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The Relationship between Maturation Size and Maximum Tree Size from Tropical to Boreal Climates

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133

134 **The fundamental trade-off between current and future reproduction has**
135 **long been considered to result in a tendency for species that can grow**
136 **large to begin reproduction at a larger size. Due to the prolonged time**
137 **required to reach maturity, estimates of tree maturation size remain very**
138 **rare and we lack a global view on the generality and the shape of this**
139 **trade-off. Using seed production from five continents, we estimate tree**
140 **maturation sizes for 486 tree species spanning tropical to boreal climates.**
141 **Results show that a species' maturation size increases with maximum**
142 **size, but in a non-proportional way: the largest species begin reproduc-**
143 **tion at smaller sizes than would be expected if maturation were simply**
144 **proportional to maximum size. Furthermore, the decrease in relative mat-**
145 **uration size is steepest in cold climates. These findings on maturation**
146 **size drivers are key to accurately represent forests' responses to distur-**
147 **bance and climate change.**

148 *keywords:* tree fecundity | size | seed production | tree maturation | life-history | allometry

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154 **Data and code availability statement**

155 Data and code supporting our results are archived on the Open Science Framework (OSF)
156 Repository: <https://doi.org/10.17605/OSF.IO/U23VY>. All analyses used R Core Team
157 (2023) (v4.3.0) and published R packages.

158 **Author contributions**

159 V.J., G.K. and J.S.C performed analyses, led the paper, and designed the study. V.J., M.B.,
160 B.C., G.K., T.Q, and J.S.C co-wrote the paper. J.S.C compiled the MASTIF network, and
161 wrote the MASTIF model and software. All authors contributed data and revised the paper.

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171 Introduction

172 The size or age at maturity is critical for tree population fitness and forest regeneration because recruitment
173 opportunities can occur when trees are any size or age (Dietze & Clark, 2008; McDowell *et al.*, 2020; Qiu
174 *et al.*, 2021). In trees, reproduction follows an extended maturation phase (Thomas, 1996; Clark *et al.*, 2004).
175 Juvenile allocation to leaves and the roots and architecture that supports them build the large light- and water-
176 harvesting capacity characteristic of the tree life form. Allocation can then shift to include reproduction. This
177 delayed maturation of trees is linked to the fundamental trade-off between current and future reproduction
178 (Stearns, 1989).

179 On one hand, delayed reproduction sacrifices early seed production to reap future benefits. In environ-
180 ments marked by intense competition and a reliable future, delayed reproduction benefits from large size and
181 the resources that accumulate if juveniles allocate to growth and survival (Falster & Westoby, 2003; Wenk &
182 Falster, 2015). On the other hand, the advantages of large size can come with costs, including water trans-
183 port high into the crown and biomechanical risk of bole fracture or windthrow (Niklas, 1994; Koch *et al.*, 2004;
184 Dietze & Clark, 2008; Lines *et al.*, 2012). Current reproduction avoids the risks of an uncertain future, and it
185 contributes most to fitness in non-competitive or frequently disturbed environments (Charlesworth, 2000).

186 Among tree species, the potential trade-off between current and future reproduction might require a bal-
187 ance of benefits and risks and result in a positive association across species in maturation and maximum size
188 or age (Loehle, 1988; Thomas, 1996; Davies & Ashton, 1999; Westoby *et al.*, 2002; Falster & Westoby, 2003;
189 Wenk & Falster, 2015; Visser *et al.*, 2016). Our understanding of the variation of maturation size among tree
190 species is, however, extremely limited and there are no large-scale studies on this topic. We thus have a poor
191 understanding of how maturation size varies with species maximum size and the relative importance of other
192 factors such as species climate niche and functional traits.

193 In the absence of maturation estimates, earth system models (ESMs) incorporate assumptions that are
194 expected to bias lifetime reproduction. Many ESMs omit impacts of life history on disturbance response
195 entirely (see McDowell *et al.* 2020 for a review). In models that do accommodate life history, maturation size
196 – d_{mat} (for diameter) – is independent of maximum size – d_{max} (Kohler & Huth, 2004; Wallentin *et al.*, 2008;
197 Yang *et al.*, 2022) (Fig. 1, black dotted line). An alternative hypothesis is that maturation size is proportional
198 to maximum size. It is consistent with a study at Barro Colorado Island in Panama, where Visser *et al.*
199 (2016) reported that $d_{mat} = d_{max}/2$ (red dashed line in Fig. 1). This is related to the classical prediction
200 of a proportionate increase in maturation age with increased maximum age from simple optimization models
201 in animals (Charnov & Berrigan, 1990, 1991; Jensen, 1996; Thorson *et al.*, 2017) and trees (Clark, 1991).
202 Indeed, if the predictions for age also apply to size, then this **proportionate risk model** means that the
203 maturation delay incurred for increased maximum size is the same for species large and small, represented
204 by the red line in Fig. 1.

205 In fact, it would be remarkable if this relationship was the same for species of all sizes because the
206 constraints on the large size and the relative contribution to fitness of early seed production could vary widely
207 depending on the species' maximum size. If mortality risks and allocation demands change with age and size
208 (Charnov & Berrigan, 1990), then the strictly proportional relationship between maturation size (d_{mat}) and
209 maximum size (d_{max}) can be generalized to a power relationship,

$$d_{mat} = \alpha \times d_{max}^{\beta_d} \quad (1)$$

210 The proportionate model means that $\beta_d = 1$ in Eq. (1) (Fig. 1a). An **accelerating risk model** refers to
 211 the case where the maturation delay required for large species to increase maximum size is greater than for
 212 small species. If $\beta_d > 1$ (purple in Fig. 1), the relative size at maturation ($d_{rel} = d_{mat}/d_{max}$) continues to
 213 increase for species in the largest size classes (Fig. 1b). Consider, for example, an expected fitness gain
 214 from extending end-of-life reproduction that comes with increased size and age. The early life investments in
 215 structural support or defenses needed for an incremental increase in maximum size might be especially high
 216 for the largest species.

217 Alternatively, a **diminishing risk model** refers to the case where the need to further delay maturation
 218 size declines for species already at large size. If $0 < \beta_d < 1$, then species that reach large size do not incur
 219 the same proportionate delay risk as small species. As β_d approaches zero, the largest species mature at
 220 nearly the same size as the small species. Then, the relative size at maturation d_{rel} declines with maximum
 221 size (Fig. 1b).

222 Improved understanding of maturation size confronts challenges posed by slow dynamics and limited
 223 observation. Where there is a dense canopy, the reproductive status of individual trees is often not detected,
 224 and crop failures (little or no seed production in trees that have reached maturity) are common. Likewise, seed
 225 traps often fail to recover seeds from nearby reproductive trees, especially the low seed production of newly
 226 mature individuals (LaDeau & Clark, 2001). Detection error can be minimized where observations come from
 227 above the canopy or open settings like savannas, seed orchards, or common gardens (LaDeau & Clark, 2001;
 228 Caignard *et al.*, 2021). Still, a time series of observations is needed because an individual reproducing this
 229 year will have matured at some time in the past. Estimates of maturation status from time series data allow
 230 for detection error similar to the way it is used in capture-recapture models. Maturation can be treated as
 231 a hidden Markov process (see detailed Supplements to Clark *et al.* 2004, 2019). As in capture-recapture
 232 models, the probability that an individual is mature in a given year depends not only on failure to detect in the
 233 current year but also on the history and future of observations on the same individual. The more times that
 234 reproduction is not detected in the past (or future), the lower the probability that a tree is mature now. In tree-
 235 fecundity studies, the complexity is compounded by the "masting" phenomenon, where quasi-synchronous,
 236 quasi-periodic crops require observations over several years, making a large number of observations in a
 237 single year insufficient. Most studies where maturation size has been estimated focus on open-grown trees
 238 and/or have limited taxonomic breadth, habitat variation, or both (Wenk *et al.*, 2018; Thomas, 1996; Davies &
 239 Ashton, 1999; Kohyama *et al.*, 2003; Wright *et al.*, 2005; Visser *et al.*, 2016; Minor & Kobe, 2019).

240 Inferring the relationship between maturation and maximum size has also to control for the environment
 241 (Wenk & Falster, 2015) and species characteristics (Visser *et al.*, 2016). While the effects of climate on
 242 maturation size are unknown, tree fecundity responds to seasonal temperature and moisture, soils, and light
 243 availability, which depends on the local competitive environment (Clark *et al.*, 2014; Caignard *et al.*, 2017;
 244 Minor & Kobe, 2019; Le Roncé *et al.*, 2021; Qiu *et al.*, 2022; Journé *et al.*, 2022). Also, fast growth and
 245 accelerated competition that comes from long growing seasons in the wet tropics do not necessarily imply
 246 small or large maturation sizes.

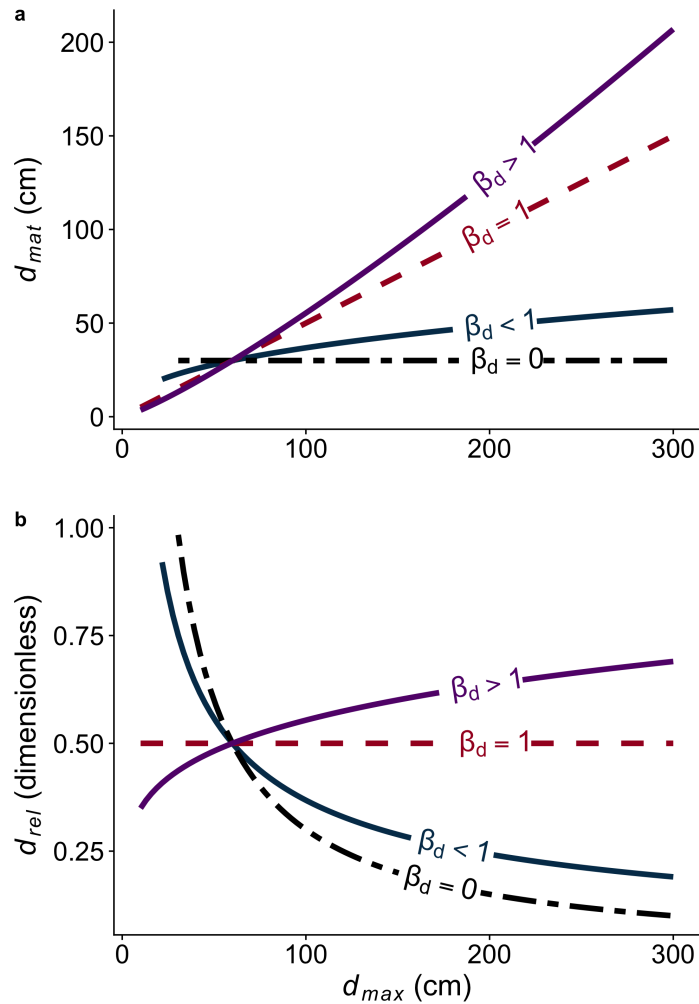


Figure 1: Hypothesized association between maturation size (d_{mat}) and maximum size (d_{max}) (**a**) and the relative size at maturation ($d_{rel} = d_{mat}/d_{max}$) (**b**) (Eq. (1)). To highlight the effects of size (parameter β_d), values of parameter α are selected to yield an equivalent diameter at $d_{max} = 60$ cm. Two "baseline" hypotheses (dashed lines) are independence between d_{mat} and d_{max} (black dotted) and proportionate delay (red dotted), the latter is expected if increased size incurs the same maturation delay at all size classes. Two alternative hypotheses are increasing (purple - accelerating risk model) or decreasing (blue - diminishing risk model) maturation delays in the largest size classes.

247 The relationship between maturation and maximum size could be associated with other plant functional
248 traits, that would reflect diverse plant strategies. Fast growth in open environments is often associated with
249 low wood density and high specific leaf area (SLA) (Moles *et al.*, 2004, 2006; Thomas *et al.*, 2015; Visser
250 *et al.*, 2016; Wenk *et al.*, 2018). However, it is unclear whether the same traits that are involved in fast growth
251 are also associated with maturation at a small size. Furthermore, if large-seeded species need to accumulate
252 resource reserves, then there could be a positive association between seed size and maturation size (Moles
253 *et al.*, 2004). Relatedly, high reproductive expenditures, measured as seed size \times seed number (Qiu *et al.*,
254 2022), might be associated with delayed maturation size. Due to their co-dependence, it is necessary to
255 model all of these traits jointly, while accounting for the effects of habitat and phylogenetic groups (Clark,
256 2016; Seyednasrollah & Clark, 2020; Bogdziewicz *et al.*, 2023; Qiu *et al.*, 2023).

257 In this study, we provide the first comprehensive estimates of tree maturation size, obtained for 486 tree
258 species on five continents, incorporating effects of the environment over a large range of tree diameters
259 and habitats. We use the Masting Inference and Forecasting (MASTIF) network and modeling framework
260 to accommodate the dependence between observations between trees and within trees over time (Clark
261 *et al.*, 2021; Sharma *et al.*, 2022; Qiu *et al.*, 2022; Journé *et al.*, 2022). Based on MASTIF estimates we
262 derive maturation size as tree diameter at the onset of female reproductive function allowing us to compare
263 maturation sizes across species that vary in reproductive biology (e.g., Pinaceae commonly produce male
264 cones earlier than female cones; many species have no such separation) and where pollen production can
265 be hard to quantify. We first evaluate how maturation varies with species' maximum size and test the three
266 alternative models of Fig. 1 with our estimates of maturation size and estimates of species' maximum size.
267 Then, we evaluate how the relationship between maturation size and maximum size is influenced by climate
268 and its association with other plant functional traits.

269 **Materials and Methods**

270 Our analysis includes three elements (Fig. 2). We first parameterize a model for individual maturation status
271 and fecundity based on diameter, shade conditions, and environmental variables (Fig. 2a). The year in which
272 an individual achieves maturity is almost never observed. Instead, seeds counted in traps or in crowns vary
273 from year to year. Successive observations represent a time series for every tree. This first step estimates
274 maturation status and conditional fecundity (seeds per tree per year given that it is mature) for all trees in
275 the network. From this fitted model, we generate predictive distributions of maturation status across diameter
276 with other variables held at intermediate values to estimate d_{mat} from the model. Again, this prediction
277 from the model is necessitated by the fact that true maturation status is an estimate, not a state that is directly
278 observed. Second, we estimated the model of Fig. 1 to obtain estimates of α and β_d (Fig. 2b), while controlling
279 for other variables that could affect their relationship. Finally, we evaluate the species-level trait relationship
280 that includes maturation size (Fig. 2c). The following section describes these elements of the analysis.

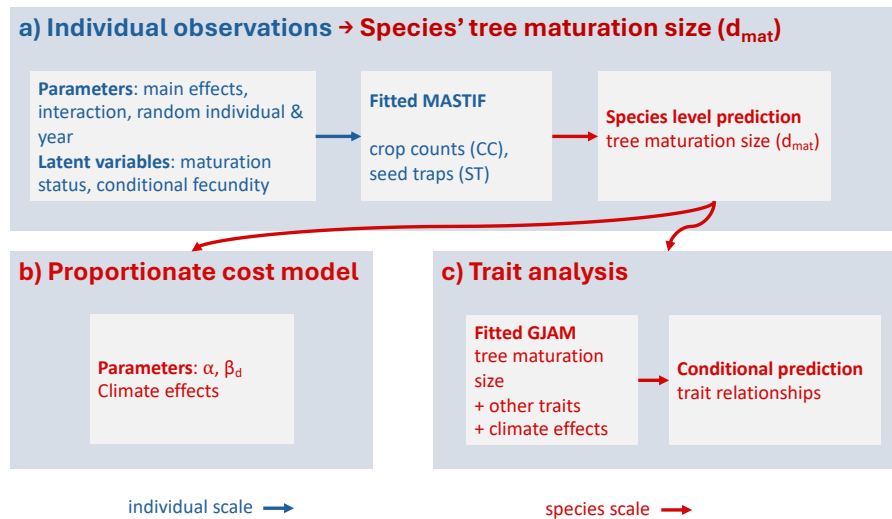


Figure 2: Three elements of the analysis include a) an individual-scale analysis (blue) to estimate maturation status each year and to parameterize relationships that control maturation. This fitted model is the basis for species-level prediction of maturation size (red). b) Species-level expected maturation size based on the proportionate risk model, controlling for species' differences in their climate domains. c) Analysis of species-level trait relationships with maturation size.

MASTIF data and model

281

282 The MASTIF model and data summarized here are detailed in Clark *et al.* (2019) and its extended Supplement
 283 (see also Qiu *et al.* 2021, 2022; Journé *et al.* 2022). Data are of two types, crop counts on trees and seed traps
 284 in mapped inventory plots (MASTIF) (Clark *et al.*, 2019) (Fig. S1). The initial sample size is approximately 12
 285 million tree-years from five continents on 898 species and 112 families. The majority of observations (99%)
 286 are derived from longitudinal studies, involving repeated observations of all trees on a plot or individual trees.
 287 The remaining crop count observations (1%) are collected opportunistically through the iNaturalist project
 288 MASTIF (Clark *et al.*, 2019). The number of species observed per plot ranges from 1 to 221 species. The
 289 number of species observations is larger for seed trap monitoring (476 species in total, 22,929 tree-year
 290 observations on average) than for crop count monitoring (130 species in total, 1,058 tree-year observations
 291 on average). Most plots are localized in North America and central Europe (97%), whereas most species
 292 observations are coming from South America (54%). On average, 75% of individual tree year observation are
 293 coming from the tropics. Additional information is provided in Table S1 and Supplementary Files 1 and 2. For
 294 both data types, observations include species, diameter, shade class (ranging from "full sun", class 1, to "full
 295 shade", class 5), number of fruiting structures, and an estimate of the fraction of the total crop represented
 296 by the count. For crop counts, the data model is beta-binomial, with binomial uncertainty for the counts given
 297 crop fraction, and beta uncertainty for crop fraction. The seed traps data additionally include mapped locations
 298 of trees and seed traps, which is used to jointly estimate fecundity, dispersal, and, for seeds identified only to

299 genus, species identity. For seed traps, the data model is Poisson for counts given dispersal and species, a
 300 bivariate Student's t (i.e. 2Dt) redistribution kernel for dispersal (Clark *et al.*, 1999), and a multinomial species
 301 probability (many seeds are identified only to genus level).

302 The MASTIF model is a dynamic model for year-to-year and tree-to-tree seed production. The model
 303 allows for conditional independence in crop counts and seed traps data through latent states. It estimates
 304 maturation state and conditional fecundity (seed production given the individual is mature), which depend
 305 on tree size, shading, local climate, and soil conditions. Random effects on individuals and years allow for
 306 wide variation between trees and over time. The posterior distribution includes the parameters and latent
 307 states presented in Clark *et al.* (2019), and summarized in Qiu *et al.* (2022) and Journé *et al.* (2022). Model
 308 fitting was accomplished with Gibbs sampling, a Markov chain Monte Carlo technique based on sampling
 309 from conditional distributions. Model structure and methodology are implemented with the R package Mast
 310 Inference and Forecasting (`mastif`, v1.0.1) (Clark *et al.*, 2019).

311 Derivation of tree maturation size from fitted MASTIF model

312 Tree maturation size (d_{mat}) is derived from an individual-scale model fitted to each species with MASTIF. We
 313 define tree maturation size (d_{mat}) as the diameter when a tree is mature and has the capacity to produce
 314 enough seed to construct one fruiting structure, f_{min} . For species that produce one-seeded fruits (e.g.,
 315 *Quercus*, *Juglandaceae*), $f_{min} = 1$. For species that produce cones (e.g., Pinaceae, Cupressaceae), pods
 316 (e.g., Fabaceae, Bignoniaceae), or other capsules that house multiple seeds (e.g., *Fagus* capsules), f_{min}
 317 is the number of seeds contained in that structure. The data and definitions we use to determine d_{mat}
 318 differ from those employed in previous studies (e.g. Visser *et al.* 2016), as we use both crop count and
 319 seed trap observation and not only maturation status. The estimation of individual fecundities, obtained
 320 through MASTIF model, is also included, taking into account tree characteristics and environment (Clark
 321 *et al.*, 2021; Qiu *et al.*, 2021; Journé *et al.*, 2022). MASTIF models the effects of environmental predictors on
 322 conditional fecundity (given mature status), because immature trees do not respond to predictors (it is always
 323 zero). [Modeling environmental effects on (unconditional) fecundity would make no more sense than including
 324 immature individuals in studies of masting intervals or synchronicity.] Conditional fecundity ψ is represented
 325 by a log-normal distribution, which allows for the effects of the environment. The log-normal is undefined
 326 for zero seeds. Zeros are accommodated by the fact that trees can be in the immature state ($\rho = 0$), or
 327 conditional fecundity can be below the threshold f_{min} , as in a failed seed crop (Clark *et al.*, 2004, 2019),

$$f = \begin{cases} \psi & \rho = 1 \\ 0 & (\rho = 0) + (\rho = 1)(\psi < f_{min}) \end{cases} \quad (2)$$

328 An individual is immature until the first time fecundity rises above the threshold for producing fruit, i.e., ($\rho_{i,t} =$
 329 $1)(\psi_{i,t} > f_{min})$). Specifically for tree i in year t ,

$$\begin{aligned}
f_{i,t} &= \psi_{i,t} \times \rho_{i,t} \\
\rho_{i,t} | \rho_{i,t-1}, \rho_{i,t+1} &\sim \text{Bernoulli}(\rho_{i,t-1} + (1 - \rho_{i,t-1})\rho_{i,t+1}\Phi(\beta_0^p + \beta_1^p d_{i,t})) \\
\log \psi_{i,t} &\sim N(\mathbf{x}'_{i,t}\boldsymbol{\beta}^x + \dots, \sigma^2)
\end{aligned} \tag{3}$$

330 where $\Phi(\cdot)$ is the standard normal cumulative distribution function for the probit probability of transitioning to
331 the mature state, depending on tree diameter $d_{i,t}$. Importantly, $\Phi(\beta_0^p + \beta_1^p d_{i,t})$ it is the probability of making
332 the transition for an individual that is now in the immature state. For this reason, the coefficients β_0^p, β_1^p for
333 maturation in the second line of Eq. (3) engage only for the transition tree-years, $[\rho_{i,t} | \rho_{i,t-1} = 0, \rho_{i,t+1} = 1]$.
334 Predictors in the design vector for conditional fecundity $\mathbf{x}'_{i,t}$ include the mean climate variables (defined at
335 the species level) tested here and competition by neighbors, and $\boldsymbol{\beta}^x$ is the estimated parameter vector. The
336 ellipses (...) in Eq. (3) includes individual effects (subscript i) and year effects (subscript t) (Clark *et al.*,
337 2019). The variance not assigned to predictors is $s^2 = \sigma^2 + \text{Var}(\text{individuals}) + \text{Var}(\text{years})$.

338 Setting all other fitted variables at their mean values and intermediate shade (shade class 3 on the
339 scale from 1 to 5), we obtained (unconditional) fecundity f from the fitted model. We first factored the joint
340 distribution of conditional fecundity and maturation,

$$[\psi > f_{min}, \rho = 1] = [\psi > f_{min} | \rho = 1][\rho = 1] \tag{4}$$

341 Using Bayes' theorem, the cumulative distribution function for maturation diameter is

$$\begin{aligned}
[d_{matr} > d | \psi > f_{min}, \rho = 1] &\propto [\psi > f_{min}, \rho = 1 | d][d] \\
&= [\psi > f_{min} | \rho = 1, d][\rho = 1][d] \\
&= \Phi(z_1) \Phi(z_2) [d]
\end{aligned} \tag{5}$$

342 where $z_1 = \frac{\log f_{min} - \mathbf{x}'\boldsymbol{\beta}^p}{s}$ (log normal fecundity), $z_2 = \beta_0^p + \beta_1^p d$ (probit maturation), and again, s^2 is the
343 marginal variance for conditional fecundity. We have taken the diameter distribution $[d]$ to be uniform. The
344 distribution of maturation size is obtained using inverse distribution sampling from Eq. (5), and we estimated
345 \bar{d}_{mat} as the mean of this distribution. We selected species for which maturation and fecundity schedules
346 could be estimated with confidence. The selection was based on estimates of maturation status from the
347 MASTIF model, and we retained species with at least 10 immature and 10 mature individuals. This included
348 486 species observed over a range of values for diameters.

349 Trait and climate data

350 Like maximum tree height or age, maximum tree diameter is a useful concept, despite the fact that it cannot
351 be known. To incorporate the concept of size differences, we use extreme sizes available from literature and
352 our inventory data, recognizing that the concept of a maximum becomes most meaningful with large sample
353 sizes, which are not available for all species. For the final analysis here, we kept the highest estimates

354 of d_{max} . Sources in Table S3 include tropical species from large plots in central Panama (189 species)
 355 and French Guyana (33 species), which together represent 45.7% of values. Estimates extracted from the
 356 internet (e.g. encyclopedia, online flora) include 173 species (35.6%) (Table S3). For species not estimated
 357 in other sources, we used forest inventory data, evaluated by two approaches, both based on order statistics.
 358 We avoided using the absolute largest reported value in forest/MASTIF inventories due to the high noise
 359 levels associated with extremes. Order statistics were preferred over quantiles, the latter being determined
 360 by whether there are huge numbers of small trees in the data set; quantiles are based on the entire stand
 361 structure, whereas here the goal is to estimate the largest sizes, regardless of whether there are few or
 362 many small trees. For species present in national forest inventories we estimated d_{max} following Qiu *et al.*
 363 (2021) by using the tenth largest order statistic (38 species, 7.8%). For the remaining species present in
 364 MASTIF inventories, and with at least more than 90 unique individuals, we used the fifth largest order statistics
 365 (representing in total 8.4%). For species having only maximal plant height (Liu *et al.*, 2019), but no d_{max} ,
 366 we converted them to d_{max} using allometric equations of Feldpausch *et al.* (2011) (12 species, <2.5%).
 367 Observations of d_{max} coming from the internet are usually higher than data from National Forest Inventories,
 368 allometric predictions, and MASTIF inventories (Fig. S2). Seed size estimates came from measurements in
 369 our lab (Clark *et al.*, 2021), the primary literature, and the [TRY Plant Trait Database](#) (Kattge *et al.*, 2011).
 370 Wood density and SLA are from the compilation of Carmona *et al.* (2021). We used genus- or family-level
 371 means for seed size, SLA, and wood density values that were missing at the species level (15%, 28%, and
 372 26%, respectively). We defined a species' seed productivity as (mass per seed) \times (mean seeds per tree
 373 basal area) (Qiu *et al.*, 2022).

374 For species' climate, we extracted average temperature (in $^{\circ}$ C) and moisture deficit (evapotranspiration
 375 minus precipitation, in mm) for each species based on all occurrences in the Global Biodiversity Information
 376 Facility ([GBIF](#)) through the R package `rgbif` (Chamberlain & Boettiger, 2017). The GBIF request is available
 377 from reference GBIF.org (2022). For species that are absent from GBIF, we extracted temperature and deficit
 378 from the MASTIF sites where those species were reported (162 species, 33%). Climate variables were
 379 obtained from [CHELSA](#) (Karger *et al.*, 2017).

380 Maturation and maximum size

381 To test the alternative hypotheses that the maturation diameter decreases ($\beta_d < 1$) or increases ($\beta_d > 1$) with
 382 maximum species size (Fig. 2b), we estimated parameters in Eq. (1) with the model

$$\begin{aligned} \log_{10}(d_{mat_s}) &= \log_{10}(\alpha) + \beta_d \times \log_{10}(d_{max_s}) + \dots + \epsilon_s \\ \epsilon &\sim N(0, \sigma^2) \end{aligned} \quad (6)$$

383 for species s , where the ellipsis includes climatic variables (moisture deficit and temperature) and their
 384 interactions with d_{max} . We tested alternative models including independence between maturation and max-
 385 imum size (fitted α with β_d fixed at zero), proportionate increase (fitted α with $\beta_d = 1$), and changing rela-
 386 tionship with size (both α and β_d estimated). Models were fitted with regression by using species average

387 estimates of d_{mat} as a response, and we included the inverse of the standard error of d_{mat} as weights. Model
388 selection and fit were evaluated with AIC and root-mean-square error (RMSE). Regression dilution could
389 cause underestimation of the strength between here d_{mat} and d_{max} when a predictor (i.e. d_{max}) contains
390 errors (Frost & Thompson, 2000; Detto *et al.*, 2019). We thus ran additional analyses to test the robustness
391 of our results to the regression dilution effect (see Supplementary material A.2). First, we corrected the pa-
392 rameter $\hat{\beta}_d$ from measurement error by using the R package `mecor` (Nab, 2021) (v1.0). Secondly, we tested
393 if the relationship between d_{mat} and d_{max} varies depending on the origin of d_{max} .

394 **Joint trait analysis**

395 We evaluated the association between maturation size and other species' traits from the ability of d_{mat} to pre-
396 dict other trait values while allowing for climate and phylogeny effects (Fig. 2c). The marginal correlations that
397 are commonly used for this purpose do not account for the many ways that traits can be related to one another.
398 For instance, maturation size might be associated with maximum size because both tend to be high in warm
399 climates, or in the phylogenetic groups that tend to occur in warm climates. To accommodate co-dependence
400 between trait values we used Generalized Joint Attribute Modeling (GJAM) with traits as responses (Clark
401 2016). To account for phylogeny in the joint traits model, we diverged from traditional assumptions concerning
402 residual covariance. Instead, we adopted a direct inference of the effects of phylogenetic groups. Traditional
403 approaches of phylogenetic correction build on highly specific assumptions for the residual variance (random
404 walk, or more complex models representing stabilizing selection such as the Ornstein–Uhlenbeck model).
405 Our departure from these assumptions stems from the recognition that natural selection does not operate
406 uniformly, neither within a given species pair nor across a broad spectrum of species. Our GJAM analysis
407 explored phylogenetic contributions, with species groups treated as random effects and covariance that is
408 unconstrained by assumptions on divergence rates (Qiu *et al.*, 2023). Explanatory variables included temper-
409 ature, moisture deficit, and their interaction. Traits included wood density (g m^{-3}), specific leaf area (SLA)
410 ($\text{mm}^2 \text{mg}^{-1}$), species seed productivity (kg m^{-2} basal area), seed size (g), maximum diameter (d_{max}) (cm),
411 and maturation diameter (d_{mat}) (cm). All traits were log-transformed. We included a random phylogenetic
412 group effect in the joint trait analysis (Qiu *et al.*, 2022; Bogdziewicz *et al.*, 2023; Qiu *et al.*, 2023). For species
413 in speciose genera (more than 10 species), genus was used as the phylogenetic group. For species in less
414 speciose genera but belonging to families with more than five species, family was used as the phylogenetic
415 group. For the remaining species (<25% of the total), an 'other' category was used. To estimate the direct
416 effect of traits (i.e. SLA, wood density, species seed productivity, seed size) and climatic variables on d_{mat} , we
417 report conditional parameters from GJAM. Conditional parameters are estimated by extracting the parameters
418 of the conditional distribution of traits conditioned on d_{mat} . Conditional parameters estimate the direct associ-
419 ations between traits while accounting for climate and phylogeny. Conditional parameters were obtained with
420 the `gjam` R package (v2.6.2) (Supplementary Material, Section A.1).

421 **Relation of d_{mat} along the phylogeny**

422 We visualized how d_{rel} varies across species phylogeny by making a phylogenetic tree plot. We used the
 423 phylogeny from Zanne *et al.* (2014), and retrieved phylogenetic information for 400 out of the 486 studied
 424 species. Of the species missing from the phylogeny (i.e. 86 species), the relative proportion of missing
 425 phylogenetic information is about 13.2% for temperate species and about 19.4% for tropical species. We then
 426 tested for a phylogenetic signal in d_{rel} and d_{mat} using Pagel's λ (Pagel, 1999) (which test for a Brownian
 427 motion evolutionary signal), with values close to 0 indicating low phylogenetic signal and values close to 1
 428 suggesting a phylogenetic correlation. We plotted the phylogenetic tree with `ggtree` R package (v3.8) (Yu
 429 *et al.*, 2017). We estimated the Pagel's λ by using the `phylosig` function from `phytools` (v1.5) (Revell, 2012).

Table 1: Coefficient estimates and fit to Eq. (6). The selected model with the lowest AIC (bold font at top) includes temperature (β_T) and the interaction between d_{max} and temperature (β_{dT}). The proportional cost model has β_d fixed at 1. The independence model has β_d fixed at 0. Additional models that include moisture deficit and temperature have higher AIC values (Table S4).

α	β_d	β_T	β_{dT}	σ	AIC	RMSE
3.71 [1.94, 7.07]	0.30 [0.15, 0.46]	-0.023 [-0.035, -0.011]	0.012 [0.0058, 0.019]	0.089	-62	10.2
1.08 [0.93, 1.25]	0.59 [0.55, 0.63]	-	-	0.090	-52	10.0
0.24 [0.23, 0.26]	1	-	-	0.12	248	18.8
9.25 [8.69, 9.85]	0	-	-	0.15	447	15.4

430 **Results**

431 Maturation size is associated with maximum size, but not proportionately so (Fig. 3a). Large inter-specific
 432 variation in d_{mat} estimates had 95% quantiles that ranged from 4.0 to 51 cm, with relative maturation size
 433 ($d_{rel} = d_{mat}/d_{max}$) quantiles of (0.07, 0.65). Contrary to the baseline independence model ($\beta_d = 0$), trees
 434 did not start to reproduce at a constant size (dashed black line in Fig. 3a). If we force proportionality (fix
 435 β_d at 1), the estimate of $\hat{\alpha} = 0.24(0.23, 0.26)$ (line 3 of Table 1) is consistent with Loehle's (1988) range for
 436 hardwoods (1/5 to 1/4), but far outside his range for conifers (1/15 to 1/10). The 95% CI that is well below 0.5.
 437 This differs from the Visser *et al.* (2016)'s estimate of 1/2 for Barro Colorado Island (N = 60 species), Panama,
 438 and with Minor & Kobe (2019) La Selva, Costa Rica (N = 16 species). It is crucial to acknowledge that the
 439 aforementioned authors employed a distinct definition of d_{mat} and estimated larger d_{mat} (Fig. S3). Moreover,
 440 this proportional cost model ($\beta_d = 1$) fits poorly, with twice the RMSE and a higher AIC than the best-fitting
 441 model (Table 1).

442 Fitting both α and β_d (line 2 of Table 1) shows strong support for the diminishing risk model ($0 < \hat{\beta}_d < 1$).
 443 Allowing for environmental predictors further decreases the estimate to $\hat{\beta}_d = 0.30$ (0.15, 0.46). The exponent
 444 $0 < \beta_d < 1$ means that relative size at maturation (d_{rel}) decreases in large species (blue in Fig. 3a).

445 The best-fitting model (lowest AIC and RMSE) includes a negative effect of temperature (maturation at
 446 small size for species most common in cold climates) and a positive interaction between temperature T and
 447 d_{max} (Table 1). This positive interaction means that the relationship between maturation and maximum size

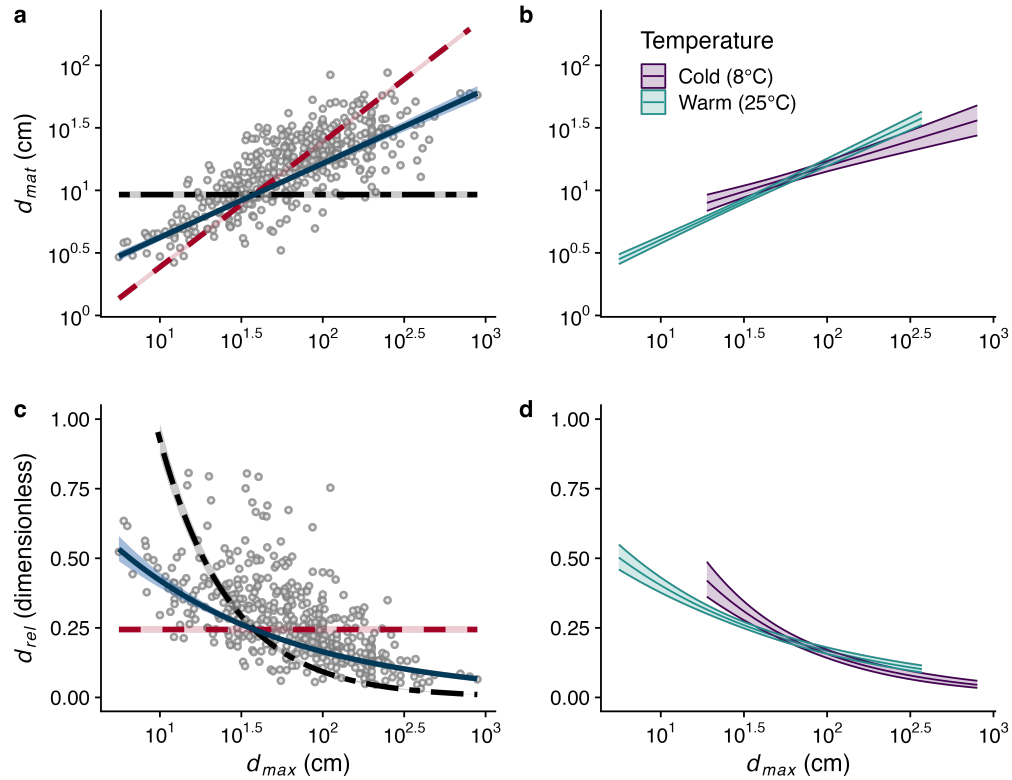


Figure 3: Tree maturation size (a, b), and relative size at maturation (c, d) for 486 species. Each dot represents one species. Alternative models are dashed lines, black for independence between maturation size and maximum size ($\beta_d = 0$), and red for the proportional cost model ($\beta_d = 1$). The best fitting model (blue with 95%CI) supports the diminishing risk model ($\beta_d < 1$, Table 1). Panels b and d are predictions from the fitted model with an interaction between continuous d_{max} and temperature (line 1 of Table 1). This model gives a continuous surface plot of maturation size as a function of maximum size and temperature (see Fig. S4). However, for clarity, we represent only the prediction at cold (8°C, purple) and warm temperatures (25°C, green) spanning observed diameter ranges.

448 tends to steepen for species in warm climates (Fig. 3b, d), approaching the proportionate risk model (Table 1);
 449 the rise in d_{mat} with d_{max} increases with temperature. However, the main plus interaction effect remains below
 450 1 even in warm climates showing that the diminishing risk model is supported across this temperature range.
 451 The β_d remained below 1 even when we restricted the analysis to a single source of d_{max} (Table A1 and
 452 Figure A1, see Supplementary Section 2). After correcting for risks of regression dilution, the average value
 453 of β_d remained below 1, with corrected $\beta_d = 0.73$, however, the confidence interval is between 0.03 to 1.43
 454 (Table A2, see Supplementary Section 2).

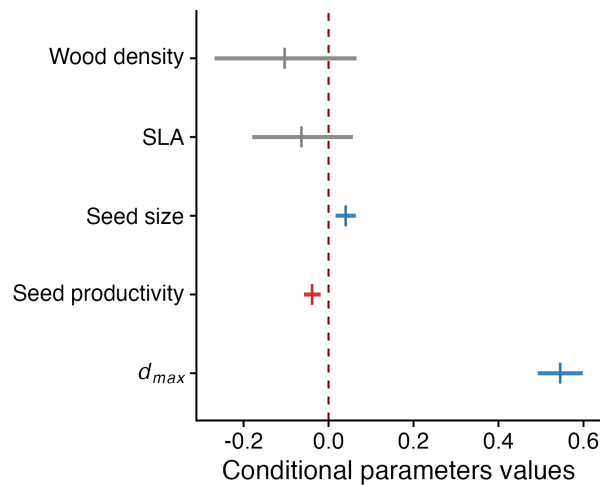


Figure 4: Conditional parameter estimates for the direct effect of traits on tree size at maturation diameter (d_{mat}) while accounting for trait covariance, climate, and phylogeny. Conditional parameters are evaluated on a standardized scale (predictors are centered and standardized) making trait effects on d_{mat} respective to their variation in the data set. Shown are posterior means and 95% credible intervals. Blue and red represent positive and negative associations where 95% of the posterior does not include zero. SLA = specific leaf area

455 The joint trait model incorporating random phylogenetic group and climate exhibits a root mean square
 456 prediction error 1.17 units smaller compared to the model that includes only climate. Conditional parameter
 457 estimates from the joint trait analysis show that d_{max} has a stronger effect on d_{mat} than other traits. There is
 458 a weak positive association with seed size, and a negative association with species fecundity (see Methods,
 459 Trait and climate data section) (Fig. 4). There are no meaningful associations with wood density or SLA. The
 460 joint trait analysis also confirms the absence of a direct climate effect on d_{mat} after accounting for d_{max} in the
 461 conditional trait analysis (see Table S5 for joint trait model and Table S6 for conditional parameters). Previous
 462 linear models showed that temperature was significant only in the interaction with d_{max} (Table S4). Joint trait
 463 analysis indicates that the temperature effect on maturation size in Fig. 2c could be due to the abundance of
 464 small species (small d_{max}) in warm climates (Figure S5). The trait relationships do not depend on the source
 465 of climatic data: i) GBIF species occurrence in Fig. 4 or ii) more narrowly, where they occur in the MASTIF
 466 data network (Fig. S6).

467 Both maturation (d_{mat}) and relative size (d_{rel}) show evidence of phylogenetic conservation ($\lambda_{mat} = 0.83$,
 468 $p < 0.0001$; $\lambda_{rel} = 0.51$, $p < 0.0001$, $n = 400$, Fig. S7a), yet with substantial variation within some groups.

469 The two-sample t-test for unequal variances shows differences between gymnosperms and angiosperms.
470 Gymnosperms have high mean values for both d_{mat} and d_{max} and low mean values for d_{rel} (all $p < 0.0001$).
471 Within gymnosperms, Pinales and Cupressaceae mature at large size, but large d_{max} gives them lower d_{rel}
472 than most angiosperms (Fig. S8, S9). Most Pinaceae (*Picea*, *Pinus*) and Cupressaceae (*Thuja*, *Sequoia*),
473 Fagaceae (*Quercus* and *Fagus*), and Juglandaceae have low d_{rel} (Fig. S10). Plant groups with both tree
474 and shrub habits, such as Rosales, Magnoliales, Rubiaceae, and Fabaceae, have mixed d_{rel} . However, we
475 did not find a significant effect of tree versus shrub habit on d_{rel} , possibly due to high variation in the data
476 (Fig. S10). Shrubs may tend to have high d_{rel} , but higher d_{rel} is also observed in trees genera like *Magnolia*
477 and *Poulsenia*.

478 Discussion

479 Our analysis suggests a diminishing risk model for the relationship between maturation and maximum size
480 (i.e. d_{mat} and d_{max}). The novelty here comes from the low coupling we find. Indeed, the coefficient $\hat{\beta}_d = 0.30$
481 in Table 1 that we found is closer to zero (no relationship) than one. In contrast, the estimated exponent values
482 fitted to vertebrates are greater than 1/2 (Prothero, 1993; Herculano-Houzel, 2019), twice the value of $\hat{\beta}_d$ we
483 find for trees. Nevertheless, the comparison across groups is complex due to the uncertainty on maximum
484 size (d_{max}), which could influence the value of the exponent $\hat{\beta}_d$, but this issue remained unexplored in other
485 taxa. The biological difference of $\hat{\beta}_d$ may arise because trees differ from other species groups in the gains that
486 come from allocation to growth, as the gain is due to the relative difference in height with other competitive
487 individuals. In most tree species, individuals in the understory produce no seed at all, while dominant stature
488 can yield multi-order-of-magnitude gains in fecundity over crowded neighbors (Clark *et al.*, 2004). In contrast,
489 in vertebrates, improved parental condition and size can translate to incremental increases in clutch size or
490 survival of well-provisioned offspring. Gestation times and physical limits on clutch size (e.g., one offspring)
491 may allow only muted near-term benefits of reproductive delay.

492 In trees, large size comes with uncertainty that could weaken the potential benefit of delaying maturation.
493 Wind exposure and risk of hydraulic failure both increase with size (Bennett *et al.*, 2015; Jackson *et al.*,
494 2021; Gardiner, 2021; Barrere *et al.*, 2023). The vanishing probability that a seed survives to large size,
495 combined with the fact that fecundity can plateau and even decline late in life (Qiu *et al.*, 2021) means that
496 the competitive advantages of extremely large size can rarely make up for lost benefits of early reproduction.
497 At a stand scale, the risk of stand-replacing disturbances can increase with stand age and development (e.g.,
498 accumulated fuels increase fire risk), such that species that fail to reach minimum reproductive size before
499 the next disturbance can be excluded from communities (Clark, 1991; McDowell *et al.*, 2020). The fact that
500 maturation size increases with maximum size means that the two are not independent. But the cost is not
501 proportionate (Fig. 3).

502 The fact that some correlation exists does not conflict with a disproportionate importance of near-term
503 gains that can follow delayed maturation. Instead, it suggests that the benefits of large size probably do not
504 come at the end of life. The capacity to reach a large size pays benefits throughout life, contributing with many
505 other variables to current size and fecundity, not just as a tree approaches the maximum.

506 Both climate and species traits contribute to the relationships between maturation and maximum size.
507 The negative main effect of temperature and its positive interaction steepens the relationship with maximum
508 size in warm climates (Fig. 3), where growth and mortality rates are generally higher than in temperate forests
509 (Stephenson & Van Mantgem, 2005; Locosselli *et al.*, 2020). Abundant resources may offer a disproportionate
510 advantage to early maturation (van Noordwijk & de Jong, 1986; Kozłowski, 1992; Wenk & Falster, 2015). Long
511 growing seasons in warm climates might have similar effects. However, intense competition on nutrient-rich
512 sites might also favor delayed reproduction as trees compete for canopy access. Theoretical studies (Falster
513 *et al.*, 2017; Detto *et al.*, 2022) have shown that a trade-off between maximum size and maturation size can
514 promote niche diversification and maintain species coexistence, and can be typically observed in tropical
515 where there is a wide range of maximum sizes forests (Falster *et al.*, 2017).

516 We did not find that high specific leaf area (SLA) is associated with maturation at small size (Visser
517 *et al.*, 2016) or early age (Wenk *et al.*, 2018). The relationship reported in Wenk *et al.* (2018) includes leaf
518 area from one year and one site, and the correlation estimated in that study does not appear to control for
519 phylogeny. Similarly, lack of association with wood density in our study does not agree with suggestions that
520 shade-tolerant species with high wood density mature at small size (Thomas *et al.*, 2015). The inclusion of a
521 wider range of plant species may reveal a different pattern of traits. For example, a comparison over a large
522 number of perennial plant species such as herbs, graminoids, shrubs, and trees shows that traits that promote
523 longevity are associated with greater variability in seed production (Journé *et al.*, 2023). The fact that species
524 that produce large seeds also allocate more to reproductive effort (Qiu *et al.*, 2022) could contribute in a small
525 way to delayed maturation. The differences between our result and previous work may be due to the larger
526 species coverage, and to the control of the effect of climate and phylogeny in our joint analysis.

527 Results highlight the importance of large data sets and how they are modelled. This first compilation of
528 tree maturation size for hundreds of species on five continents shows strong support for a diminishing risk
529 model –trees that can get big can still mature at relatively small sizes. The result is a decline in the relative
530 size of maturation for large trees (Fig. 3d). The benefits of extensive data here parallel the shift from early
531 theory that argued for a constant relative maturation size (d_{rel}) in fish (Charnov & Berrigan, 1990), followed
532 by studies showing an exponent that is less than one (Froese & Binohlan, 2000; Tsikliras & Stergiou, 2014;
533 Thorson *et al.*, 2017). It is, however, important to acknowledge that our coverage of tree species diversity
534 is still patchy, with most data coming from Europe and North America and limited spatial coverage in Africa,
535 South America, Asia, and Oceania as data are concentrated in a few large plots in these areas (Daru &
536 Rodriguez, 2023).

537 New insight from this analysis comes first from extending observations beyond a small number of tropical
538 sites, few species, or limited sample size (Thomas, 1996; Wright *et al.*, 2005; Thomas, 2011; Visser *et al.*,
539 2016; Minor & Kobe, 2019). The expanded coverage of species and sites permitted the incorporation of
540 climatic drivers into the analysis of d_{mat} in relation to d_{max} , which influenced the estimation of α and β_d .
541 Secondly, this study also benefited from accommodating detection and temporal dependence to infer mat-
542 uration. The estimation of d_{mat} was possible by combining diverse datasets, either based from direct crop
543 measurement and seed trap monitoring and by the use of MASTIF model which could estimate jointly a prob-
544 ability of maturation and individual fecundities. For instance, estimates of d_{mat} from Visser *et al.* (2016) are,
545 on average, approximately 1.8 times larger than our estimates for the species in common in the two studies

546 (Fig. S3). This discrepancy could be attributed to a different definition of size at maturation and methods of
547 analysis, as our method also includes the number of seeds produced.

548 Due to the high juvenile mortality, the maturation sizes quantified here are expected to impact predictions
549 from demographic vegetation models, including earth system models (ESMs) that include effects of maturation
550 size. In one ESM study that considered the effects of maturation height, variation in a single value applied
551 to all species did not have a large impact on simulated stand productivity (Raczka *et al.*, 2018). However,
552 when differences in species maturation size are accounted for in models, the effect can be larger. Few
553 individuals survive to large size and, thus, their ability to reproduce early can be important. The fact that
554 species capable of large size tend to retain this capacity to reproduce while still small highlights the importance
555 of understanding maturation size. Accurate estimation of maturation size (d_{mat}) is likewise important for
556 assessing response to disturbance regimes, especially as the time to maturity begins to exceed the interval
557 between disturbances. For instance, several species that compared pairs of species found that species with
558 smaller size at maturation can have better post-disturbance dynamics than species with larger maturation size
559 (Alfaro-Sánchez *et al.*, 2022; Andrus *et al.*, 2020). Our results provided the data to test such hypotheses at
560 a much larger scale. This effect can even scale up at the ecosystem scale. In boreal habitats, exposure to
561 more frequent disturbances that exceed the tree maturation time can completely change a tree community to
562 a grass-dominated community without a return to a forest stand within centuries (Buma *et al.*, 2013).

563 Current ESMs suffer from limited information on allocation to reproduction (Wenk & Falster, 2015), in-
564 cluding empirical data (Hanbury-Brown *et al.*, 2022b). Similarly, management actions intended to assure
565 regeneration from seed also need to consider if the minimum harvest diameter is smaller than maturation
566 size (Ouédraogo *et al.*, 2018). Maturation size may play an important role in the ability of species to respond
567 to disturbance and climate change (McDowell *et al.*, 2020) when tree maturation can be reached faster un-
568 der elevated CO_2 exposure (LaDeau & Clark, 2001). Considering the difference in maturation size between
569 species may be crucial, although it can be more challenging to comprehend due to the impact of CO_2 on
570 maturation size. Understanding how fecundity strategies differ between species and phylogenetic groups,
571 such as lower relative size at maturation (d_{rel}) for gymnosperms than angiosperms, may open a new avenue
572 to better understand species diversification and responses to disturbances (Bond, 1989; Verdu, 2002; Qiu
573 *et al.*, 2022). Developing a model that represents the size at which a species begins to produce seeds could
574 improve the representation of the regeneration of each functional type (Hanbury-Brown *et al.*, 2022a) and
575 colonization rates (Snell, 2014) and improve our understanding of species coexistence. Our study contributes
576 to the maturation sizes needed for each of these objectives.

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Competing interests

The authors declare no competing interests

Supplementary Materials

Section A1 - A2

Table S1 – S6

Fig S1 - S9

790 Supplementary material

791 A.1 Conditional parameters

792 One way to evaluate relationships between traits is to ask how well a trait like d_{mat} predicts other traits, while
793 controlling for effects of climate and phylogeny. We start with the joint distribution of M traits for each species
794 $s = 1, \dots, S$ fitted with GJAM (Methods). All traits were log-transformed. The joint distribution is

$$\begin{aligned} [\mathbf{T}_s | P, X] &= MVN_M(\mathbf{T}_s | \mathbf{B}'\mathbf{x}_s + \mathbf{g}[s], \Sigma) \\ \mathbf{g} &\sim MVN(\mathbf{0}, \Omega) \end{aligned} \quad (\text{A1})$$

795 where MVN is the multivariate normal distribution, $\mathbf{g}[s]$ is a random vector for the phylogenetic group to which
796 s belongs, and Ω is the $M \times M$ covariance between traits taken over phylogenetic groups (Clark *et al.*, 2016).
797 With this fitted model, we consider the effects of d_{mat} on all other traits, organized in the vector $\mathbf{T} = [\mathbf{u}, \mathbf{d}]$,
798 where \mathbf{d} is the length- S vector of maturation sizes, and \mathbf{u} is a $S \times M - 1$ matrix holding all traits in \mathbf{T} other
799 than d_{mat} .

800 We partition the coefficients in \mathbf{B} and trait covariance Σ as

$$\mathbf{B} = \begin{bmatrix} \mathbf{B}_u \\ \mathbf{B}_d \end{bmatrix}, \Sigma = \begin{bmatrix} \Sigma_{u,u} & \Sigma_{u,d} \\ \Sigma_{d,u} & \Sigma_{d,d} \end{bmatrix} \quad (\text{A2})$$

801 For M traits and Q climate predictors in \mathbf{x}_s , \mathbf{B}_u is the $Q \times M - 1$ matrix of climate effects on traits other
802 than d_{mat} , \mathbf{B}_d is the $Q \times 1$ vector of climate effects on d_{mat} , with similar partition of Σ . We then write the
803 conditional distribution of responses in \mathbf{u} as

$$\begin{aligned} \mathbf{u}_s | d_{mat,s} &\sim MVN(\mathbf{A}d_{mat,s} + \mathbf{C}\mathbf{x}_s + \mathbf{g}[s], \mathbf{P}) \\ \mathbf{A} &= \Sigma_{u,d}\Sigma_{d,d}^{-1} \\ \mathbf{C} &= \mathbf{B}'_u - \mathbf{A}\mathbf{B}'_d \\ \mathbf{P} &= \Sigma_{u,u} - \mathbf{A}\Sigma_{d,u} \end{aligned} \quad (\text{A3})$$

804 \mathbf{A} is the vector of effects of d_{mat} on each response in \mathbf{u} , \mathbf{C} holds the effects of \mathbf{x} , and \mathbf{P} is the conditional
805 residual covariance. Other applications can be found in Qiu *et al.* (2021); Bogdziewicz *et al.* (2023). We report
806 in Fig. 4 the estimates from \mathbf{A} .

807 **A.2 Impact of error on estimates of maximum size (d_{max})**

808 **A.2.1 Robustness of the model relating maturation size to maximum size to data**
 809 **sources**

810 In this additional analysis, we aimed to test the relationship between maturation size (d_{mat}) and maximum
 811 size (d_{max}) using different data sources for d_{max} . The estimates d_{max} used in the main analysis are based
 812 on online open sources and are on average higher than other sources of d_{max} (Figure S2) which could
 813 underestimate the parameter β_d . The analysis was restricted to the most abundant data source of d_{max} . We
 814 conducted separate regression analyses using d_{max} estimates from unpublished data (J. Wright, N = 233
 815 species), National Forest Inventories (N = 158 species), and MASTIF inventories (N = 346 species) based on
 816 the model from Equation (6). In the three different models (i.e. one model per data source of d_{max}), we used
 817 the inverse of the standard error of d_{mat} as weights in the models. We then extracted coefficient estimates
 818 for all three models. Results are reported in Table A1 and visualized in Figure A1.

Table A1: Coefficient estimates from the model Eq. (6) according to the origin of d_{max} . Data sources of d_{max} are National Forest Inventories (NFI), MASTIF inventories, and unpublished field tropical measurements.

Origin of d_{max}	α	β_d	σ
NFI	1.40 [0.89, 2.20]	0.56 [0.45, 0.68]	0.089
MASTIF	1.30 [1.10, 1.60]	0.64 [0.58, 0.70]	0.078
Unpublished	0.88 [0.73, 1.10]	0.65 [0.60, 0.70]	0.090

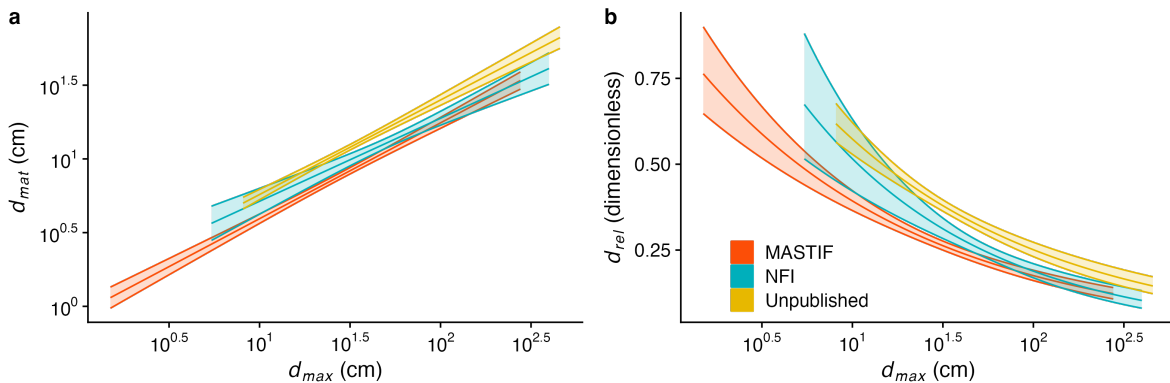


Figure A1: Tree maturation size and relative size at maturation relationship to maximum size according to the origin of maximum size observations. The orange line represents predictions from the regression between d_{mat} and d_{max} based on unpublished data (obtained from J. Wright field observation, N = 233 species). In blue, the prediction from the regression between d_{mat} and d_{max} comes only from National Forest Inventories estimates (N = 158 species). In yellow, the prediction from the regression between d_{mat} and d_{max} comes only from MASTIF inventories (N = 346 species).

819 **A.2.2 Correction of maximum size error measurement**

820 Measurement error in a covariate is common and often ignored which could have implications in the estimation
 821 of the relationship between a response and a covariate (Nab *et al.*, 2021). Indeed, the true value of a covariate,
 822 here of d_{max} , is not available, and using a log-log model exposed to regression dilution could flatten the slope
 823 (β_d) (Detto *et al.*, 2019). To correct for measurement error we benefit here from the R package `mecor` (Nab,
 824 2021) by using additional observation of our variable d_{max} . We specified here the error-prone measurement of
 825 d_{max} , coming from the highest estimates of d_{max} . We then used here four different additional observations of
 826 d_{max} , where this covariate can be obtained from Online Open-access resources, National Forest Inventories,
 827 Unpublished data, and MASTIF inventories. We ran the analysis on a simple model from Equation (6), that
 828 would include only d_{max} , or both d_{max} and temperature as covariates. The function does not allow to take into
 829 account weights in the analysis. To make a fair comparison, we reported here both coefficients, uncorrected
 830 and corrected (Table A2).

Table A2: Coefficient estimates uncorrected and corrected from measurement errors fitted to Eq. (6). Values are reported with a mean estimate and 95% CI.

Model	Coefficient Parameter	Uncorrected value	Corrected value
$d_{max}; T$	α	1.404 [1.092, 1.804]	0.826 [0.022, 31.637]
	β_d	0.58 [0.53, 0.62]	0.732 [-0.049, 1.51]
	β_T	-0.0005 [-0.0029, 0.0019]	-0.0003 [-0.012, 0.011]
d_{max}	α	1.357 [1.132, 1.627]	0.810 [0.048, 13.555]
	β_d	0.582 [0.539, 0.625]	0.733 [0.031, 1.434]

831 **Supplementary Tables and Figures**

Table S1: Numbers of species, plots, tree-year observations coming from crop count and seeds traps, and individual species tree year observations according to region. Additional details about MASTIF network are provided in Supplementary Files 1 and 2, and in Table S2.

Region	Nb. of plots	Nb. of species	Crop count x year	Seed-trap x year	Nb. Ind/Year
Africa	2	19	416	9,705	12
Asia	4	59	0	1,589,946	1,475
Eastern North America	155	92	20,983	1,389,998	142
Western North America	280	29	83,042	715,132	576
Europe	156	21	30,763	158,991	28
South America	7	267	2,280	7,050,620	863

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Table S2: MASTIF plots listed by WWF eco-regions, with principal investigator list and references. The column ST/CC indicates seed traps (ST) and crop counts (CC) sites.

Eco-region	Plot	PI(s)	lon	lat	ST/CC	Citation
A/W Turkey sclerophyllous/mixed						
	PNPG	E. Daskalaku	24	38	CC	Daskalaku <i>et al.</i> (2019)
Alps conifer/mixed forests						
	ROTH	G. Gratzler	15	48	ST	
	BELLE	G. Kunstler; B. Courbaud	6	45	ST CC	
	RNNPT	L. Dormon	7	45	CC	Dormont <i>et al.</i> (2006)
	PNPP	D. Ascoli; R. Motta; R. Berretta; G. Vacchiano	12	46	ST	Hacket-Pain <i>et al.</i> (2019)
Appalachian-Blue Ridge forests						
	BCEF	C. Greenberg	-83	35	CC	Rose <i>et al.</i> (2012)
	CWT	J. S. Clark	-83	35	ST CC	Clark <i>et al.</i> (2004)
	EPENN	M. Steele	-76	41	CC	
	GRAN	C. Greenberg	-82	36	CC	Rose <i>et al.</i> (2012)
	GRSM	J. S. Clark	-83	36	ST	
	MARS	J. S. Clark; S. Pearson	-83	36	ST CC	Clark <i>et al.</i> (2014)
	MLBS	J. S. Clark	-81	37	ST CC	
	PISG	C. Greenberg	-83	35	CC	Rose <i>et al.</i> (2012)
	SCBI	B. McShea	-78	39	ST	Bourg <i>et al.</i> (2013)
Appalachian mixed mesophytic forests						
Arizona Mountains forests						
	MOPA	M. Redmond	-106	33	CC	Redmond <i>et al.</i> (2012)
	REMO	A. Whipple; C. Gering; T. Whitham	-112	36	CC	Whipple <i>et al.</i> (2019)
	SICI	A. Wion; M. Redmond	-108	33	CC	
	WHIT	A. Wion; M. Redmond	-109	33	CC	
	WINO	A. Whipple; C. Gering; T. Whitham	-111	35	CC	Whipple <i>et al.</i> (2019)

Table S2 – continued from previous page

Eco-region	Plot	PI(s)	lon	lat	ST/CC	Citation
Atlantic coastal pine barrens	BARBEAU	N. Delpierre; D. Berveiller	3	48	ST	
Atlantic mixed forests						
Balkan mixed forests						
Baltic mixed forests						
British Columbia mainland coastal forests	GLCR1	J. Franklin	-122	49	CC	
	GLCR2	J. Franklin	-122	49	CC	
	HEME	J. Franklin	-122	49	CC	
	STPA	J. Franklin	-121	47	CC	
California Central Valley grasslands						
California interior chaparral/woodlands						
California montane chaparral/woodlands	HNHR	J. Knops; W. Koenig	-122	36	CC	Knops & Koenig (2012)
Carpathian montane forests	BGNP	M. Zywiec; L. Piechnik; B. Seget; M. Ledwon	20	50	CC	
Cascade Mountains leeward forests	TUCR	J. Franklin	-121	48	CC	
Celtic broadleaf forests	BENWE	A. Hacket-Pain	-2	55	CC	Bogdziewicz <i>et al.</i> (2020)
	CONGL	A. Hacket-Pain	-2	53	CC	Bogdziewicz <i>et al.</i> (2020)
	GILLF	A. Hacket-Pain	-2	54	CC	Bogdziewicz <i>et al.</i> (2020)
	HIMLE	A. Hacket-Pain	-2	53	CC	Bogdziewicz <i>et al.</i> (2020)
	KEELE	A. Hacket-Pain	-2	53	CC	Bogdziewicz <i>et al.</i> (2020)
	KILLE	A. Hacket-Pain	-3	51	CC	Bogdziewicz <i>et al.</i> (2020)
	RIPON	A. Hacket-Pain	-1	54	CC	Bogdziewicz <i>et al.</i> (2020)
	SPENN	A. Hacket-Pain	-2	55	CC	Bogdziewicz <i>et al.</i> (2020)

Table S2 – continued from previous page

Eco-region	Plot	PI(s)	lon	lat	ST/CC	Citation
	WOODB	A. Hacket-Pain	-3	51	CC	Bogdziewicz <i>et al.</i> (2020)
Central Canadian Shield forests						
	COCH	Y. Bergeron; Y. Messaoud	-81	49	CC	Messaoud <i>et al.</i> (2007)
	LDUPT	Y. Bergeron; Y. Messaoud	-79	48	CC	Messaoud <i>et al.</i> (2007)
	MASK	Y. Bergeron; Y. Messaoud	-79	50	CC	Messaoud <i>et al.</i> (2007)
Central European mixed forests						
Central forest-grasslands transition						
	UKFS	J. S. Clark	-95	39	ST CC	
	WUSL	J. Myers	-91	39	ST	
Central Pacific coastal forests						
	MAPK	J. Franklin	-124	45	CC	
Central Ranges xeric scrub						
	LS	B. Wright	132	-24	CC	Wright & Zuur (2014)
Central tall grasslands						
Central/S Cascades forests						
	BAMT	J. Franklin	-122	46	ST	
	BERK	J. Franklin	-122	43	CC	
	BLLK	J. Franklin	-122	46	CC	
	DECU	J. Franklin	-122	45	CC	
	IRMT	J. Franklin	-122	44	CC	
	MOLK	J. Franklin	-122	46	CC	
	MORA	J. HilleRisLambers	-122	47	ST	
	PEPR	J. Franklin	-122	46	CC	
	SAMT	J. Franklin	-122	44	CC	Redmond <i>et al.</i> (2012)
	SAPA	J. Franklin	-122	45	CC	
	SIRK	J. Franklin	-122	46	CC	
	SLBE	J. Franklin	-122	46	CC	

Table S2 – continued from previous page

Eco-region	Plot	PI(s)	lon	lat	ST/CC	Citation
	STMT	J. Franklin	-122	46	CC	
	TIRD	J. Franklin	-122	46	CC	
	WIMT1	J. Franklin	-122	44	CC	
	WIMT2	J. Franklin	-122	44	CC	
	WISP	J. Franklin	-122	43	CC	
	WREF	J. S. Clark; J. HilleRisLambers	-122	46	ST CC	
Chihuahuan desert						
	FOBA	M. Redmond	-108	33	CC	Redmond <i>et al.</i> (2012)
Colorado Plateau shrublands						
	ALBU	A. Wion; M. Redmond	-106	35	CC	Wion <i>et al.</i> (2020)
	CEBO	A. Wion; M. Redmond	-106	36	CC	Rodman <i>et al.</i> (2020)
	DOLO	A. Wion; M. Redmond	-109	38	CC	Rodman <i>et al.</i> (2020)
	GLPA	A. Wion; M. Redmond	-109	39	CC	Rodman <i>et al.</i> (2020)
	HOND	A. Wion; M. Redmond; K. Rodman	-106	37	CC	
	HOTC	A. Wion; M. Redmond; K. Rodman	-108	39	CC	Rodman <i>et al.</i> (2020)
	LASA	A. Wion; M. Redmond	-109	39	CC	Rodman <i>et al.</i> (2020)
	MAGD	A. Wion; M. Redmond	-107	34	CC	Rodman <i>et al.</i> (2020)
	MONT	A. Wion; M. Redmond	-108	38	CC	Rodman <i>et al.</i> (2020)
	NATU	A. Wion; M. Redmond	-109	38	CC	Rodman <i>et al.</i> (2020)
	SEV	R. Zlotin; D. Macias	-107	34	CC	Parmenter <i>et al.</i> (2018)
	SUCR	A. Whipple; C. Gering; T. Whitham	-111	36	CC	Whipple <i>et al.</i> (2019)
Colorado Rockies forests						
	BOCA	I. Pearse	-105	40	CC	
	CANJ	A. Wion; M. Redmond	-106	36	CC	Rodman <i>et al.</i> (2020)
	HAYM	A. Wion; M. Redmond	-105	39	CC	
	LAK	K. Rodman	-106	36	CC	Rodman <i>et al.</i> (2020)
	LV	M. Redmond	-105	36	CC	Redmond <i>et al.</i> (2012)

Table S2 – continued from previous page

Eco-region	Plot	PI(s)	lon	lat	ST/CC	Citation
	MG	K. Rodman	-106	36	CC	Rodman <i>et al.</i> (2020)
	MON	K. Rodman	-106	36	CC	Rodman <i>et al.</i> (2020)
	MR	K. Rodman	-106	36	CC	Rodman <i>et al.</i> (2020)
	MVG	K. Rodman	-106	36	CC	Rodman <i>et al.</i> (2020)
	NIWO	J. S. Clark	-106	40	ST CC	
	PC	K. Rodman	-106	36	CC	Rodman <i>et al.</i> (2020)
	PECO	M. Redmond	-106	36	CC	Redmond <i>et al.</i> (2012)
	POND	A. Wion; M. Redmond	-107	36	CC	Wion <i>et al.</i> (2020)
	RATN	M. Redmond	-104	37	CC	Redmond <i>et al.</i> (2012)
	SAFE	A. Wion; M. Redmond	-106	36	CC	Rodman <i>et al.</i> (2020)
	WACA	A. Wion; M. Redmond	-105	39	CC	
	WEMO	A. Wion; M. Redmond	-105	38	CC	
	Cross-Sanaga-Bioko coastal forests					
	KNP	J. Norghauer	9	5	CC	Norghauer & Newbery (2015)
	Dinaric Mountains mixed forests					
	E Cascades forests					
	E forest-boreal transition					
	LMONT	Y. Bergeron; Y. Messaoud	-79	48	CC	Messaoud <i>et al.</i> (2007)
	E Great Lakes lowland forests					
	English Lowlands beech forests					
	BEECH	A. Hacket-Pain	0	52	CC	Bogdziewicz <i>et al.</i> (2020)
	BUCKH	A. Hacket-Pain	-2	52	CC	Bogdziewicz <i>et al.</i> (2020)
	FISHH	A. Hacket-Pain	-2	52	CC	Bogdziewicz <i>et al.</i> (2020)
	NETTL	A. Hacket-Pain	-1	52	CC	Bogdziewicz <i>et al.</i> (2020)
	PAINS	A. Hacket-Pain	-2	52	CC	Bogdziewicz <i>et al.</i> (2020)
	PATCH	A. Hacket-Pain	-0	51	CC	Bogdziewicz <i>et al.</i> (2020)
	STP	M. Fenner M. Hanley	-1	51	CC	Hanley <i>et al.</i> (2018)

Table S2 – continued from previous page

Eco-region	Plot	PI(s)	lon	lat	ST/CC	Citation
Great Basin shrub steppe	DSP	M. Redmond	-119	39	CC	
Iberian sclerophyllous/semi-deciduous	CARB	C. Perez-Izquierdo	-6	40	CC	
	HUEC	R. Bonal	-4	40	CC	
	SIOE	R. Calama	-4	40	CC	
	VALT	J. Espelta	-4	41	CC	
Illyrian deciduous forests						
Interior Alaska-Yukon lowland taiga	EAPL	J. Johnstone	-137	66	CC	Viglas <i>et al.</i> (2013)
	BONA	J. Johnstone	-148	65	ST	
	FAIR	J. Johnstone	-148	65	CC	Viglas <i>et al.</i> (2013)
	LAGE	J. Johnstone	-145	64	CC	Viglas <i>et al.</i> (2013)
	LELA	J. Johnstone	-138	64	CC	Viglas <i>et al.</i> (2013)
	SMR	J. Johnstone	-141	64	CC	Viglas <i>et al.</i> (2013)
Interior Yukon-Alaska alpine tundra	CHIC	J. Johnstone	-143	63	CC	Viglas <i>et al.</i> (2013)
Isthmian-Atlantic moist forests	BCI	S.J. Wright	-80	9	ST	
Italian sclerophyllous/semi-deciduous						
Klamath-Siskiyou forests	ASRN	J. Franklin	-123	42	CC	
	MEOV	J. Franklin	-123	42	CC	
Mid Atlantic coastal forests	BLSF	D. Brockway	-79	35	CC	Chen <i>et al.</i> (2018)
	CALL	J. S. Clark	-79	35	ST CC	
	CROA	S. Cohen	-77	35	CC	

Table S2 – continued from previous page

Eco-region	Plot	PI(s)	lon	lat	ST/CC	Citation
	GRSW	J. S. Clark	-78	34	ST	
	SASF	D. Brockway	-81	34	CC	Chen <i>et al.</i> (2018)
Mississippi lowland forests						
	CHICK	J. Straub; T. Leininger	-90	36	CC	Straub <i>et al.</i> (2016)
	DELTA	J. Straub; T. Leininger	-91	33	CC	Straub <i>et al.</i> (2016)
	MINGO	J. Straub; T. Leininger	-90	37	CC	Straub <i>et al.</i> (2016)
	TENAS	J. Straub; T. Leininger	-91	32	CC	Straub <i>et al.</i> (2016)
	WHITE	J. Straub; T. Leininger	-91	34	CC	Straub <i>et al.</i> (2016)
Montana Valley/Foothill grasslands						
N California coastal forests						
	UCSC	G. Gilbert; Kai Zhu	-122	37	ST	
N Central Rockies forests						
	WBP	E. McIntire	-114	48	CC	
N short grasslands						
NE coastal forests						
NE Spain/S France Mediterranean						
	ISS	H. Davi	6	44	CC	Davi <i>et al.</i> (2016)
	PCMEJEAN	T. Curt	3	44	CC	Debain <i>et al.</i> (2003)
	PUECHEXP1	J. Limousin; J. Ourcival	4	44	ST	
	RBI	T. Boivin	5	44	CC	Doublet <i>et al.</i> (2019)
	RBLL	H. Davi	6	44	CC	Davi <i>et al.</i> (2016)
	VALLI	F. Lefevre; F. Courbet	5	44	CC	
	VEN	H. Davi	5	44	CC	Davi <i>et al.</i> (2016)
	VENT	H. Davi	5	44	CC	Davi <i>et al.</i> (2016)
	VES	H. Davi	7	44	CC	Davi <i>et al.</i> (2016)
New England-Acadian forests						
	ASWP	C. Moore; J. S. Clark	-69	45	ST CC	

Table S2 – continued from previous page

Eco-region	Plot	PI(s)	lon	lat	ST/CC	Citation
	BART	I. Fer; M. Dietze	-71	44	ST	
	COMPT	W. Schlesinger	-67	45	CC	
	HARV	J. S. Clark	-72	42	ST CC	
	HBEF	T. Fahey; N. Cleavitt	-72	44	ST	Cleavitt & Fahey (2017)
Nihonkai montane deciduous forests						
	KANU	K. Hoshizaki	141	39	ST	
	JNP	Q. Han; D. Kabeya; K. Noguchi	139	37	ST	Han <i>et al.</i> (2014)
NW Congolian lowland forests						
	CONGO	J. Poulson; C. Nunez	16	2	ST	
Pannonian mixed forests						
Peruvian Yungas						
	ABERG	M. Silman; W. Farfan	-72	-13	ST	
Piney Woods forests						
	KINF	D. Brockway	-92	31	CC	Chen <i>et al.</i> (2018)
Pontic steppe						
Puerto Rican dry forests						
	GUA	M. Uriarte	-67	18	ST	Uriarte <i>et al.</i> (2012)
Puerto Rican moist forests						
	LUQ	M. Uriarte	-66	18	ST	Uriarte <i>et al.</i> (2012)
Puget lowland forests						
Pyrenees conifer/mixed forests						
	PNVO	J. Camarero	-1	43	ST	de Andrés <i>et al.</i> (2014)
	PNP	S. Delzon; T. Caignard	-0	43	CC	Caignard <i>et al.</i> (2017)
Rodope montane mixed forests						
S Central Rockies forests						
	YELL	J. S. Clark	-110	45	ST CC	
S Great Lakes forests						

Table S2 – continued from previous page

Eco-region	Plot	PI(s)	lon	lat	ST/CC	Citation
SE conifer forests	ANNA	I. Ibanez	-84	42	ST	Redmond <i>et al.</i> (2012)
	APNF	D. Brockway	-85	30	CC	Chen <i>et al.</i> (2018)
	BRSF	D. Brockway	-87	31	CC	Chen <i>et al.</i> (2018)
	DSNY	J. S. Clark	-81	28	ST CC	
	EAFB	D. Brockway	-87	30	CC	Chen <i>et al.</i> (2018)
	EEF	D. Brockway	-87	31	CC	Chen <i>et al.</i> (2018)
	JERC	D. Brockway	-84	31	CC	Chen <i>et al.</i> (2018)
	OSBS	J. S. Clark	-82	30	ST CC	
	STCB	D. Brockway	-85	31	CC	Chen <i>et al.</i> (2018)
	TTRS	D. Brockway	-86	31	CC	Chen <i>et al.</i> (2018)
SE mixed forests	DUKE	J. S. Clark	-79	36	ST CC	Berdanier & Clark (2016)
	FBMB	D. Brockway	-85	32	CC	Chen <i>et al.</i> (2018)
	SERC	J. S. Clark	-77	39	ST CC	van Mantgem <i>et al.</i> (2006)
	TALL	J. S. Clark	-87	33	ST CC	
Sierra Nevada forests	SEQU	A. Das; N. Stephenson	-119	37	ST	van Mantgem <i>et al.</i> (2006)
	SOAP	J. S. Clark	-119	37	ST CC	
	YOSE	A. Das; N. Stephenson	-120	38	ST	van Mantgem <i>et al.</i> (2006)
SW Iberian Mediterranean S/M	ALCO	I. Perez-Ramos	-6	36	CC	Pérez-Ramos <i>et al.</i> (2014)
	PNLA	A. Hampe	-6	37	CC	Hampe & Bairlein (2000)
	SJDV	F. Rodriguez-Sanchez	-6	37	CC	
Taiwan subtropical evergreen forests						
	FFDF	C. Chang-Yang; I-Fang Sun	122	25	ST	
Upper Midwest forest-savanna transition						

Table S2 – continued from previous page

Eco-region	Plot	PI(s)	lon	lat	ST/CC	Citation
Valdivian temperate forests						
	LNP	J. Sanguinetti; T. Kitzberger	-71	-39	CC	Sanguinetti & Kitzberger (2008)
	ARAU	M. Aravena; S. Donoso Calderon	-71	-38	CC	
W European broadleaf forests						
W Great Lakes forests						
	CADI	R. Kobe	-86	44	ST CC	
	MANI	R. Kobe	-86	44	ST CC	
	MICH	J. LaMontagne	-88	47	CC	
	PAFA	J. LaMontagne	-90	46	CC	
	TREE	J. S. Clark	-90	45	ST CC	
	UMBS	I. Ibanez	-85	46	ST	
	UNDE	J. S. Clark	-90	46	ST CC	
	WILW	J. LaMontagne	-90	46	CC	
	WORU	J. LaMontagne	-90	46	CC	
W Gulf coastal grasslands						
W short grasslands						
	CMNM	M. Redmond	-104	37	CC	Redmond <i>et al.</i> (2012)
	KENT	M. Redmond	-103	37	CC	Redmond <i>et al.</i> (2012)
Willamette Valley forests						
	CAMT	J. Franklin	-123	45	CC	
Wyoming Basin shrub steppe						
	NORT	A. Wion; M. Redmond	-109	41	CC	

Table S3: Origin of maximum diameter (d_{max}), with the number of species for each data source retained for the analysis used in this study.

Data source of d_{max}	Nb of species	Comments
National Forest Inventories	38	Used near maximum diameter forest inventory and analysis in the United States (Gray <i>et al.</i> , 2012); forest inventory in Europe (Kunstler <i>et al.</i> , 2021); tree census data in Japan (Ishihara <i>et al.</i> , 2011).
Unpublished field tropical measurements	222	Maximum diameter value observed from French Guyana (33 species) and from Panama (189 species).
Allometric equation	12	Maximum trait height (Liu <i>et al.</i> , 2019; Carmona <i>et al.</i> , 2021) and allometric equation from pan-tropical for Africa region, South America equation for South America region and Asia equation for Asia region.
MASTIF inventories	41	Used tree size observations and near maximum diameter for species with > 90 individual unique diameter.
Online open sources	173	Wikipedia, https://www.wikipedia.org/ ; American conifers society, https://conifersociety.org/ ; Monumental trees https://www.monumentaltrees.com/en/ ; iPlantz, https://www.iplantz.com/ , Useful tropical plants, https://tropical.theferns.info/)

Table S4: Summary of all fitted linear models between maturation size (d_{mat}) and maximum size (d_{max}) in \log_{10} - \log_{10} testing alternative effects of climatic variables. The mean value of estimates with a confidence interval of 95%, and their p-values (p) are reported. All models have the initial structure $\log_{10}(d_{mat_s}) = \alpha + \beta_d \times \log_{10}(d_{max_s})$ represented here by the ellipse (...). Other parameters included are temperature (T) and deficit (D).

Parameters	Estimate	2.5%	97.5%	p	AIC
... + $\beta_T \times T + \beta_{dT} \times T \times \log_{10}(d_{max_s})$					
α	3.7100	1.94000	7.0700	< 0.001	-62.84
β_d	0.3050	0.15100	0.4590	< 0.001	
β_T	-0.0233	-0.03520	-0.0114	< 0.001	
β_{dT}	0.0126	0.00586	0.0193	< 0.001	
... + $\beta_D \times D + \beta_{dD} \times D \times \log_{10}(d_{max_s}) + \beta_T \times T + \beta_{dT} \times T \times \log_{10}(d_{max_s})$					
α	4.15e+00	1.99e+00	8.65e+00	< 0.001	-59.29
β_d	2.81e-01	1.09e-01	4.53e-01	< 0.001	
β_T	-2.43e-02	-3.66e-02	-1.20e-02	< 0.001	
β_D	2.73e-05	-7.98e-05	1.34e-04	0.617000	
β_{dT}	1.31e-02	6.18e-03	2.00e-02	< 0.001	
β_{dD}	-1.29e-05	-7.62e-05	5.03e-05	0.688000	
...					
α	1.080	0.929	1.250	0.325	-52
β_d	0.592	0.552	0.631	< 0.001	
... + $\beta_D \times D + \beta_{dD} \times D \times \log_{10}(d_{max_s})$					
α	1.06e+00	8.17e-01	1.38e+00	0.657	-48.12
β_d	5.93e-01	5.27e-01	6.59e-01	< 0.001	
β_D	-6.10e-06	-1.13e-04	1.01e-04	0.910	
β_{dD}	1.40e-06	-6.18e-05	6.47e-05	0.964	
... + $\beta_D \times D + \beta_T \times T$					
α	1.19e+00	9.32e-01	1.51e+00	0.165	-49.48
β_d	5.83e-01	5.42e-01	6.25e-01	< 0.001	
β_D	-3.90e-06	-2.53e-05	1.75e-05	0.721	
β_T	-1.59e-03	-4.29e-03	1.10e-03	0.246	
... + $\beta_D \times D$					
α	1.07e+00	9.09e-01	1.25e+00	0.433	-50.12
β_d	5.92e-01	5.53e-01	6.31e-01	< 0.001	
β_D	-3.70e-06	-2.52e-05	1.77e-05	0.732	
... + $\beta_T \times T$					
α	1.20000	0.94800	1.52000	0.129	-51.35
β_d	0.58300	0.54100	0.62500	< 0.001	
β_T	-0.00159	-0.00429	0.00111	0.248	
$\alpha + 1 \times \beta_d$					
α	0.244	0.232	0.257	0	248.1
β_d	1	-	-	-	-
α					
α	9.25	8.69	9.85	0	447.83
β_d	0	-	-	-	-

Table S5: Summary of the best joint trait model. The best model has been selected based on the lowest DIC value (Table S7). Traits have been included as responses (d_{max} , d_{mat} , SLA, Wood density, seed size, and species seed productivity), with temperature (T), deficit (D), and their interaction ($T : D$) as predictors, with genus as a random effect. For each response, estimate, standard error (SE), and credible interval (95%) with significance are reported (CI does not overlap 0).

Climate variable	Estimate	SE	2.5%	97.5%	significance
d_{max}					
T	-0.230	0.068	-0.360	-0.097	*
D	0.150	0.050	0.054	0.250	*
T:D	-0.096	0.065	-0.220	0.031	
d_{mat}					
T	-0.190	0.065	-0.320	-0.064	*
D	0.077	0.049	-0.018	0.170	
T:D	0.010	0.064	-0.110	0.140	
SLA					
T	-0.006	0.073	-0.150	0.140	
D	0.190	0.051	0.083	0.280	*
T:D	-0.047	0.065	-0.180	0.079	
Wood density					
T	0.160	0.067	0.030	0.300	*
D	0.064	0.050	-0.033	0.160	
T:D	0.019	0.064	-0.110	0.150	
Seed size					
T	0.046	0.071	-0.093	0.180	
D	-0.180	0.050	-0.270	-0.078	*
T:D	-0.075	0.064	-0.200	0.054	
Seed productivity					
T	-0.130	0.061	-0.250	-0.012	*
D	-0.061	0.048	-0.150	0.032	
T:D	-0.037	0.064	-0.160	0.085	

Table S6: Summary of conditional parameters for the effect on d_{mat} from the GJAM joint trait model. Conditioning was done on SLA, wood density, species seed productivity, seed size, and d_{max} . Standardized coefficient values are coming from matrix **A**, for direct trait effect, and **C**, for direct climate effect.

Conditional variable	Estimate	SE	2.5%	97.5%	significance
Traits					
d_{max}	0.5460	0.0266	0.4940	0.5960	*
SLA	-0.0569	0.0576	-0.1720	0.0552	
Wood density	-0.1300	0.0856	-0.3020	0.0384	
Seed size	0.0403	0.0120	0.0169	0.0639	*
Seed productivity	-0.0385	0.0100	-0.0574	-0.0180	*
Climate					
Intercept	8.36e-01	2.69e-01	3.22e-01	1.36e+00	*
T	4.11e-03	4.66e-03	-4.93e-03	1.33e-02	
D	-1.59e-04	9.53e-05	-3.49e-04	3.28e-05	
T:D	8.30e-06	4.60e-06	-8.00e-07	1.73e-05	

Table S7: Joint traits model selection (based on the lowest DIC values). GJAM models ran with different combinations of climate covariates (T , temperature, and D , deficit).

Climatic predictors in GJAM	DIC
$T \times D$	20,575
$T + D$	20,603
T	20,661
D	20,898

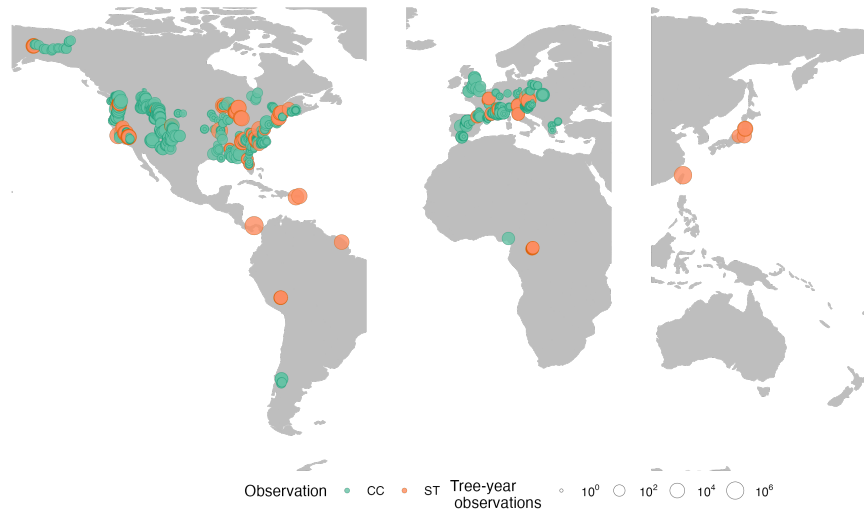


Figure S1: MASTIF data network, including seed traps data and crop count data limited here to species-genus used. The dot size represents the number of initial tree-year observations at the log10 scale. Crop count data (green dots, CC) includes 137,484 tree years observations and seed traps (orange dots, ST) 10,914,392 observations in total.

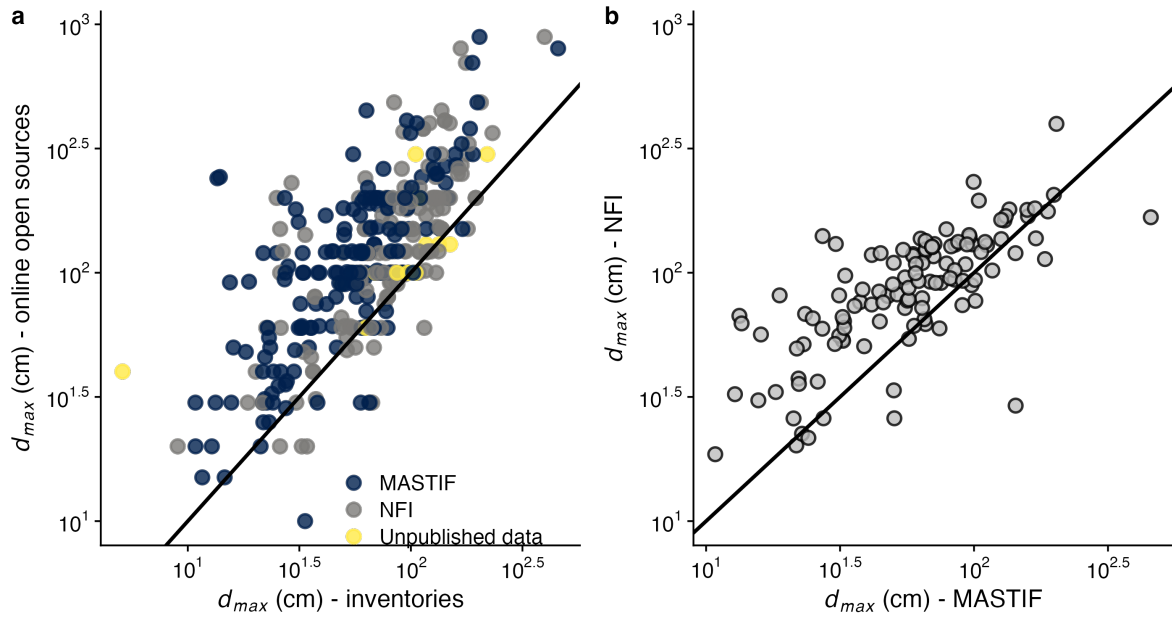


Figure S2: a) Comparison of d_{max} obtained from online open sources to d_{max} obtained from National Forest Inventories (NFI), MASTIF inventories, and from the unpublished dataset (n=191 species). b) Comparison of d_{max} obtained from National Forest Inventories (NFI) to d_{max} obtained from MASTIF inventories (N = 118 species). For both panels, the black line is the 1:1 relationship.

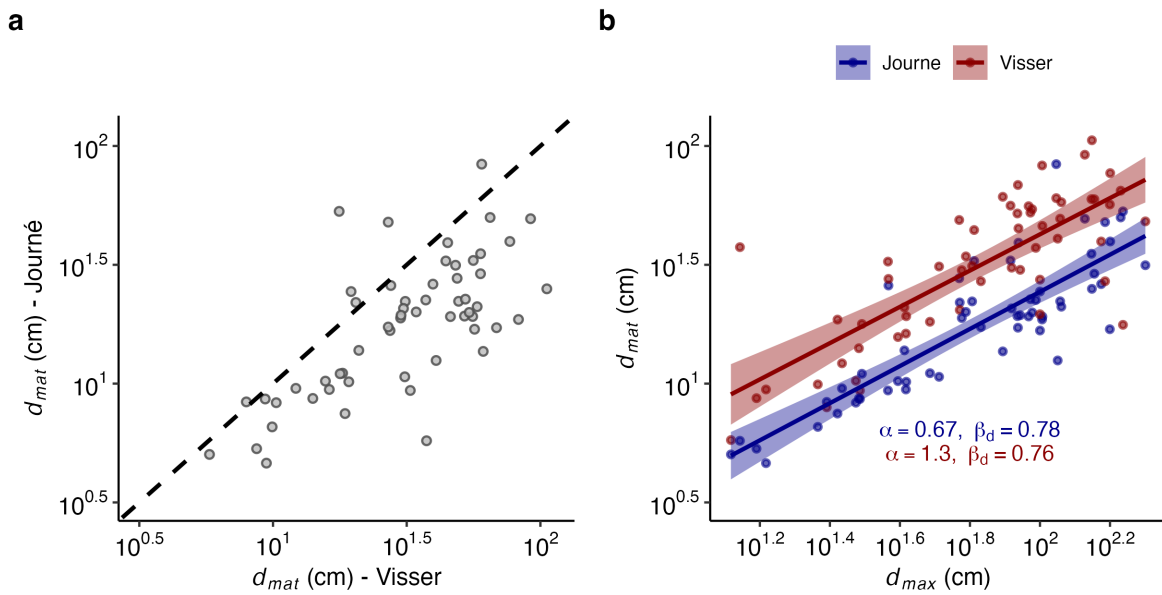


Figure S3: a) Comparison of maturation size (d_{mat}) from the main analysis (probability to produce the first fruiting structure) to maturation size (probability to reproduce at 50%) based on the reference in Visser *et al.* (2016), restricted to Barro Colorado Island, Panama. Each dot represents a single species, with the black dotted line indicating a 1:1 relationship (N = 56 species). b) Relationship between d_{mat} and d_{max} restricted to species used by Visser *et al.* (2016). The model fitted between d_{mat} and d_{max} is shown in blue for the model based on our estimates of d_{mat} and in red for estimates of d_{mat} from Visser *et al.* (2016). The regressions are reported with a confidence interval of 0.95. The average parameters α and β_d are reported for both models.

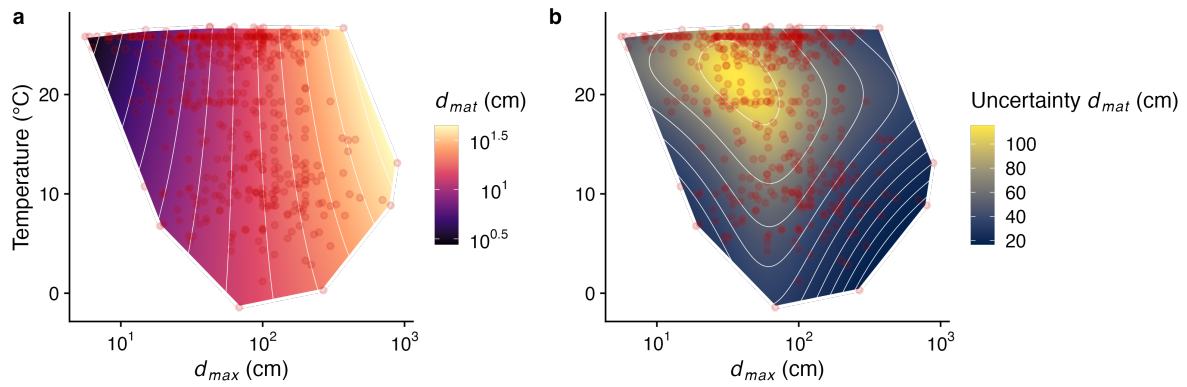


Figure S4: a) Maturation size response to d_{max} and temperature and b) Uncertainty of maturation size. Convex hulls are defined by observations (red), including the 486 tree species. In b) the surface scale color decreases as the inverse of the predictive standard error—blue edges reflect increased uncertainty at data extremes.

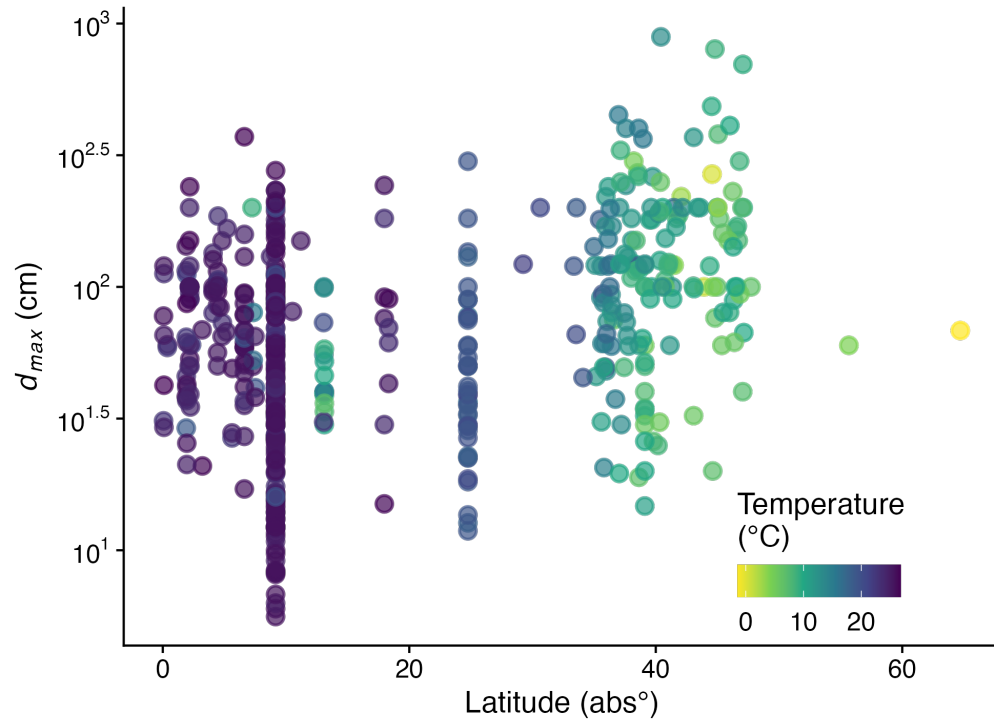


Figure S5: Relationship between d_{max} with latitude (in absolute degree) across species. The color gradient represents the average temperature (in °C). The average latitude for each species was determined by using MASTIF inventories. Each dot represents one species.

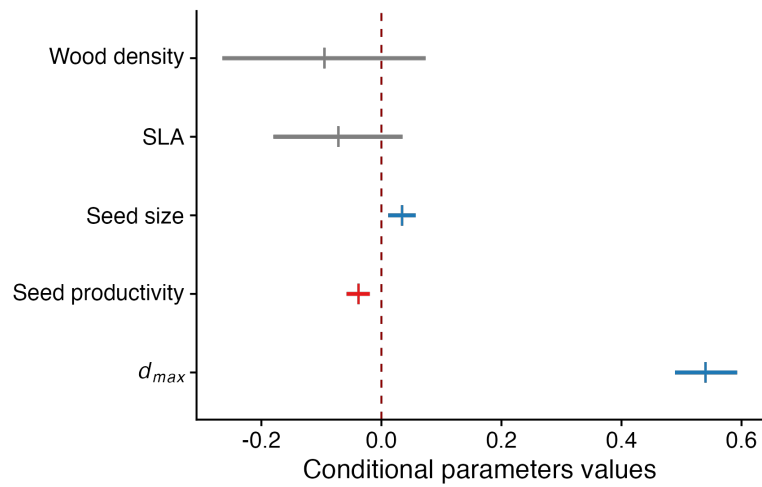


Figure S6: Conditional parameter estimates for the direct effect of traits on maturation size (d_{mat}), while accounting for trait covariance, climate and phylogeny. The climate used here has been extracted from the MASTIF inventories. Conditional parameters are evaluated on a standardized scale, making trait effects on d_{mat} respective to their variation in the data set. Points represent the posterior mean with their 95% credible intervals. Blue and red represent positive and negative associations where 95% of the posterior does not include zero. SLA, specific leaf area.

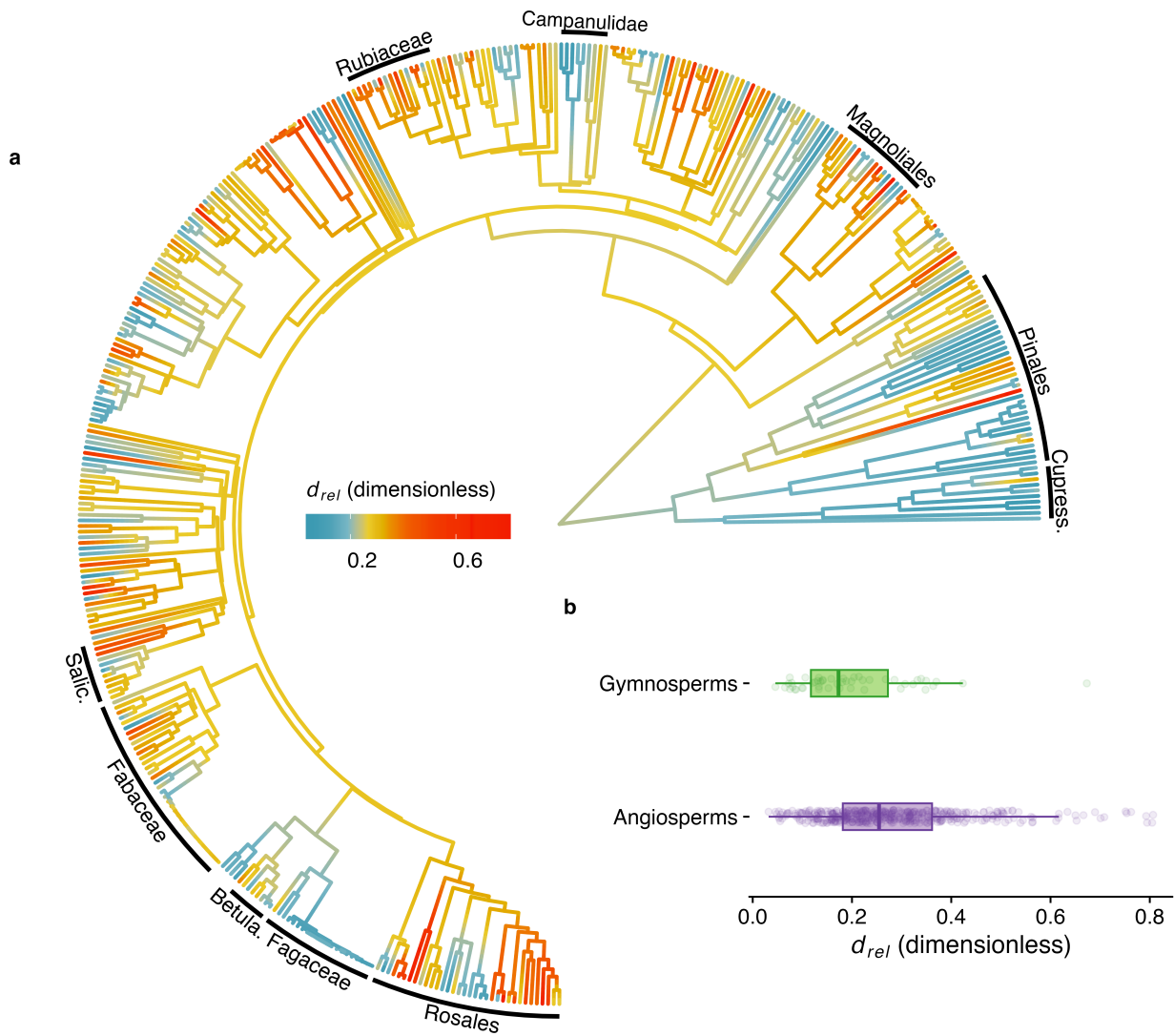


Figure S7: (a) Relative size at maturation (d_{rel}) includes a phylogenetic signal (400 species in our data have phylogenies in Zanne *et al.* 2014, Pagel's $\lambda = 0.51$, $p < 0.0001$). (b) Boxplot of relative size at maturation (d_{rel}) for gymnosperms and angiosperms (number of species is 48 for gymnosperm and 438 for angiosperm).

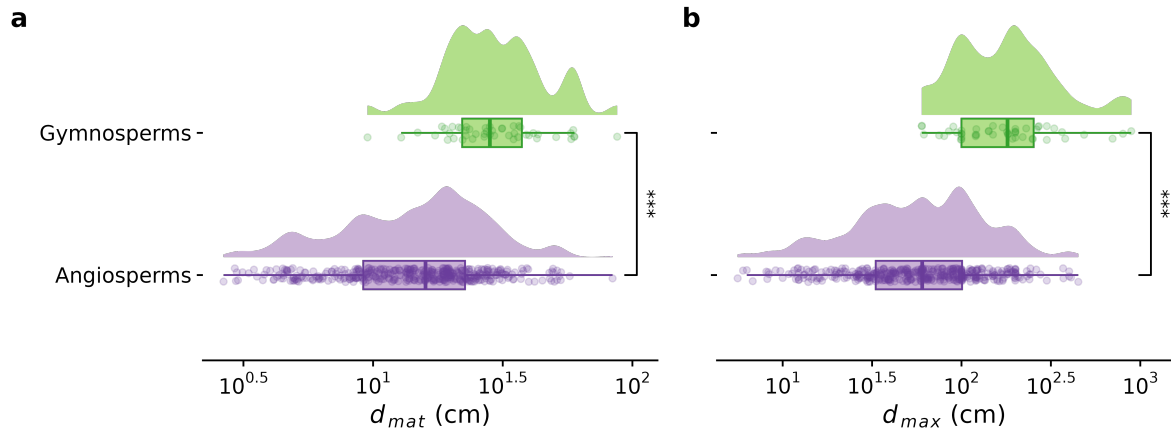


Figure S8: Boxplot of a) d_{mat} and b) d_{max} for gymnosperms ($n = 48$) and angiosperms ($n = 438$). *** indicates $p < 0.0001$ based on the sample t-test for unequal variances.

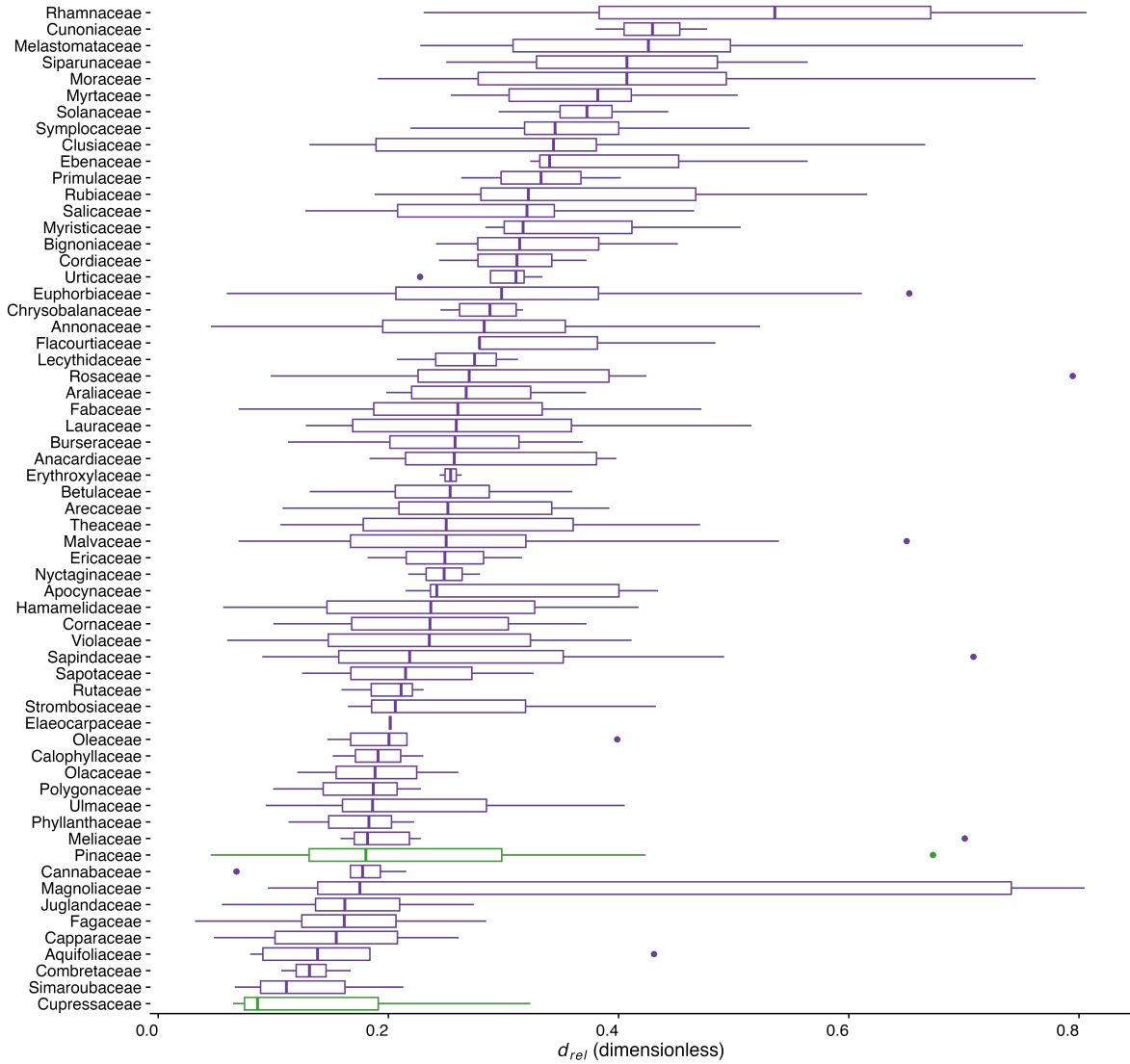


Figure S9: Boxplot of d_{rel} for families with more than one species. Green is for gymnosperms and purple for angiosperms.

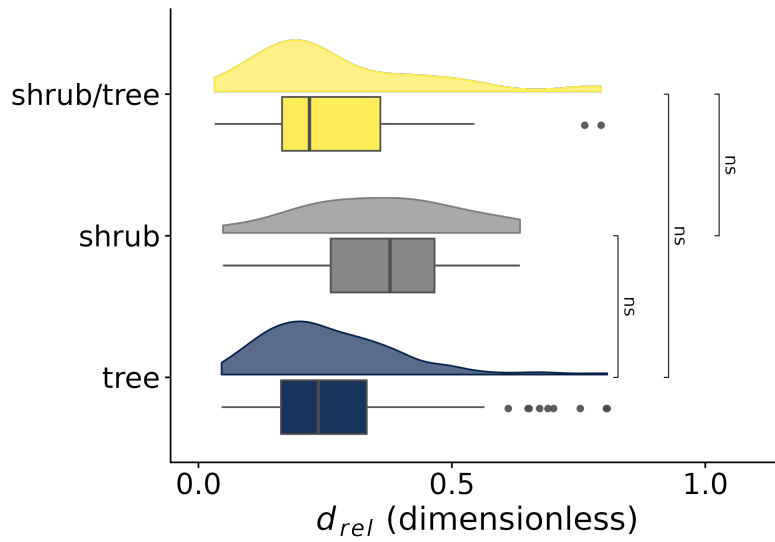


Figure S10: Boxplot with violin of variation of d_{rel} across growth forms ($n = 419$ species). The violin here is a mirrored density plot and showed the distribution of the data. Growth form follows a compilation from Díaz *et al.* (2022), with samples: trees, $n = 361$ species; shrubs, $n = 17$ species; shrub/tree $n = 41$ species. Groups were compared with a t-test for unequal variance and detected no differences according to plant growth forms (non-significant adjusted p-values with $p > 0.05$).

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