

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

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<sup>1</sup> *I think this is should be 2*

## Abstract

13 Species' distributions and abundances are shifting in response to climate change. Most species  
14 harbor microbial symbionts that have the potential to influence these responses. Mutualistic  
15 microbial symbionts may provide resilience to environmental change by protecting their hosts  
16 from increasing stress. However, environmental change that disrupts these interactions may  
17 lead to declines in hosts or symbionts. Microbes preserved within herbarium specimens offer a  
18 unique opportunity to quantify changes in microbial symbiosis across broad temporal and spatial  
19 scales. We asked how the prevalence of seed-transmitted fungal symbionts of grasses (*Epichloë*  
20 endophytes), which can protect hosts from abiotic stress, have changed over time in response to  
21 climate change, and how these changes vary across host species' ranges. Specifically, we analyzed  
22 2,346 herbarium specimens of three grass host species collected over the last two centuries (1824  
23 – 2019) for the presence or absence of endophyte symbiosis, and evaluated spatial and temporal  
24 trends in endophyte prevalence. We found that endophytes have increased in prevalence over  
25 the last two centuries from ca. 25% prevalence to ca. 75% prevalence, on average, across the  
26 three host species. We also found that changes in prevalence were associated with observed  
27 changes in seasonal climate drivers<sup>2</sup> corresponding to each host species' peak growing season.  
28 Our analysis performed favorably in an out-of-sample predictive test, however we identified  
29 XXX as suggesting the model fusion may be an important step moving forward. Our results  
30 provide novel evidence for a cryptic biological response to climate change that may contribute to  
31 the resilience of host-microbe symbiosis through context-dependent benefits that confer a fitness  
32 advantage to symbiotic hosts under environmental change.<sup>3</sup>

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<sup>2</sup>Describe "changes" – warming? drying?

<sup>3</sup>I like this and the abstract in general. I agree with Tom and I think we have some space to add these details. Abstract : 300

## Introduction

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

43 Natural history specimens, which were originally collected to study and preserve taxonomic  
44 diversity, present a unique opportunity to explore long-term changes in ecological interactions  
45 across broad spatial and temporal scales (Meineke et al., 2018). Natural history collections, built  
46 and maintained by the efforts of thousands of scientists, are invaluable time machines, primarily  
47 comprised of physical specimens of organisms along with information about the time and place  
48 of their collection. These specimens often preserve physical legacies of ecological processes and  
49 species' interactions from dynamically changing environments across time and space. For exam-  
50 ple, previous researchers have used plant collections (herbaria) to document shifts in phenology  
51 (Berg et al., 2019; Park et al., 2019; Willis et al., 2017), pollination (Duan et al., 2019; Pauw and  
52 Hawkins, 2011), and herbivory (Meineke et al., 2019) related to anthropogenic climate change.  
53 However, few previous studies have leveraged biological collections to examine climate change-  
54 related shifts in a particularly common type of interaction: microbial symbiosis.

55 Microbial symbionts are common to all macroscopic organisms and can have important ef-  
56 fects on their hosts' survival, growth and reproduction (McFall-Ngai et al., 2013; Rodriguez et al.,  
57 2009). Many microbial symbionts act as mutualists, engaging in reciprocally beneficial interac-  
58 tions with their hosts that can ameliorate environmental stress. For example, bacterial symbionts

59 of insects, such as *Wolbachia*, can improve their hosts' thermal tolerance (Renoz et al., 2019; Truitt  
60 et al., 2019), and arbuscular mycorrhizal fungi, documented in 70-90% of families of land plants  
61 (Parniske, 2008), allow their hosts to persist through drought conditions by improving water and  
62 nutrient uptake (Cheng et al., 2021). On the other hand, changes in the mean and variance of  
63 environmental conditions may disrupt microbial mutualisms by changing the costs and bene-  
64 fits of the interaction for each partner, leading the interaction to deteriorate (Aslan et al., 2013;  
65 Fowler et al., 2024). Coral bleaching (the loss of symbiotic algae) due to temperature stress (Sully  
66 et al., 2019) is perhaps the best known example, but this phenomenon is not unique to corals.  
67 Lichens exposed to elevated temperatures experienced loss of photosynthetic function along with  
68 changes in the composition of their algal symbiont community (Meyer et al., 2022). How com-  
69 monly and under what conditions microbial mutualisms deteriorate or strengthen under climate  
70 change remain unanswered questions. Previous work suggests that these alternative responses  
71 may depend on the intimacy and specialization of the interaction as well as the physiological  
72 tolerances of the mutualist partners (Rafferty et al., 2015; Toby Kiers et al., 2010; Warren and  
73 Bradford, 2014).

74 Understanding of how microbial symbioses are affected by climate change is additionally  
75 complicated by spatial heterogeneity in the direction and magnitude of environmental change  
76 (IPCC, 2021). Beneficial symbionts are likely able to shield their hosts from environmental stress  
77 in locations that experience a small degree of change, but symbionts in locations that experience  
78 changes of large magnitude may be pushed beyond their physiological limits (Webster et al.,  
79 2008). Additionally, symbionts are often unevenly distributed across their hosts' distribution.  
80 Facultative symbionts may be absent from portions of the host range (Afkhami et al., 2014),  
81 and hosts may engage with a diversity of partners (different symbiont species or locally-adapted  
82 strains) across their environments (Frade et al., 2008; Rolshausen et al., 2018). Identifying broader  
83 spatial trends in symbiont prevalence is therefore an important step in developing predictions  
84 for where to expect changes in the symbiosis in future climates.

85 *Epichloë* fungal endophytes are specialized symbionts of cool-season grasses, which have been

86 documented in ~ 30% of cool-season grass species (Leuchtmann, 1992). They are transmitted ver-  
87 tically from maternal plants to offspring through seeds. Vertical transmission creates a feedback  
88 between the fitness of host and symbiont (Douglas, 1998; Fine, 1975; Rudgers et al., 2009). Over  
89 time, endophytes that act as mutualists should rise in prevalence within a host population (Don-  
90 ald et al., 2021). *Epichloë* are known to improve their hosts' drought tolerance (Decunta et al.,  
91 2021) and protect their hosts against herbivores (Crawford et al., 2010) and pathogens (Xia et al.,  
92 2018) likely through the production of a diverse suite of alkaloids and other secondary metabo-  
93 lites. The fitness feedback induced by vertical transmission leads to the prediction that endophyte  
94 prevalence should be high in populations where these fitness benefits are most important. Pre-  
95 vious contemporary survey studies have documented large-scale spatial patterns in endophyte  
96 prevalence structured by environmental gradients (Afkhami, 2012; Bazely et al., 2007; Granath  
97 et al., 2007; Sneck et al., 2017). We predicted that prevalence should track temporal changes in  
98 environmental drivers that elicit these fitness benefits.

99 Early research on *Epichloë* used herbarium specimens to describe the broad taxonomic di-  
100 versity of host species that harbor these symbionts (White and Cole, 1985), establishing that  
101 endophyte symbiosis could be identified in plant tissue from as early as 1851.<sup>4</sup> However, no  
102 subsequent studies, to our knowledge, have used the vast resources of biological collections to  
103 quantitatively assess spatio-temporal trends in endophyte prevalence and their environmental  
104 correlates. Grasses are commonly collected and identified based on the presence of their re-  
105 productive structures, meaning that preserved specimens typically contain seeds, conveniently  
106 preserving the fungi along with their host plants on herbarium sheets. This creates the oppor-  
107 tunity to leverage the unique spatio-temporal sampling of herbarium collections to examine the  
108 response of the symbiosis to historical climate change. Research using historical collections has  
109 clearly demonstrated other ecological signatures of a changing climate. However the predictive  
110 ability of these historical analyses is rarely tested against contemporary data (Lee et al., 2024).  
111 Identifying the ways in which these analyses fall short is a crucial step for the field move from

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<sup>4</sup>Edited this a bit. This is the earliest year we have in the database that was part of JFWhites original paper.

112 reading signatures in the past to forecasting ecological dynamics into the future.<sup>5</sup>

113 In this study, we assessed the long-term responses of endophyte symbiosis to climate change  
114 through the use of herbarium specimens of three North American host grass species (*Agrostis*  
115 *hyemalis*, *Agrostis perennans*, and *Elymus virginicus*). We first address questions describing spatial  
116 and temporal trends in endophyte prevalence: (i) How has endophyte prevalence changed over  
117 the past two centuries? and (ii) How spatially variable are temporal trends in endophyte preva-  
118 lence across eastern North America? We then address how climate change may be driving trends  
119 in endophyte prevalence by asking: (iii) What is the relationship between variation in temporal  
120 trends in endophyte prevalence and changes in climate drivers? We predicted that aggregate en-  
121 dophyte prevalence would increase over time in tandem with climate warming, and that hotspots  
122 of endophyte change would correspond spatially to hotspots of climate change. Finally, we eval-  
123 uated the performance of models built on data from historic specimens with an out-of-sample  
124 test, data on endophyte prevalence from contemporary surveys of host populations. To answer  
125 these questions we examined a total of 2,346 specimens collected across eastern North America  
126 between 1824 and 2019.<sup>6</sup>

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## Methods

128

### *Focal species*

129 Our surveys focused on three native North American grasses: *Agrostis hyemalis*, *Agrostis peren-*  
130 *nans*, and *Elymus virginicus*. Both *Agrostis* species host *Epichloë amarillans* (Craven et al., 2001;  
131 Leuchtmann et al., 2014), while *Elymus virginicus* typically hosts *Epichloë elymi* (Clay and Schardl,  
132 2002). These C<sub>3</sub> grass species are commonly represented in natural history collections with broad  
133 distributions covering much the eastern United States. *A. hyemalis* is a small short-lived perennial

5what do you think of this? trying to presage the out-of-sample test without over promising and without saying outright that our analysis sucks. Is this the right place for this? I had imagined some of this material will be really developed in the discussion.

6I think the consensus was to keep the out-of-sample validation which should absolutely go into the Intro as an important element of novelty. Should go in the Abstract too.

<sup>134</sup> species that germinates in the spring and typically flowers between March and July (most com-  
<sup>135</sup> mon collection month: May). *A. perennans* is of similar stature but is longer lived than *Agrostis*  
<sup>136</sup> *hyemalis* and flowers in late summer and early autumn (most common collection month: Septem-  
<sup>137</sup> ber). *A. perennans* is more sparsely distributed, tending to be found in shadier and more moist  
<sup>138</sup> habitats, while *A. hyemalis* is commonly found in open and recently disturbed ground. Both  
<sup>139</sup> *Agrostis* species are recorded from throughout the Eastern US, but *A. perennans* has a slightly  
<sup>140</sup> more northern distribution, whereas *A. hyemalis* is found rarely as far north as Canada and is  
<sup>141</sup> listed as a rare plant in Minnesota. *E. virginicus* is a larger and relatively longer-lived species that  
<sup>142</sup> is more broadly distributed than the *Agrostis* species. It begins flowering as early as March or  
<sup>143</sup> April but continues throughout the summer (most common collection month: July).

<sup>144</sup> *Herbarium surveys*

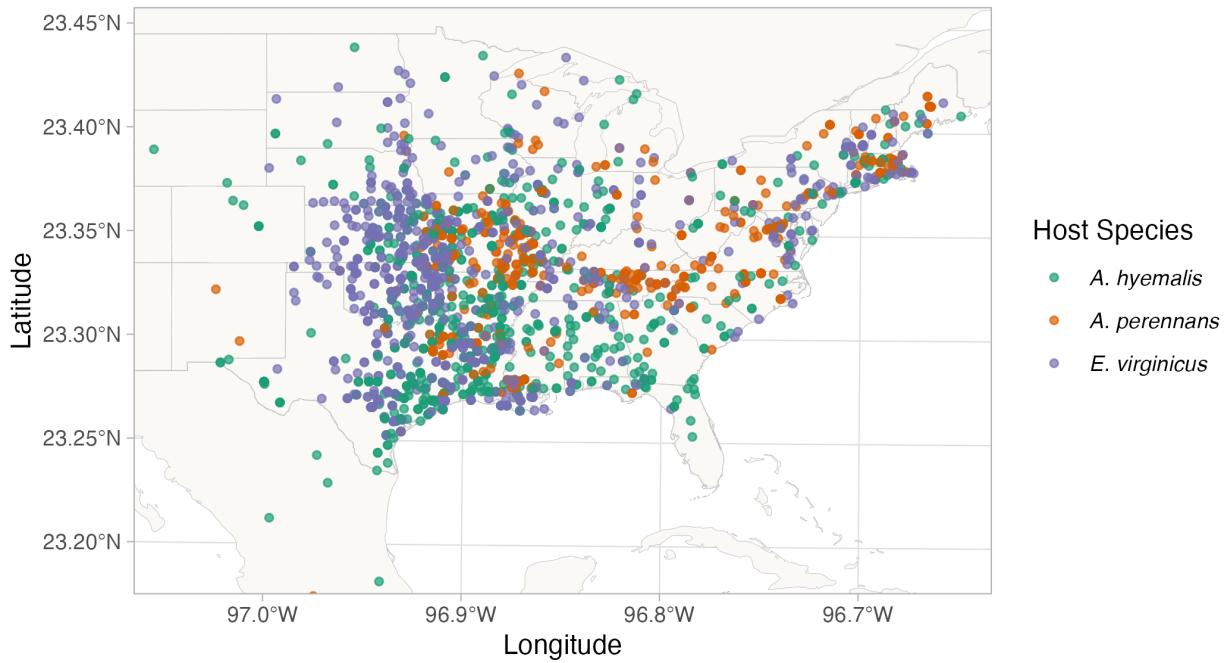
<sup>145</sup> We visited nine herbaria between 2019 and 2022 (see Table A1 for a summary of specimens in-  
<sup>146</sup> cluded from each collection). With permission from herbarium staff, we acquired seed samples  
<sup>147</sup> from 1135 *A. hyemalis* specimens collected between 1824 and 2019, 357 *A. perennans* specimens  
<sup>148</sup> collected between 1863 and 2017, and 854 *E. virginicus* specimens collected between 1839 and  
<sup>149</sup> 2019 (Fig. 1, Fig. 2A, Fig. A1). We chose our focal species in part because they are commonly  
<sup>150</sup> represented in herbarium collections, and produce high numbers of seeds, meaning that small  
<sup>151</sup> samples would not diminish the value of the specimens for future studies. We collected 5-10  
<sup>152</sup> seeds per specimen after examining the herbarium sheet under a dissecting microscope to en-  
<sup>153</sup> sure that we collected mature seeds, not florets or unfilled seeds, fit for our purpose of identifying  
<sup>154</sup> fungal endophytes with microscopy. We excluded specimens for which information about the  
<sup>155</sup> collection location and date were unavailable. Each specimen was assigned geographic coor-  
<sup>156</sup> dinates based on collection information recorded on the herbarium sheet using the geocoding  
<sup>157</sup> functionality of the ggmap R package (Kahle et al., 2019). Many specimens had digitized collec-  
<sup>158</sup> tion information readily available, but for those that did not, we transcribed information printed  
<sup>159</sup> on the herbarium sheet. Collections were geo-referenced to the nearest county centroid, or near-

<sup>160</sup> est municipality when that information was available. For a few of the oldest specimens, only  
<sup>161</sup> information at the state level was available, and so we used the state centroid.

<sup>162</sup> After collecting seed samples, we quantified the presence or absence of *Epichloë* fungal hy-  
<sup>163</sup> phae, which grow intercellularly, in each specimen using microscopy. We first softened seeds  
<sup>164</sup> with a 10% NaOH solution, then stained the seeds with aniline blue-lactic acid stain and squashed  
<sup>165</sup> them under a microscope cover slip. We examined the squashed seeds for the presence of fungal  
<sup>166</sup> hyphae at 200-400X magnification (Bacon and White, 2018). In some cases, the tissues examined  
<sup>167</sup> during microscopy came from flowers or otherwise non-viable seeds, which were excluded for  
<sup>168</sup> that specimen. On average we scored 4.7 seeds per specimen of *A. hyemalis*, 4.2 seeds per spec-  
<sup>169</sup> imen of *A. perennans*, and 3.8 seeds per specimen of *E. virginicus*; we scored # seeds in total. .  
<sup>170</sup> Due to imperfect vertical transmission (Afkhami and Rudgers, 2008), it is possible that symbiotic  
<sup>171</sup> host-plants produce a mixture of symbiotic and non-symbiotic seeds. We therefore designated a  
<sup>172</sup> specimen as endophyte-symbiotic if *Epichloë* hyphae were observed in one or more of its seeds,  
<sup>173</sup> or non-symbiotic if hyphae were observed in none of its seeds. To capture uncertainty in the  
<sup>174</sup> endophyte scoring process, we recorded both a "liberal" and a "conservative" endophyte status  
<sup>175</sup> for each plant specimen. When we identified potential endophytes with unusual morphology,  
<sup>176</sup> low uptake of stain, or a small amount of fungal hyphae across the scored seeds, we recorded a  
<sup>177</sup> positive liberal status (more likely to be endophyte-positive) and a negative conservative status  
<sup>178</sup> (less likely to be endophyte-positive). 89% of scored plants had matching liberal and conservative  
<sup>179</sup> scores, reflecting high confidence in endophyte status. The following analyses in the main text  
<sup>180</sup> used the liberal status, but we repeated all analyses with the conservative status which yielded  
<sup>181</sup> qualitatively similar results (Fig. ??)

<sup>182</sup> *Modeling spatial and temporal changes in endophyte prevalence*

<sup>183</sup> We assessed spatial and temporal changes in endophyte prevalence across each host distribution,  
<sup>184</sup> quantifying the "global" temporal trends, aggregating across space, and then examining spatial  
<sup>185</sup> heterogeneity in the direction and magnitude of endophyte change (hotspots and coldspots)



**Figure 1: Collection locations of herbarium specimens of three grass host species across eastern North America that were sampled for *Epichloë* endophyte presence or absence.**

across the spatial extent of each host's distribution. To appropriately account for the spatial non-independence of geo-referenced occurrences<sup>7</sup>, we used an approximate Bayesian method, Integrated Nested Laplace Approximation (INLA), to construct spatio-temporal models of endophyte prevalence. INLA provides a computationally efficient method of ascertaining parameter posterior distributions for certain models that can be formulated as latent Gaussian Models (Rue et al., 2009). Many common statistical models, including structured and unstructured mixed-effects models, can be represented as latent Gaussian Models. We incorporated spatial heterogeneity into this analysis using spatially-structured intercept and slope parameters implemented as stochastic partial differential equation (SPDE) approximations of a continuous spatial Gaussian process. This SPDE approach is a flexible method of smoothing across space while explicitly accounting for spatial dependence between data-points (Bakka et al., 2018; Lindgren

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<sup>7</sup> spelling?

<sup>197</sup> et al., 2011). Fitting models with structured spatial effects is possible with MCMC sampling but  
<sup>198</sup> can require long computation times, making INLA an effective alternative, which has been used  
<sup>199</sup> to model spatial patterns in flowering phenology (Willems et al., 2022), the abundance of bird  
<sup>200</sup> species (Meehan et al., 2019) and butterflies (Crossley et al., 2022), the distribution of temperate  
<sup>201</sup> trees (Engel et al., 2022) as well as the population dynamics of endangered amphibians (Knapp  
<sup>202</sup> et al., 2016) and other ecological processes (Beguin et al., 2012).

<sup>203</sup> We estimated global and spatially-varying trends in endophyte prevalence using a joint-  
<sup>204</sup> likelihood model. For each host species  $h$ , endophyte presence/absence of the  $i^{th}$  specimen ( $P_{[h]i}$ )  
<sup>205</sup> was modeled as a Bernoulli response variable with expected probability of endophyte occurrence  
<sup>206</sup>  $\hat{P}_{[h]i}$ . We modeled  $\hat{P}_{[h]i}$  as a linear function of intercept  $A_{[h]i}$  and slope  $T_{[h]}$  defining the global trend  
<sup>207</sup> in endophyte prevalence specific to each host species as well as with spatially-varying intercepts  
<sup>208</sup>  $\alpha_{[h_1]l[i]}$  and slopes  $\tau_{[h_1]l[i]}$  associated with location ( $l[i]$ , a unique latitude-longitude combination).  
<sup>209</sup> The joint-model structure allowed us to share variance terms across focal species to account for  
<sup>210</sup> dependence associated with the collection of specimens and identification of endophytes. Shared  
<sup>211</sup> variance terms included the spatially-dependent random effect  $\delta_{l[i]}$ , intended to account for resid-  
<sup>212</sup> ual spatial variation, and  $\chi_{c[i]}$  and  $\omega_{s[i]}$  i.i.d.-random effects indexed for each collector identity  
<sup>213</sup> ( $c[i]$ ), and scorer identity ( $s[i]$ ) of the  $i^{th}$  specimen.

$$\text{logit}(\hat{P}_{[h_1]i}) = A_{[h_1]i} + T_{[h_1]} * \text{year}_i + \alpha_{[h_1]l[i]} + \tau_{[h_1]l[i]} * \text{year}_i + \delta_{l[i]} + \chi_{c[i]} + \omega_{s[i]} \quad (1a)$$

$$\text{logit}(\hat{P}_{[h_2]i}) = A_{[h_2]i} + T_{[h_2]} * \text{year}_i + \alpha_{[h_2]l[i]} + \tau_{[h_2]l[i]} * \text{year}_i + \delta_{l[i]} + \chi_{c[i]} + \omega_{s[i]} \quad (1b)$$

$$\text{logit}(\hat{P}_{[h_3]i}) = A_{[h_3]i} + T_{[h_3]} * \text{year}_i + \alpha_{[h_3]l[i]} + \tau_{[h_3]l[i]} * \text{year}_i + \delta_{l[i]} + \chi_{c[i]} + \omega_{s[i]} \quad (1c)$$

$$(1d)$$

<sup>214</sup> Previous work suggests that behavior of historical botanists and uneven sampling may intro-  
<sup>215</sup> duce biases into ecological inferences made from historic collections (Kozlov et al., 2020). Prolific  
<sup>216</sup> collectors who contribute thousands of specimens may be more or less likely to collect certain  
<sup>217</sup> species, or specimens with certain traits (Daru et al., 2018). Similarly, the process of scoring seeds

218 for hyphae involved several student researchers who, even with standardized training, may vary  
219 in their likelihood of positively identifying *Epichloë* hyphae. By including a random effect for  
220 collectors and for scorers, we attempted to account for variance across individual researchers  
221 that may bias our predictions of changes in endophyte prevalence.

222 We performed model fitting using the inlabru R package (). Global intercept and slope pa-  
223 rameters A, and T, were given vague priors. Scorer and collector random effects,  $\chi$  and  $\omega$ , were  
224 given penalized complexity priors, with distributions approximating a Normal distribution with  
225 standard deviation of 5. Each spatially-structured parameter depended on a covariance matrix  
226 according to the proximity of each collection location (Bakka et al., 2018; Lindgren et al., 2011).  
227 The covariance matrix was approximated using a Matérn covariance function, with each data  
228 point assigned a location according to the nodes of a mesh of non-overlapping triangles encom-  
229 passing the study area (Fig. A2). Priors, termed "range" and "variance", define the distance of  
230 spatial decay described by the Matérn covariance function. Priors for results presented in the  
231 main text reflect a range of XX<sup>8</sup> kilometers. We found that model results were sensitive to this  
232 choice, and so tested a range of priors (from XX kilometers to XX kilometers) and meshes (Sup-  
233 plemental Material), finding that model results were qualitatively similar, i.e. the same direction  
234 of effects across space, but that the magnitude and uncertainty varied.

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

236 We evaluated the predictive ability of the model using both in-sample training data from the  
237 herbarium surveys, and with out-of-sample test data from contemporary endophyte surveys, **an**  
238 **important but rarely used strategy in ecological studies (Tredennick et al., 2021).**<sup>9</sup> <sup>10</sup> We used  
239 data from contemporary surveys of endophyte prevalence in *A. hyemalis* and *E. virginicus* in Texas  
240 and the southern US. Surveys of *E. virginicus* were conducted in 2013 as described in Sneed et al.

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8

<sup>9</sup> *This is the type of thing to emphasize in the intro? Are there any other collections-based papers that have done anything like this?? None to my knowledge.*

<sup>10</sup> *Add Benjamin lee paper, maybe? it's not just herbaria, but kind of related*

<sup>241</sup> (2017), and surveys of *A. hyemalis* took place between 2015 and 2020<sup>11</sup>. Population surveys of *A.*  
<sup>242</sup> *hyemalis* were initially designed to cover longitudinal variation in endophyte prevalence towards  
<sup>243</sup> its range edge, while surveys of *E. virginicus* were designed to cover latitudinal variation along its  
<sup>244</sup> range edge. In total, we visited 43 populations of *A. hyemalis* and 20 populations of *E. virginicus*  
<sup>245</sup> across the south-central US, with emphasis on Texas and neighboring states (Fig A11). During  
<sup>246</sup> surveys, we collected seeds from up to 30 individuals per location (average number of plants  
<sup>247</sup> sampled: 22.9). We quantified the endophyte status of each individual with staining microscopy  
<sup>248</sup> as described for the herbarium surveys (with 5-10 seeds scored per individual), and calculated  
<sup>249</sup> the prevalence of endophytes within the population (proportion of symbiotic plants divided by  
<sup>250</sup> the number of sampled plants). For each population, we compared the observed fraction of  
<sup>251</sup> endophyte-symbiotic hosts to the predicted probability of endophyte occurrence  $\hat{P}$  derived from  
<sup>252</sup> the model based on location and year. The contemporary survey period (2013-2020) is at the most  
<sup>253</sup> recent edge of the time period encompassed by the historical observations used for model fitting.  
<sup>254</sup> We compared the model's prediction for these locations to the observed population prevalence.

<sup>255</sup> *Assessing the role of climate drivers*

<sup>256</sup> We assessed how the magnitude of climate change may have driven changes in endophyte preva-  
<sup>257</sup> lence by assessing correlations between changes in climate and changes in endophyte prevalence  
<sup>258</sup> predicted from our spatial model at evenly spaced pixels across the study area. We first down-  
<sup>259</sup> loaded monthly temperature and precipitation rasters from the PRISM climate group (Daly and  
<sup>260</sup> Bryant, 2013) covering the time period between 1895 and 2020 using the 'prism' R package (Hart  
<sup>261</sup> and Bell, 2015). Prism provides reconstructions of historic climate variables across the United  
<sup>262</sup> States by spatially-interpolating weather station data (Di Luzio et al., 2008). We calculated 30-  
<sup>263</sup> year climate normals for seasonal mean temperature and cumulative precipitation for the recent  
<sup>264</sup> (1990 to 2020) and historic (1895 to 1925) periods. We used three four-month seasons within

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<sup>11</sup> *We have added more recent AGHY survey data. I am not sure if you have access to this but you should definitely use it. Karl or I can point you to the right file.*

265 the year (Spring: January, February, March, April; Summer: May, June, July, August; Autumn:  
266 September, October, November, December). This division of seasons allowed us to quantify dif-  
267 ferences in climate associated with the two “cool” seasons, when we expected our focal species  
268 to be most biologically active (*A. hyemalis* flowering phenology: spring; *E. virginicus*: spring and  
269 summer; *A. perennans*: autumn). In addition to mean climate conditions, environmental vari-  
270 ability itself can influence population dynamics (Tuljapurkar, 1982) and changes in variability  
271 are a key prediction of climate change models (IPCC, 2021; Stocker et al., 2013). Therefore, we  
272 calculated the standard deviation for each annual and seasonal climate driver across each 30-  
273 year period. We then took the difference between recent and historic periods for the mean and  
274 standard deviation for each climate driver (Figs. A12-A14). All together, we assessed twelve  
275 potential climate drivers: the mean and standard deviation of spring, summer, and autumn temper-  
276 ature, as well as the mean and standard deviation of spring, summer, and autumn cumulative  
277 precipitation, cumulative precipitation, and cumulative precipitation.

278 To evaluate whether areas that have experienced the greatest changes in endophyte preva-  
279 lence (hotspots of endophyte change) are associated with high degrees of change in climate  
280 (hotspots of climate change), we modeled spatially varying slopes of endophyte change through  
281 time ( $\tau_{[h]l}$  as a linear function of environmental covariates, with a Gaussian error distribution.<sup>12</sup>  
282 Data from each host species was analysed separately. Fitting regressions to many pixels across  
283 the study region risks artificially inflating confidence in our results due to large sample sizes, and  
284 so we performed this analysis using only a random subsample of 250 pixels across the study  
285 region, which provided results qualitatively similar to analysis of the full set of pixels<sup>13,14</sup>.

286 15

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<sup>12</sup>I think we need to account for uncertainty in the slopes. They are outputs of a (quasi) Bayesian model so we should be able to propagate all the uncertainty in the posterior distribution.

<sup>13</sup>100 seems like a low number to me. What if we did this for all of the herbarium collection locations?

<sup>14</sup>I upped the number of points. I don't think conceptually we need to only do collection locations, but I can work on that as an alternative.

<sup>15</sup>I cut the notation for the Gaussian model for now because it is a pretty simple model and the notation may be overkill, plus because I changed your tau's to beta's there were betas on both sides of the tilde, which was confusing/annoying. Happy have the

287

## *Modeling distributions of host species*

288 We modeled the distribution of each host species to generate maps on which we predicted the  
 289 dynamics of *Epichloë* symbionts. We followed the ODMAP (overview, data, model, assessment,  
 290 prediction) protocol (Crossley et al., 2022), using presence-only observations of the host species  
 291 from GBIF between 1990 to 2020<sup>16</sup>. To reduce the potential influence of sampling bias and spa-  
 292 tial autocorrelation, we thinned the occurrences to the spatial scale ()<sup>17</sup> of our selected climatic  
 293 predictors. We selected climate variables that aligned with our analysis of climatic influences on  
 294 trends in endophyte prevalence described above. We calculated the mean and standard deviation  
 295 of seasonal temperature and precipitation across 1990 to 2020. Among this suite of variables,  
 296 we chose to include mean spring temperature, mean spring precipitation, and mean summer  
 297 temperature<sup>18</sup>, which were uncorrelated (Variance Inflation Factor > 0.7) and allowed us to pre-  
 298 dict the occurrence probability of each host species in space and time. We fit maximum entropy  
 299 (MaxEnt) models using the maxent function in the package dismo (Hijmans et al., 2017). Max-  
 300 Ent is preferred because it has been shown to generate response curves with less unpredictable  
 301 behavior when applied to new climates (Hijmans and Graham, 2006).<sup>19</sup> We generated 10,000  
 302 pseudo-absences as background points, and split the occurrence data into 75% for model train-  
 303 ing and 25% for model testing. The performance of models was evaluated with AUC AUC<sup>20</sup>  
 304 (Jiménez-Valverde, 2012). To convert the continuous predicted probabilities into binary presence  
 305 - absence maps, we used the training sensitivity (true positive rate) and specificity threshold  
 306 (true negative rate) (Liu et al., 2005). These binary maps serve as boundaries in presented maps  
 307 of change in endophyte prevalence, and outline the set of pixels used in our analysis of climate

*notation back if you prefer it. I am also a little confused because the appendix has spearman correlations but there are no methods here for where those come from.*

<sup>16</sup>How many data points does this end up being?

<sup>17</sup>I think this is 4km, but need to check

<sup>18</sup>is this list accurate? my re-running my climate analysis means we ought to re-run the sdm's, and use SD instead of CV, so we can update this list based on whatever is appropriate

<sup>19</sup>possibly could remove this sentence?

<sup>20</sup>can we add these values?

<sup>308</sup> correlates with trends in endophyte prevalence

<sup>309</sup> **Results**

<sup>310</sup> *How has endophyte prevalence changed over time?*

<sup>311</sup> We found that endophyte prevalence increased within the examined specimens over the last two  
<sup>312</sup> centuries for all three host species (Fig. 2). On average, modeling indicated that endophytes of *A.*  
<sup>313</sup> *perennans* and *E. virginicus* increased from ~ 40 % to 70% prevalence across the study region, and  
<sup>314</sup> that of *A. hyemalis* increased from ~ 25% to over 50% prevalence. Our model indicates a high  
<sup>315</sup> certainty that overall temporal trends are positive across species (99% probability of a positive  
<sup>316</sup> overall year slope in *A. hyemalis*, 92% probability of a positive overall year slope in *A. perennans*,  
<sup>317</sup> and 91% probability of a positive overall year slope in *E. virginicus*) (Fig. A6)

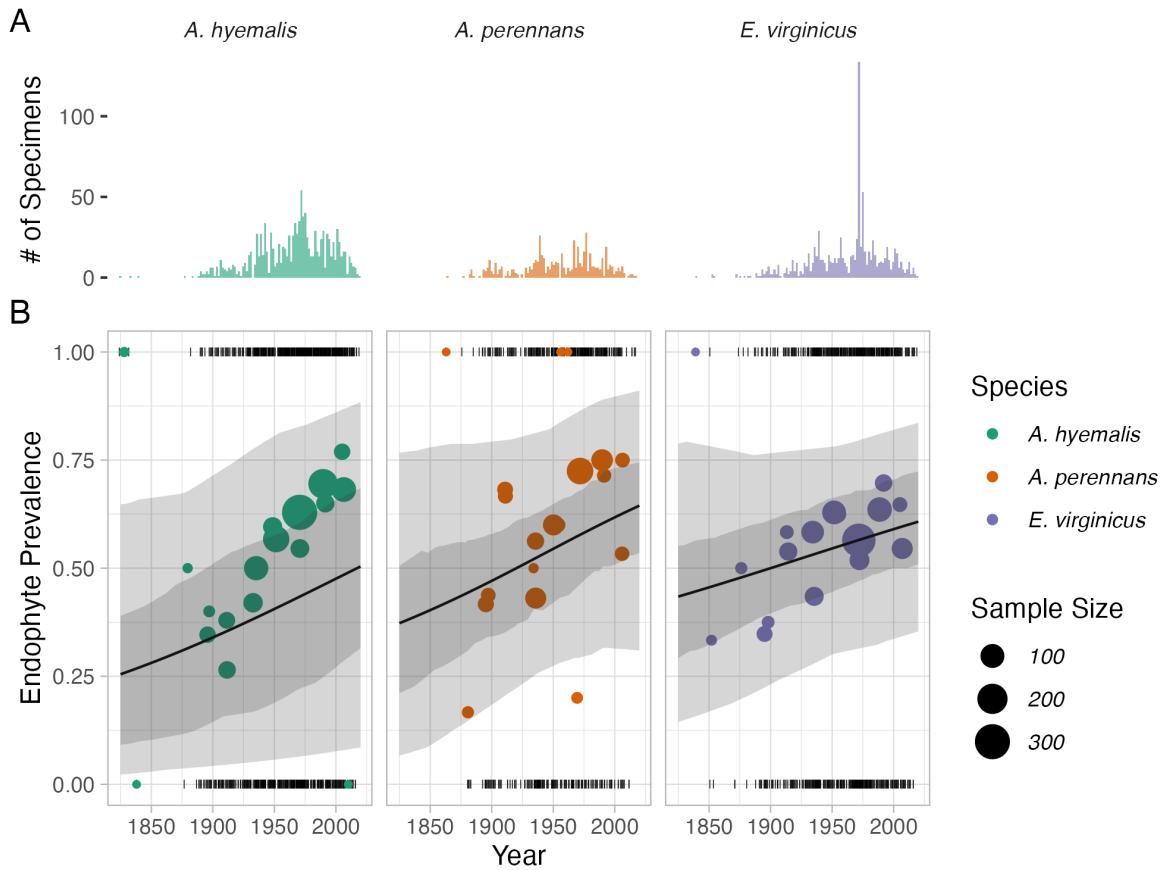


Figure 2: Temporal trends in endophyte prevalence. (A) Histograms show the frequency of scored specimens through time for each host species. (B) Lines show predicted mean endophyte prevalence over the study period along with the 50% and 95% CI bands incorporating uncertainty associated with collector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

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

Our model revealed hotspots of change in endophyte prevalence. While there was an overall increase in endophyte prevalence, these changes varied across the host species' ranges (Fig. 3). In some regions, posterior estimates of spatially varying temporal trends,  $\tau$ , indicate that *A.*

322 *hyemalis* and *A. perennans* experienced increases in percent prevalence by as much as 2% per  
 323 year over the study period, while *E. virginicus* experienced increases up to around 1% per year.  
 324 Compared to *E. virginicus*, which had a weaker overall increase in endophytes and less spatial  
 325 variability, maps of both *Agrostis* species show areas of strong increase and areas of declining  
 326 prevalence. Notably, endophytes increased towards the western range edge of *A. hyemalis* (Fig.  
 327 3A) and across the northeastern US for *A. perennans* (Fig. 3B). Posterior estimates of uncertainty  
 328 in spatially varying slopes indicate that these hotspots of change may have experienced increases  
 329 of up to 5% per year while declines in prevalence may be as great as 4% per year for *A. hyemalis*  
 330 and *A. perennans*. For *E. virginicus*, uncertainty ranges between 3.5% increases and 2.5% decreases  
 331 (Fig. A7).

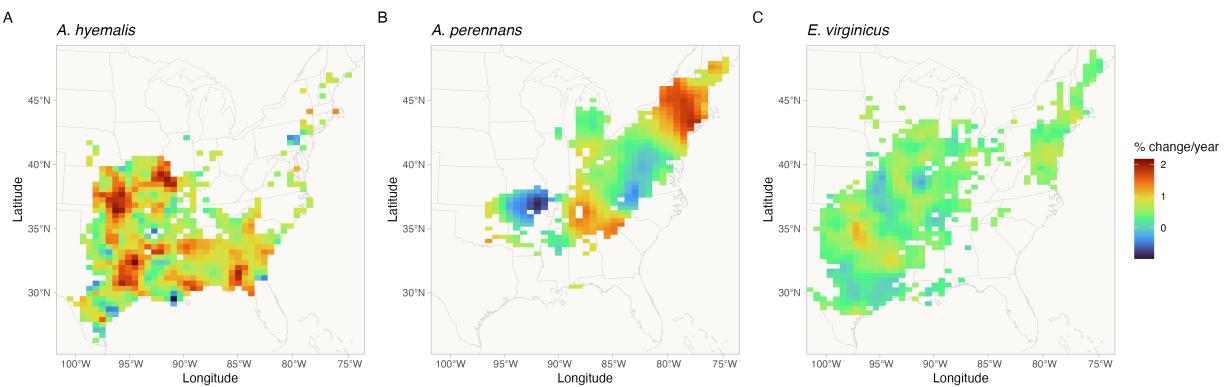


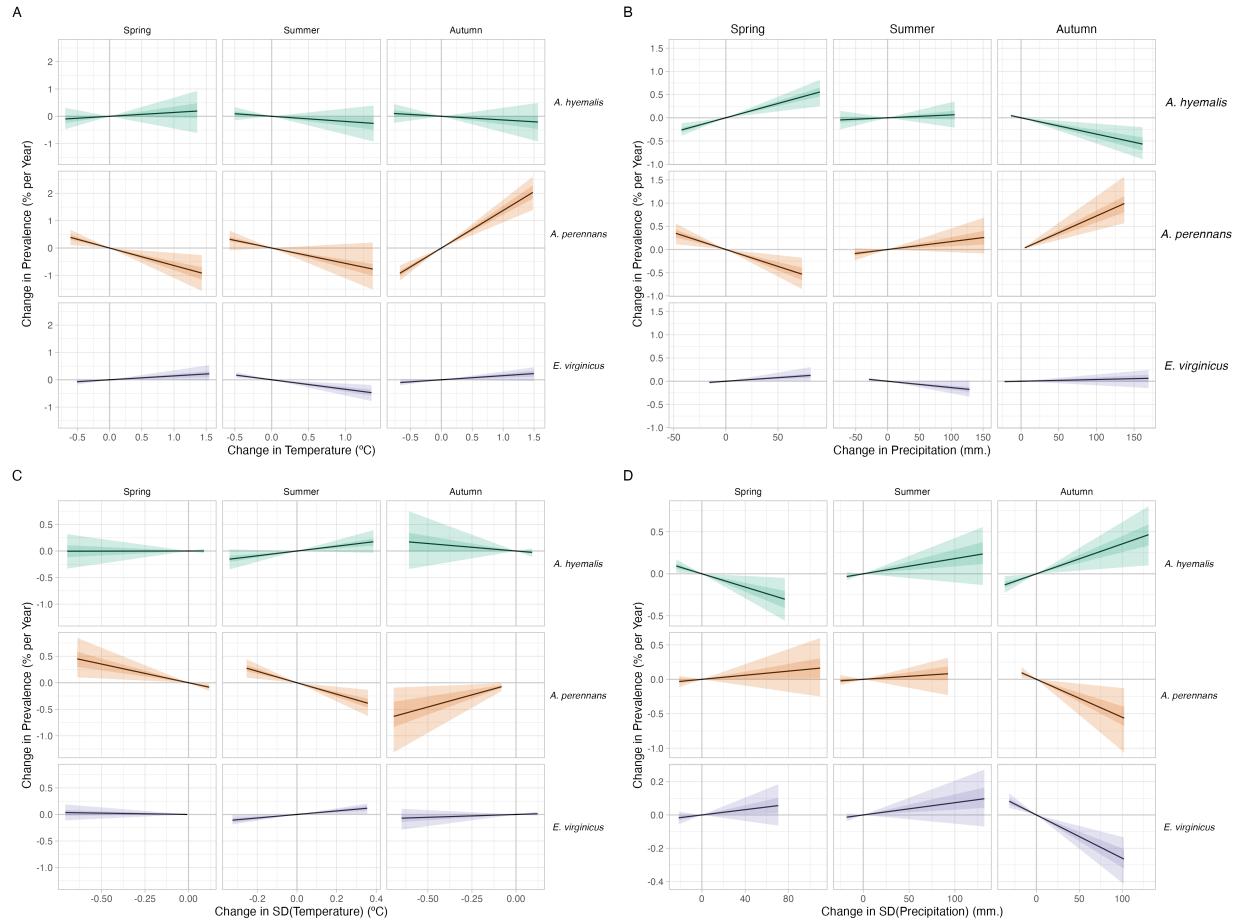
Figure 3: Predicted posterior mean of spatially-varying slopes representing change in endophyte prevalence for each host species. Color indicates the relative change in predicted endophyte prevalence.

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

334 We found that trends in endophyte prevalence were strongly associated with seasonal climate  
 335 change drivers (Fig. 4). For the majority of the study region, the climate has become wetter and

336 cooler over the last century (Fig. A12-A14), a consequence of regional variation in global climate  
337 change (IPCC, 2021). Within the study region, spatial variation in climate trends were predic-  
338 tive of trends in endophyte prevalence. For example, strong increases in prevalence within *A.*  
339 *perennans* were most associated with autumn climate drivers that coincide with its Aug-Sep active  
340 growing season. For this species, warmer and wetter autumn climates showed particularly strong  
341 relationships, however other seasonal drivers may also contribute to increasing endophyte preva-  
342 lence (drier springs and cooler summers). Trends in endophyte prevalence for *A. hyemalis* were  
343 most strongly associated with changes in precipitation variability were the strongest predictors.  
344 Endophyte prevalence increased the most in regions that experienced greater spring precipita-  
345 tion along with increasing variability in summer and autumn precipitation. While this species  
346 actively grows and reproduces in the late spring and early summer, climate effects outside of the  
347 growing season may indicate that endophytes play a role in persistence during dormant periods  
348 through summer droughts or contribute to the ability to successfully germinate. Prevalence of  
349 endophytes of *E. virginicus* were least influenced by climate, but decreasing autumn temperature  
350 variability and less precipitation in autumn were the strongest predictors.

351 Correlations assessed using all pixels across each species distribution were qualitatively sim-  
352 ilar to these results (Fig. A11).

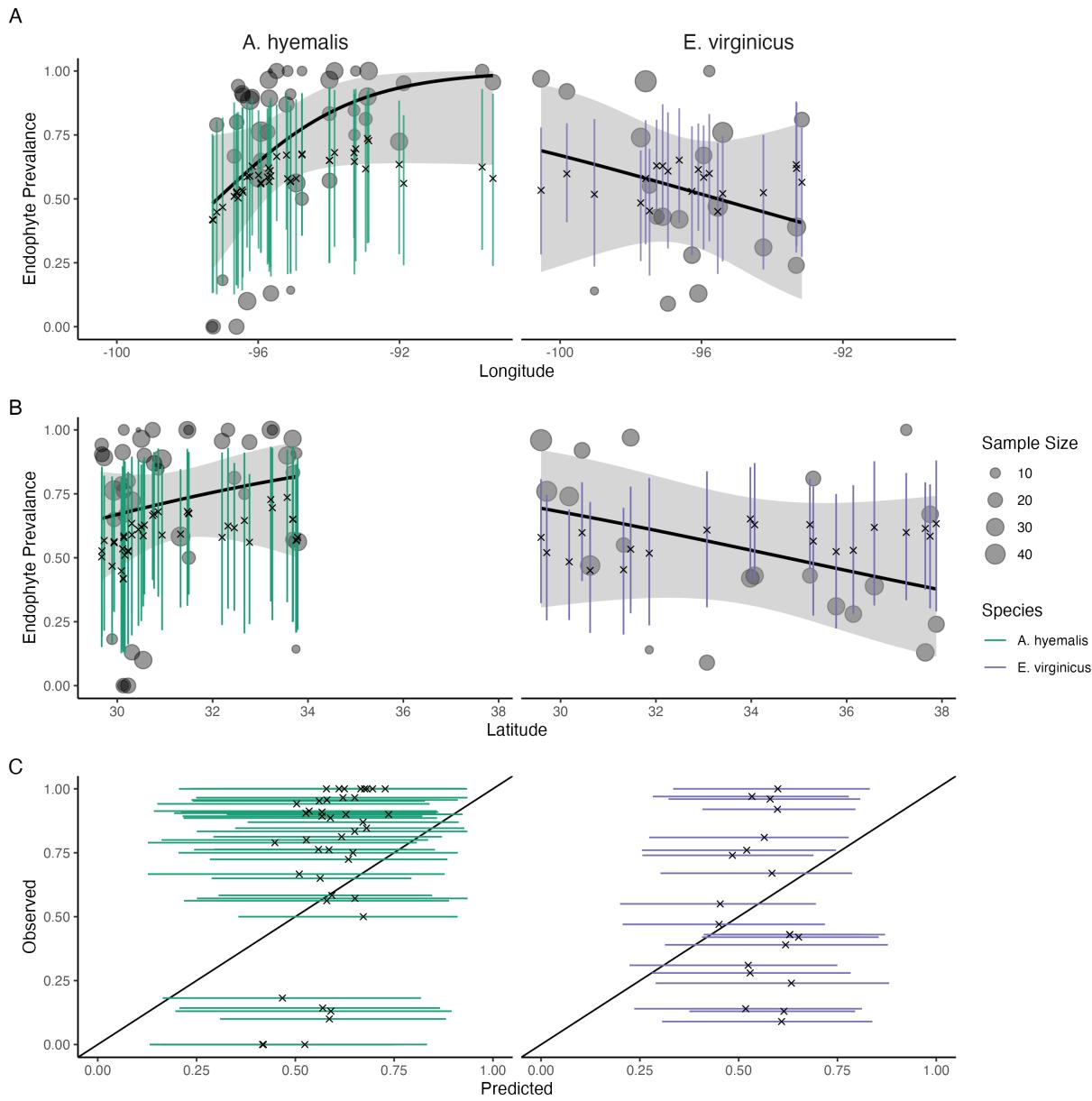


**Figure 4: Relationships between changes in seasonal climate drivers and predicted marginal trends in endophyte prevalence.** Lines show relationships between seasonal climate (A: mean temperature, B: cumulative precipitation, C: standard deviation in temperature, D: standard deviation in precipitation) and spatially-varying trends in endophyte prevalence for each host species, along with 50 and 95% CI.

353 *Performance on test data*

354 We found that model performance, as judged by AUC, was similar between historic herbarium  
 355 specimens used as training data and the out-of-sample test data from contemporary surveys (0.79  
 356 and 0.77 respectively; Fig. A5-A4). The model successfully captured broader regional trends  
 357 in endophyte prevalence present in the contemporary survey data, such as decline endophyte

<sup>358</sup> prevalence towards western longitudes in *A. hyemalis* (Fig. 5A). However, the contemporary  
<sup>359</sup> data contains additional variability at smaller scales not captured by our sampling of herbarium  
<sup>360</sup> specimens. We interpreted this to mean that the model captured regional spatial dynamics, but  
<sup>361</sup> underpredicts local scale dynamics. We discuss potential model improvements in the Discussion.



**Figure 5: Predicted vs observed endophyte prevalence for contemporary test data.** (A) The model, trained on historic herbarium collection data, performed modestly at predicting contemporary endophyte prevalence in *A. hyemalis*, as indicated by some overlap of predicted 95% CI with the 1:1 line, however contemporary test data generally had more variance between populations than model predictions. The model did recapitulate broader regional trends across (B) longitude and (C) latitude. Point size in panels B and C reflect sample sizes of contemporary endophyte population surveys.

362 Assessing collector and scorer influences on predicted endophyte prevalence

363 Our modeling effort quantified temporal and spatial trends in endophyte prevalence while ac-  
364 counting for potential biases introduced by collectors and by individual scorers who quantified  
365 endophyte presence/absence within specimens with the use of random effects. We found no  
366 evidence that collector biases influenced our results. Collector random effects were consistently  
367 small (Fig. A9), and models fit with and without this random effect provide qualitatively simi-  
368 lar results. The identity of individual scorers did contribute to observed patterns in endophyte  
369 prevalence. For example, 3 of the 25 scorers were more consistently likely than average to assign  
370 positive endophyte status, as indicated by 95% credible intervals greater than zero) (Fig. A10).  
371 This may have been driven by differences in scorers biases during the seed scoring process or  
372 by unintended spatial clustering of the specimens scored by each scorer (Clayton et al., 1993;  
373 Urdangarin et al., 2023). Interpreting our models with the inclusion of variance associated with  
374 the scorer effect thus provides conservative estimates of the absolute magnitude of changes in  
375 endophyte prevalence.

## Discussion

377 Our examination of historic plant specimens revealed a cryptic biotic response to climate change.  
378 For the three host species we examined, there have been clear increases in fungal endophyte  
379 prevalence over the last two centuries. Increases in prevalence of *Epichloë*, which are vertically  
380 transmitted, can potentially be interpreted as adaptive changes that improve the fitness of their  
381 hosts under stressful conditions. This interpretation is in line with theory predicting that the  
382 positive fitness feedback caused by vertical transmission leads beneficial symbionts to rise in  
383 prevalence within a population (Fine, 1975). We found that trends in endophyte prevalence var-  
384 ied across the distribution of each species in association with observed changes in climate drivers,  
385 suggesting that the endophytes have contributed to host resilience under environmental change.  
386 Taken together, this suggests a strengthening of the mutualism over the last two centuries.

387 Differences between the responses of each host species underscore that while all of these  
388  $C_3$  grasses share similar broad-scale distributions, each engages in unique biotic interactions  
389 and has unique niche requirements. We identified hotspots of change for *A. perennans*, which  
390 experienced the strongest absolute changes in endophyte prevalence (Fig. 3). Declines in the  
391 southern portion of its range and increases in the north suggest a potential poleward range shift  
392 of endophytic plants. Based on previous work demonstrating that endophytes can shield their  
393 hosts from drought stress (Decunta et al., 2021), we generally predicted that drought conditions  
394 could be a driver of increasing endophyte prevalence. In contrast to this expectation, increasing  
395 prevalence for this species was associated with increasing autumn temperature and precipitation  
396 (Fig. 4). To our knowledge, the response of the symbiosis in *A. perennans* to drought has not been  
397 examined experimentally, but in a greenhouse experiment, endophytes had a positive effect on  
398 host reproduction under shaded, low-light conditions (Davitt et al., 2010). Our results also hint  
399 that it may be useful to investigate whether lagged climate effects are important predictors of  
400 host fitness in this system (Evers et al., 2021). Endophyte prevalence of the spring-flowering *A.*  
401 *hyemalis* was most strongly linked to increasing variability in precipitation across summer and  
402 autumn. Endophytes could be playing a role helping hosts weather autumn-season droughts  
403 while the species is dormant. Previous work has demonstrated drought benefits in a greenhouse  
404 manipulation with this species (Davitt et al., 2011), and early life stages may be particularly  
405 vulnerable to prolonged droughts. For *E. virginicus*, which experienced the most modest changes  
406 in endophyte prevalence overall, we only modest associations with changes in climate drivers.  
407 Surveys by Sneck et al. (2017), used as part of the test data in this study, identified a drought index  
408 (SPEI) that integrates precipitation with estimated evapotranspiration as an important predictor  
409 of endophyte prevalence. *Epichloë* endophytes have also been connected to a suite of non-drought  
410 related fitness benefits including herbivore protection (Brem and Leuchtmann, 2001), salinity  
411 resistance (Wang et al., 2020), and mediation of the soil microbiome (Roberts and Ferraro, 2015)  
412 These effects are potentially mediated by the diverse bioactive alkaloids and other signaling  
413 compounds they produce (Saikonen et al., 2013). Increases in symbionts could be explained, at

414 least in part, by these diverse benefits that may help hosts weather a world made increasingly  
415 stressful by changes in climate and other anthropogenically introduced stressors. While we show  
416 consistent increasing trends in prevalence between the three species, the mechanisms that explain  
417 these changes may be diverse and idiosyncratic.

418 Our spatially-explicit model predicted regions of both high and low endophyte prevalence,  
419 suggesting that symbiotic and non-symbiotic host plants have overlapping, but non-identical  
420 niche requirements. Endophytes fitness benefits potentially explain the spatial distribution of  
421 prevalence by allowing their hosts to persist in environments where they otherwise could not  
422 (Afkhami et al., 2014; Kazenel et al., 2015). For example, fitness benefits of the symbiosis could  
423 explain historically low prevalence in *A. hyemalis* towards its western range edge coinciding with  
424 a strong aridity gradient. Previous population surveys for endophytes, which were used as  
425 test data for our model, found similar regional trends in prevalence for endophyte host species  
426 (Rudgers and Swafford, 2009; Sneck et al., 2017). While the model recreated these large-scale  
427 spatial trends, test data contained more population-to-population variability in prevalence. Val-  
428 idating our model predictions in this way allows us to evaluate places to improve the model's  
429 out-of-sample predictive ability, which will be particularly important for predicting host and  
430 symbiont niche-shifts under future climate change. Lack of information on local variability may  
431 simply be a feature of data derived from herbarium specimens. They are samples from local pop-  
432 ulations, but they are single specimens that are aggregated over in broad-scale model estimates.  
433 Poor predictive ability at local scales in this grass-endophyte system is not surprising, as previ-  
434 ous studies have found that local variation, even to the scale of hundreds of meters can structure  
435 endophyte-host niches (Kazenel et al., 2015). Other studies have found factors including land-  
436 use history (Vikuk et al., 2019) and the biotic environment, including herbivory (Rudgers et al.,  
437 2016), and host genotype Sneck et al. (2017), to be important predictors of endophyte ecology.  
438 Incorporating available climatic and soil layers as covariates is an obvious first step that could  
439 improve predictions. Another important step would be integrating data from local and regional  
440 scales through modeling to constrain estimates of local and regional variation. These steps will

<sup>441</sup> bridge gaps that often exist between large but broad bioclimatic and biodiversity data and small  
<sup>442</sup> but local data on biotic interactions, and move towards the goal of predicting the dynamics of  
<sup>443</sup> microbial symbioses under climate change (Isaac et al., 2020; Miller et al., 2019).

<sup>444</sup> Our analysis advances the use of herbarium specimens in global change biology in two ways.  
<sup>445</sup> First and foremost, this is the first study to link long-term changes in microbial symbioses to  
<sup>446</sup> changes in climate using specimens from natural history collections. The responses of micro-  
<sup>447</sup> bial symbioses are a rich target for future studies within museum specimens, particularly those  
<sup>448</sup> that take advantage of advances in sequencing technology. While we used relatively coarse  
<sup>449</sup> presence/absence data based on fungal morphology, other studies have examined historic plant  
<sup>450</sup> microbiomes using molecular sequencing and sophisticated bioinformatics techniques, but these  
<sup>451</sup> studies have so far been limited to relatively few specimens at limited spatial extents (Bieker  
<sup>452</sup> et al., 2020; Bradshaw et al., 2021; Gross et al., 2021; Heberling and Burke, 2019; Yoshida et al.,  
<sup>453</sup> 2015). Continued advances in capturing historic DNA and in filtering out potential contami-  
<sup>454</sup> nation during specimen storage (Bakker et al., 2020; Daru et al., 2019; Raxworthy and Smith,  
<sup>455</sup> 2021) will be imperative in the effort to scale up these efforts. This scaling up will be essential  
<sup>456</sup> to be able to quantify changes not just in the prevalence of symbionts, but also in symbionts'  
<sup>457</sup> intraspecific variation and evolutionary responses to climate change, as well as in changes in the  
<sup>458</sup> wider microbial community. Answering these questions as well as the unknown questions that  
<sup>459</sup> future researchers may ask also reiterates the value in capturing meta-information during ongo-  
<sup>460</sup> ing digitization efforts at herbaria around the world and during the accession of newly collected  
<sup>461</sup> specimens (Edwards et al.; Lendemer et al., 2020). Second, we accounted for several potential  
<sup>462</sup> biases in the data observation process that may be common to many collections-based research  
<sup>463</sup> questions by using a spatially-explicit random effects model. Spatial autocorrelation (Willems  
<sup>464</sup> et al., 2022), potential biases introduced by the sampling habits of collectors (Daru et al., 2018),  
<sup>465</sup> and variation between contemporary researchers during the collection of trait data, if not cor-  
<sup>466</sup> rected for could lead to over-confident inference about the strength and direction of historic  
<sup>467</sup> change. Previous studies that have quantified the effects of collector biases typically find them

<sup>468</sup> to be small (Davis et al., 2015; Meineke et al., 2019), and we similarly did not find that collector  
<sup>469</sup> has a strong effect on the results of our analysis.

<sup>470</sup> Ultimately, a central goal of global change biology is to generate predictive insights into the  
<sup>471</sup> future of natural systems. While this survey of historic endophyte prevalence is necessarily cor-  
<sup>472</sup> relative, it serves as a foundation to develop better predictive models of the response of microbial  
<sup>473</sup> symbioses to climate change. Combining the insights from this type of regional-scale survey with  
<sup>474</sup> field experiments and physiological data could be invaluable. While we found that climate is  
<sup>475</sup> strongly correlated with endophytes' temporal responses, we do not know why trends in preva-  
<sup>476</sup> lence were weak in some areas or how endophytes would respond to more extreme changes in  
<sup>477</sup> climate. For example, transplanting symbiotic and non-symbiotic plants beyond the range edge  
<sup>478</sup> of *A. hyemalis* could tell us whether persistent low endophyte prevalence in that area is a result of  
<sup>479</sup> environmental conditions that lead the symbiosis to negative fitness consequences, or is a result  
<sup>480</sup> of some historical contingency or dispersal limitation that has thus far limited the presence of  
<sup>481</sup> symbiotic hosts from a region where they would otherwise flourish and provide resilience. While  
<sup>482</sup> we observed evidence of mutualism resilience, more extreme environmental changes than those  
<sup>483</sup> observed in our study could potentially push one or both partners beyond their physiological  
<sup>484</sup> limit, leading to the collapse of the mutualism. Our analysis thus far is agnostic to changes in the  
<sup>485</sup> distributions of hosts. Mechanistic models could connect the responses of both host and sym-  
<sup>486</sup> bionts to abiotic climate drivers integrating dispersal processes. Beyond host-microbe symbioses,  
<sup>487</sup> building these types of models would work towards quantitatively attributing biotic responses  
<sup>488</sup> to anthropogenically driven climate change, similar to methods in climate science and economics  
<sup>489</sup> (Carleton and Hsiang, 2016; Stott et al., 2010).

<sup>490</sup> **Acknowledgments**

<sup>491</sup> We thank Jessica Budke for help in drafting our initial destructive sampling plan, and to the  
<sup>492</sup> many members of herbarium staff who facilitated our research visits, as well as to the hundreds

493 of collectors who contributed to the natural history collections. Several high schooler and un-  
494 dergraduate researchers contributed to data collection, including A. Appio-Riley, P. Bilderback,  
495 E. Chong, K. Dickens, L. Dufresne, B. Gutierrez, A. Johnson, S. Linder, E. Scales, B. Scherick,  
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497 National Science Foundation (grants 1754468 and 2208857) and by funding from the Texas Ecolab  
498 Program.

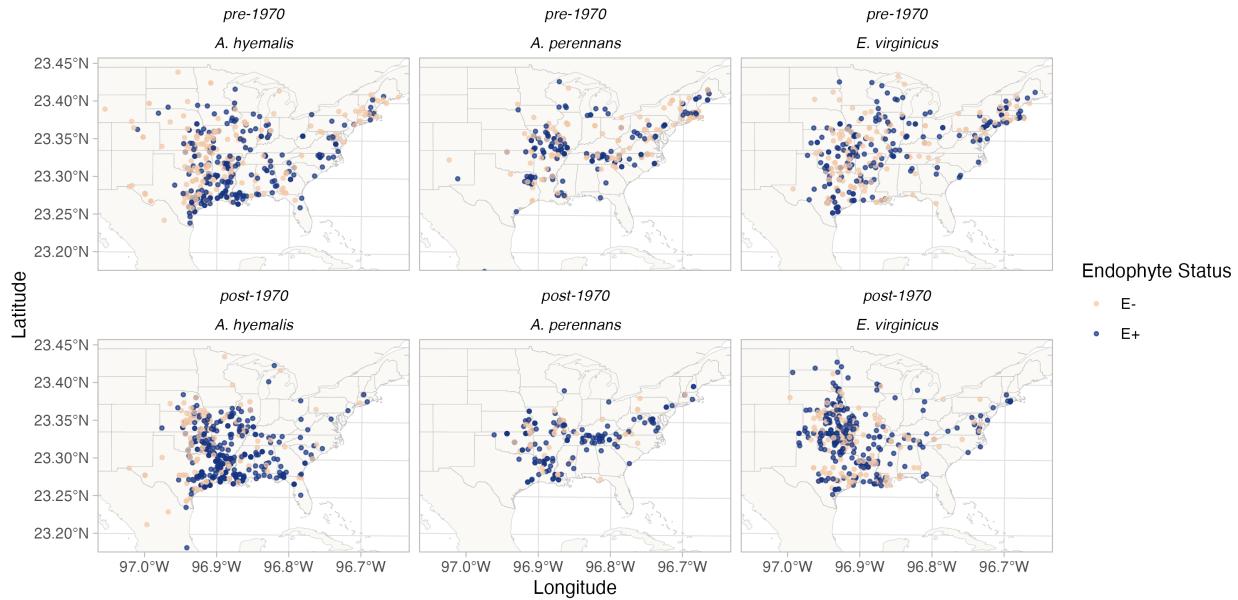
499 **Statement of Authorship**

500 J.C.F. contributed to research conception, data collection, data analysis, and led manuscript draft-  
501 ing. J.M. contributed to data analysis and manuscript manuscript revisions. T.E.X.M. contributed  
502 to research conception, data collection, data analysis, and manuscript revisions.

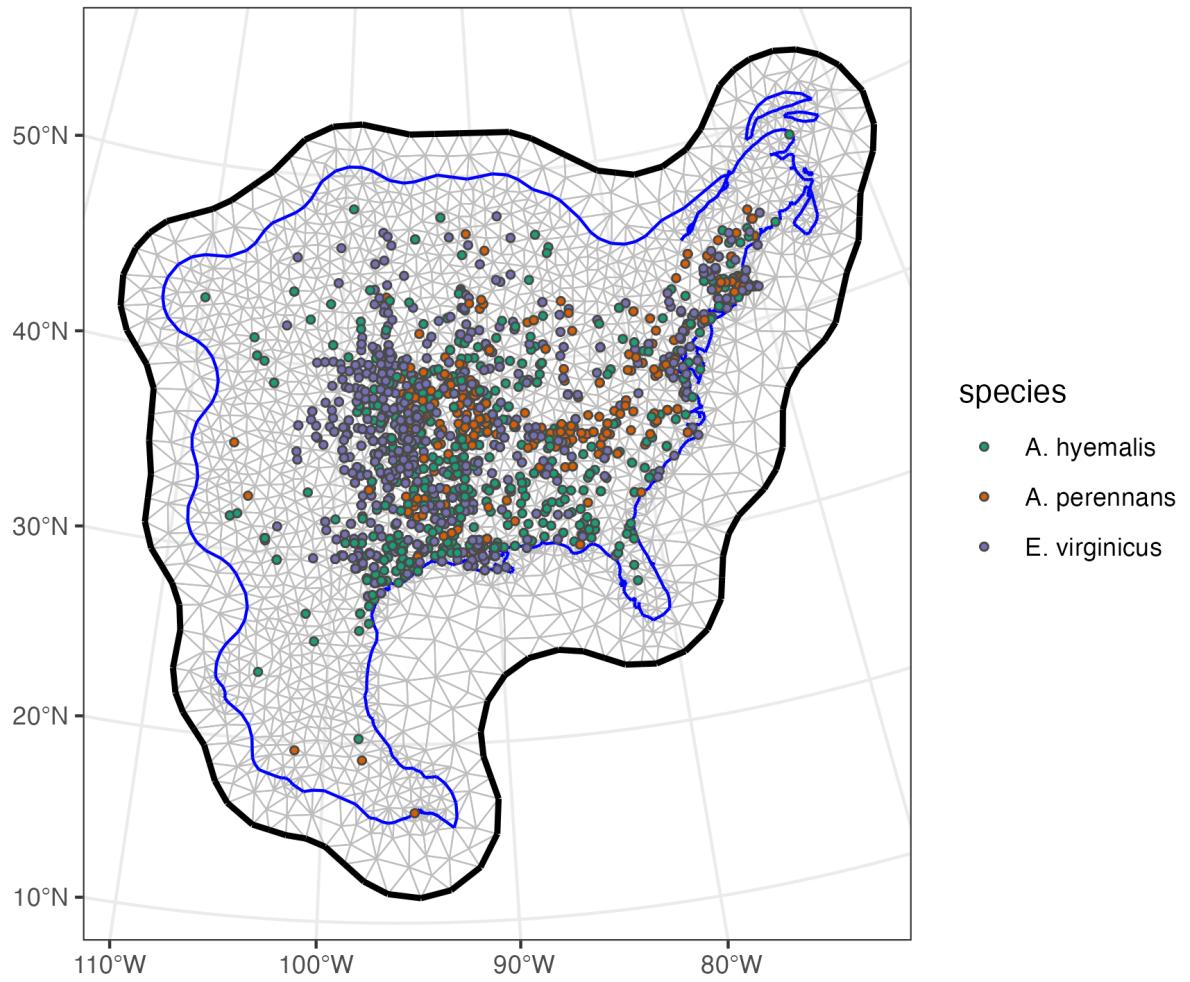
503 **Data and Code Availability**

504 On initial submission, you may use this section to provide a URL for editors and reviewers that  
505 is 'private for peer review'. After acceptance, this section must be updated with correct, working  
506 DOIs for data deposits (typically on the Dryad Digital Repository, ) and code deposits (such as  
507 in Zenodo).

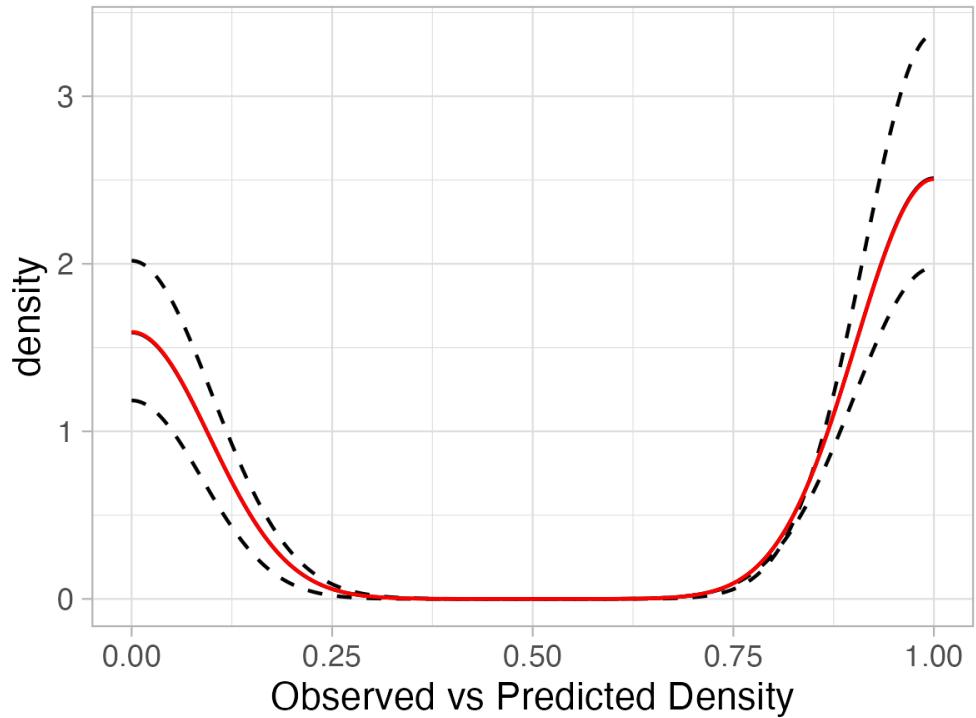
## Appendix A



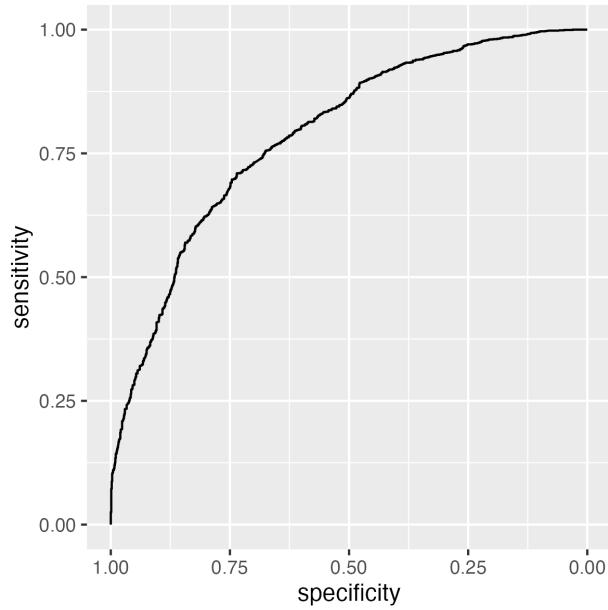
**Figure A1: Endophyte presence/absence in specimens of each host species.** Points show collection locations colored according to whether the specimen contained endophytes ( E+; blue points) or did not contain endophytes (E-, tan points) and are faceted based on collection period.



**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: Consistency between real data and simulated values indicate that the fitted model accurately describes the data.** Graph shows density curves for the observed data (red) along with the mean(solid) and 95% CI (dashed) of simulated values (black).



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

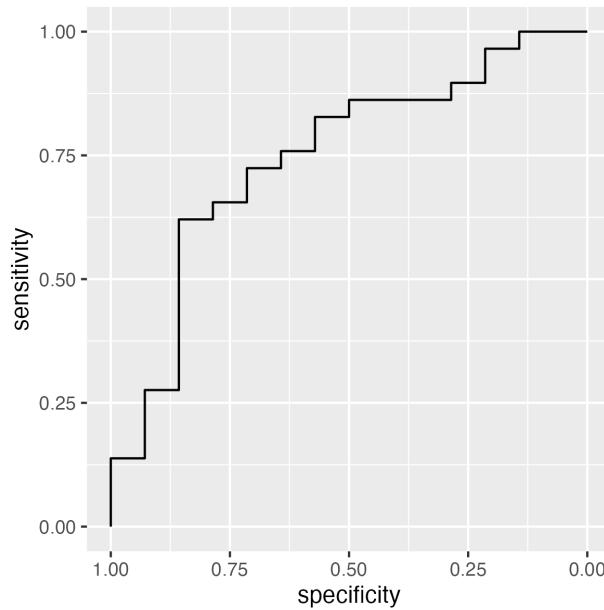


Figure A5: **ROC plot showing model performance classifying observations according to endophyte status within the out-of-sample data.** The curves show adequate model performance for test data. The AUC value is 0.77.

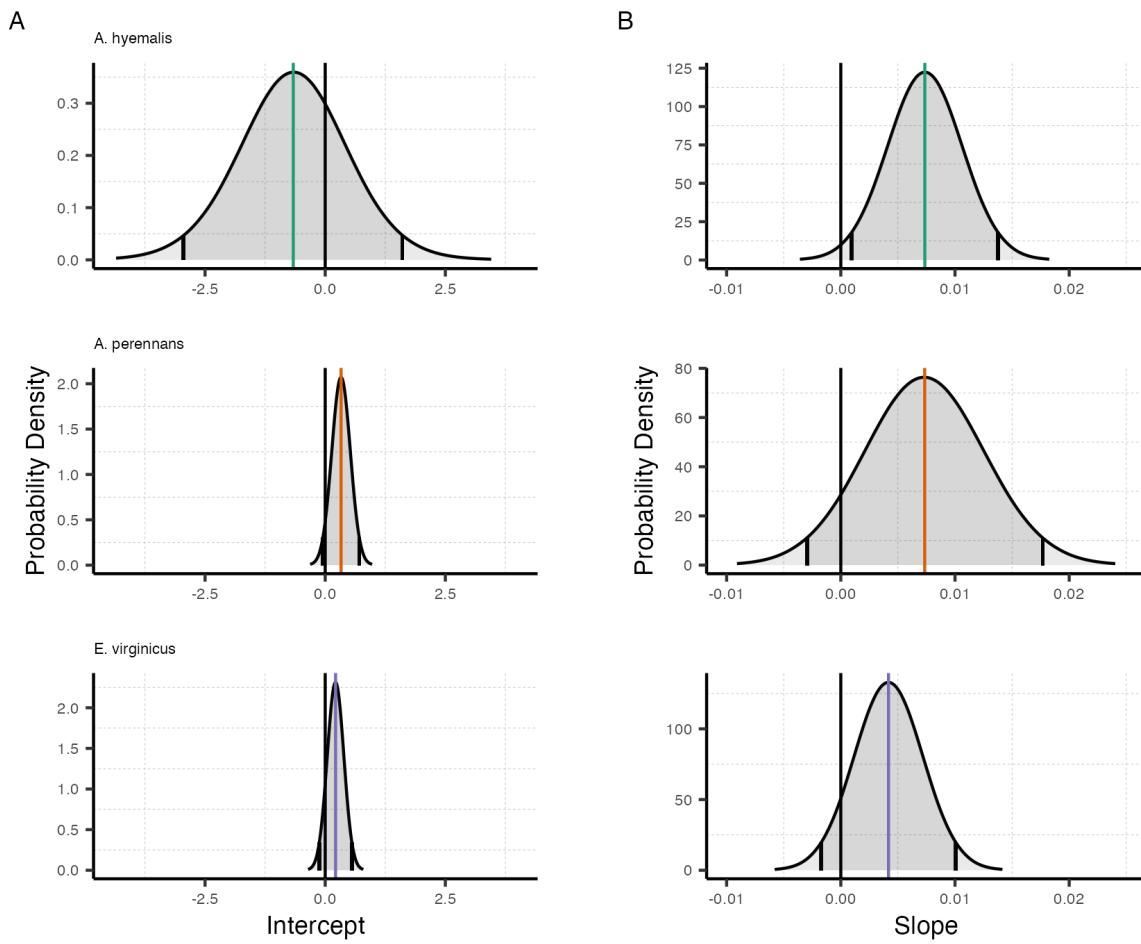


Figure A6: Density curves show the probability density along with mean (colored line) and 95% CI (black lines) for the (A) intercept and (B) slope terms, **A** and **T** respectively. Colors represent each host species

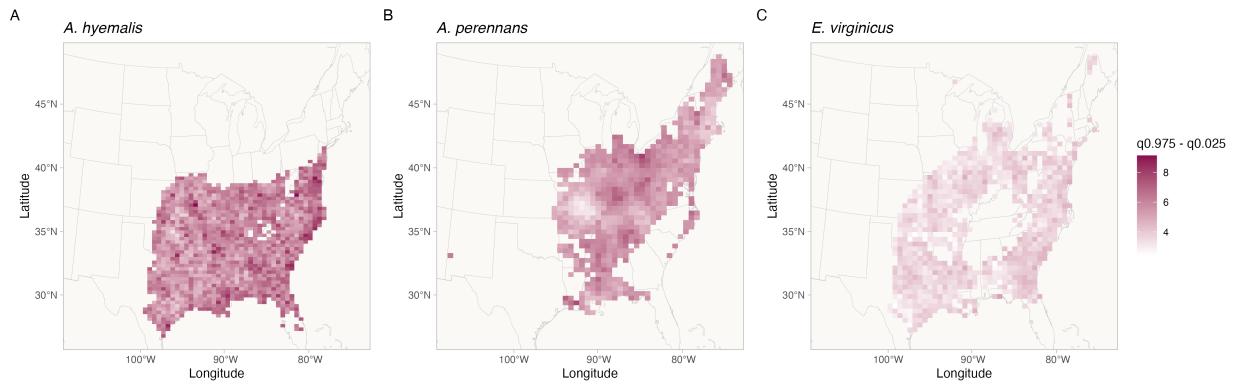


Figure A7: Shading represents the range of the 95% posterior credible interval for spatially varying slopes,  $\tau$ .

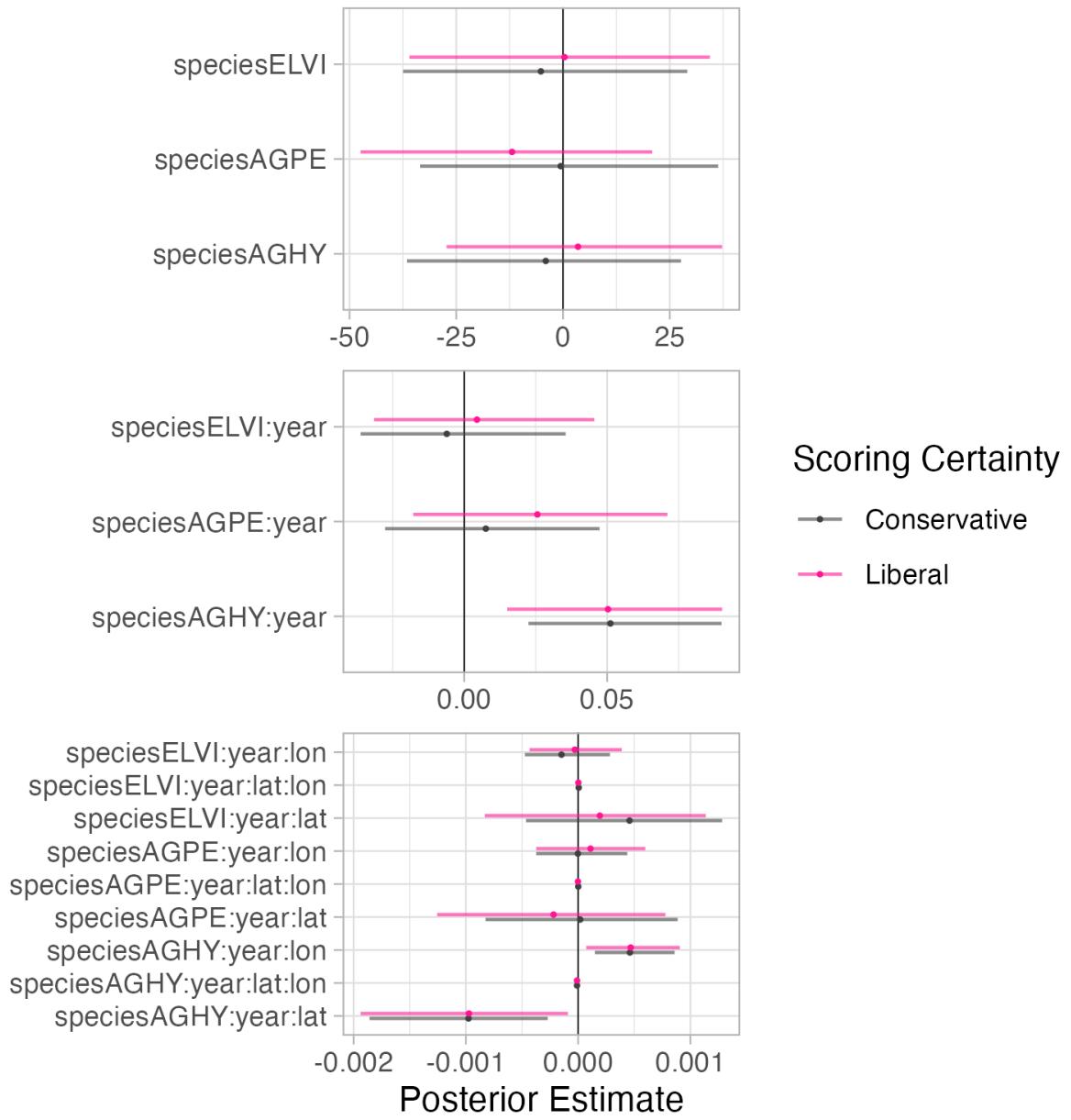
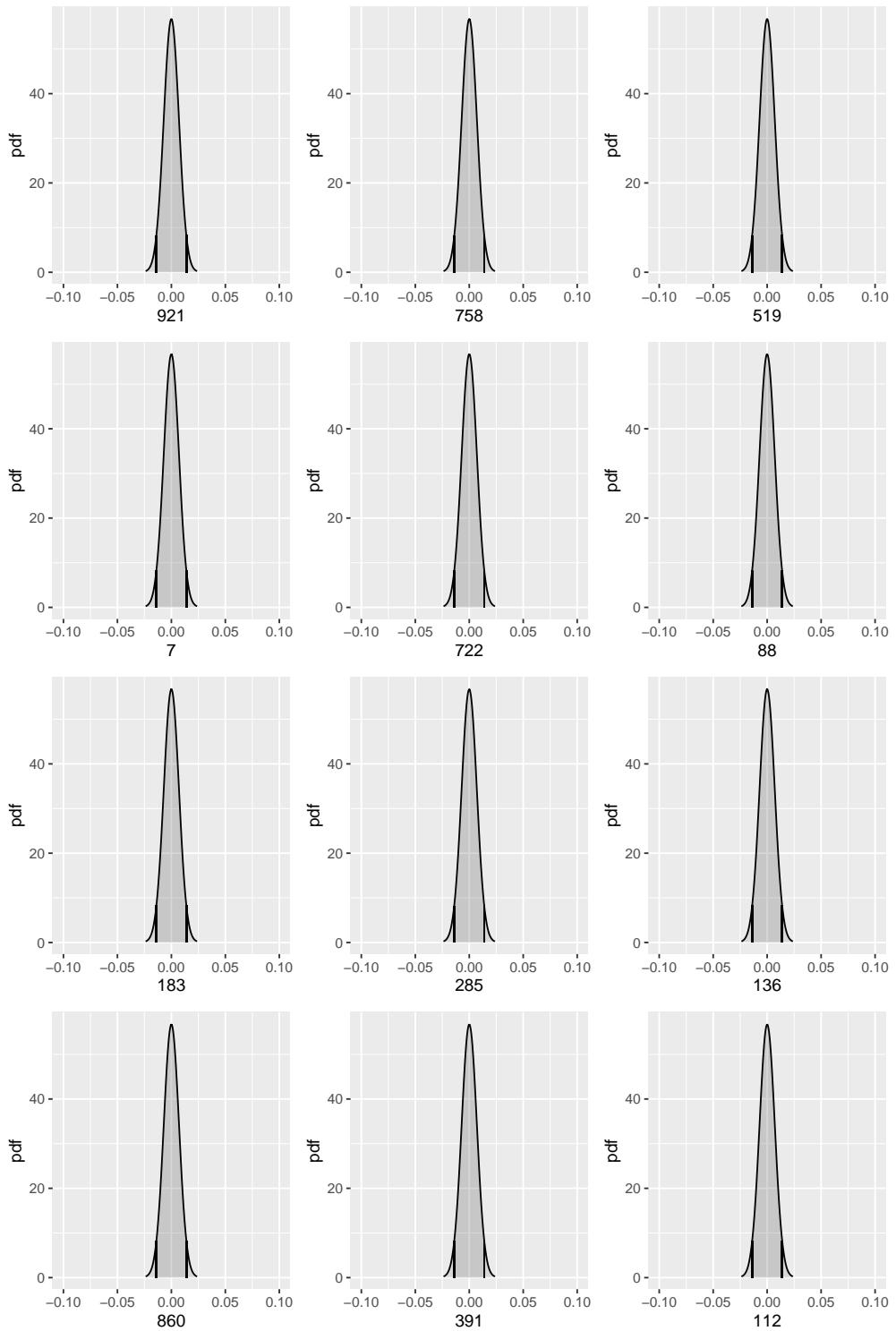
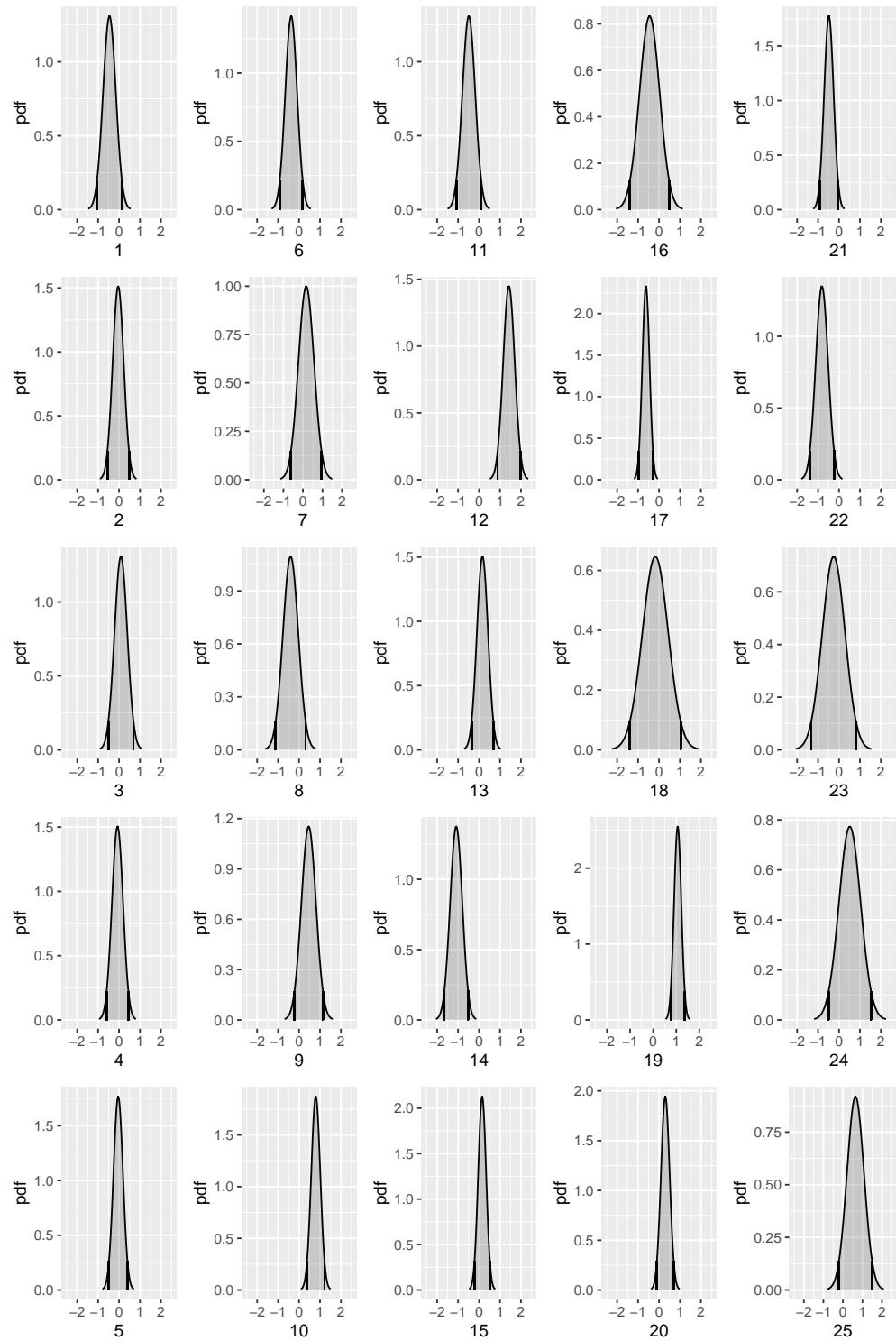


Figure A8: Comparison of posterior estimates of fixed effects when using Liberal or Conservative endophyte scores.



**Figure A9: Posterior estimates of collector random effects.** Density curves show the posterior estimate along lines indicating the 95% CI for 12 randomly selected collectors.



**Figure A10: Posterior estimates of scorer random effects.** Density curves show the posterior estimate along lines indicating the 95% CI for 25 scorers.

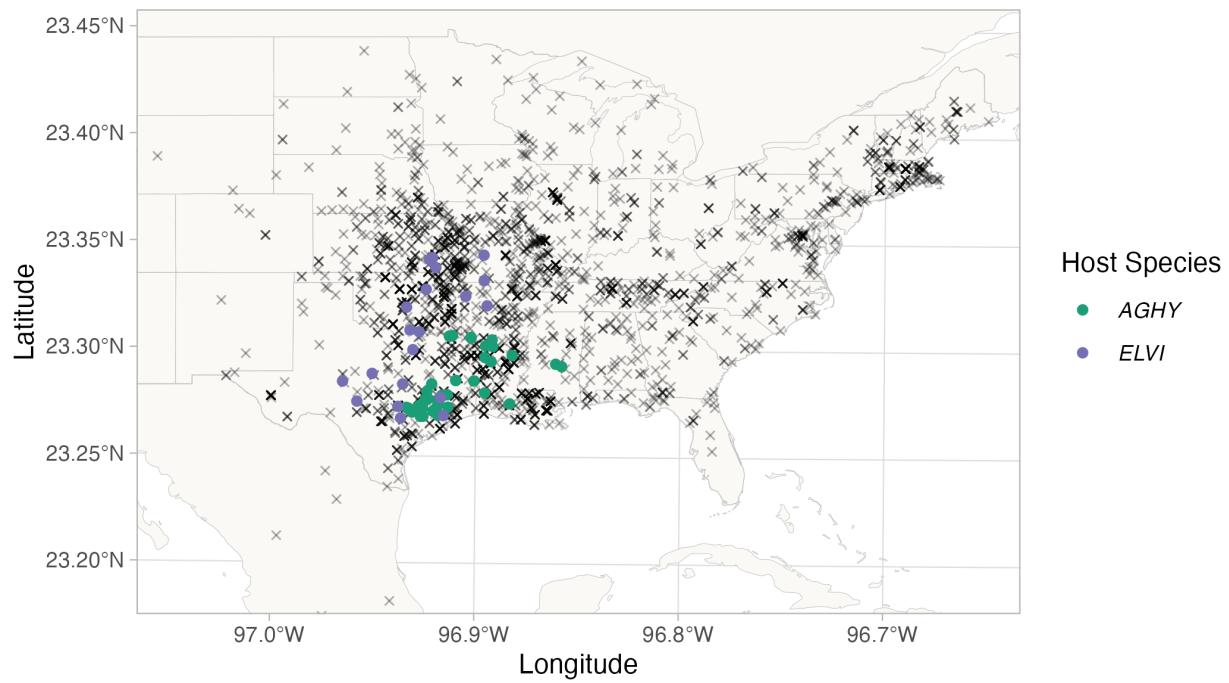
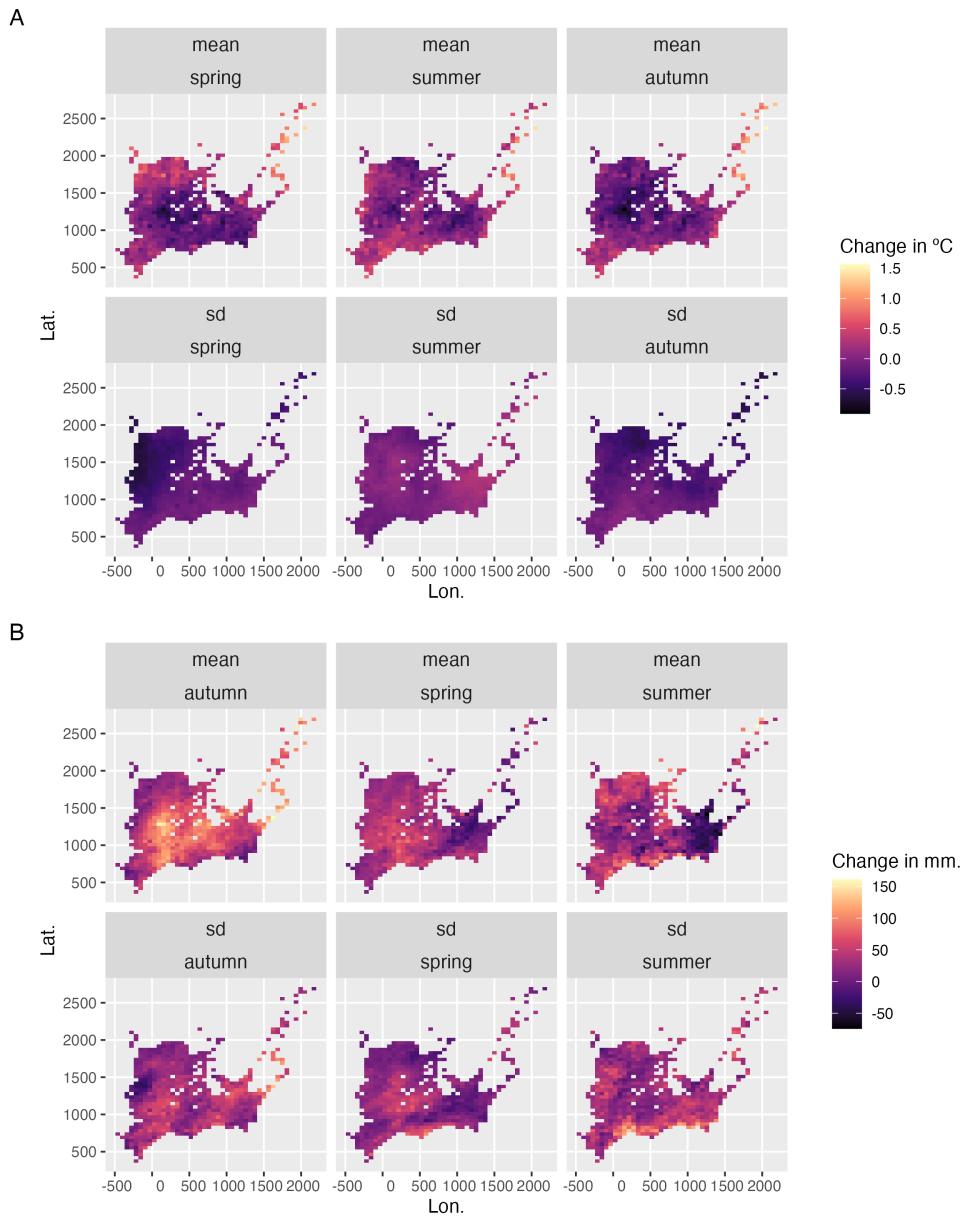
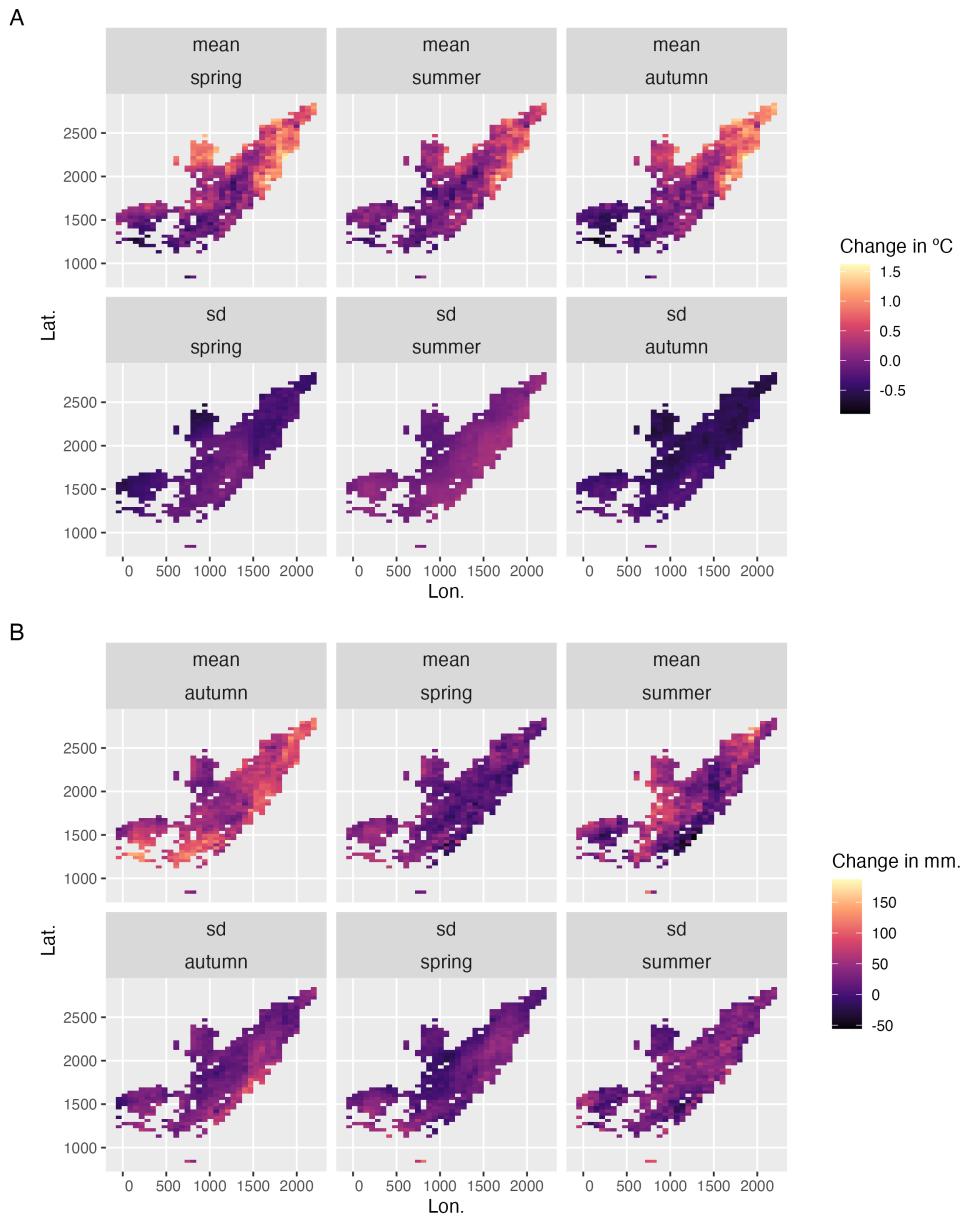


Figure A11: Locations of contemporary surveys of endophytes in *A. hyemalis* used as "test" data (red points), relative to the historical collection data (black crosses).

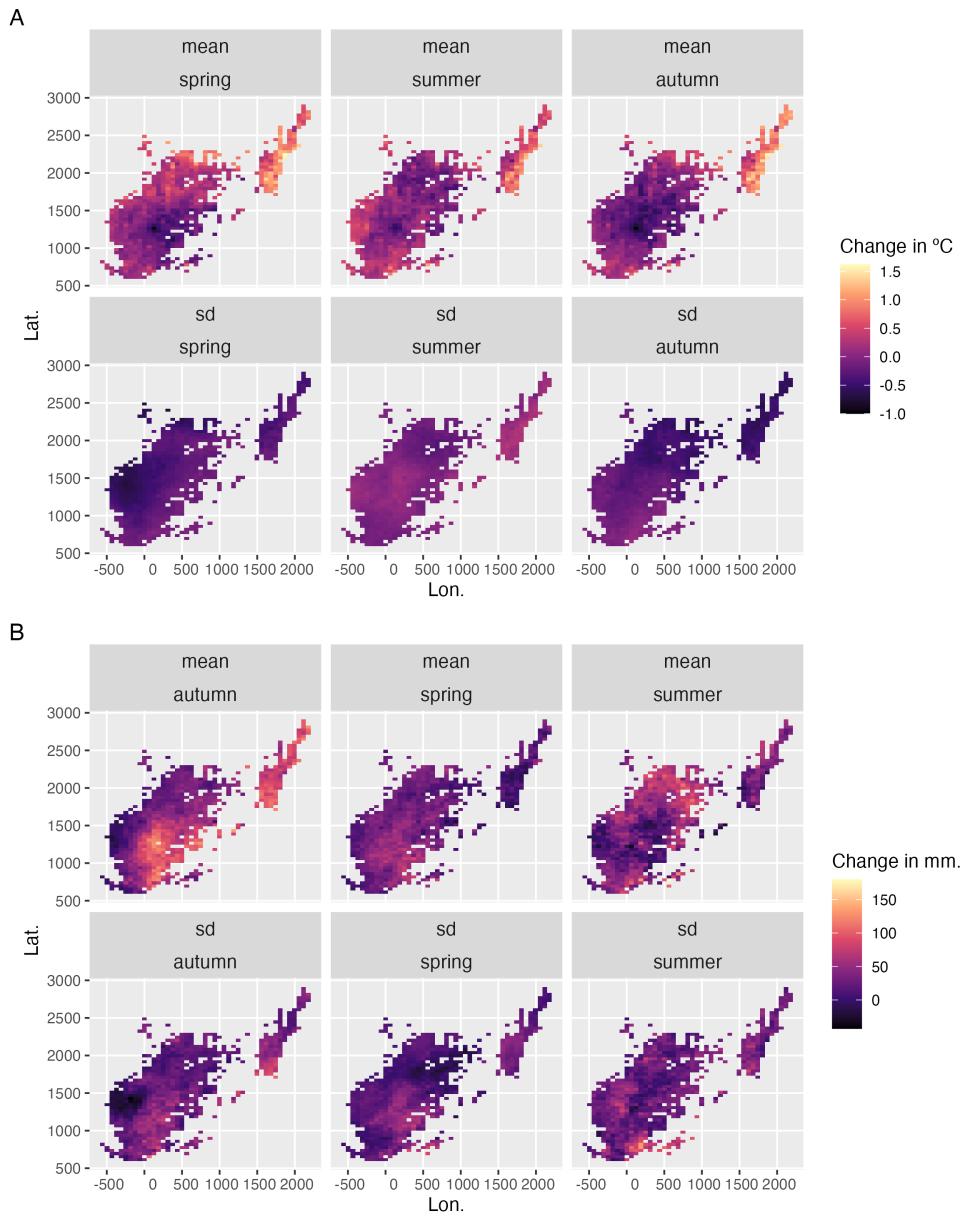


**Figure A12: Change in seasonal climate variables between the periods 1895-1925 and 1990-2020.** Color represents change in (A) seasonal temperature and (B) seasonal precipitation. Maps show pixels covering the modeled distribution of *A. hyemalis* used in post-hoc climate correlation analysis.



**Figure A13: Change in seasonal climate variables between the periods 1895-1925 and 1990-2020.**

Color represents change in (A) seasonal temperature and (B) seasonal precipitation. Maps show pixels covering the modeled distribution of *A. perennans* used in post-hoc climate correlation analysis.



**Figure A14: Change in seasonal climate variables between the periods 1895-1925 and 1990-2020.** Color represents change in (A) seasonal temperature and (B) seasonal precipitation. Maps show pixels covering the modeled distribution of *E. virginicus* used in post-hoc climate correlation analysis.

Table A1: Summary of herbarium samples across collections

Herbarium Collection	AGHY	AGPE	ELVI
Botanical Research Institute of Texas	341	189	176
Louisiana State University	71	–	61
Mercer Botanic Garden	3	–	6
Missouri Botanic Garden	78	39	31
Texas A&M	73	–	49
University of Kansas	134	–	20
University of Oklahoma	65	30	91
University of Texas & Lundell	169	41	99
Oklahoma State University	30	–	69

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