

Forecasting range shifts of a dioecious plant species under climate change

Jacob K. Moutouama ^{*1}, Aldo Compagnoni², and Tom E.X. Miller¹

¹Program in Ecology and Evolutionary
Biology, Department of BioSciences, Rice University, Houston, TX USA

²Institute
of Biology, Martin Luther University Halle-Wittenberg, Halle, Germany; and
German Centre for Integrative Biodiversity Research (iDiv), Leipzig, Germany

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^{*}Corresponding author: jmoutouama@gmail.com

¹ Abstract

² Rising temperatures and extreme drought events associated with global climate change have
³ triggered an urgent need for predicting species response to climate change. Currently, the
⁴ vast majority of theory and models in population biology, including those used to forecast
⁵ biodiversity responses to climate change, ignore the complication of sex structure. To address
⁶ this issue, we developed a climate-driven population matrix model using demographic data of
⁷ dioecious species (Texas bluegrass), past and future climate (different gas emission scenarios)
⁸ to forecast and backcast the effect of climate change on range shifts. Our results show a sex
⁹ specific demographic response to climate change. Female individuals have a demographic
¹⁰ advantage (higher vital rate) over males. Female demographic advantage led to a slight
¹¹ decline in population viability under future climate assuming moderate gas emission and
¹² a drastic reduction in population viability under future climate assuming high gas emission.
¹³ Despite a change in species range, climate change can alter population viability in dioecious
¹⁴ species. Overall, our work provides a framework for predicting the impact of climate on
¹⁵ dioecious species using population demography.

¹⁶ Introduction

¹⁷ Rising temperatures and extreme drought events associated with global climate change are
¹⁸ leading to increased concern about how species will become redistributed across the globe
¹⁹ under future climate conditions (Bertrand et al., 2011; Gamelon et al., 2017; Smith et al., 2024).
²⁰ Dioecious species (most animals and many plants) might be particularly vulnerable to the
²¹ influence of climate change because they often display skewed sex ratios that are generated or
²² reinforced by sexual niche differentiation (distinct responses of females and males to shared cli-
²³ mate drivers) (Tognetti, 2012). Accounting for such a niche differentiation within a population
²⁴ is a long-standing challenge in accurately predicting which sex will successfully track envi-
²⁵ ronmental change and how this will impact population viability and range shifts (Gissi et al.,
²⁶ 2023a; Jones et al., 1999). The vast majority of theory and models in population biology, includ-
²⁷ ing those used to forecast biodiversity responses to climate change, ignore the complication of
²⁸ sex structure (Ellis et al., 2017; Pottier et al., 2021). As a result, accurate forecasts of colonization-
²⁹ extinction dynamics for dioecious species under future climate scenarios are limited.

³⁰ Climate change can influence dioecious populations via shifts in sex ratio.¹ Females and
³¹ males may respond differently to climate change, especially in species where there is sexual
³² niche differentiation (Gissi et al., 2023a,b; Hultine et al., 2016). This sex-specific response to
³³ climate change may help one sex to succeed in extreme climatic conditions rather than the
³⁴ other sex (Bürli et al., 2022; Zhao et al., 2012) leading to a skewness in the operational sex ratio
³⁵ (relative number of males and females as available mates) (Eberhart-Phillips et al., 2017). For
³⁶ example, experiments in two populations of Atlantic marine copepods (*Acartia tonsa*) revealed
³⁷ that male survival was more sensitive to increasing temperatures than female survival (Sasaki
³⁸ et al., 2019). In other species, such as *Pteropus poliocephalus* or *Populus cathayana*, females
³⁹ showed lower survival than males in response to high temperature (Welbergen et al., 2008;
⁴⁰ Zhao et al., 2012). Sex-specific responses to climate drivers have the potential to influence
⁴¹ population viability under global change because skew in the operational sex ratio can limit
⁴² reproduction through mate scarcity (Petry et al., 2016).

⁴³ Species's range limits, when not driven by dispersal limitation, should generally reflect
⁴⁴ the limits of the ecological niche (Lee-Yaw et al., 2016). For most species, niches and geographic
⁴⁵ ranges are often limited by climatic factors including temperature and precipitation (Sexton
⁴⁶ et al., 2009). Therefore, any substantial changes in the magnitude of these climatic factors in a
⁴⁷ given location across the range could impact population viability, with implications for range
⁴⁸ shifts based on which regions become more or less suitable (Davis and Shaw, 2001; Pease

¹This paragraph is really good but notice that the topic sentence (and much that follows) is largely redundant with the first paragraph. I would suggest creating clearer distinction between paragraphs.

49 et al., 1989). Forecasting range shifts for dioecious species is complicated by the potential for
50 each sex to respond differently to climate variation (Morrison et al., 2016; Pottier et al., 2021).
51 Populations in which males are rare under current climatic conditions could experience low
52 reproductive success due to sperm or pollen limitation that may lead to population decline in
53 response to climate change that disproportionately favors females (Eberhart-Phillips et al., 2017).
54 In contrast, climate change could expand male habitat suitability (e.g. upslope movement),
55 which might increase seed set for pollen-limited females and favor range expansion (Petry
56 et al., 2016). Although the response of species to climate warming is an urgent and active area
57 of research, few studies have disentangled the interaction between sex and climate drivers
58 to understand their combined effects on population dynamics and range shifts.

59 Our ability to track the impact of climate change on the population dynamics of
60 dioecious plants and the implication of such impact on range shift depends on our ability
61 to build mechanistic models that take into account the spatial and temporal context in which
62 sex specific response to climate change affects population viability (Czachura and Miller, 2020;
63 Davis and Shaw, 2001; Evans et al., 2016). For example, structured models that are built from
64 long-term demographic data collected from common garden experiments have emerged as
65 powerful technic to study the impact of climate change on species range shift (Merow et al.,
66 2017; Schwinning et al., 2022). These structured models are increasingly utilized for two
67 reasons. First, they enable the manipulation of treatments that can isolate spatial and temporal
68 correlations between environmental factors, thus overcoming a main disadvantage with many
69 types of correlative studies (Leicht-Young et al., 2007). Second, they link individual-level
70 demographic trait to population demography allowing the investigation of the demographic
71 mechanisms behind vital rates (e.g. survival, fertility, growth and seed germination) response
72 environmental variation (Dahlgren et al., 2016; Louthan et al., 2022). Third, these structured
73 models can be used to identify which aspect of climate is more important for population
74 dynamics. For example, Life Table Response Experiment (LTRE) build from structured
75 models is an approach that has become widely used to understand how a given treatment
76 (eg. temperature or precipitation) could affect population dynamics (Caswell, 1989; Iler et al.,
77 2019; Morrison and Hik, 2007; O'Connell et al., 2024).

78 In this study, we used a mechanistic approach by combining geographically-distributed
79 field experiments, hierarchical statistical modeling, and two-sex population projection
80 modeling to understand the demographic response of dioecious species to climate change and
81 its implications for future range dynamics. Our study system is a dioecious plant species (*Poa*
82 *arachnifera*) distributed along environmental gradients in the south-central US corresponding
83 to variation in temperature across latitude and precipitation across longitude. A previous
84 study on the same system showed that, despite a differentiation of climatic niche between

85 sexes, the female niche mattered the most in driving the environmental limits of population
86 viability (Miller and Compagnoni, 2022b). However that study did not use climate variables
87 preventing us from backcasting and forecasting the impact of climate change on dioecious
88 species. Here, we asked four questions:

- 89 1. What are the sex-specific vital rate responses to variation in temperature and precipitation
90 across the species' range?
- 91 2. How sex-specific vital rates combine to determine the influence of climate variation on
92 population viability (λ)?
- 93 3. What are the historical and projected changes in climate across the species range?
- 94 4. What are the back-casted and fore-casted dynamics of this species' geographic niche
95 ($\lambda \geq 1$) and how does accountind for sex structure modify these predictions?

96 Materials and methods

97 Study species

98 Texas bluegrass (*Poa arachnifera*) is a dioecious perennial, summer-dormant cool-season (C3)
99 grass that occurs in the south-central U.S.(Texas, Oklahoma, and southern Kansas) (Hitchcock,
100 1971). Average temperatures along the distribution of the species tend to decrease northward
101 as a result of the influence of latitude: lower latitudes receive more heat from the sun over
102 the course of a year. Similarly the average precipitation decrease eastward as a result of
103 the influence of longitude: lower longitudes receive less precipitation over the year. Texas
104 bluegrass grows between October and May (growing season), with onset of dormancy often
105 from June to September (dormant season) (Kindiger, 2004). Flowering occurs in May and
106 the species is wind pollinated (Hitchcock, 1971). [The male heads are smooth, while those
107 of the female appear fuzzy.](#)

108 Common garden experiment

109 We set up a common garden experiment throughout and beyond the range of Texas bluegrass
110 to enable study of sex-specific demographic responses to climate and the implications for range
111 shifts. The novelty of this study lies in the fact that we use a precise climate variable to build
112 a mechanistic model to forecast the response of species to climate change. Details of the exper-
113 imental design are provided in Miller and Compagnoni (2022b); we provide a brief overview
114 here. The common experiment was installed at 14 sites across a climatic gradient (FigX). At

115 each site, we established 14 blocks. For each block we planted three female and three male indi-
116 viduals that were clonally propagated from eight natural source populations of Texas bluegrass.
117 The experiment was established in November 2013 and was census annually through 2016, pro-
118 viding both spatial and inter-annual variation in climate. Each May (2014-2016), we collected
119 individual demographic data including survival (alive or dead), growth (number of tillers),
120 flowering status (reproductive or vegetative), and fertility (number of panicles, conditional on
121 flowering). For the analyses that follow, we focus on the 2014-15 and 2015-16 transitions years.

122 Climatic data collection

123 We downloaded monthly temperature and precipitation from Chelsa to describe observed
124 climate conditions during our study period (Karger et al., 2017). These climate data were used
125 as covariates in vital rate regressions, which allowed us to forecast and back-cast demographic
126 responses to climate change based on observations across the common garden experiment.
127 We aligned the climatic years to match demographic transition years (**May 1 – April 30**)²
128 rather than calendar years. Based on the natural history of this summer-dormant cool-season
129 species, we divided each transition year into growing and dormant seasons. We define June
130 through September as the dormant season and the rest of the year as the growing season.
131 Across years and sites, the experiment included substantial variation in growing and dormant
132 season temperature and precipitation (**Figure**³).

133 To back-cast and forecast changes in climate, we downloaded projection data for three
134 30-year periods: past (1901-1930), current (1990-2019) and future (2070-2100). Data for these
135 climatic periods were downloaded from four general circulation models (GCMs) selected
136 from the Coupled Model Intercomparison Project Phase 5 (CMIP5). The GCMs are MIROC5,
137 ACCESS1-3, CESM1-BGC, CMCC-CM and were downloaded from chelsa (Sanderson
138 et al., 2015). We evaluated future climate projections from two scenarios of representative
139 concentration pathways (RCPs): RCP4.5, an intermediate-to-pessimistic scenario assuming
140 a radiative forcing to amount to 4.5 Wm^{-2} by 2100, and RCP8.5, a pessimistic emission
141 scenario which project a radiative forcing to amount to 8.5 Wm^{-2} by 2100 (Schwalm et al.,
142 2020; Thomson et al., 2011).

143 Sex ratio experiment

144 We conducted a sex-ratio experiment on a site close (1 km) to a natural population of the
145 focal species at the center of the range to estimate the effect of sex-ratio variation on female

²I am not sure if these are actually the right dates.

³I think we should have a figure, maybe just for the appendix, that visualizes this.

¹⁴⁶ reproductive success. Details of the experiment are provided in Compagnoni et al. (2017) and
¹⁴⁷ Miller and Compagnoni (2022b). In short, we established 124 experimental populations on
¹⁴⁸ plots measuring 0.4 x 0.4m and separated by at least 15m from each other at that site. We chose
¹⁴⁹ 15m because our pilot data show that more than 90% of wind pollination occurred within 13m.
¹⁵⁰ We varied population density (1-48 plants/plot) and sex ratio (0%-100% female) across the ex-
¹⁵¹ perimental populations, and we replicated 34 combinations of density-sex ratios. We collected
¹⁵² the number of panicles from a subset of females in each plot and collected the number of
¹⁵³ seeds in each panicle. Since the number of panicles (proxy of reproduction effort) does not nec-
¹⁵⁴ essarily reflect reproduction success in *Poar arachnifera*, we accessed reproduction success (seed
¹⁵⁵ fertilized) using greenhouse-based germination and trazolium-based seed viability assays.

¹⁵⁶ We used the sex-ratio to estimate the probability of viability and the germination rate.
¹⁵⁷ Seed viability was modeled with a binomial distribution where the probability of viability
¹⁵⁸ (v) was given by:

$$v = v_0 * (1 - OSR^\alpha) \quad (1)$$

¹⁶⁰ where OSR is the operational sex ratio (proportion of panicles that were female) in the
¹⁶¹ experimental populations. The properties of the above function is supported by our previous
¹⁶² work (Compagnoni et al., 2017). Here, seed viability is maximized at v_0 as OSR approaches
¹⁶³ zero (strongly male-biased) and goes to zero as OSR approaches 1 (strongly female-biased).
¹⁶⁴ Parameter α controls how viability declines with increasing female bias.

¹⁶⁵ We used a binomial distribution to model the germination data from greenhouse trials.
¹⁶⁶ Given that germination was conditional on seed viability, the probability of success was given
¹⁶⁷ by the product $v * g$, where v is a function of OSR (Eq. 1) and g is assumed to be constant.

¹⁶⁸ Sex specific demographic responses to climate

¹⁶⁹ We used individual level measurements of survival, growth (number of tillers), flowering, num-
¹⁷⁰ ber of panicles to independently develop Bayesian mixed effect models describing how each
¹⁷¹ vital rate varies as a function of sex, size, precipitation of growing and dormant season and tem-
¹⁷² perature of of growing and dormant season. We fit vital rate models with second-degree poly-
¹⁷³ nomial functions for the influence of climate. We included a second-degree polynomial because
¹⁷⁴ we expected that climate variables would affect vital rates through a hump-shaped relationship.

¹⁷⁵ We centered and standardized all predictors to facilitate model convergence. We included
¹⁷⁶ site, source, and block as random effect. All the vital rate models used the same linear and
¹⁷⁷ quadratic predictor for the expected value (μ) (Eq. 2). However, we applied a different
¹⁷⁸ link function ($f(\mu)$) depending on the distribution the vital rate. We modeled survival and

179 flowering data with a Bernoulli distribution. We modeled the growth (tiller number) with
 180 a zero-truncated Poisson inverse Gaussian distribution. Fertility (panicle count) was model
 181 as zero-truncated negative binomial.

$$\begin{aligned}
 f(\mu) = & \beta_0 + \beta_1 \text{size} + \beta_2 \text{sex} + \beta_3 \text{pptgrow} + \beta_4 \text{pptdorm} + \beta_5 \text{tempgrow} + \beta_6 \text{tempdorm} \\
 & + \beta_7 \text{pptgrow} * \text{sex} + \beta_8 \text{pptdorm} * \text{sex} + \beta_9 \text{tempgrow} * \text{sex} + \beta_{10} \text{tempdorm} * \text{sex} \\
 & + \beta_{11} \text{size} * \text{sex} + \beta_{12} \text{pptgrow} * \text{tempgrow} + \beta_{13} \text{pptdorm} * \text{tempdorm} \\
 & + \beta_{14} \text{pptgrow} * \text{tempgrow} * \text{sex} + \beta_{15} \text{pptdorm} * \text{tempdorm} * \text{sex} + \beta_{16} \text{pptgrow}^2 \\
 & + \beta_{17} \text{pptdorm}^2 + \beta_{18} \text{tempgrow}^2 + \beta_{19} \text{tempdorm}^2 + \beta_{20} \text{pptgrow}^2 * \text{sex} \\
 & + \beta_{21} \text{pptdorm}^2 * \text{sex} + \beta_{22} \text{tempgrow}^2 * \text{sex} + \beta_{23} \text{tempdorm}^2 * \text{sex} + \phi + \rho + \nu
 \end{aligned} \tag{2}$$

182 where β_0 is the grand mean intercept, $\beta_1 \dots \beta_{13}$ represent the size and climate dependent slopes.
 183 size was on a natural logarithm scale. pptgrow is the precipitation of the growing season
 184 (standardized to mean zero and unit variance), tempgrow is the temperature of the growing
 185 season (standardized to mean zero and unit variance), pptdorm is the precipitation of the
 186 dormant season (standardized to mean zero and unit variance), tempdorm is the temperature
 187 of the dormant season (standardized to mean zero and unit variance). The model also
 188 includes normally distributed random effects for block-to-block variation ($\phi \sim N(0, \sigma_{block})$) and
 189 source-to-source variation that is related to the provenence of the seeds used to establish the
 190 common garden ($\rho \sim N(0, \sigma_{source})$), site to site variation ($\nu \sim N(0, \sigma_{site})$). We fit survival, growth,
 191 flowering models with generic weakly informative priors for coefficients ($\mu = 0, \sigma = 1.5$) and
 192 variances ($\gamma [0.1, 0.1]$). [We fit fertility model with different generic weakly informative priors for coefficients \(\$\mu = 0, \sigma = 0.15\$ \)](#). We ran three chains for 1000 samples for warmup and 4000
 193 for interactions, with a thinning rate of 3. We accessed the quality of the models using trace
 194 plots and predictive check graphs (Piironen and Vehtari, 2017) (Supporting Information S-2).
 195 To understand the effect of climate on vital rates, we got the 95 % credible interval of the
 196 posterior distribution. Then we assumed that there is 95 % probability that the true (unknown)
 197 estimates would lie within that interval, given the evidence provided by the observed data
 198 for each vital rate. All models were fit in Stan (Stan Development Team, 2023).

201 Population growth rate responses to climate

202 To understand the effect of climate on population growth rate, we used the vital rate estimated
 203 earlier to build a matrix projection model (MPM) structured by size (number of tillers),
 204 sex and climate (dormant and growing) as covariate. Let $F_{x,z,t}$ and $M_{x,z,t}$ be the number of
 205 female and male plants of size x in year t present at a location that has z as climate, where

206 $x \in \{1, 2, \dots, U\}$ and U is the maximum number of tillers a plant can reach (here 95th percentile
 207 of observed maximum size). Let F_t^R and M_t^R be the new recruits, which we assume do not
 208 reproduce in their first year. We assume that the parameters of sex ratio-dependent mating
 209 (Eq. 1) do not vary with climate. For a pre-breeding census, the expected numbers of recruits
 210 in year $t+1$ is given by:

$$211 \quad F_{t+1}^R = \sum_{x=1}^U [p^F(x, z) \cdot c^F(x, z) \cdot d \cdot v(\mathbf{F}_t, \mathbf{M}_t) \cdot m \cdot \rho] F_{x,z,t} \quad (3)$$

$$212 \quad M_{t+1}^R = \sum_{x=1}^U [p^F(x, z) \cdot c^F(x, z) \cdot d \cdot v(\mathbf{F}_t, \mathbf{M}_t) \cdot m \cdot (1 - \rho)] F_{x,z,t} \quad (4)$$

213 where p^F and c^F are flowering probability and panicle production for females of size x , d
 214 is the number of seeds per female panicle, v is the probability that a seed is fertilized, m is
 215 the probability that a fertilized seed germinates, and ρ is the primary sex ratio (proportion
 216 of recruits that are female), z is the climate. Seed fertilization depends on the OSR of panicles
 217 (following Eq. 1) which was derived from the $U \times 1$ vectors of population structure \mathbf{F}_t and \mathbf{M}_t :

$$218 \quad v(\mathbf{F}_t, \mathbf{M}_t) = v_0 * \left[1 - \left(\frac{\sum_{x=1}^U p^F(x, z) c^F(x, z) F_{x,z,t}}{\sum_{x=1}^U p^F(x, z) c^F(x, z) F_{x,z,t} + p^M(x, z) c^M(x, z) M_{x,z,t}} \right)^\alpha \right] \quad (5)$$

219 Thus, the dynamics of the size-structured component of the population are given by:

$$220 \quad F_{y,t+1} = [\sigma \cdot g^F(y, x=1, z)] F_t^R + \sum_{x=1}^U [s^F(x, z) \cdot g^F(y, x, z)] F_{x,z,t} \quad (6)$$

$$221 \quad M_{y,t+1} = [\sigma \cdot g^M(y, x=1, z)] M_t^R + \sum_{x=1}^U [s^M(x, z) \cdot g^M(y, x, z)] M_{x,z,t} \quad (7)$$

222 In the two formula above, the first term indicates seedlings that survived their first year and en-
 223 ter the size distribution of established plants. Instead of using *P. arachnifera* survival probability,
 224 we used the seedling survival probability (σ) from demographic studies of the hermaphroditic
 225 congener *Poa autumnalis* in east Texas (T.E.X. Miller and J.A. Rudgers, *unpublished data*), and we
 226 assume this probability was constant across sexes and climatic variables. We did this because
 227 we had little information on the early life cycle transitions of greenhouse-raised transplants.
 228 We also assume that $g(y, x=1)$ is the probability that a surviving seedlings reach size y ,
 229 the expected future size of 1-tiller plants from the transplant experiment. The second term
 230 represents survival and size transition of established plants from the previous year, where
 231 s and g give the probabilities of surviving at size x and growing from sizes x to y , respectively,
 232 and superscripts indicate that these functions may be unique to females (F) and males (M).

233 Since the two-sex MPM is nonlinear (vital rates affect and are affected by population
234 structure) we estimated the asymptotic geometric growth rate (λ) by numerical simulation,
235 and repeated this across a range of climate.

236 Identifying the mechanisms of population growth rate sensitivity to climate

237 ⁴ To identify which aspect of climate is most important for population viability, we use
238 a "random design" Life Table Response Experiment (LTRE). We used the RandomForest
239 package to fit a regression model with θ as predictors and λ_c as response (Ellner et al., 2016;
240 Liaw et al., 2002). The LTRE approximates the variation in λ in response to climate covariates
241 and their interaction (Caswell, 2000; Hernández et al., 2023):

$$242 \quad Var(\lambda_c) \approx \sum_{i=-1}^n \sum_{j=1}^n Cov(\theta_i, \theta_j, \theta_{ij}) + Var(\epsilon) \quad (8)$$

243 where, θ_i , θ_j , θ_{ij} represent respectively the fitted regression slope for the covariate of the
244 dormant season, j the covariate of the growing season and ij the covariate of their interactions.

245 Because LTRE contributions are additive, we summed across vital rates to compare the
246 total contributions of female and male parameters.

247 Impact of climate change on niche and range shifts

248 A species' ecological niche can be defined as the range of resources and conditions (physical
249 and environmental) allowing the species to maintain a viable population ($\lambda > 1$). To
250 understand the impact of climate change on species niche shifts, we estimated the conditional
251 probability of the population viability being more than one across two environmental axes
252 (Diez et al., 2014). In this study, the environmental axes are temperature and precipitation
253 of the dormant season or temperature and precipitation of the growing season. Averaging
254 projection of population growth rates was used to reduce uncertainty across climate
255 projections (general circulation models).

256 All the analysis were performed in R 4.3.1 (R Core Team, 2023)

⁴I don't think the LTRE analysis is adequately motivated by the Intro.

257 **Results**

258 **Sex specific demographic response to climate change**

259 Most vital rates were strongly climate dependent, but the magnitude of their response differed
260 between sexes suggesting a sex-specific demographic response to climate. Survival and
261 flowering were strongly more dependent on climate than growth (number of tillers) and repro-
262 duction (number of panicles) (Fig.1; Supporting Information S-3). We found opposite patterns
263 in the direction of the effect on seasonal climate on the probability of survival and flowering.
264 The growing season (precipitation) has a negative effect on the probability of survival, number
265 of tillers, and the probability of flowering, whereas the dormant season has a positive effect
266 on these vital rates. Unlike the other seasonal variables, temperature had different effects on
267 different vital rates. Temperature of the growing season has a positive effect of the probability
268 of survival, a negative effect of the probability of flowering, and the number of tillers, but no
269 significant effect on the number of panicles. Further, there was a female survival and flowering
270 advantage across both climatic seasons (Figures. 3A-3D, 3I-3K). On the contrary, there was
271 a male panicle advantage across all climatic variables (Figure3M-3P). Counter-intuitively, there
272 was no significant sex growth advantage in all season climatic variables (Figures. 3E-3H).

273 **Population growth rate response to climate change**

274 We estimated the predicted response to population growth rate (population fitness) to seasonal
275 climate gradients using a model assuming a female dominant model and another model using
276 the two sexes. Consistent with the effect of climate on the individual vital rate, we found a
277 strong effect of seasonal climate on population fitness (Fig.2). For both models (female domi-
278 nant and two sexes), population fitness decreased with an increase of precipitation of growing
279 season. In contrast population fitness increased with precipitation of the dormant season. Fur-
280 thermore, population fitness was maximized between 23 and 17 degrees Celsius and decreases
281 to zero just beyond 32 degrees Celsius during the growing season. Similarly population fitness
282 was maximized between 13 and 17 degrees Celsius and decreases to zero just beyond 20 de-
283 grees Celsius during the growing season. We have also detected a strong effect of the past and
284 future climate on population growth rate. However, for future climate, the magnitude of that ef-
285 fect was different between gas-scenario emissions. A moderate emission gas scenario (RCP4.5)
286 has a moderate effect on the population growth rate, while a high emission scenario (RCP8.5)
287 has a strong effect on the population growth rate. High-emission scenario (RCP8.5) will lead

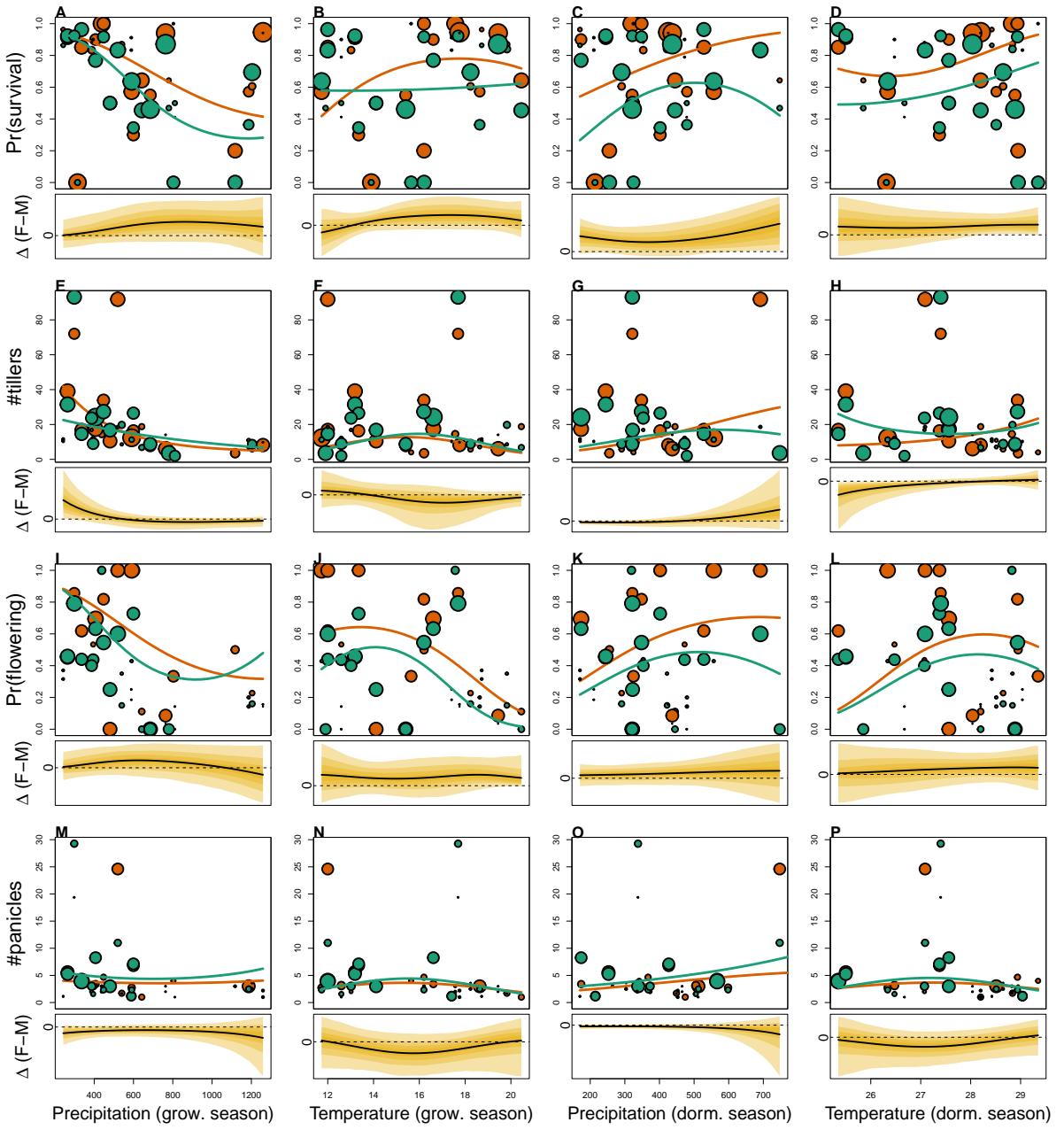


Figure 1: Sex specific demographic response to climate across species range: A–D, inter-annual probability of survival; E–H, inter-annual growth (change in number of tillers); I–L, probability of flowering; M–P, number of panicles produced given flowering. Points show means by site for females (orange) and males (green). Point size is proportional to the sample size of the mean. Lines show fitted statistical models for females (yellow) and males (green) based on posterior mean parameter values. Lower panels below each data panel show the posterior distribution of the difference between females and males as a function of climate (positive and negative values indicate female and male advantage, respectively); dashed horizontal line shows zero difference.

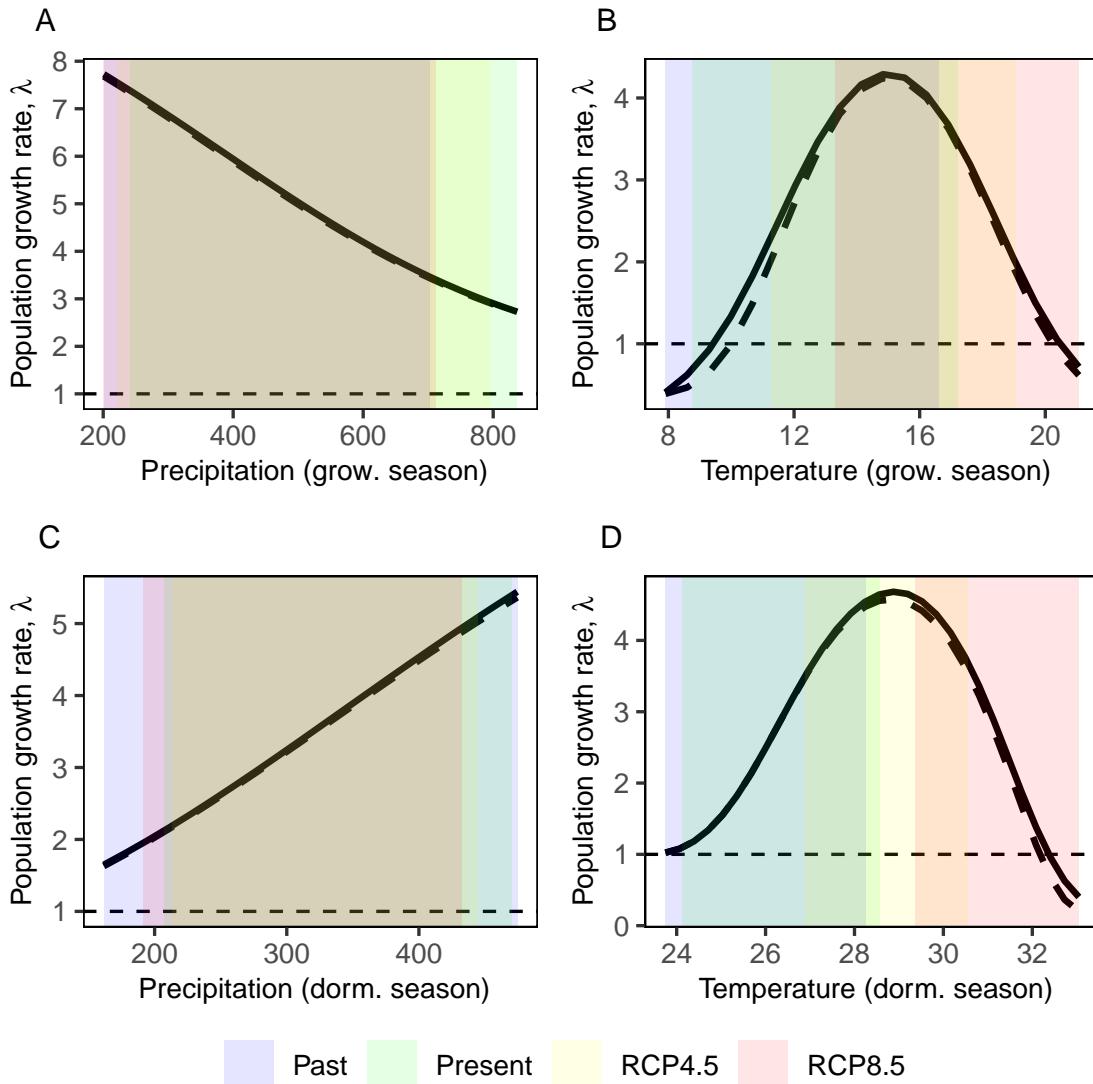


Figure 2: Population growth rate (λ) as a function of climate (past climate, present and predicted future climates). For future climate, we show a Representation Concentration Pathways 4.5 and 8.5. Values of (λ) are derived from the mean climate variables across 4 GCMs. The solid bold curve shows prediction by the two-sex matrix projection model that incorporates sex-specific demographic responses to climate with sex ratio dependent seed fertilization. The bold dashed curve represents the prediction by the female dominant matrix projection model. The dashed horizontal line indicates the limit of population viability ($\lambda = 1$)

288 to an alteration of population viability. Under past climate conditions, population growth rate
 289 decreased below one for temperature of the growing season and the dormant season.

290 **Climatic niches and range predictions**

291 Our demographically based range predictions broadly captured the known distribution of
 292 the species (Fig. 1). More specifically, the predicted population viable ($\lambda > 1$) matches the

²⁹³ presence and absence of the species. Furthermore, viable populations of *P. arichnifera* were
²⁹⁴ only predicted at the center of the range for current climatic conditions (Fig1). Future and
²⁹⁵ past projections of climate change showed a north-west range shift compared to current
²⁹⁶ distributions. Although *P. arichnifera* was predicted to have suitable habitat in the center of the
²⁹⁷ range under the current climate, future warming is predicted to reduce much of the suitable
²⁹⁸ habitat in the southern part (Figure).

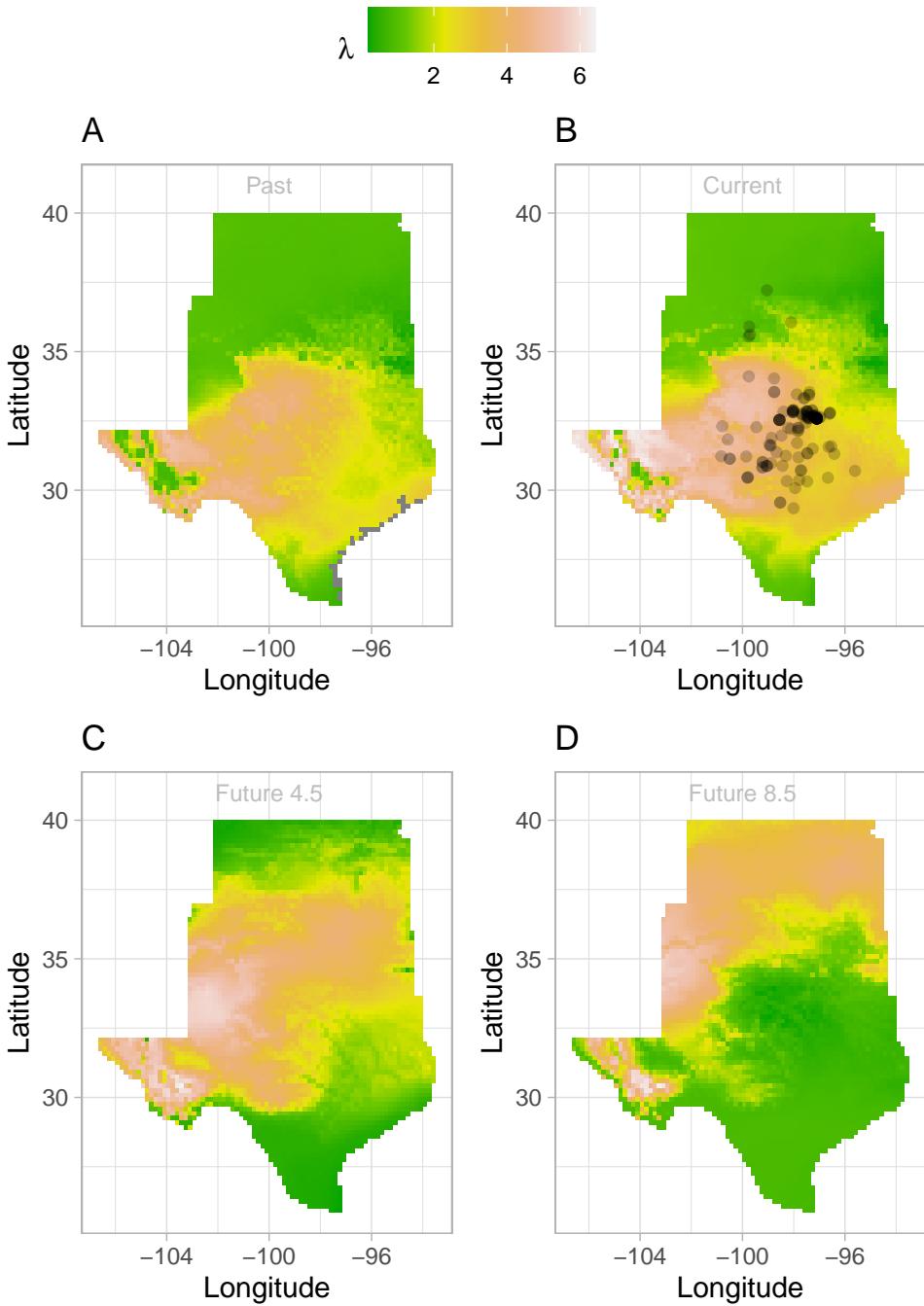


Figure 3: Past (A), Current (B), Future (2070–20100) (C and D) predicted range shift based on population growth rate. Future projections were based on the average population growth rate in four GCMs. The black circles on panel B indicate all known presence points collected from GBIF from 1990 to 2019, which corresponds to the current condition in our prediction. The occurrences of GBIFs are distributed inwith higher population fitness habitat ($\lambda > 1$) , confirming that our study approach can reasonably predict range shifts.

²⁹⁹ **Discussion**

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Supporting Information

426 S.1 XX

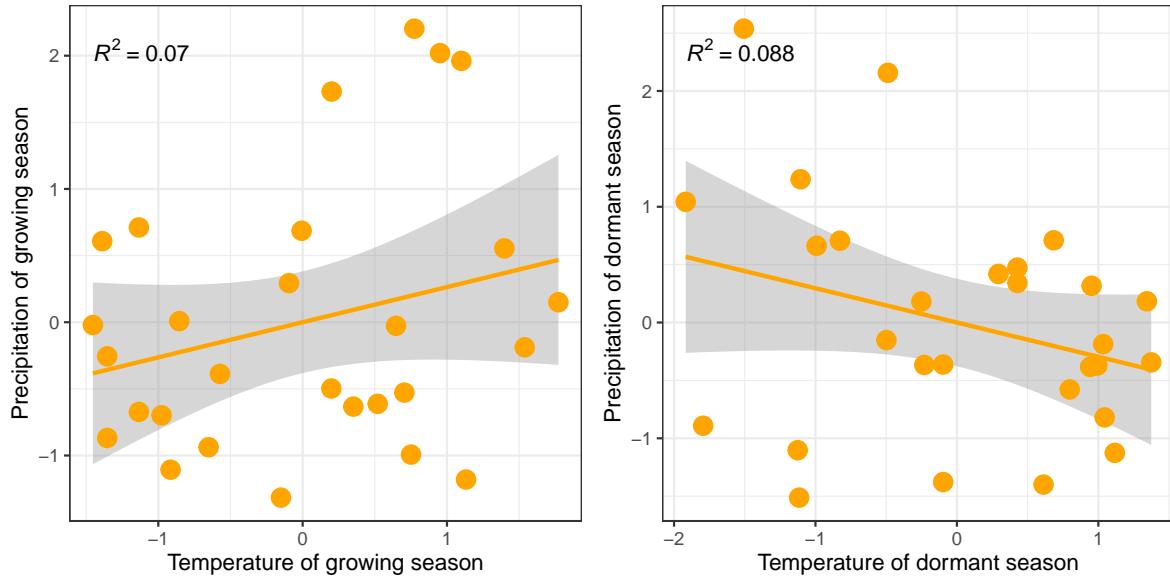


Figure S-1: Relation between precipitation and temperature for each season (growing and dormant). R^2 indicates the value of proportion of explained variance between the temperature and precipitation

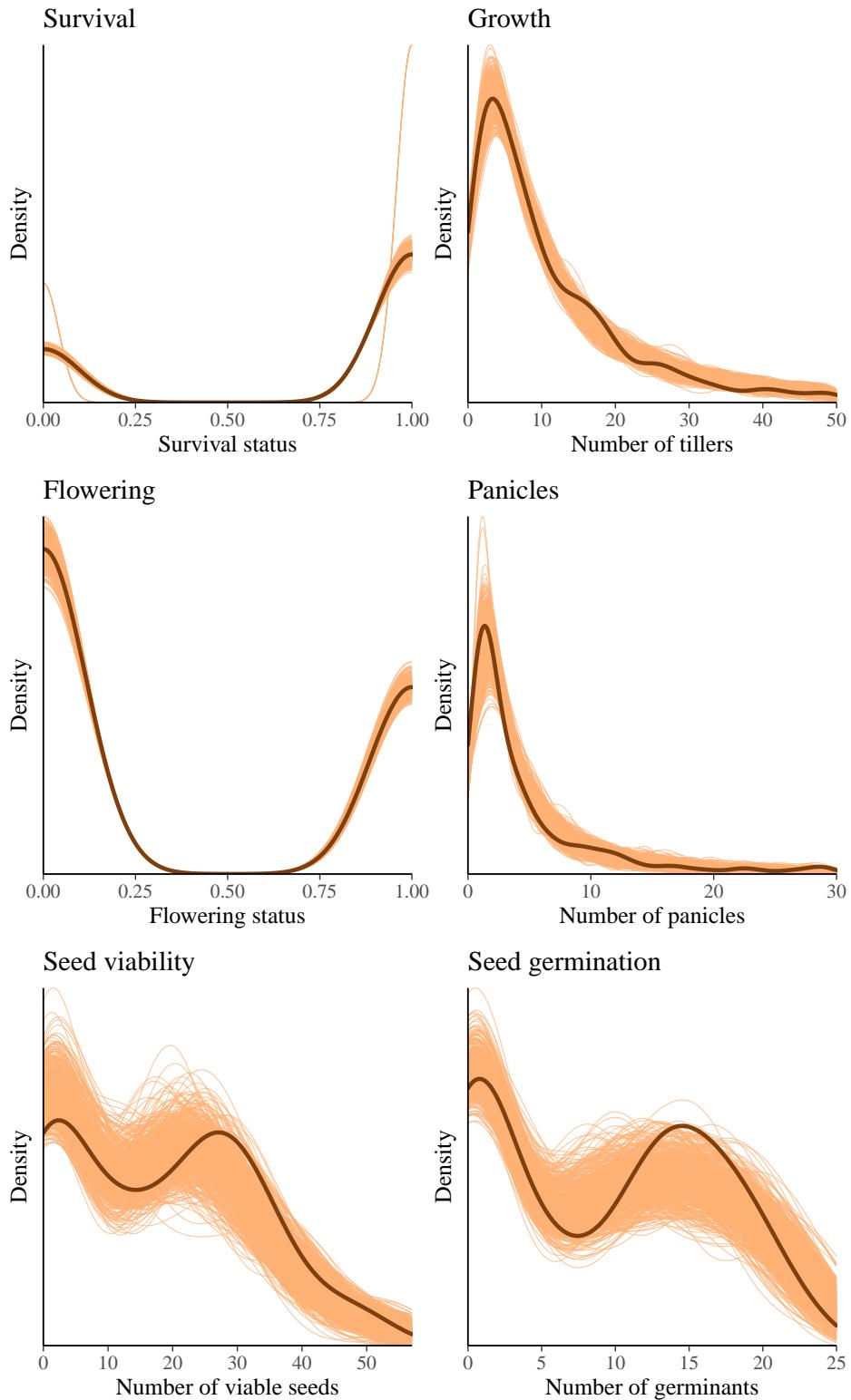


Figure S-2: Consistency between real data and simulated values suggests that the fitted model accurately describes the data. Graph shows density curves for the observed data (light blue) along with the simulated values (dark blue). The first column shows the linear models and the second column shows the 2 degree polynomial models.

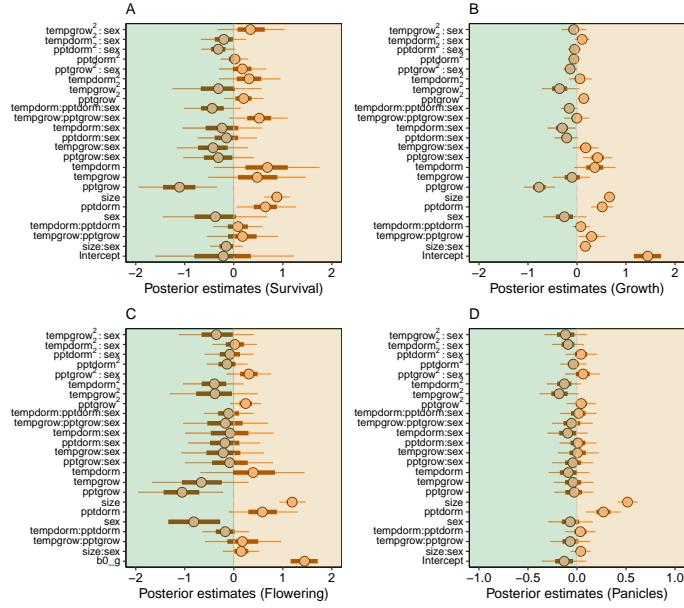


Figure S-3: Mean parameter values and 95% credible intervals for all vital rates.

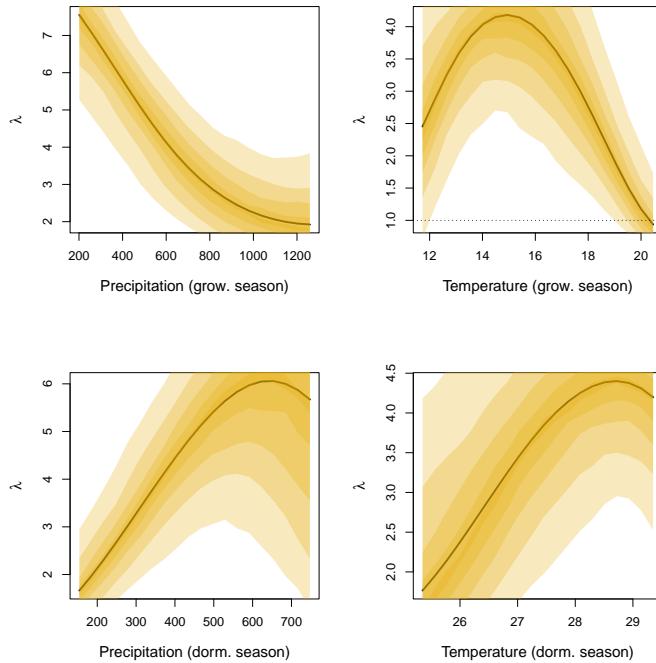


Figure S-4: Population growth rate (λ) as a function of seasonal climate (2016-2017), predicted by the two-sex matrix projection model that incorporates sex-specific demographic responses to climate with sex ratio-dependent seed fertilization. We show the mean posterior distribution of λ in solid lines, and the 5, 25, 50, 75, and 95% percentiles of parameter uncertainty in shaded gold color. The dashed horizontal line indicates the limit of population viability ($\lambda = 1$)

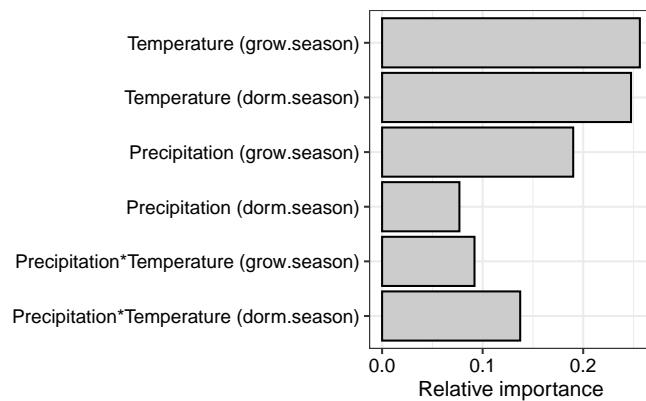


Figure S-5: XXX