse experiment, endophytes had a positive effect on host  
494 reproduction under shaded, low-light conditions (Davitt et al., 2010). Our results also hint that it  
495 may be useful to investigate whether lagged climate effects are important predictors of host fitness  
496 in this system (Evers et al., 2021). Endophyte prevalence of the autumn-flowering *A. perennans* was  
497 strongly linked with decreasing spring precipitation, and that of the spring-flowering *A. hyemalis*  
498 was associated with decreasing autumn precipitation (Fig. 5B). For *A. hyemalis*, endophytes could  
499 be playing a role helping hosts weather autumn-season droughts, which is likely also an important

time for the species' germination. Previous work demonstrated drought benefits in a greenhouse manipulation with this host-symbiont pair (Davitt et al., 2011), and early life stages may be particularly vulnerable to prolonged droughts. For *E. virginicus*, which experienced the weakest changes in endophyte prevalence overall (ranging between 1.1% increases and 0.2% decreases), we only found modest associations with changes in climate drivers. Surveys by Sneck et al. (2017), used as part of the test data in this study, identified a drought index (SPEI) that integrates precipitation with estimated evapotranspiration as an important predictor of contemporary endophyte prevalence in this species. The diverse relationships we detect between trends in endophyte prevalence and climate drivers suggest a more complicated picture than the simple explanation that drought alone, as measured through changes in annual precipitation, causes increasing endophyte prevalence through context-dependent fitness benefits.

While we show consistent increasing trends in prevalence between the three species, the mechanisms that explain these changes may be diverse and idiosyncratic. First, climate change responses may depend on genotype-specific responses that are not considered in our current analysis. While *Epichloë* symbioses are highly specialized, surveys have demonstrated genotypic and chemotypic diversity of the symbionts among and within populations (Treindl et al., 2023; von Cräutlein et al., 2021). Genotypic variation in *Epichloë* endophytes, particularly in genes responsible for alkaloid production, produces "chemotypes" with differing benefits for hosts against insect or mammalian herbivores mediated by environmental conditions (Ambrose et al., 2014; Saikkonen et al., 2013; Schardl et al., 2012). Genotypic variation of the hosts themselves can also influence interaction outcomes (Gundel et al., 2011a; Parker et al., 2017). Whether hotspots of change in endophyte prevalence reflect selection for genotype-pairings with particularly strong fitness benefits is an unanswered question. Additionally, *Epichloë* endophytes have been connected to a suite of non-drought related fitness benefits including herbivory defense (Brem and Leuchtmann, 2001), salinity resistance (Wang et al., 2020), and mediation of pathogens (Vikuk et al., 2019) and the soil microbiome (Roberts and Ferraro, 2015). Broad changes in the distribution and abundance of natural enemies (Côté et al., 2004), along with stresses from anthropogenic changes in land management and pollution (Sage,

527 2020) likely influence the benefits of symbiosis (Rudgers et al., 2020). Changing endophyte preva-  
528 lence results from the combination of net fitness benefits playing out across the heterogeneous map  
529 of a changing climate and and its interactive effects on other anthropogenic drivers. Host species  
530 experience a world that is made increasingly stressful by a combination of global change drivers,  
531 and while historic trends that we observed suggest that symbiotic fitness benefits have helped mit-  
532 igate this stress, it is possible that at yet higher levels of stress, increasing costs of the mutualism  
533 could lead to declines in endophyte prevalence. It is also known that stressful conditions can both  
534 reduce (Gundel et al., 2011b) and increase (Gundel et al., 2020) the rate of successful transmission  
535 of *Epichloë* endophytes from mother plant to offspring. These responses likely reflect both conse-  
536 quences of host sanctions on costly symbionts and the ability of symbionts to successfully colonize  
537 seeds (Afkhami and Rudgers, 2008; Gundel et al., 2011c). While we did not investigate differences  
538 in the rate of transmission across these historic specimens due to low numbers of sampled seeds per  
539 individual, it would be valuable to conduct deeper sampling for a subset of specimens with known  
540 endophyte status and investigate how transmission itself may respond to environmental change. Ad-  
541 ditionally, we have interpreted increasing prevalence as a signature of increased host fitness driven  
542 by vertical transmission, which we expect is the predominant mode of tranmission in this system.  
543 Horizontal transmission, while rare, could also explain increasing prevalence if global change stres-  
544 sors lead symbionts to engage in increased parasitic behavior, resulting in increased dispersal and  
545 transmission at the cost of host fitness. More extreme climate stresses, which are expected more  
546 frequently in the future (Seneviratne et al., 2021) could shift the balance of interactions costs and  
547 benefits. Identifying ‘tipping points’ of mutualism breakdown under increasing environmental stress  
548 is an important area of future inquiry.

549 Our results indicate that *Epichloë* symbiosis has likely improved host fitness in stressful envi-  
550 ronments leading to increasing prevalence. What is less clear is how this will influence future range  
551 shifts. Based on our analysis, it is likely that the symbiosis will facilitate range shifts for hosts by  
552 improving population growth at range edges. Previous population surveys (Rudgers and Swafford,  
553 2009; Semmarin et al., 2015; Sneck et al., 2017) attributed environment-dependent gradients in

554 endophyte prevalence to symbiont-derived fitness benefit's allowing hosts to persist in environments  
555 where they otherwise could not (Afkhami et al., 2014; Kazenel et al., 2015). However, symbiont-  
556 facilitated range shifts require that endophytes be present in the populations to be able to contribute  
557 to population growth. For example, the arid western range edge of *A. hyemalis* has had historically  
558 low endophyte prevalence (Fig. 4), and dispersal of symbionts may limit the capacity for range  
559 shifts. A range edge population with no endophytes would require dispersal of symbionts to oc-  
560 cur, either via symbiotic seeds or horizontally-transmitted fungal spores, before the symbiosis could  
561 result in an expanding distribution (Fowler et al., 2023). At the same time, we found that endo-  
562 phyte prevalence has increased most quickly in regions with historically low endophyte prevalence  
563 (Fig. A11), suggesting strong selection for symbiotic hosts when they are present. These factors  
564 potentially contribute to the ability of the host species to track its environmental niche. Another  
565 interesting question is the degree to which symbiotic and non-symbiotic hosts, which occupy over-  
566 lapping but distinct niches, are likely to experience distribution shifts in tandem or at different rates  
567 in the future.

568 *Steps towards forecasts of host-microbe symbioses*

569 The combination of a spatially-explicit model and historic herbarium specimens allowed us  
570 to identify regions of both increasing and decreasing endophyte prevalence. We see several next  
571 steps toward the goal of predicting host and symbiont niche-shifts in response to future climate  
572 change. While the model successfully predicted large-scale spatial trends observed in the out-  
573 of-sample contemporary population surveys, these data contained more population-to-population  
574 variability in prevalence than could be explained by the model. We interpret this to mean that  
575 the model captures coarse-scale spatial and temporal trends reasonably well, but is not equipped  
576 to capture local-scale nuances that generate population-to-population differences. Validating our  
577 model predictions with this test, a rare extra step in collections-based studies, allows us to identify  
578 ways in which the model's out-of-sample predictive ability could be improved. Lack of information  
579 on local variability in symbiont prevalence may simply be a feature of data derived from herbarium

580 specimens. Natural history collectors sample one or a few specimens from local populations, and  
581 these observations are aggregated by the model to derive broad-scale estimates. This suggests that  
582 increasing local replication should be a factor considered in future collection efforts of natural history  
583 specimens, balancing the required time and effort along with limitations on storage space within  
584 collections. Herbarium collections were predominately used for taxonomic research in the past,  
585 but use of specimens to understand ongoing global change would benefit from increased collection  
586 efforts and expansion of herbarium collections. An alternative validation test would be to hold-out  
587 samples from the historic data set. Such a test would more clearly match the conditions of the  
588 training data (i.e., in spatial scale and climate conditions), however the trade-off between training  
589 and testing the model with a limited number of sampled specimens held us back from exploring this  
590 option. Splitting datasets can negatively impact model estimates, and the choice of how to split  
591 the data for model validation is not trivial (Bergmeir and Benítez, 2012; James et al., 2013).

592 Another key consideration in forecasting the dynamics of host-microbe symbioses is the spatial  
593 scale of both specimen georeferencing and available climate data. For this analysis, most specimen  
594 localities were assigned coordinates at county or city centroids, and the climate data examined  
595 was on 4 km grid cells. Georeferencing of specimens as accurately as possible is a key priority  
596 of herbarium specimen digitization efforts (Davis, 2023; Soltis, 2017). While the INLA modeling  
597 approach that we used allows for predictions at arbitrarily small spatial scales, and would simplify  
598 connecting model predictions to the scale of a given climate driver, the coarse scale inherent to our  
599 analysis may obscure some local-scale ecological processes. Poor predictive ability at local scales in  
600 this grass-endophyte system is not surprising, as previous studies have found that local variation  
601 (e.g., in soil conditions, in microclimate), even to the scale of hundreds of meters can structure  
602 endophyte-host niches (Gundel et al., 2024; Kazenel et al., 2015). Local adaptation in either the  
603 host or symbiont to microclimate or soil conditions could cause populations to differ from broad  
604 regional trends. The choice of prior distributions for spatially-varying random effects also impacts  
605 the model's flexibility to capture spatial trends. Our exploration of model sensitivity to prior choice  
606 (presented in the *Supplemental Methods*) reveals qualitatively similar results across a broad range

607 of priors. An important next step would be integrating data from local and regional scales through  
608 modeling to constrain estimates of local and regional variation.

609 Predicting future niche-shifts of hosts and symbionts will require considering the coupled dynam-  
610 ics of host-symbiont dispersal in addition to fitness benefits. For example, transplanting symbiotic  
611 and non-symbiotic plants beyond the range edge of *A. hyemalis* could tell us whether low endophyte  
612 prevalence in that area (Fig. 4A) is a result of environmental conditions that lead the symbiosis  
613 to have negative fitness consequences, or is a result of some historical contingency or dispersal lim-  
614 itation that has thus far limited the presence of symbiotic hosts from a region where they would  
615 otherwise flourish and provide resilience. Incorporating available climatic and soil layers as covari-  
616 ates is another obvious step that could improve predictions. These steps will bridge gaps that often  
617 exist between large but broad bioclimatic and biodiversity data and small but high-resolution data  
618 on biotic interactions, and move towards the goal of predicting the dynamics of microbial symbioses  
619 under climate change (Isaac et al., 2020; Miller et al., 2019).

620 *Herbaria for global change research*

621 Our analysis advances the use of herbarium specimens in global change biology in two ways.  
622 First and foremost, this is one of a growing number of studies to examine microbial symbiosis  
623 using specimens from natural history collections, and the first, to our knowledge, to link long-term  
624 changes in symbioses to changes in climate. The responses of microbial symbioses are a rich target  
625 for future studies within historic specimens, particularly those that take advantage of advances  
626 in sequencing technology. While we used relatively coarse presence/absence data based on fungal  
627 morphology, other studies have examined historic plant microbiomes using molecular sequencing  
628 and sophisticated bioinformatics techniques, but these studies have so far been limited to relatively  
629 few specimens at limited spatial extents (Bearchell et al., 2005; Bieker et al., 2020; Bradshaw et al.,  
630 2021, 2023; Gross et al., 2021; Heberling and Burke, 2019; Yoshida et al., 2015). Much of this work  
631 highlights the important role that historic specimens can play in tracking pathogens, a particularly  
632 important area as climate change facilitates the spread of new diseases (Ristaino, 2020; Singh et al.,  
633 2023) Continued advances in capturing historic DNA and in filtering out potential contamination  
634 during specimen storage (Bakker et al., 2020; Daru et al., 2019; Raxworthy and Smith, 2021) will  
635 be imperative in the effort to scale up these efforts. This scaling up will be essential to be able  
636 to quantify changes not just in the prevalence of symbionts, but also in symbionts' intraspecific  
637 variation and evolutionary responses to climate change, as well as in changes in the wider host  
638 microbiome. With improved molecular insights from historic specimens, we could ask whether  
639 the broad increases in endophytes that we have identified reflect selection for particular genetic  
640 strains or chemotypes and how this selection varies across space. Answering these questions as well  
641 as the unknown questions that future researchers may ask also reiterates the value in capturing  
642 meta-information during ongoing digitization efforts at herbaria around the world and during the  
643 accession of newly collected specimens (Edwards et al.; Lendemer et al., 2020).

644 The second major advance in this analysis is in accounting for several potential biases in the data  
645 observation process that may be common to many collections-based research questions by using a

646 spatially-explicit random effects model. Potential biases introduced by the sampling habits of col-  
647 lectors (Daru et al., 2018), and variation between contemporary researchers during the collection of  
648 trait data, if not corrected for could lead to over-confident inference about the strength and direction  
649 of historic change (Fig. 2). Previous studies that have quantified the effects of collector biases typ-  
650 ically find them to be small (Davis et al., 2015; Meineke et al., 2019), and we similarly did not find  
651 that collector has a strong effect on the results of our analysis, but that scorer identity did impact  
652 results. It is difficult to distinguish whether the impact of scorers was driven by true differences  
653 in scorers' biases or by unintended spatial or temporal clustering of the specimens examined by  
654 each scorer (Clayton et al., 1993; Urdangarin et al., 2023). By under-weighting endophyte-positive  
655 samples that are clustered spatially or by collector or observer, the endophyte prevalence model is  
656 appropriately accounting for nuisance variables and providing a conservative inference of endophyte  
657 change relative to the raw data. Spatial autocorrelation is another phenomenon likely common  
658 in data derived from herbarium specimens (Willems et al., 2022), which our spatially-explicit anal-  
659 ysis models among samples. Beyond spatial autocorrelation of outcomes, systematic differences in  
660 sampling across space can result in spatial bias.

661 One strength of herbaria as vehicles for global change research is the relative ease with which  
662 specimens from many distinct geographic locations can be examined. We visited just nine institu-  
663 tions in the central southern United States, and we were able to sample seeds from specimens across  
664 an area spanning over 300,000 sq. km, including specimens from Mexico and Canada. Despite this  
665 advantage, the specimens we examined are concentrated in the south-central United States, with  
666 fewer specimens in the rapidly warming northeastern United States reflecting the regional focus of  
667 herbaria. We provide a simulation analysis exploring the potential impact of spatially and tempo-  
668 rally biased sampling (Appendix A - Supporting Methods). We found that the spatially-varying  
669 coefficient model had a strong ability to re-capitulate temporal trends across space in simulated  
670 data, and that this result was robust to relatively high levels of spatial bias (80% of data missing  
671 from one spatial region). Simulation analyses that extend this work to consider the myriad ways  
672 herbarium data may be biased (i.e. testing different spatial arrangements and scales of spatial

673 bias, or testing different sample sizes) would be extremely valuable (Daru et al., 2018; Erickson and  
674 Smith, 2021; Gaul et al., 2020; Meineke and Daru, 2021; Schmidt et al.).

675 *Conclusion*

676 Ultimately, a central goal of global change biology is to generate predictive insights into the future of  
677 natural systems on a rapidly changing planet. Beyond host-microbe symbioses, detecting ecological  
678 responses to anthropogenic global change and attributing their causes would inform public policy  
679 decision-makers and adaptive management strategies. Natural history specimens, such as the plant  
680 hosts examined in this study, have a clear role to play in informing global change biodiversity  
681 science, including building understanding of the dynamics of host-symbiont interactions (Davis,  
682 2023). This survey of historic endophyte prevalence is necessarily correlative, yet it serves as a  
683 foundation to develop better predictive models of the response of microbial symbioses to climate  
684 change. Combining the insights from this type of regional-scale survey with field experiments and  
685 physiological performance data could be invaluable to identify mechanisms driving shifts in host-  
686 symbiont dynamics. Evidence is strong that certain dimensions of climate change correlated with  
687 endophytes' temporal responses, however we do not know why trends in prevalence were weak  
688 in some areas or how endophytes would respond to more extreme changes in climate. The "time  
689 machine" of natural history collections revealed evidence of mutualism resilience for grass-endophyte  
690 symbioses in the face of environmental change, but more extreme changes could potentially push  
691 one or both partners beyond their physiological limits, leading to the collapse of the mutualism;  
692 more research is needed to understand what those limits might be.

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703 **Statement of Authorship**

704 J.C.F. contributed to research conception, data collection, data analysis, and led manuscript draft-  
705 ing. J.M. contributed to data analysis and manuscript revisions. T.E.X.M. contributed to research  
706 conception, data collection, data analysis, and manuscript revisions.

707 **Data and Code Availability**

708 Data from this publication can be found through a publicly available repository  
709 (<https://doi.org/10.5061/dryad.rn8pk0pn0>). Code for analyses can be found through a publicly  
710 available repository (<https://github.com/joshuacfowler/EndoHerbarium>) that will be permanently  
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712

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## Appendix A

1078

1079     *Appendix to "Increasing Prevalence of plant-fungal symbiosis across two*  
1080                 *centuries of environmental change"*

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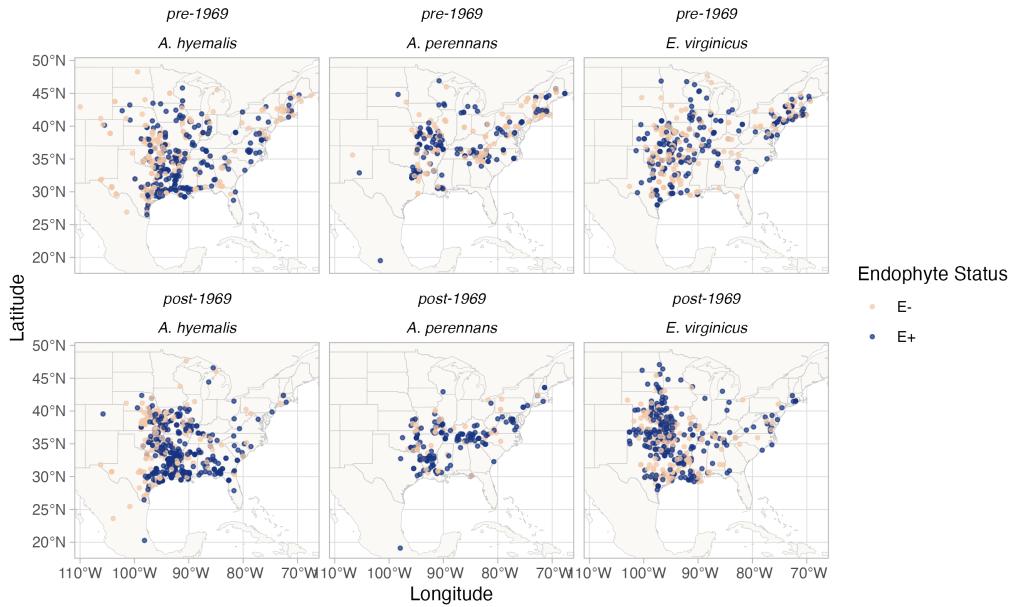
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1089     **Contents:**

1090     Appendix A includes: Figure A1 - Figure A15, Table A1, and Supporting Methods).

1091

## Supplemental Figures



**Figure A1: Endophyte presence/absence in specimens of each host species.** Points show collection locations colored according to whether the specimen contained endophytes ( E+; blue points) or did not contain endophytes (E-, tan points). To visualize temporal change, the data are faceted before and after the median year of collection. Map lines delineate study areas and do not necessarily depict accepted national boundaries.

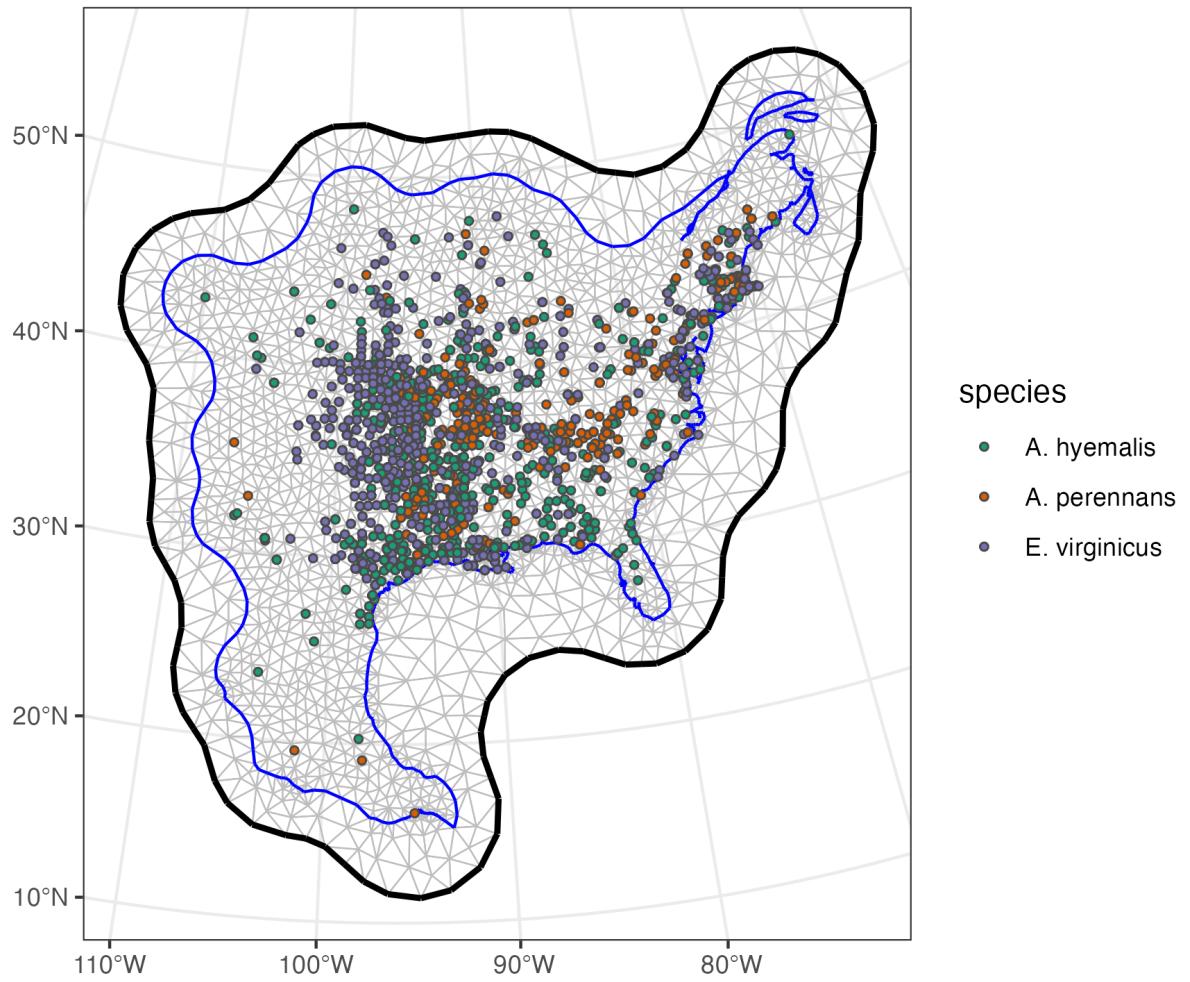


Figure A2: Triangulation mesh used to estimate spatial dependence between data points.

Grey lines indicate edges of triangles used to define distances between observations. Colored points indicate locations of sampled herbarium specimens for each host species, and the blue line shows the convex hull and coastline used to define the edge of the mesh around the data points. The thick black line shows the convex hull defining a buffer space around the edge of the mesh to reduce the influence of edge effects on model estimates.

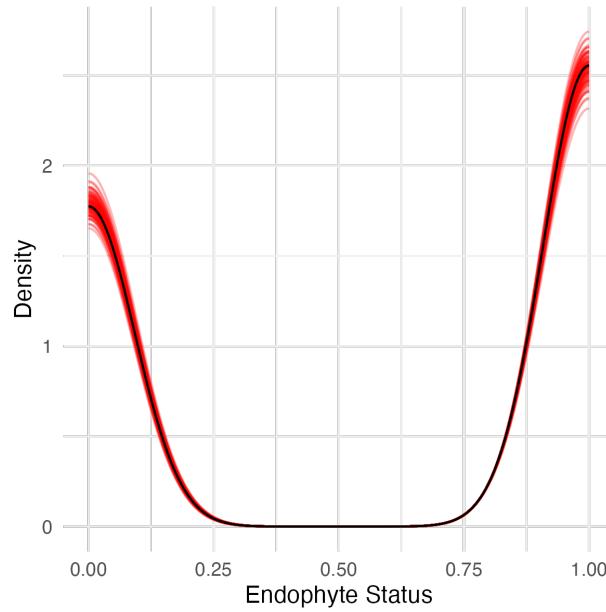
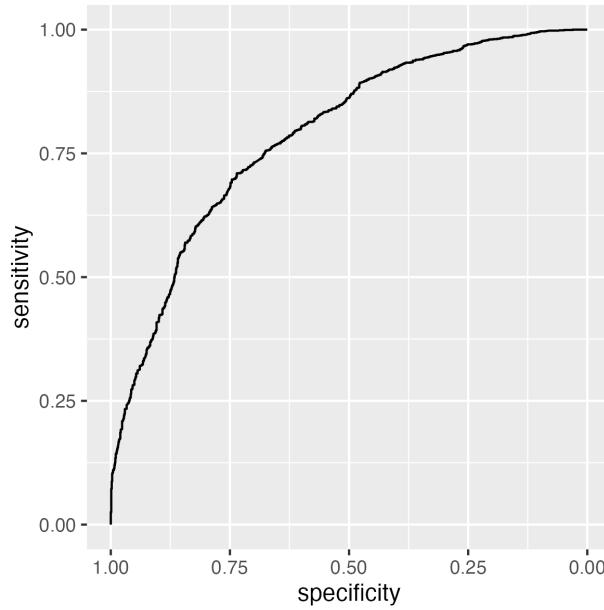
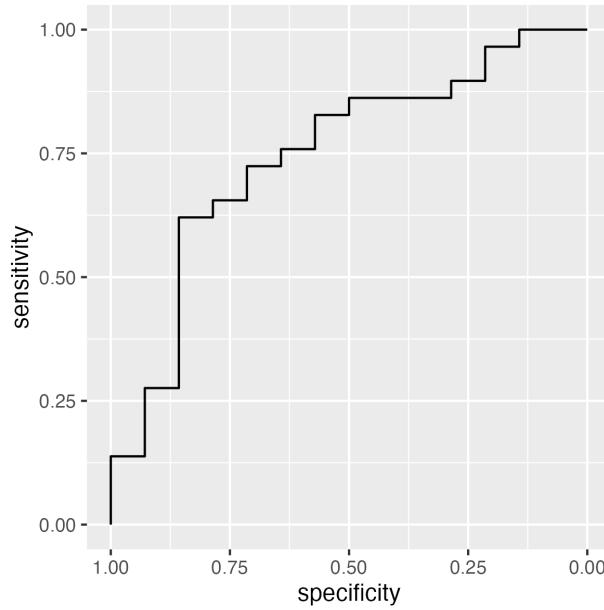


Figure A3: **Graphical posterior predictive check of the endophyte prevalence model fit.**

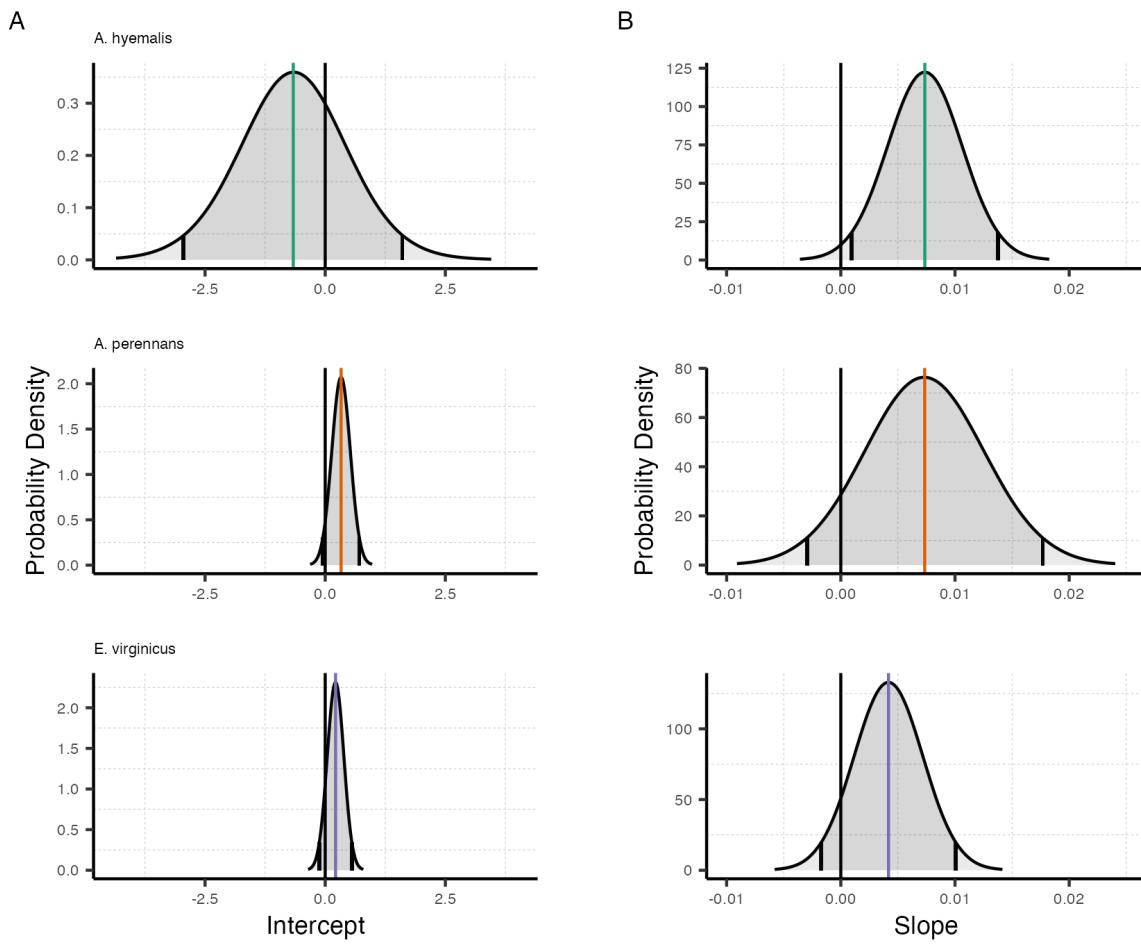
Consistency between observed data and predicted values indicate that the fitted model accurately describes the data. Graph shows density curves for the observed data (black) along with 100 predicted datasets (red).



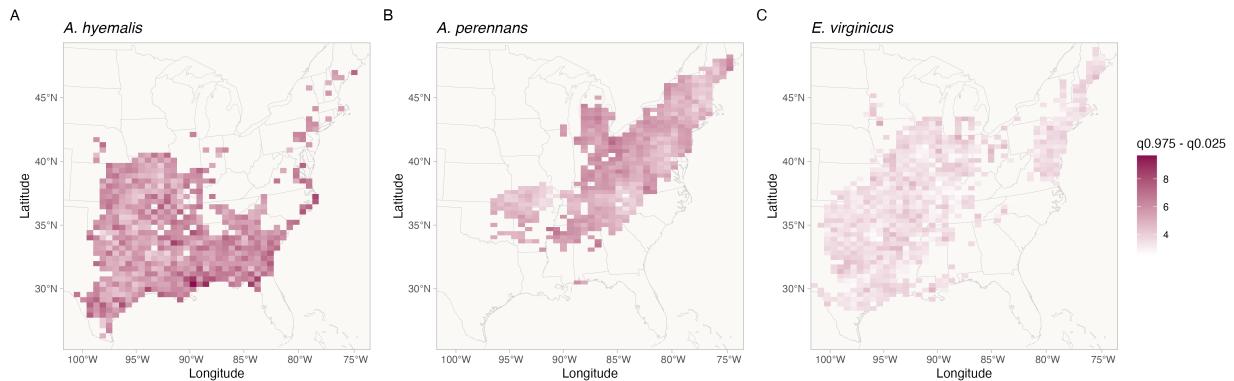
**Figure A4: ROC plot showing performance of the endophyte prevalence model in classifying observations according to endophyte status within the in-sample training data from herbarium collections.** The curves show adequate model performance for observed data. The AUC value is 0.79.



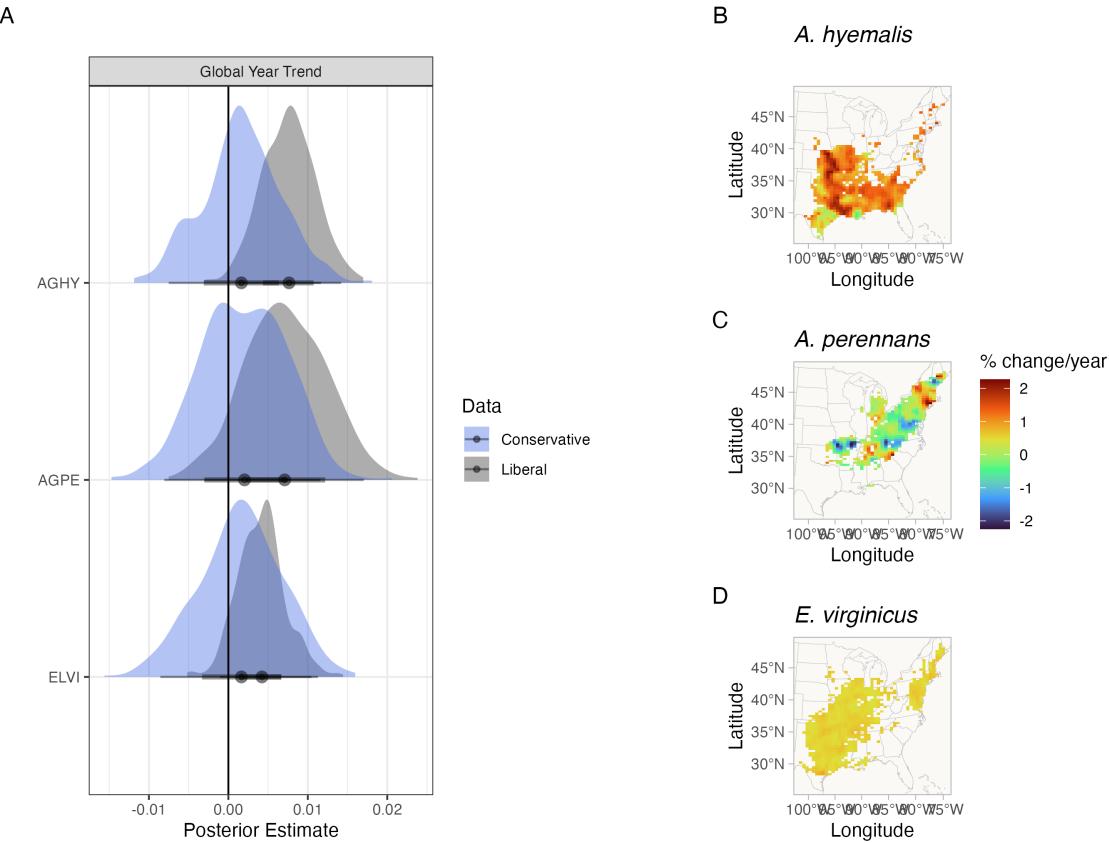
**Figure A5: ROC plot showing performance of the endophyte prevalence model in classifying observations according to endophyte status within the out-of-sample test data from contemporary surveys.** The curves show adequate model performance for test data. The AUC value is 0.77.



**Figure A6: Posterior estimates of parameters describing global intercept and temporal trends from the endophyte prevalence model.** Density curves show the probability density along with mean (colored line) and 95% CI (black lines) for the (A) intercept and (B) slope terms,  $A$  and  $T$  respectively from Eqn. 1. Colors represent each host species



**Figure A7: Credible interval width of temporal trends in endophyte prevalence across the distribution of each host species estimated from the endophyte prevalence model.**  
 Shading represents the range of the 95% posterior credible interval given in units of *% change in prevalence/year* for spatially varying slopes,  $\tau$  from Eqn. 1. Map lines delineate study areas and do not necessarily depict accepted national boundaries.



**Figure A8: Comparison of endophyte prevalence model estimates fit to data with liberal versus conservative endophyte scores.** Liberal and conservative scores document uncertainty in the endophyte identification process. Each specimen was given both a liberal and conservative scores. In cases of uncertain identification, the liberal status assumed a potential endophyte identification was more likely to be endophyte-positive while the conservative status assumed that the potential endophyte identification was less likely to be endophyte-positive. (A) Posterior estimates of global temporal trend ( $T$  from Eqn. 1) for the endophyte prevalence model fit to liberal scores (grey) and to conservative scores (blue). Maps show the spatially varying temporal trend estimates ( $\tau$  from Eqn. 1) from the endophyte prevalence model fit to conservative scores for (B) *A. hyemalis*, (C) *A. perennans*, and (D) *E. virginicus*. Note that the color scale differs between this visualization and Fig. 3 that shows estimates fit using liberal endophyte scores.

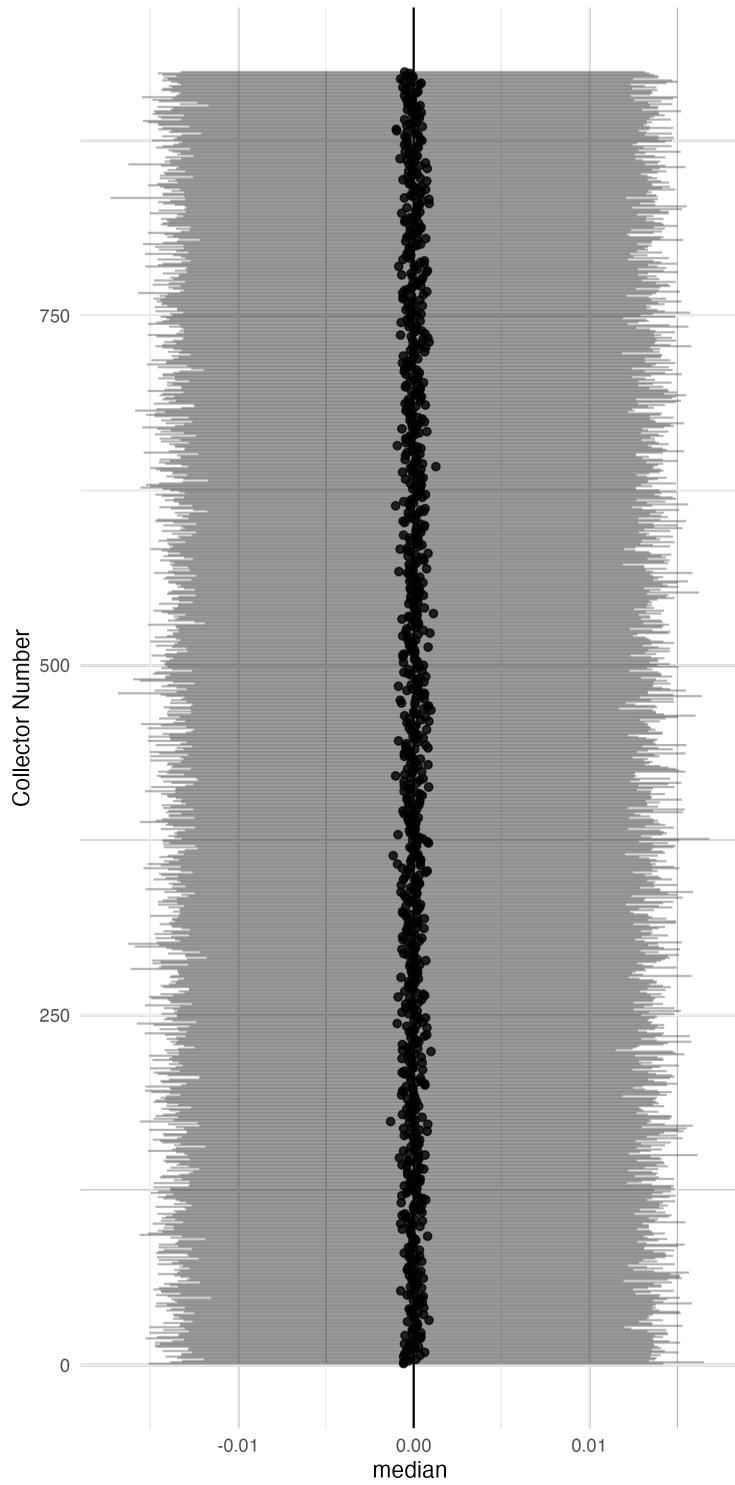
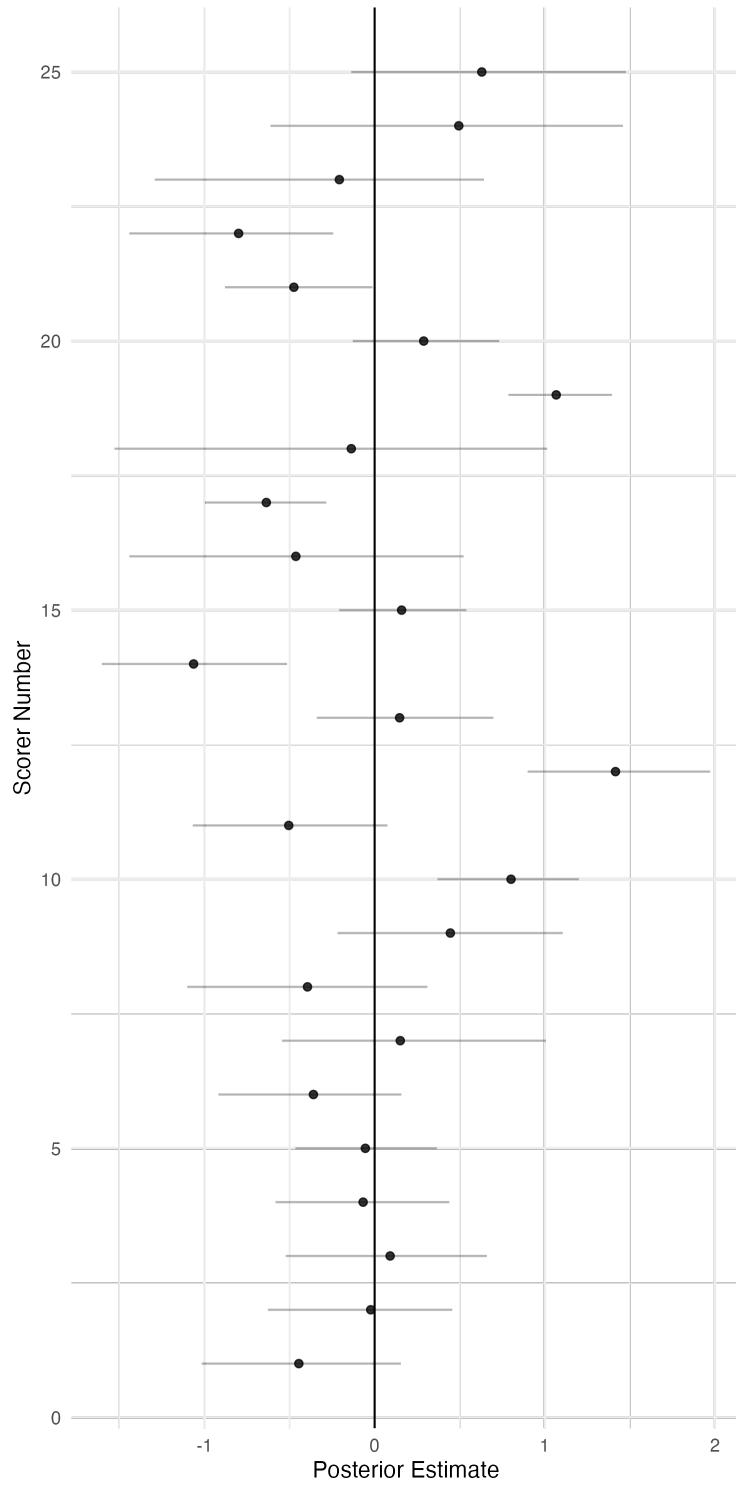
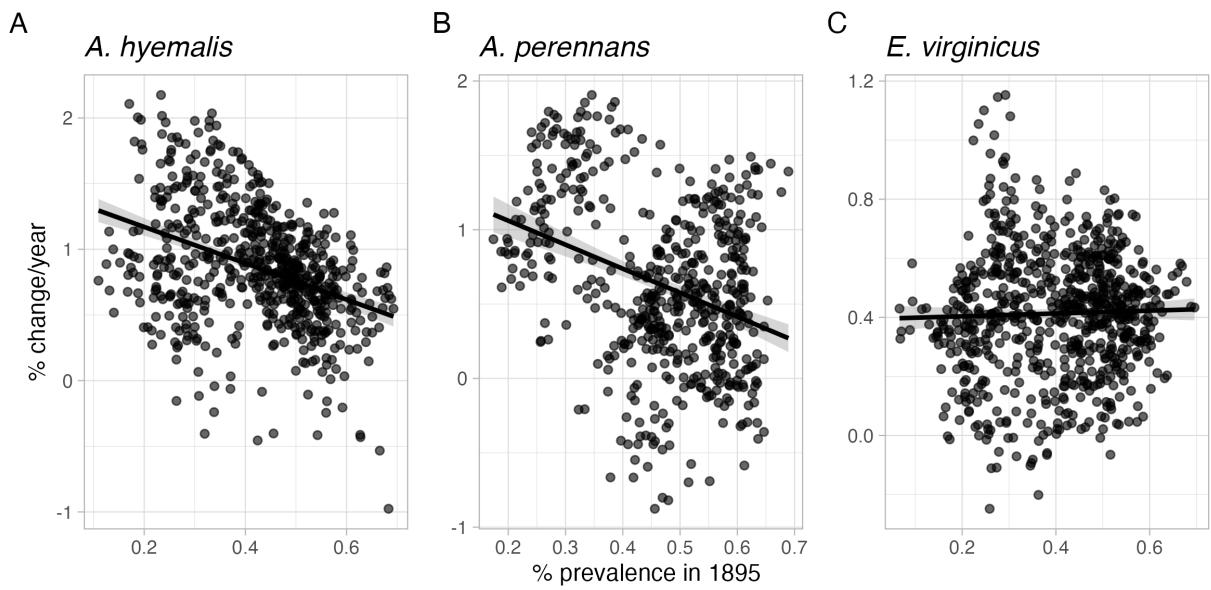


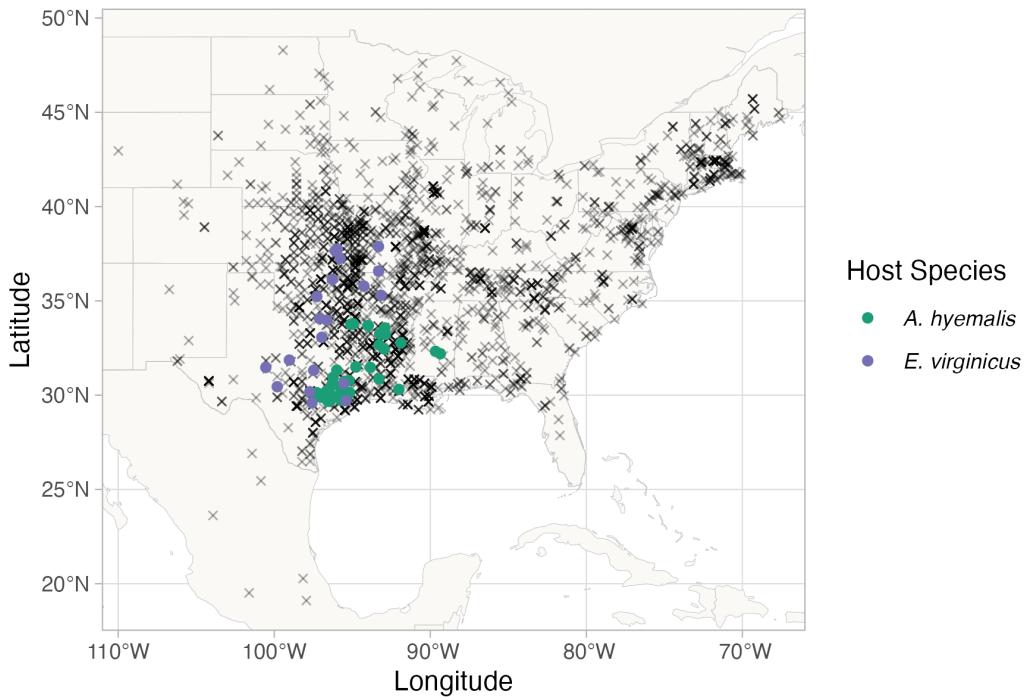
Figure A9: **Posterior estimates of collector random effects from endophyte prevalence model.** Collector random effects are denoted  $\chi$  in Eqn. 1 and represent variance associated with researchers who collected historic herbarium specimens. Points show posterior median along with 95% CI for each of 924 individual collectors.



**Figure A10: Posterior estimates of scorer random effects from endophyte prevalence model.** Scorer random effects are denoted  $\omega$  in Eqn. 1 and represent variance associated with researchers who identified *Epichloë* endophytes within herbarium specimen tissue samples. Points show posterior median along with 95% CI for each of 25 individual scorers.



**Figure A11: Relationship between initial prevalence and temporal trends in prevalence estimated from the endophyte prevalence model.** Points show predicted posterior mean temporal trend for each species at pixels across each host distribution ((A) *A. hyemalis*, (B) *A. perennans*, and (C) *E. virginicus*). along with a linear regression and shaded ribbon showing 95% confidence interval.



**Figure A12: Locations of contemporary surveys of endophytes used as "test" data to evaluate predictive ability of the endophyte prevalence model.** Points are locations of host populations surveyed between 2013 and 2019 for endophytes, colored by species (*A. hyemalis*: green, *E. virginicus*: purple). Black crosses show the historical herbarium collection locations used as "training" data for the endophyte prevalence model.

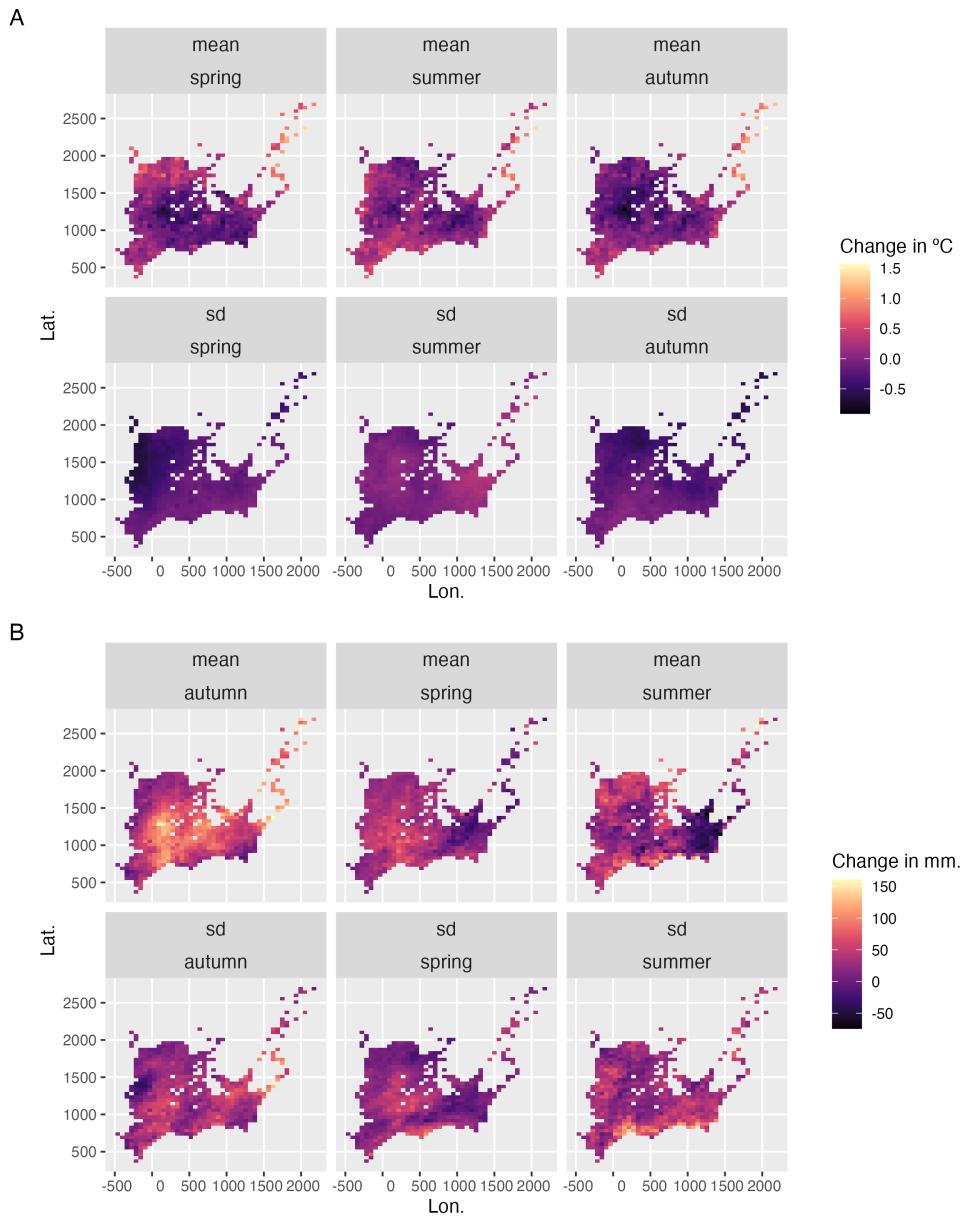
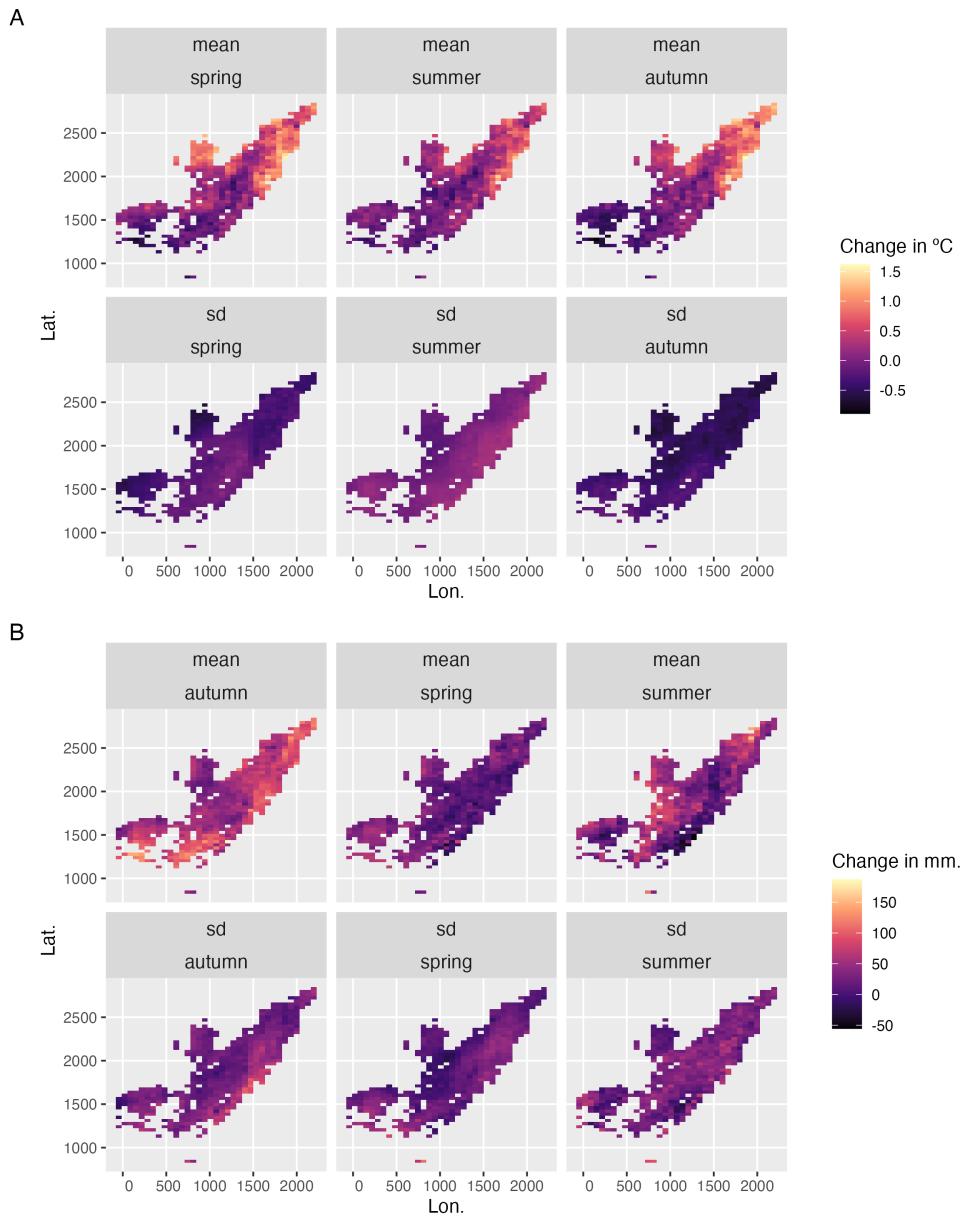


Figure A13: **Change in seasonal climate variables between the periods 1895-1925 and 1990-2020 across the distribution of *A. hyemalis*.** Color represents change in (A) seasonal temperature ( $^{\circ}\text{C}$ ) and (B) seasonal precipitation (mm.). Maps show pixels covering the modeled distribution of *A. hyemalis* used in *post hoc* climate regression analysis.



**Figure A14: Change in seasonal climate variables between the periods 1895-1925 and 1990-2020 across the distribution of *A. perennans*.** Color represents change in (A) seasonal temperature ( $^{\circ}\text{C}$ ) and (B) seasonal precipitation (mm.). Maps show pixels covering the modeled distribution of *A. perennans* used in *post hoc* climate regression analysis.

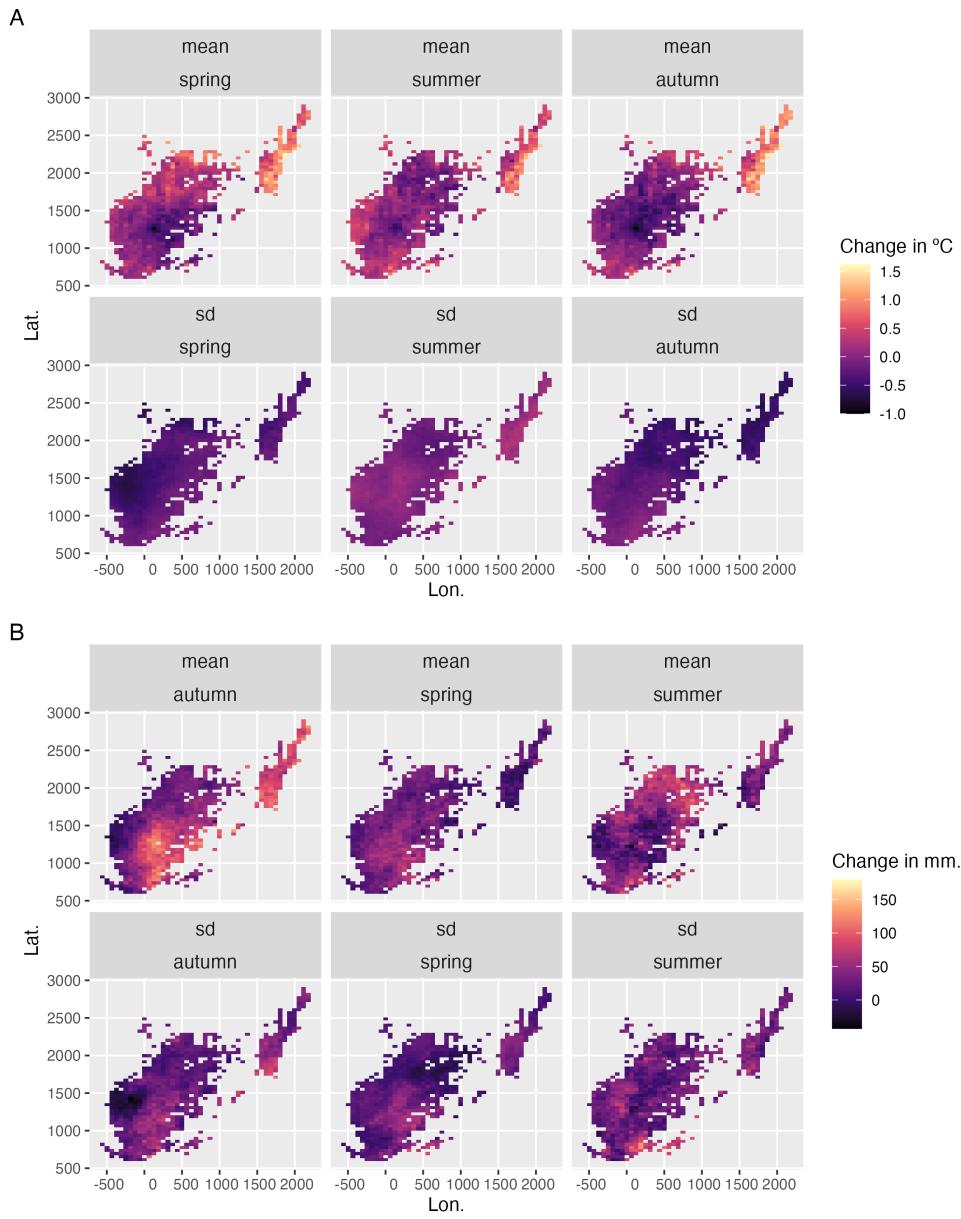


Figure A15: **Change in seasonal climate variables between the periods 1895-1925 and 1990-2020 across the distribution of *E. virginicus*.** Color represents change in (A) seasonal temperature ( $^{\circ}\text{C}$ ) and (B) seasonal precipitation (mm.). Maps show pixels covering the modeled distribution of *E. virginicus* used in *post hoc* climate regression analysis.

Table A1: Summary of herbarium samples across collections (no. of specimens)

Herbarium Collection	<i>A. hyemalis</i>	<i>A. perennans</i>	<i>E. virginicus</i>
Botanical Research Institute of Texas	350	190	198
Louisiana State University	72	38	62
Mercer Botanic Garden	3	0	6
Missouri Botanic Garden	210	205	122
Texas A&M	100	0	72
University of Kansas	134	34	197
University of Oklahoma	85	34	95
University of Texas & Lundell	183	91	102
Oklahoma State University	51	10	74

1093

## Supporting Methods

1094

### ODMAP Protocol

1095 [Overview](#)

1096 **Model purpose:** Mapping current distribution of *Epichloë* host species.

1097 **Target species:** *Agrostis hyemalis*, *Agrostis perennans*, and *Elymus virginicus*.

1098 **Study area:** Eastern North America

1099 **Spatial extent:** -125.0208, -66.47917, 24.0625, 49.9375 (xmin, xmax, ymin, ymax).

1100 **Spatial resolution:** 0.04166667, 0.04166667 (x, y).

1101 **Temporal extent:** 1990 to 2020.

1102 **Boundary:** Natural.

1103 [Data](#)

1104 **Observation type:** Occurrence records from Global Biodiversity Information Facility and

1105 herbarium collection across eastern North America. We used 713 occurrences records for *Agrostis*  
1106 *hyemalis*, 656 occurrence records for *Agrostis perennans* and 2338 for *Elymus virginicus*.

1107 **Response data type:** occurrence record, presence-only.

1108 **Coordinate reference system:** WGS84 coordinate reference system (EPSG:4326 code)

1109 **Climatic data:** raster data extracted from PRISM; 30-year normal mean and standard deviation  
1110 of temperature and of precipitation for three four-month seasons within the year (Spring: January,  
1111 February, March, April; Summer: May, June, July, August; Autumn: September, October,  
1112 November, December).

1113 **Model**

1114 **Model assumption:** We assumed that the target species are at equilibrium with their environ-  
1115 ment.

1116 **Algorithms:** Maximum entropy (maxent)

1117 **Workflow:** We described the workflow in the methods section of the manuscript.

1118 **Software:** All statistics were performed using Maxent 3.3.4 and R4.3.1 with packages terra, usdm,  
1119 spThin and dismo.

1120 **Code availability:** Available through this link: <https://github.com/joshuacfowler/EndoHerbarium>

1121 **Data availability:** Data was accessed through open-source R packages *rgbif*. *A. hyemalis*  
1122 (GBIF.Org, 2025a), *A. perennans* (GBIF.Org, 2025b), *E. virginicus* (GBIF.Org, 2025c)

1123 **Assessment**

1124 We used AUC to test model performance.

1125 **Prediction**

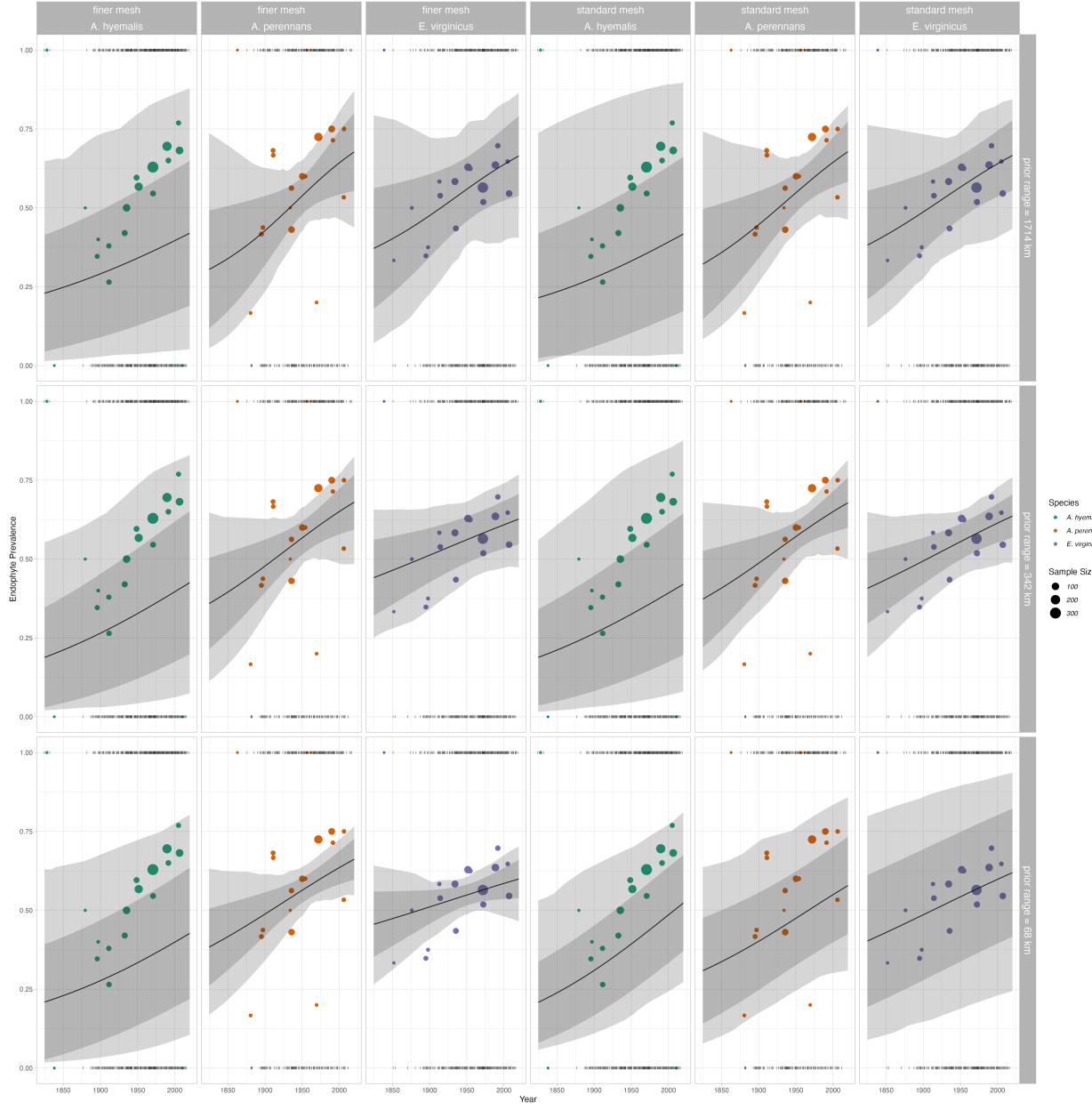
1126 We predicted the probability of presence of the host species as a binary maps (presence or absence)

## 1127 *Mesh and Prior Sensitivity Analysis*

1128 To test the influence that the triangulation mesh and choice of priors has on results, we compared  
1129 model results across a range of meshes and priors. We re-ran our model for the mesh used in main  
1130 body of the text (Fig. A2), which we refer to as the "standard mesh", and with a mesh with smaller

minimum vertices (finer mesh). Finer scale meshes increase computation time. For each of these meshes, we ran the model with a range of priors defining the spatial range of our spatial random effects: 342km (the prior used for presented results), as well as ranges five times smaller (68 km) and five times larger (1714 km). We found generally that these choices did not alter the direction of model predictions, but did influence the associated uncertainty and magnitude of some effects.

For overall temporal trends, we found that models with differing priors predicted consistently positive relationships over time (Fig. A16).



**Figure A16: Overall trend in endophyte prevalence evaluated for endophyte prevalence models with different range priors on spatially structured random effects, and for two different triangulation meshes.** Data used in model fitting is the same across all panels and as in the main text. Note that these plots, as compared to Fig. 2 in main text, show mean trends and do not incorporate variance associated with collector and scorer random effects.

1138 For spatially-varying temporal trends, we found that models with different priors predicted  
1139 consistent spatial patterns in temporal trends, although the range of this prediction varied depending  
1140 on the prior and mesh (Fig. A17 - A18). One noteworthy result of this analysis is that combinations  
1141 of prior choice and mesh can introduce instability in model fitting. This is evident in A17 panel B  
1142 and A18 panel B, where the prior range is smaller than the minimum vertex length of the mesh.  
1143 Model fitting takes an extended time period and the model struggles to identify variation across  
1144 space. Results with a set of prior ranges (Fig. A17 - A and C; Fig. A18 - A and C) result in  
1145 models that estimate trends across space of the same direction and order of magnitude, although  
1146 the "smoothness" of these predictions vary.

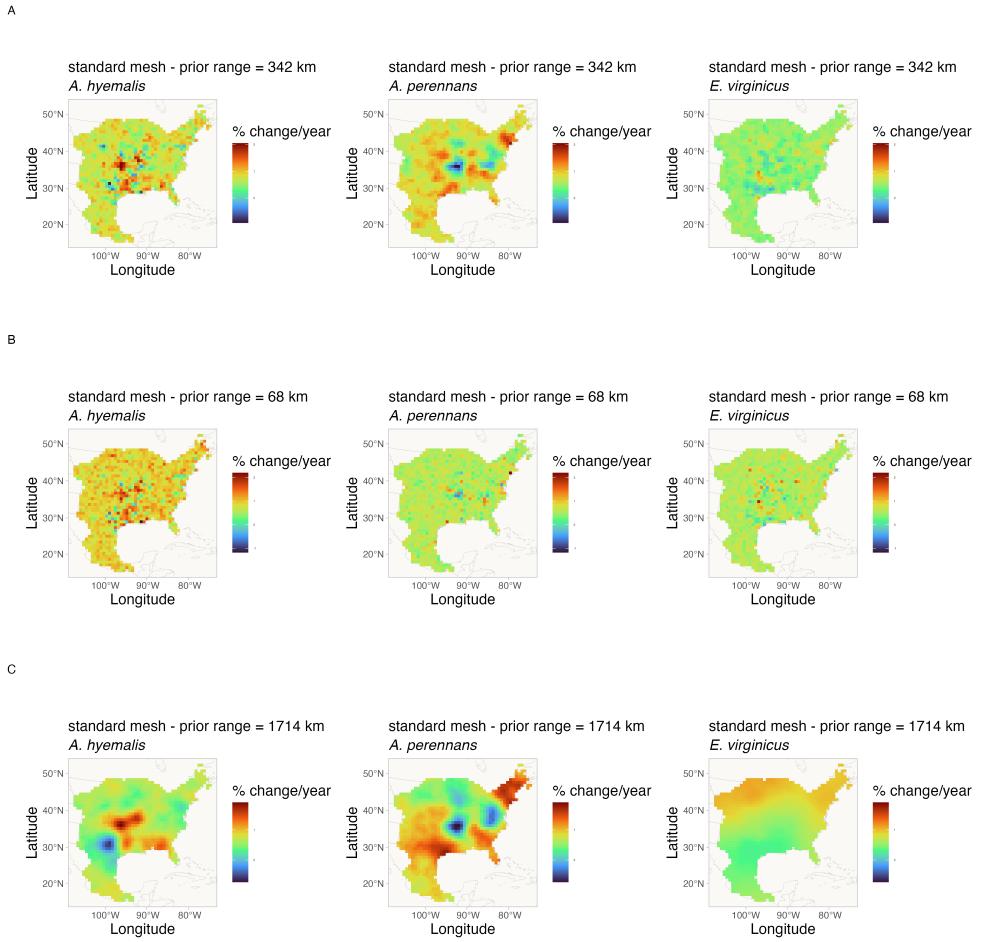
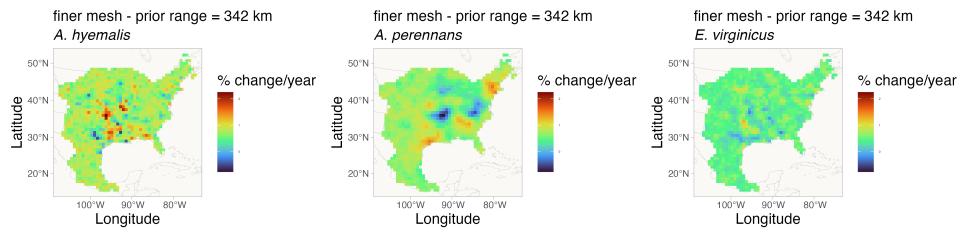
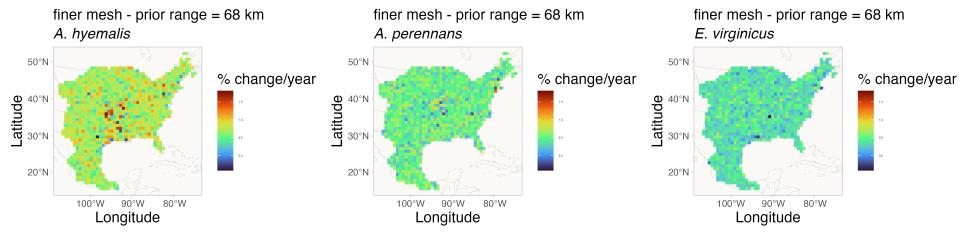


Figure A17: **Spatially-varying trends in endophyte prevalence evaluated for the endophyte prevalence model with different range priors on spatially structured random effects, and for the "standard" mesh.** Data used in model fitting is the same across all panels and as in the main text. Shading indicates the magnitude and direction of predicted trends for each of three host species for each of three prior ranges (rows A-C). Note that each plot has an individual scale bar.

A



B



C

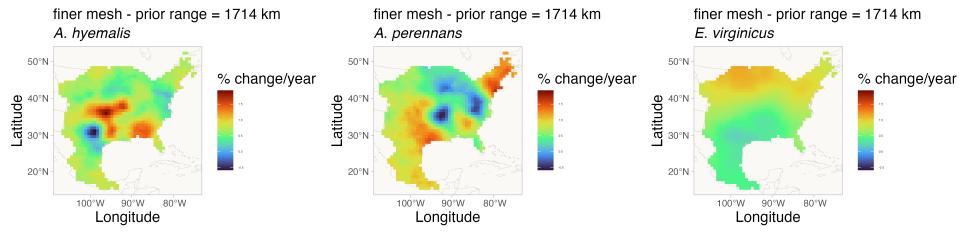


Figure A18: **Spatially-varying trends in endophyte prevalence evaluated for the endophyte prevalence model with different range priors on spatially structured random effects, and for the "finer" mesh.** Data used in model fitting is the same across all panels and as in the main text. Shading indicates the magnitude and direction of predicted trends for each of three host species for each of three prior ranges (rows A-C). Note that each plot has an individual scale bar.

1147 *Spatially-biased Sample Size Simulation Analysis*

1148 To examine how data that is unevenly distributed across host distributions may influence interpreta-  
1149 tion of spatially-varying coefficients, we performed a simulation analysis. Our focal species, *Agrostis*  
1150 *hyemalis*, *Agrostis perennans*, and *Elymus virginicus*, are widely distributed grasses across the east-  
1151 ern United States that host *Epichloë* fungal endophytes. For logistical reasons, our sampling visits  
1152 to herbaria focused on herbaria in the central southern U.S., which resulted in unevenly distributed  
1153 data across each host species' range. This is particularly noteable for *Agrostis perennans* which has  
1154 the most northern distribution and relatively fewer total collected specimens compared to the other  
1155 focal species. Thus, a significant portion in the northeast of this species' range is relatively sparsely  
1156 sampled. Our analysis presented in the main text identified this region as having strong increase in  
1157 endophyte prevalence. Future visits to herbaria with regional focuses in the Northeastern US would  
1158 certainly garner new specimens that could provide valuable insights into shifting host and symbiont  
1159 distributions.

1160 *Simulation of spatially-biased symbiont occurrence data*

1161 We simulated datasets with varying levels of missing-ness to examine how this missing-ness influ-  
1162 enced the estimation of spatially-varying trend estimates. We first generated 300 data points for  
1163 each of three hypothetical species at random positions across an area approximating the scale of  
1164 our focal data. Each data point was randomly assigned a year of collection across 200 years. We  
1165 then simulated data from a Bernoulli process with trends alternating across nine regions (Fig. A19)  
1166 in a 3X3 grid pattern. This grid pattern was intended to create a complex spatial layout of trends,  
1167 where trends were either an increase of 1% per year or a decrease of 1% per year.

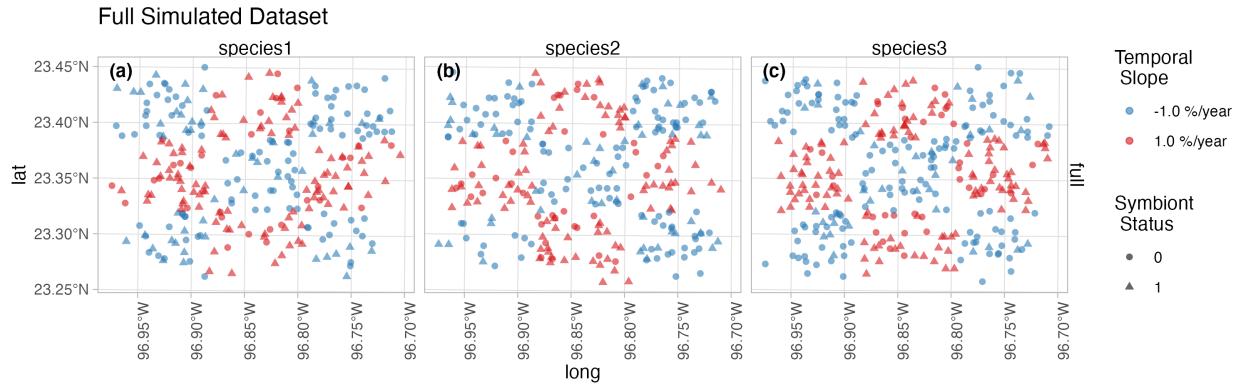
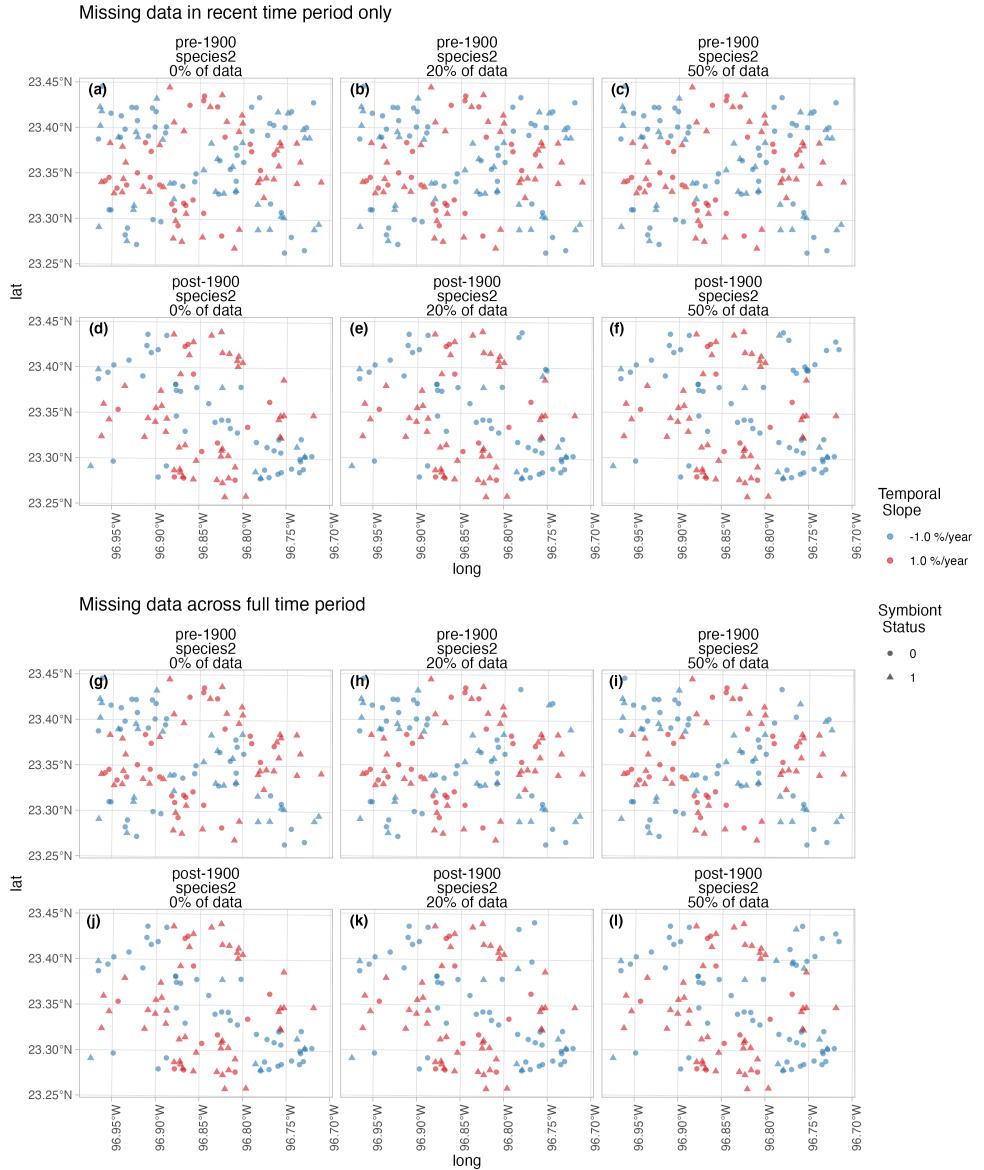


Figure A19: **Full simulated dataset of symbiotic association with spatially-varying temporal trends.** Color indicates the slope parameter used to simulate trends in endophyte status across nine "regions" for three species. Data are assigned collection years across a period of 200 years. Shape indicates the presence (1) or absence (0) of a symbiont.

From this full data, we generated six additional datasets with missing-ness in the northeast region of the simulated data for hypothetical species 2. The data remained the same for Species 1 and for species 3 across all datasets. For these six datasets, we removed data points at random in six ways: 0% of datapoints in northeast region, 0% of recent datapoints, only 20% of datapoints, only 20% of recent datapoints, only 50% of datapoints, and only 50% of recent datapoints (Fig. A20). We define the datapoints as part of the recent time period if they occur later than the median year. The result is 6 scenarios exploring degrees of spatial and temporal bias.



**Figure A20: Six simulated datasets representing scenarios of spatially-baised missingness for Species 2.** Missingness was imposed in the northeast region for six scenarios: 0% of recent datapoints available (a,d); only 20% of recent datapoints (b,e); only 50% of recent datapoints (c,f); 0% of datapoints across the full time period available (g,j); only 20% of datapoints across the full time period (h,k); and only 50% of datapoints across the full time period(i,l). Missingness was imposed only for hypothetical Species 2; Species 1 and 3 remain as in Figure A19. Color indicates the slope parameter used to simulate trends in endophyte status across 9 regions in a 3x3 grid. Shape indicates the presence (1) or absence (0) of a symbiont.

1175 *Statistical analysis*

1176 We analyzed each dataset with a model given by Eqn. A1 similar in construction to that used in  
1177 our central analysis.

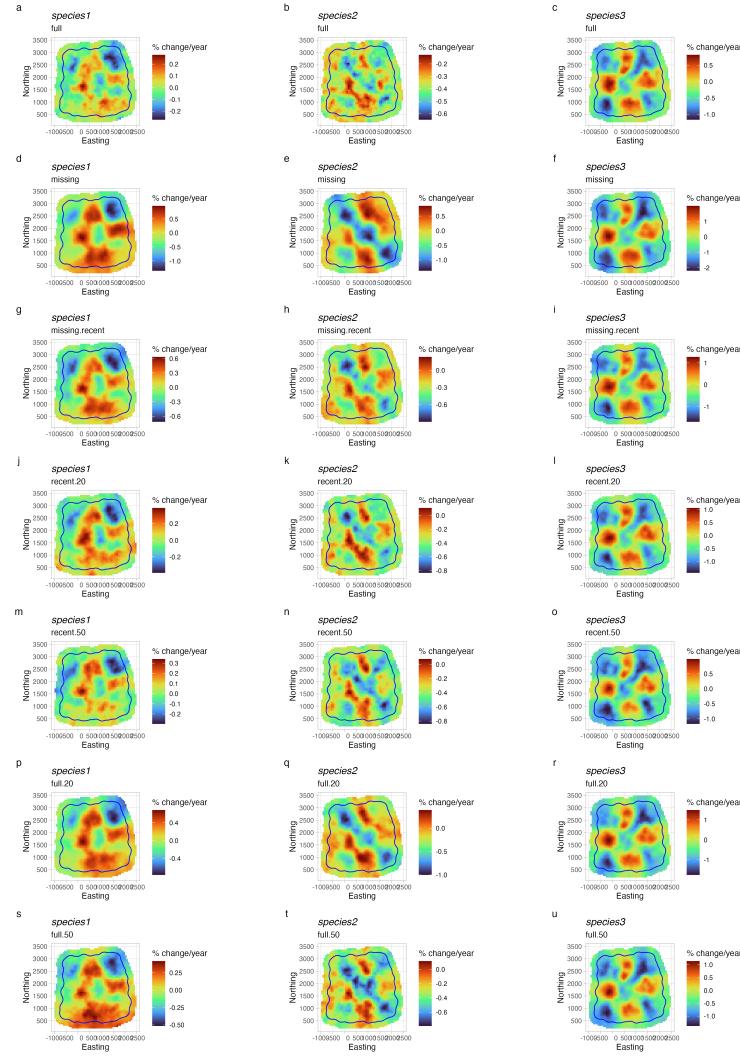
$$\text{logit}(\hat{P}_{h,i}) = A_h + T_h * \text{year}_i + \alpha_{h,l_i} + \tau_{h,l_i} * \text{year}_i + \delta_{l_i} \quad (\text{A1})$$

1178 Where symbiont presence/absence of the  $i^{th}$  specimen ( $P_{h,i}$ ) was modeled as a Bernoulli re-  
1179 sponse variable with expected probability of symbiont occurrence  $\hat{P}_{h,i}$  for each host species  $h$ . We  
1180 modeled  $\hat{P}_{h,i}$  as a linear function of intercept  $A_h$  and slope  $T_h$  defining the global trend in endophyte  
1181 prevalence specific to each host species as well as with spatially-varying intercepts  $\alpha_{h,l_i}$  and slopes  
1182  $\tau_{h,l_i}$  associated with location ( $l_i$ , the unique latitude-longitude combination of the  $i$ th observation).  
1183 Similar to the SVC model of our central analysis (Eqn. 1), we estimated a shared variance term  
1184 with the spatially-dependent random effect  $\delta_{l_i}$ , intended to account for residual spatial variation.  
1185 However in this analysis we omit i.i.d.-random effects terms associated with collector and scorer  
1186 identity ( $\chi_{c_i}$  and  $\omega_{s_i}$  in Eqn. 1) for the sake of simplicity.

1187 *Influence of spatially-biased sampling on model interpretation*

1188 Our analysis of the full simulated data shows that our model is suitably flexible to capture complex  
1189 spatial patterns in temporal trends (Fig. A21 a-c). Beyond this, the model also qualitatively  
1190 captures the spatial patterns in temporal trends even with large amounts of data missingness (i.e  
1191 missing up to 80% of the datapoints (Fig. A21 p-r)).

1192 While this analysis is not an exhaustive examination of the influence of sampling bias on our  
1193 results for several reasons (including not examining how different strengths in temporal trends,  
1194 different spatial arrangements of missing-ness influence model estimates, or different sample sizes  
1195 influence results), it demonstrates that the spatially-varying modelling framework implemented in  
1196 INLA we employ can suitably recover regional trends even with significant spatially-bias within  
1197 data collection, and further the analysis is likely robust to temporally-structured bias (missing data



**Figure A21: Mean predicted spatially-varying trend in symbiont prevalence across datasets with different levels of missingness.** Color indicates the estimated mean temporal trend within each pixel across the simulated data. Panels show estimates for models fit to different levels of missing data for species 2 in the northeast region ((a-c) the full dataset, (d-f) missing all datapoints across entire temporal period, (g-i) missing all datapoints only during the recent period, (j-l) missing 80% of the datapoints only during the recent period, (m-o) missing 50% of the datapoints only during the recent period, (p-r) missing 80% of the datapoints across the entire temporal period, (s-u) missing 50% of the datapoints across the entire temporal period). The mesh boundary that bounds the "full" simulated dataset is plotted in each panel.

1198 within recent collection period). Future work could more fully explore the scenarios that cause  
1199 this ability to break down. We expect this simulation reflects what may be a common scenario for  
1200 research investigating global change using natural history specimens. Collection effort by trained  
1201 taxonomists and professional collectors peaked in the past, and collections contain relatively fewer  
1202 modern specimens in many regions. Additionally, most global change research necessarily involves  
1203 accessing many specimens across collections. Research efforts such as ours will be unable to access  
1204 every specimen from all possible collections. Ongoing digitization efforts will make it possible to  
1205 more clearly assess how much data is missing from a particular study compared to the actual  
1206 holdings of natural history collections, but ultimately, the decision of what data and collections to  
1207 include is a question of sample size and study design.