



Supplementary Materials for

The pace of life for forest trees

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Materials and methods

1: Forest inventory data

The dataset we used for this project was developed by a global community of network partners, including members of the ForestPlots (18), TreeMort, and ForestGeo networks (19–21), and includes dynamic tree data from thousands of long-term research plots and datasets from National Forest Inventory networks (table S1). Combining and quality controlling this network of dynamic tree data was led by the Global Forest Dynamics team, initiated by the TreeMort project, and the ForestPlots network (18). The compiled dataset includes the following information: tree ID, diameter at breast height (dbh) at 1.3 m of trunk height, status (alive or dead), plot ID, plot coordinates, census year, and management history. Tree species names were standardized across the datasets using The World Consensus on Vascular Plants backbone (57) and the *Treemendous* R package (58). The point of dbh measurement differed by > 30 cm in a few cases for predominantly tropical trees, in which case we excluded the census points. To standardize our life history trait comparisons among species, we excluded tree observation < 10 cm dbh. The time interval between census periods varied from 1 to 36 years, with the highest occurrence of a 5-year census interval. Since time intervals greater than 10 years were not represented across all datasets and were sparse overall, we excluded census intervals >10 years. Thus, we focused on interval lengths that were well-represented across the forest inventory datasets. The plot size ranged from 0.07 ha to 50 ha among forest inventories. Tree observations with ‘unnatural’ modes of death (i.e., harvest, etc.) were removed from our analysis because they do not reflect ‘ambient’ life history dynamics. We limited our analysis to species with >100 unique observations and excluded species with < 5 observed deaths to maintain a sufficient sample size and excluded tree observations with unknown species identity. We also exclude species that did not have observations across species size ranges (i.e., there were only observations for large-sized individuals, with no information for smaller individuals in the 10 cm dbh size range). To balance our dataset across our biogeographic gradient, we randomly sub-sampled the North American plots to equal the number of point observations in Central and South America (see materials and methods). This allowed us to avoid potential biases due to imbalanced sampling efforts across our biogeographic gradients. These initial filters reduced the dataset from 5.6 million unique observations of 5,612 species to 3.2 million unique tree measurements for 1,127 species (i.e., tree size and status) (table S1).

All analyses were conducted in R version 4.2.0 (59). While p-values and R^2 are reported for generalized linear models, we present results in terms of ‘evidence’ versus significance levels, following (60).

2: Integral projection models

2.1 Assigning individual tree observations to hexagon grid IDs

To capture the full range of life history strategies across a latitudinal gradient, we used Google Earth Engine to assign each tree measurement (dbh and status) to equal area hexagon grids (size ~ 250,000 km²) (fig. S1). The hexagon grid ID was then included as a categorical random effect in our species-specific survival and growth models. This allowed us to incorporate intra-specific variation in tree life history traits (growth strategies, stature, and longevity) across broadscale biogeographic gradients (see material and methods, subsection 2.2-2.5). The unique hexagon grid ID were also used to calculate the demographic trait diversity (convex-hull volume in life history trait space that is occupied by species within each grid) and characterize the relationship between demographic trait diversity and above-ground net primary productivity (see material and methods, subsection 4).

2.2 Species-specific survival and growth models

To estimate size-dependent survival and growth rate coefficients for our integral projection models (IPM), we fit species-specific generalized linear mixed-effect models, using the `glmer` and the `lmer` function in the `lme4` package (61). Here y_{ij} is the response for individual i in grid cell j . The random grid cell effect, μ_j , and error, ϵ_{ij} , are added to the intercept, b_0 . The effect of size, x_{ij} , for individual i in grid cell j is measured by the slope, b_1 . Our survival model included ‘initial tree size’ (dbh) and the square of tree size (centered natural log of dbh) as predictor variables, survival at the second census interval as the response variable, and grid ID as a random effect. Similarly, for our growth model, we included initial tree size (dbh) as a predictor variable, size at the second census interval as the response variable, and grid ID as a random effect. Tree size was natural log-transformed for both models.

$$y_{ij} = \beta_0 + \beta_1 x_{ij} + \mu_j + \epsilon_{ij}$$

To account for variation in forest inventory census intervals, we standardized the survival and growth rate estimates to a one-year time-step. This was relatively straightforward for survival but more involved for growth. Specifically, for our survival model, we fit a logistic regression with a complementary log-log link function and included the census interval length as an offset, which effectively standardized the survival rate to a 1-year timestep. To standardize the time step for our growth model, we tested two approaches. First, we calculated the relative growth rate (RGR), which is the geometric mean of the ratio of log tree sizes over the time interval, $rgr = (s_t/s_0)^{1/t}$. Here, rgr is the annualized relative growth rate, s_0 is the log of the initial size, and s_t is the log of size at the end of the time interval, t . We calculated size in the next year for all initial tree observations by multiplying the initial size by the annualized growth rate, $s_1 = s_0 rgr$. This method implicitly assumes a zero intercept in the growth function. To test if the assumption of a zero intercept influenced our results, we explored a second method that directly computes the annual slope and intercept for a variable time interval. The algebraic expression that represents the compounding effect of adding an intercept in each annual estimate within a time series results in a nonlinear expression. Thus, we employed the nonlinear least squares function to estimate the following model, $s_t = b_0(1 - b_1^t)/(1 - b_1) + s_0 b_1^t$. Visual inspection of coefficient plots and model fit plots using both methods showed highly similar results. Due to the extended computation time for the nonlinear models, we chose the less complex RGR method, and converted final size, s_t , to size at one year, s_0 , before fitting our growth regressions.

Model evaluation of our vital rate regressions showed that initial tree size captured a high amount of variance for our growth models and was a significant predictor of tree size in the following timestep ($R^2=0.83-0.99$, and $p < 0.001$). Similarly, initial size was a significant predictor of survival ($p < 0.001$). It is important to note that, for nonlinear regression models, the R^2 does not represent the proportion of variance explained by the predictor variable and is thus not a useful metric for evaluating the goodness of fit for logistic regression. For this reason, we did not report this value for our survival models.

2.3 Size-dependent integral projection model

An integral projection model (IPM) is a tractable way to derive life history traits, using continuous size-based survival and growth rates. To calculate age-related traits from size-dependent probabilities, we used a key component of an IPM, the survival-growth kernel, $\mathbf{P}$, and with methods developed by (25), we projected the future fate of living individuals. By

excluding reproduction, this model captures cohort dynamics based on survival and growth rates. A change in the size-specific density of trees, $n(t)$, is projected using the following equation:

$$n(y, t + 1) = \int_L^U \mathbf{P}(y, x) n(x, t) dx$$

where the kernel $\mathbf{P}(y, x)$ is a non-negative surface of survival and growth transition probabilities of individual plants from size x at time t to size y at time $t+1$. L and U represent the minimum and maximum plant size thresholds respectively, with the lower threshold L being set to 10 cm dbh and the upper size threshold being set to the species maximal tree size. $\mathbf{P}$ is composed of two functions,

$$\mathbf{P}(y, x) = s(x)g(y, x)$$

where $s(x)$ represents the survival rate of an x -sized individual and growth $g(y, x)$ is the probability density for individuals of size x transitioning to size y over a 1-year timestep. These parameters are derived from the species- and grid-cell-specific survival and growth regression models that we parameterized with empirical field data (see materials and methods, subsection 2.2).

Our species- and grid cell-specific IPMs were informed by hundreds to thousands of unique tree measurements across a large portion of a species life cycle (from 10 cm dbh to their maximal size) and across a wide range of local conditions (light and nutrient conditions, varying levels of density dependence, etc.). This framework allowed us to explicitly account for survival-growth trade-offs that operate across species life cycles and thus provide a tractable way to calculate robust species-level mean life history trait estimates (passage time and life expectancy) across broadscale biogeographic gradients (i.e., for each species by grid cell combination).

2.4 IPM kernel integration and diagnostic checks

The relatively slow incremental growth of trees can create a sharp ridge along the diagonal of the probability surface, $\mathbf{P}$. Defining this ridge with sufficiently high resolution becomes computationally expensive when numerically integrating the kernel, $\mathbf{P}$, and failing to do so can lead to biologically unreasonable column sums, which theoretically equal the survival rate for each size class. Previous work indicates that IPM model outputs for trees (first passage times, etc.) are sensitive to the dimension used for kernel integration, whereby a small kernel size (i.e., 10 size categories) can underestimate tree age demographics and a large kernel size (i.e., 1,000 size categories) can overestimate tree age demographics. Thus, previous works show that a kernel dimension equivalent to a tree size transition rate between 0.1-1 cm in diameter is needed to produce realistic tree age demographics for trees (26). Thus, to balance the need for high biological resolution and reduced computation time and memory, a mixed kernel integration approach has been established for trees (26–28). Following this mixed kernel integration approach, we selected a moderately large resolution for the overall kernel, 600×600 , and used the standard mid-bin integration for most of these cells. Along the growth ridge, we used a Gaussian-Legendre quadrature integration, whereby each cell was divided into 420 sub-rows (i.e., along the size-dependent growth probability density) and 3 sub-columns. The result was a 600×600 kernel with a well-defined ridge and biologically reasonable column sums and element values.

2.5 Life history trait calculations and age-from-stage methods

Following numerical integration, the survival-growth kernel, $\mathbf{P}$, was used to calculate a series of life history traits, including first passage time, life expectancy from 10 cm dbh, and maximal lifespan. These life history traits were derived from survival and growth data that were collected between 1926 and 2014. These life history traits are thus representative of tree age demographics based on observed climate conditions over the last century.

Passage time: First passage time captures the number of years it takes for an x -sized individual to reach a predetermined size threshold for the first time. Using the kernel, $\mathbf{P}$, we calculated passage time τ_{ij} from initial size class j to the target size class i , following (15–17) :

$$\tau_{ij} = \frac{(\mathbf{I} - \mathbf{P}')^{-2}(i, j)}{(\mathbf{I} - \mathbf{P}')^{-1}(i, j)}$$

where $\mathbf{I}$ is an identity matrix and $\mathbf{P}'$ is identical to $\mathbf{P}$ except for column j , which is replaced with zeros in all cells. The initial size for all passage time calculations was 10 cm dbh because this is the size when all species were tagged in our standardized dataset. Throughout the main text, we refer to our passage time to target size thresholds as tree *growth strategies*.

To make biologically reasonable comparisons in growth strategies among species, we calculated first passage times to 20 cm dbh (fig. S2, path a.2) and the 70% quantile of observed maximal size (fig. S2, path a.1). The 20 cm target size threshold serves as a time-standardized rate of growth for all species in our dataset. However, the passage time from 10 to 20 cm dbh may represent the time to max size for the smallest statured species in our dataset (i.e., 20 cm size is the 95% quantile of maximum size for small trees). Conversely, this target threshold captures early life growth dynamics for larger tree species. To capture growth dynamics over a wider range of a species life cycle, we also calculated the first passage time from 10 cm DHB to the 70% quantile of the observed size distribution for each species across the full dataset. This quantile-based target size varied among species and represented an above-average size at which point a tree has approached its ultimate position in the canopy, whether that be a short-statured understory tree that reaches its maximal height in 5-years or a tall dominant canopy tree that grows for decades before reaching their ultimate position in the canopy.

Life expectancy: To examine differences in early-life tree mortality patterns and survivorship trajectories over species lifespans, we calculated life expectancy from size class i to size class j using (fig. S2, path b) (1, 15–17):

$$\eta_j = \sum_{i=1}^n (\mathbf{I} - \mathbf{P})^{-1}(i, j)$$

where $\mathbf{I}$ is an identity matrix. Life expectancy from 10 cm dbh was calculated using the equation above with $j = 1$. For total life expectancy conditional on reaching the target size classes (either 20cm dbh or the 70th quantile of a species size distribution), we determined which column, j , corresponded to the target class and then added the time to reach size class j to the remaining life expectancy for size class j , i.e., $\tau_{ij} + \eta_i$. It is important to note that life expectancy is highly left skewed by early life mortality, with smaller individuals having higher mortality than larger individuals. A low life expectancy to a given size (e.g., 20 cm dbh) does not imply that no individuals of a given species will survive to that size threshold

(i.e., it is not a maximal). It simply means that individuals that do live longer represent the lucky few, resulting in a higher proportion of smaller individuals within a population.

Maximal lifespan: We calculated the maximal lifespan as the age at which the cumulative mortality was 95%. Starting with a cohort composed exclusively of 10 cm dbh individuals, we projected the cohort through time using the recursion equation $n(t + 1) = \mathbf{P}n(t)$. The simulation limit was set to 10,000, which resulted in the exclusion of 38 species. We normalized the initial cohort to sum to one and identified the time step, x , where the sum of $n(x)$ was less than 0.05. The number of years, x , is thereby the age at which less than 5% of the initial cohort is still alive. At this maximal age, x , we also calculated the mean size from the population density, $n(x)$, which we refer to in the main text as *size at maximal age*.

Model valuation: We parameterized our IPMs using methods that were specifically developed for cross-sectional tree data (see materials and methods, subsection 2.4) (26–28) and used age-from-stage methods to calculate age-related demographics (15–17). Validation of age-related outputs would require an extensive longitudinal dataset that tracks the fate of individual trees over their life cycle (which would require decades to millennia of longitudinal data for long-lived trees). This level of longitudinal data is rarely available and is also why cross-sectional forest inventory data and age-from-stage estimates are so valuable. The next best validation method relies on tree ring data. Previous validations of IPM model outputs for trees with paired tree ring data showed that IPMs can produce realistic estimates of tree age demographics (26). Similarly, IPM model validations, using 34-year time series data, showed that IPM outputs match time series data over snapshots of species life cycles (62). Together, previous validation efforts for IPMs using time series and tree ring data suggest model outputs can accurately capture the age dynamics for long-lived species with slow growth and low mortality. We did not have such paired time series or tree ring data to compare with the wide range of species included in our analysis. Yet, while not directly comparable, the directionality of our biome-level comparisons in tree longevity was congruent with longevity estimates from tree ring data (12). Specifically, that assessment showed that the mean longevity for trees in the tropics and extratropics were 186 ± 138 and 322 ± 201 years respectively (12). In our study, we found that the mean life expectancy for trees in the tropics and extratropics were 60 and 95 years respectively (see Figure 2).

While the directionality of our biome-level patterns in tree longevity is in line with broadscale trends derived from tree ring studies, there are several reasons why it does not make conceptual sense to make one-to-one comparisons in measures of tree longevity derived from IPMs from that of tree ring-studies that differ in temporal times scales and geographical scope. First, age estimates from tree-ring studies can be heavily influenced by anthropogenic disturbance and climate-induced shifts in tree growth-longevity trade-offs. Second, the sampling framework used for tree ring studies tends to target the largest trees in areas of low anthropogenic disturbance. Yet, considering that the oldest trees can be up to half the size of the largest trees (29), it is impossible to derive standardized metrics of tree age (e.g., mean life expectancy) from tree ring studies and thus they serve as a coarse estimate of tree longevity.

3: Tree life history trade-offs and core demographic functional types

To test for broadscale tree growth- longevity-stature trade-offs, we conducted a correlation analysis, using the `cor` function in the `stats` package (59). To further contextualize the full dimensionality of growth- longevity-stature trait constellations, we conducted a standard principal component analysis (PCA) of the life history traits, using the `princomp` function

in the `stats` package (59). All traits included in the PCA were scaled to have a mean of zero and a standard deviation of one. Highly correlated traits that captured redundant trait information were dropped from the PC analysis to avoid issues of multicollinearity, resulting in the inclusion of passage time to 20 cm dbh, passage time to 70th quantile size range, size at maximal age, and life expectancy from 10 cm dbh (fig. S5). We then used the *k*-means machine learning algorithm to identify the core growth- longevity- stature groupings, setting the maximum number of iterations to 15 and the number of random starting points to 50, using the `kmeans` function in the R `stats` package. To identify the optimal number of clusters, we calculated the coefficient scores and the total within sum of squares across cluster sizes, using the `silhouette` and `wss` functions in the R `cluster` package (63). The sum of squares elbow method (`wss`) and the silhouette method both indicated that 4 was the optimal number of clusters, and the silhouette method identified 3 as the second optimal number of clusters (fig. S6).

4: The strength of tree life history trade-offs across biogeographic gradients:

To examine the independent and joint effects of soil, precipitation, and temperature on tree life history traits we used a multivariate Bayesian generalized mixed effect model, using the `MCMCglmm` package in R (38). We included the same four life history traits used above as response variables (i.e., time to 20cm, time to 70th percentile of size, size at maximal age, and life expectancy from 10cm dbh) and soil, precipitation, and temperature indexes as fixed effects (described below). To account for the signature of phylogenetic ancestry on tree life history traits, we included the phylogenetic distances between species as a random effect (38, 41). We also controlled for the covariation between our life history traits and the residual variation within each trait response to account for potential trade-offs among life history traits (38). To meet model assumptions, we scaled our life history traits and climate variables to a mean of zero standard deviation of one.

Biogeographic indexes: We included soil, precipitation, and temperature indexes in our Bayesian model because they are known to strongly regulate photosynthetic capacity and plant growth and are commonly assumed to induce life history trade-offs. To avoid issues with multicollinearity and reduce model complexity, we first extracted a comprehensive set of variables related to soil, temperature, and precipitation from WorldClim and SoilGrids (64) and calculated the mean of these variables for each grid cell, using Google Earth Engine (fig. S1 and table S4). We then assigned each variable to a categorical soil, climate, or precipitation grouping (table S4) and conducted a principal component analysis for the list of variables within each group. The first PC axis for each group (e.g., soil, precipitation, and temperature indexes) were then included as fixed effects in our Bayesian generalized mixed effect model. These soil, temperature, and precipitation indexes represent multi-year mean conditions from 1997-2013. These multi-year averages capture the mean conditions that correspond with the dynamical data used to calculate our age-related demographic traits (e.g., mean life expectancy of trees based on observation data from the 1900s-2000s).

Phylogenetic tree: We constructed the time-calibrated phylogeny for all tree species using the Qian and Jin 2016 megaphylogeny (65) for plants and the `V. Phylomaker2` (66) package in R. The three species that were missing from the phylogenetic backbone were added to the tree using the most closely related species within the same genus, following Cardoso et. Al 2013 (67).

Bayesian model construction and validation: The multivariate Bayesian models were run with 15,000 iterations, a burnin of 5,000, and a thinning rate of 10, with an effective sample size

of 1000 MCMC samples. Model convergence was assessed via inspection of trace and density plots. Posterior means and upper and lower credible intervals for the fixed and random effects were used to examine the shared influence of phylogenetic ancestry and soil, temperature, and precipitation variables on mean life history trait differences across our biogeographic gradient (figs. S12 and S14, tables S5 and S6). The estimated variance coefficients for the fixed and random effects are reported in figs. S12 and S14, tables S5 and S6. Credible intervals that do not overlap with zero are suggestive of mean trait differences across broadscale soil, temperature, and precipitation gradients. The phenotypic variance-covariance, genetic variance-covariance and residual variance-covariance, and Pagels lambda (i.e., phylogenetic heritability) are reported in table S6.

5: Demographic trait diversity across biogeographic gradients

To characterize the range of life history strategies that were occupied by species across broadscale biogeographic gradients, we first calculated the 3-dimensional convex-hull volume of tree growth-longevity-stature strategies (i.e., demographic trait diversity) using the life history trait PC scores for axes 1-3 within each grid cell (46). The convex-hull volume is a widely used method to test for macroevolutionary signatures of trait diversity and habitat filtering (46). To avoid known effects of variable plot sizes between North and South America (table S1) and minimize the potential effects of local scale disturbance events on broadscale diversity patterns, we balanced the number of individual tree observations across our biogeographic gradient (see materials and methods, section 1) and calculated the convex hull volume across equal sized hexagon grids. Four of our grid cells did not meet the minimum number of species that were needed to calculate the convex-hull volume (i.e., included < 4) and were thus excluded from our analysis.

The convex hull volume of each grid cell was then used to test for predictable variation in demographic trait diversity across biogeographic gradients, using a generalized linear model (Fig 1c, H3). We used mean annual temperature as our predictor variable because it was found to have the strongest effect on our univariate traits (see Figs. 3 and S12). We also tested for two non-mutually exclusive expectations of a positive relationship between demographic diversity and ecosystem productivity, including the expectation from an evolutionary theory perspective (i.e., productivity should drive diversification) and functional perspective (i.e., more diverse systems should be more productive). To test these non-mutually exclusive hypotheses (Fig 1c, H3), we used linear and generalized linear models. The predictor variables were scaled to a mean of zero and a standard deviation of one. We assessed the normality of the residuals and, when needed, we transformed the variable by the natural log. It is important to note that mean annual temperature and our remotely sensed estimate of above-ground net primary productivity (NPP) were based on multi-year mean conditions from 1997-2013 (47). These multi-year averages serve as coarse proxies of the conditions related to the mean pace of life for trees over the last century (life expectancies, etc.), which were derived from dynamical data collected from 1926 to 2014.

Supplementary Figures:

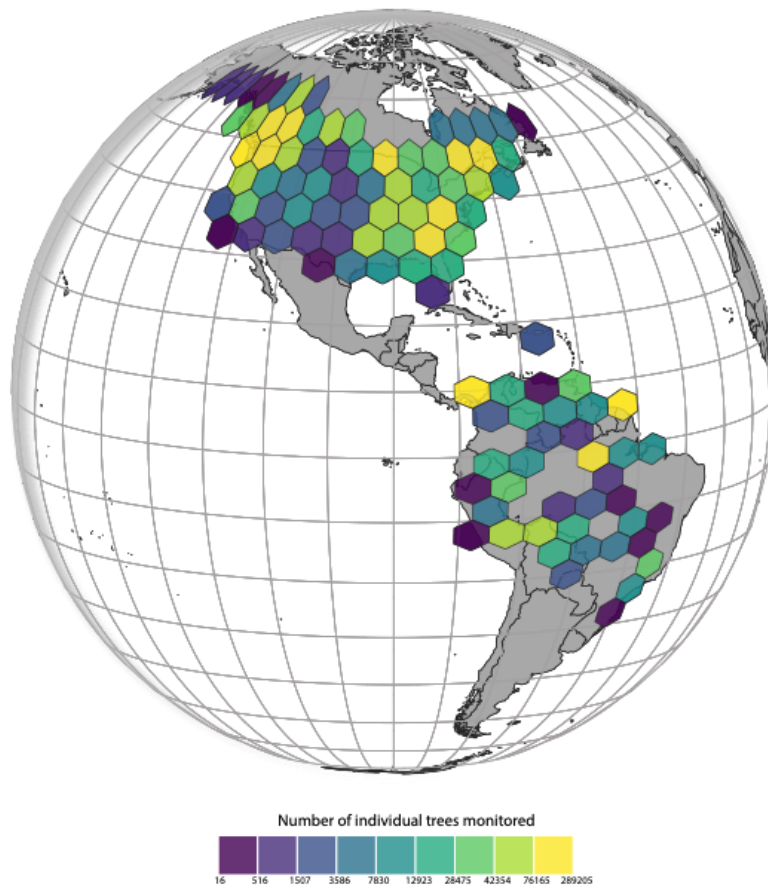


fig. S1. Map of equal area hexagon grids (size $\sim 250,000 \text{ km}^2$) that were used to calculate our species by grid ID life history traits. The heatmap represents the total number of tree observations within each grid cell.

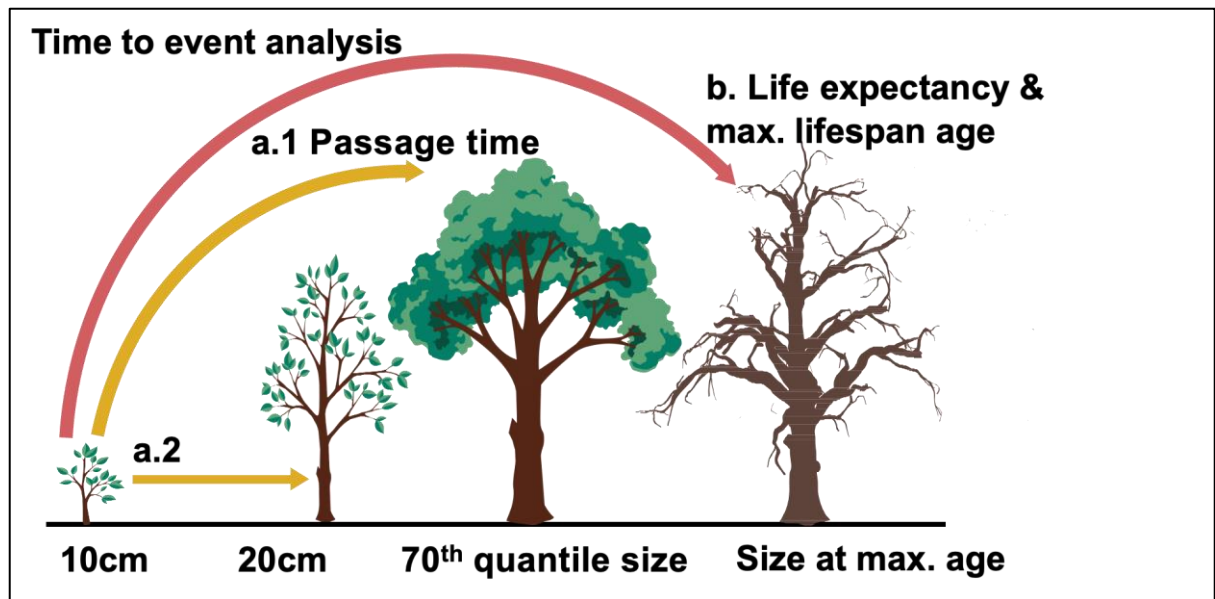


fig. S2. Visual illustration of life-history traits, including first passage times from 10 to 20 cm dbh and the 70% quantile of the observed size distribution, the life expectancy from 10 cm dbh, and the maximal lifespan age and size.

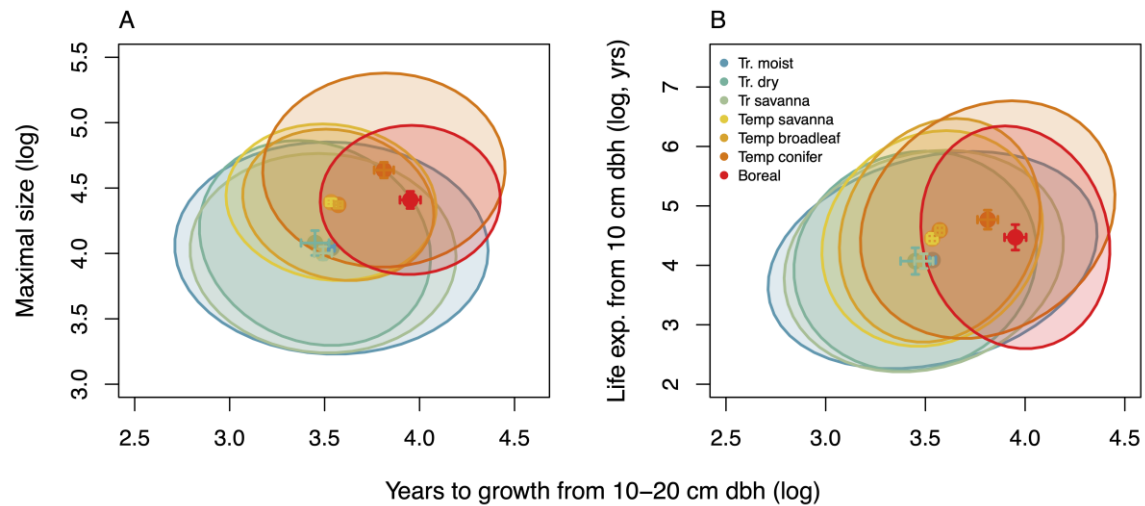


fig. S3. The relationship between growth-longevity-stature relationships across forest biomes, with means and 95% CI values. Ellipses capture the 70th quartile of trait variation among biomes (i.e., range of life history trait occupied by species across biomes).

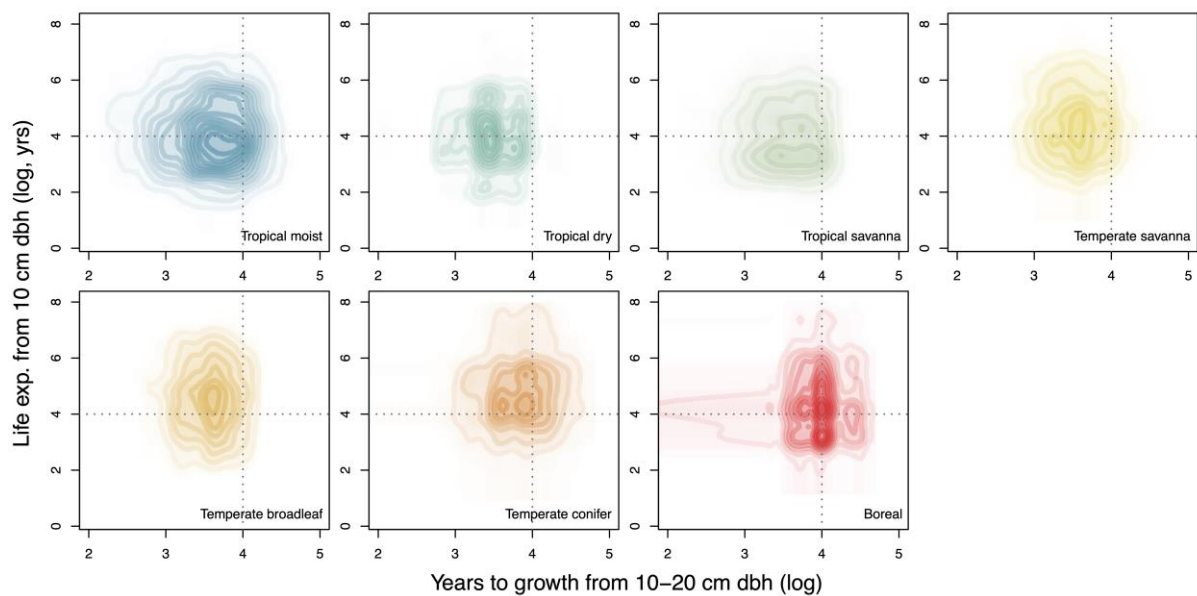


fig. S4. Heatmaps across biomes that show the relationship between tree growth strategies and the remaining life expectancies from 10 cm dbh. Color transparency represents the concentration of species with similar trait values, with less transparent colors representing a high concentration of species with similar trait values within biome.

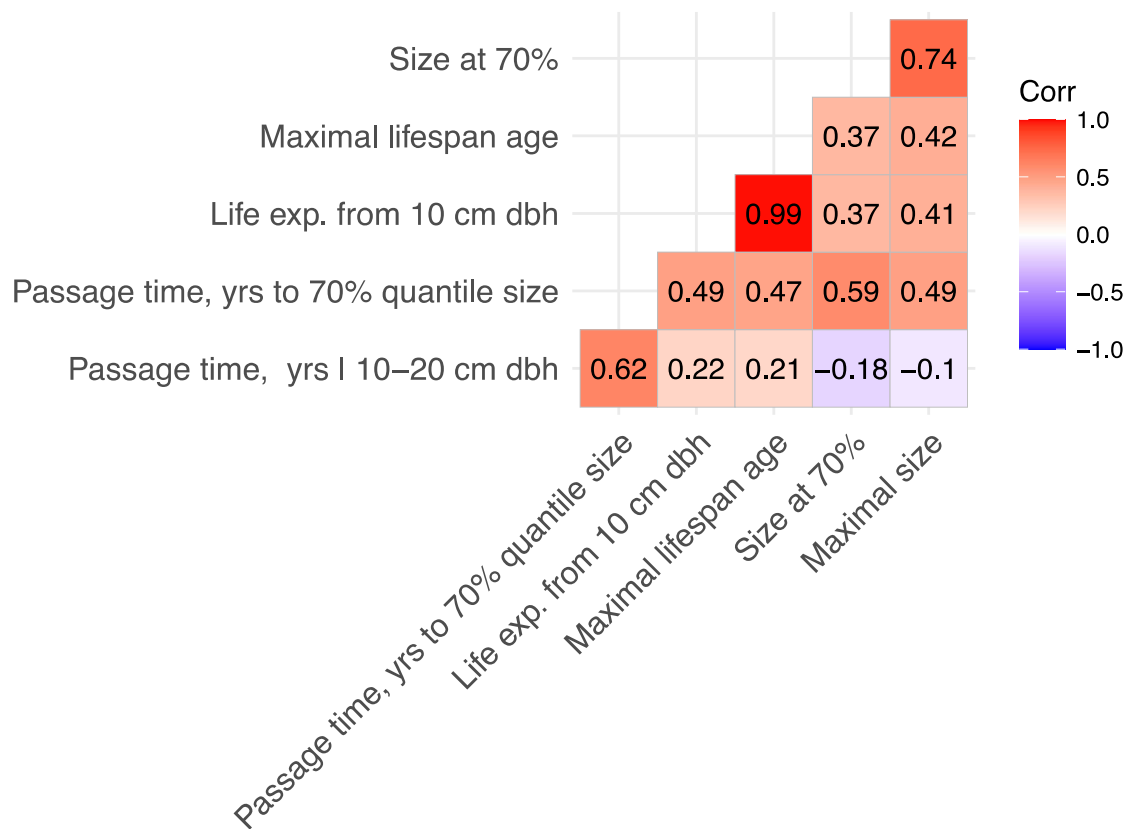


fig. S5. Life history trait correlations.

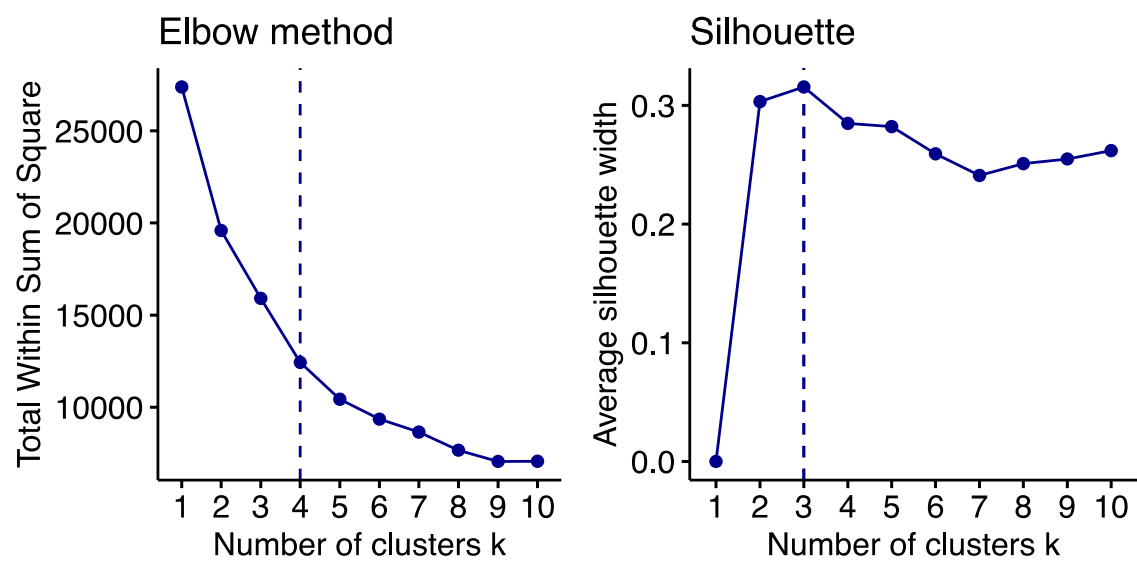


fig. S6. Optimal number of clusters using the elbow total within sum of square and Silhouette methods, including all species.

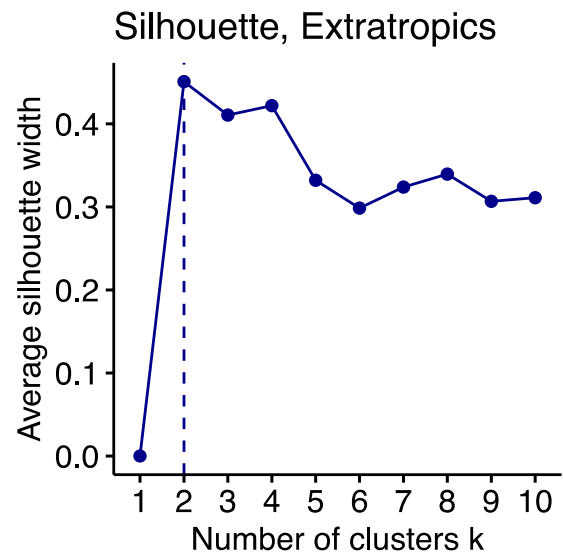
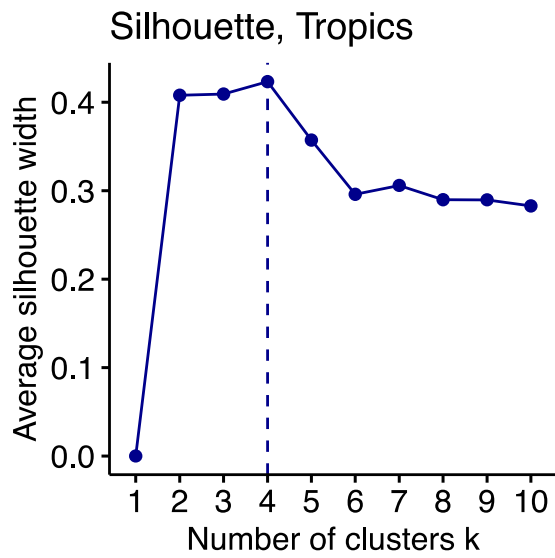
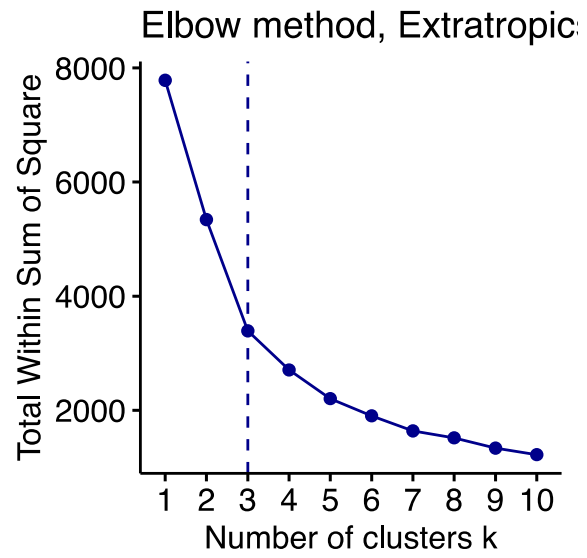
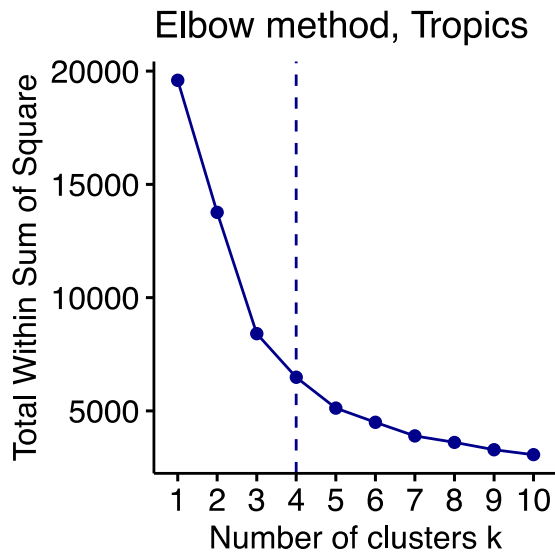


fig. S7. Optimal number of clusters using the elbow total within sum of square and silhouette methods for species in the tropics and extratropics.

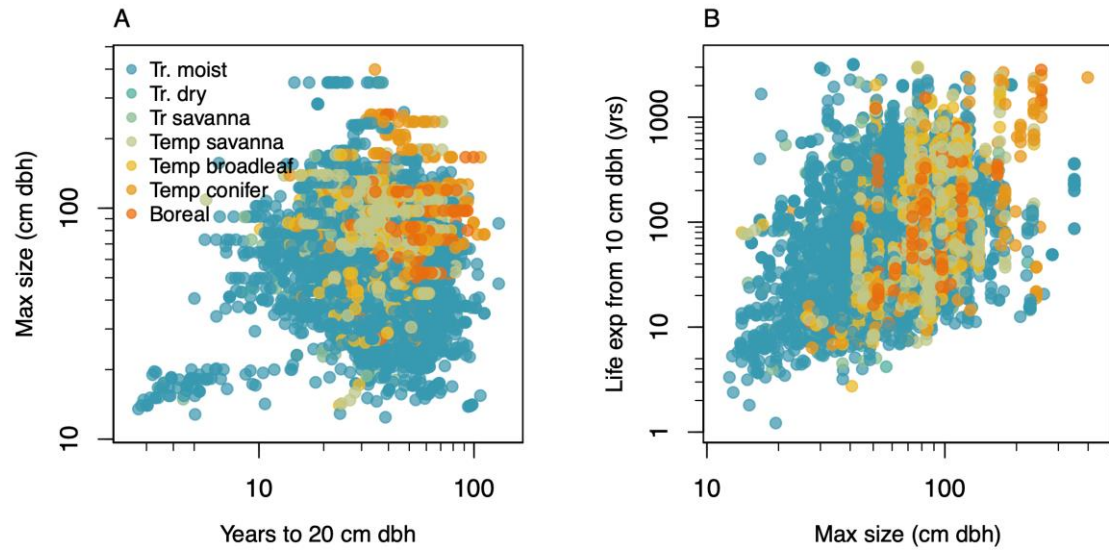


fig. S8. Visual illustration of tree growth- longevity-stature relationships for all species within each grid cell (total of 1,127 species and 6,847 trait values, i.e., species $\times$ grid).

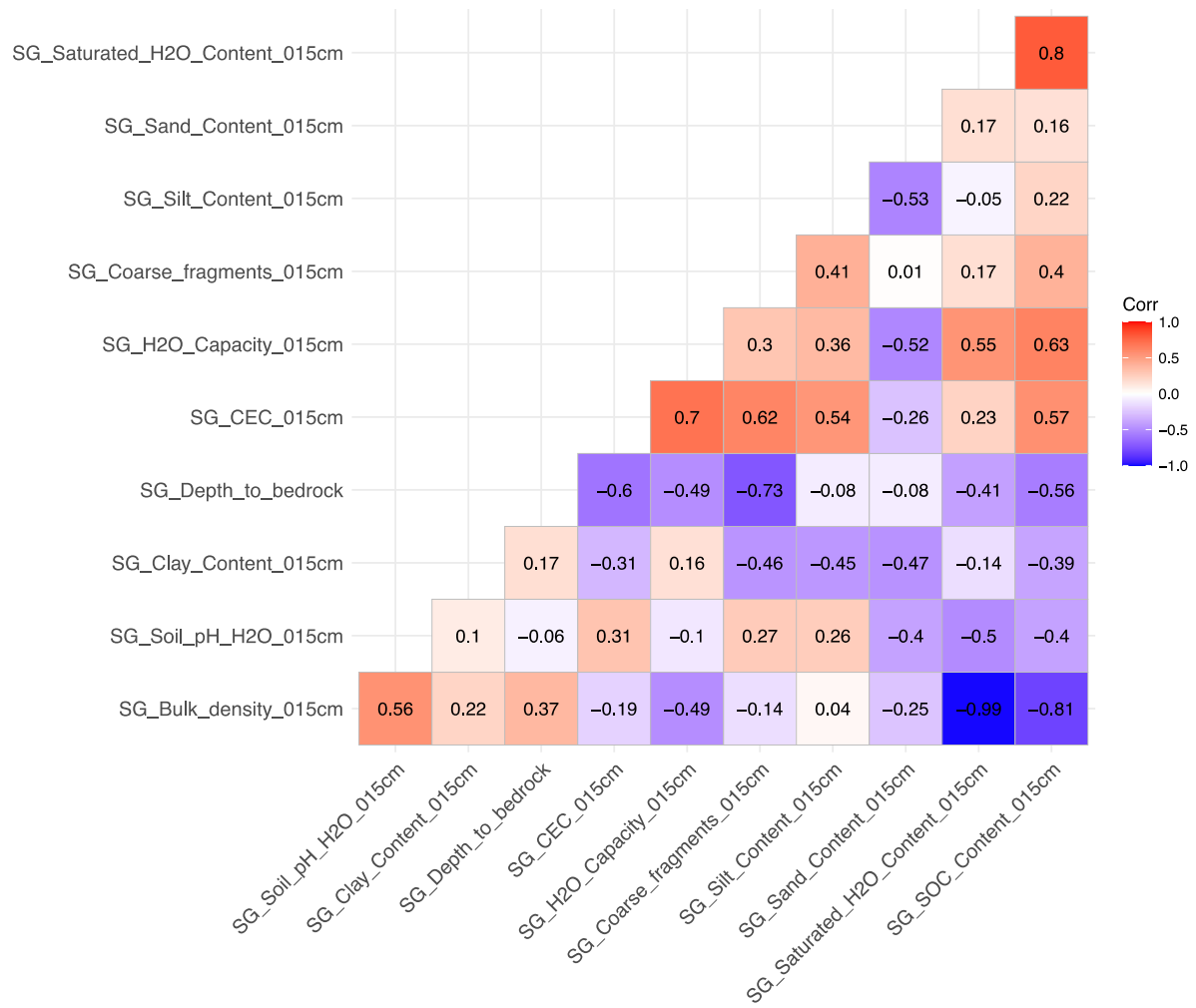


fig. S9. Correlations among soil variables, extracted from soil grids (GS)(64).

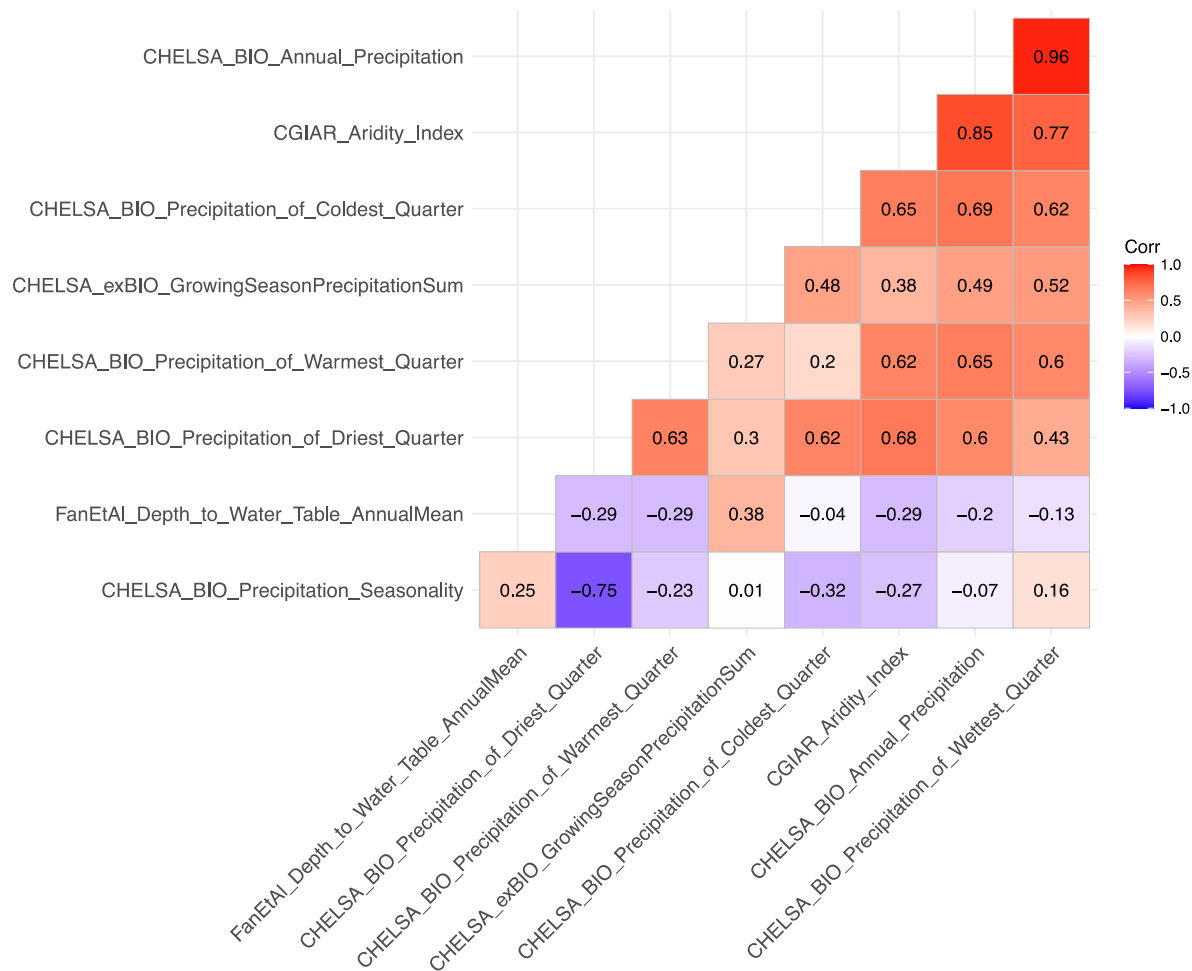
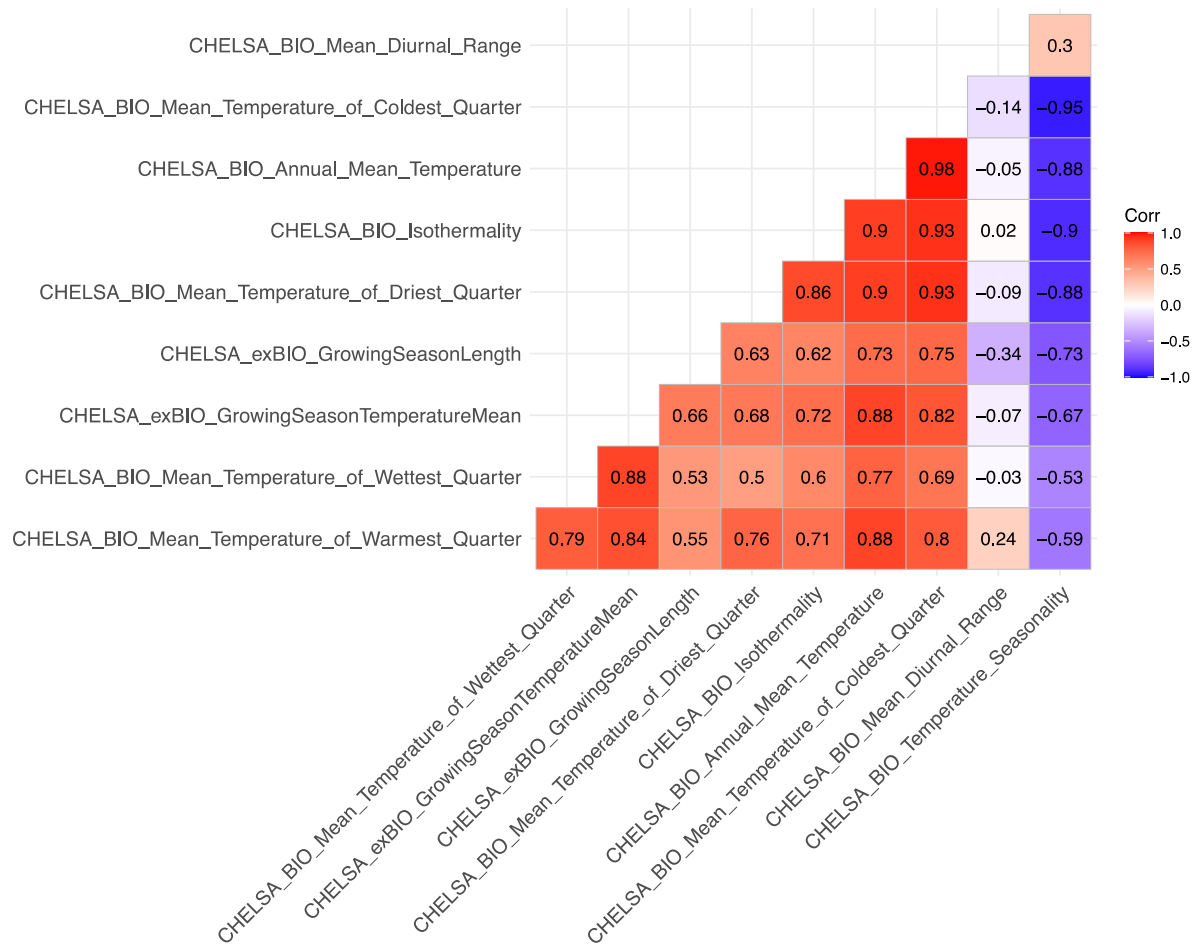


fig. S10. Correlations among precipitation variables.



fi.g S11. Correlations among temperature variables.

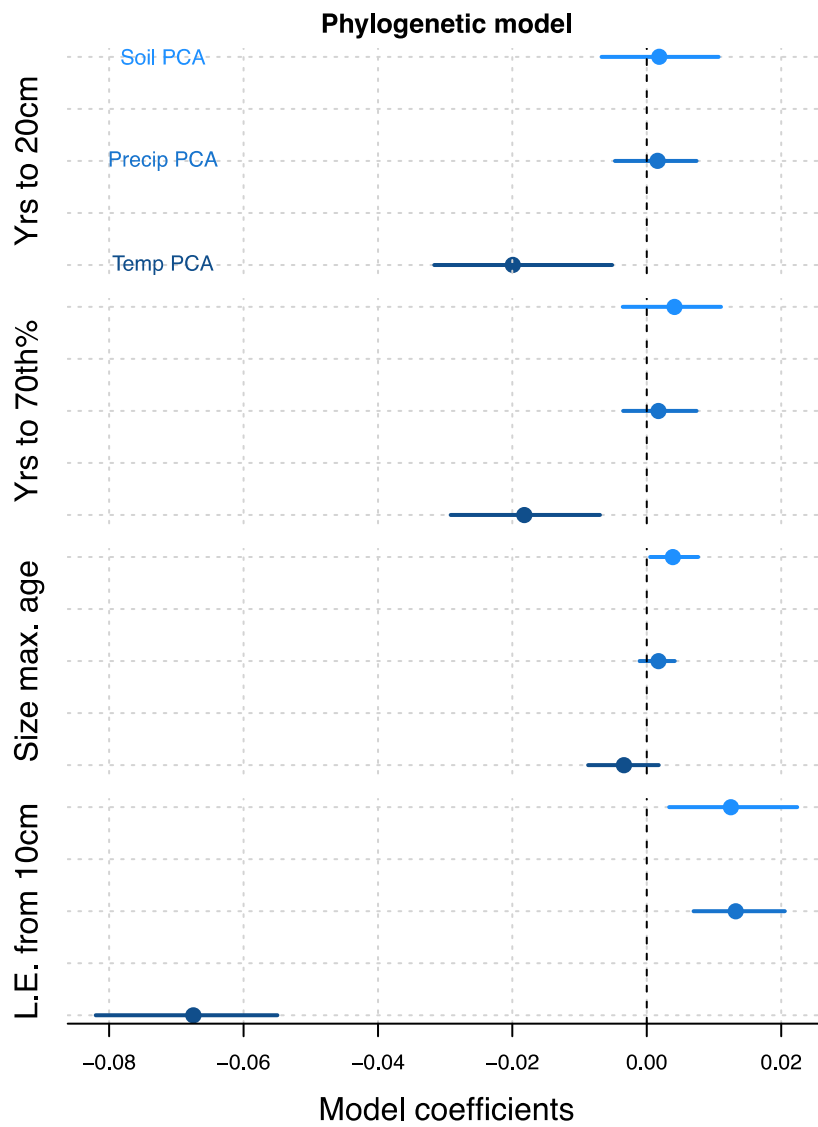


fig. S12. Estimated coefficients, with posterior mean and 95% credible intervals, for life history traits across broadscale soil, temperature, and precipitation gradients, using a multi-response Bayesian generalized mixed effect model.

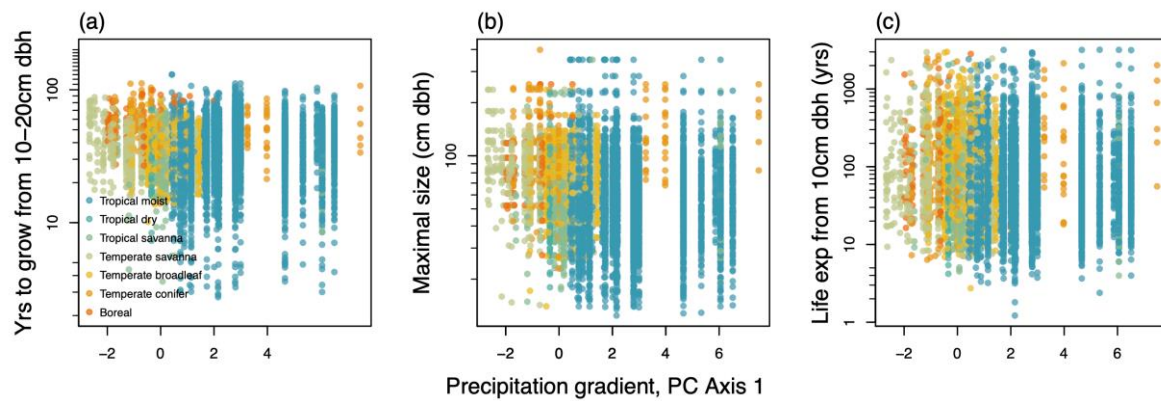


fig. S13. Life history trait variation across a precipitation gradient, which represents the first PC axis of 8 precipitation variables that we derived from WorldClim(47) and SoilGrids (64) and span a latitudinal gradient from southern Brazil to northern Canada. The Y-axis is scaled by the natural log. Data points are species- and grid-specific and are calculated using individual tree observations to fit size-based integral projection models for each species within each grid cell ID. Model coefficients of the multi-response Bayesian model are reported in fig. S12).

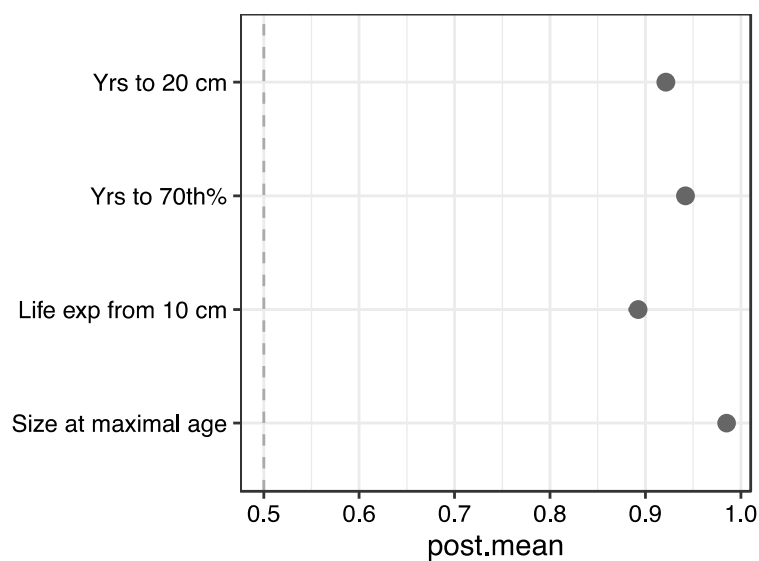


fig. S14. Estimated phylogenetic heritability from the Bayesian multiple-response mixed effect model, with posterior mean and 95% credible intervals.

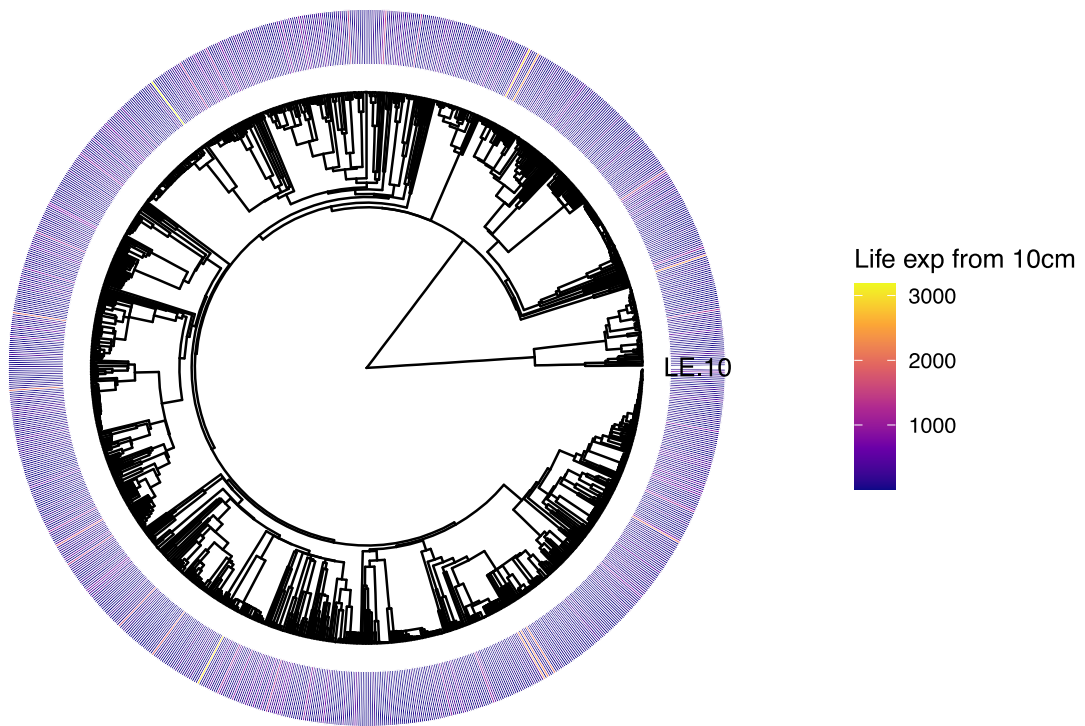


fig. S15. The phylogenetic tree for species included in our study, with a heatmap of tree life expectancies from 10 cm dbh.

Supplementary Tables:

table S1. Forest inventory network datasets used in this study.

Network name	Network regional code	# of unique tree measurements	# of species	Min census year	Max census year	Countries
ForestGeo	FGE	180,002	216	1982	2013	Panama and United States of America
ForestPlots	FPN	633,406	921	1961	2013	Bolivia, Brazil, Colombia, Ecuador, French Guiana, Guyana, Peru, Suriname, Venezuela
NFI	NAL	313,091	13	1960	2007	Canada (Alberta)
NFI	NBC	702,018	28	1926	2012	Canada (British Columbia)
NFI	NQU	252,176	34	1970	2014	Canada (Quebec)
NFI	NSA	84,207	9	1958	1999	Canada (Saskatchewan)
SYN	SYN	24,070	13	1982	2014	United States of America
FIA	FIAN	303,264	130	1999	2013	United States of America
FIA	FIANE	170,424	102	2001	2013	United States of America
FIA	FIANW	96,804	52	1995	2007	United States of America
FIA	FIARM	63,917	30	2000	2008	United States of America
FIA	FIAS	374,777	154	2000	2013	United States of America

table S2. Mean and CI values in the number of years it takes trees to go to 20 cm in diameter across biomes. The history-history traits were scaled by the natural log before calculating the mean traits and back-transformed for reporting purposes.

Life expectancy from 10 cm in diameter						
Biome	Min.	1st Qu.	Median	Mean	3rd Qu.	Max.
Boreal	10	35	73	87	186	2825
Temperate conifer	6	48	108	118	245	2674
Temperate broadleaf	3	39	100	98	253	3005
Temperate savanna	7	36	79	86	189	2976
Tropical dry	4	27	54	59	112	2037
Tropical moist	1	25	54	60	129	3195
Tropical savanna	4	23	56	59	129	2143

Growth strategy, years to grow from 10-20 cm in diameter						
Biome	Min.	1st Qu.	Median	Mean	3rd Qu.	Max.
Boreal	27	42	53	52	62	99
Temperate conifer	14	35	48	45	61	112
Temperate broadleaf	10	29	36	36	45	83
Temperate savanna	4	25	35	33	46	85
Tropical dry	7	26	32	31	41	82
Tropical moist	3	26	37	34	50	130
Tropical savanna	4	25	35	33	46	85

table S3. Principal component analysis loadings of the life history traits.

ALL species	PC 1	PC 2	PC 3	PC 4
Yrs to 20 cm dbh	0.513	0.616	0.12	0.585
Yrs to 70th max size	0.68	0.129	-0.227	-0.685
Life exp. From 10 cm dbh	0.344	-0.433	0.833	
Max size	0.395	-0.645	-0.49	0.433

Tropical species

Yrs to 20 cm dbh	0.55	0.591		0.586
Yrs to 70th max size	0.702		0.216	-0.679
Life exp. From 10 cm dbh	0.306	-0.214	-0.928	
Max size	0.333	-0.777	0.299	0.442

Extratropical species

Yrs to 20 cm dbh	0.481	0.603	0.227	0.594
Yrs to 70th max size	0.64	0.252	-0.192	-0.7
Life exp. From 10 cm dbh	0.388	-0.545	0.742	
Max size	0.456	-0.526	-0.601	0.393

table S4. List of the environmental variables included in the soil, temperature, and precipitation variables used in the multi-response Bayesian generalized mixed effect model.

Env. group	Variable name	Data source	Unit	Resolution
Soil	Bulk density 015cm	Soilgrids(64)		≈250m
Soil	Soil pH H2O 15cm	Soilgrids(64)		≈250m
Soil	Clay content 15cm	Soilgrids(64)		≈250m
Soil	Saturated H2O content 15cm	Soilgrids(64)		≈250m
Soil	Silt content 15cm	Soilgrids(64)		≈250m
Soil	CEC 15cm	Soilgrids(64)		≈250m
Soil	SOC content 15cm	Soilgrids(64)		≈250m
Soil	Sand content 15cm	Soilgrids(64)		≈250m
Soil	Coarse fragments 15cm	Soilgrids(64)		≈250m
Soil	Depth to bedrock	Soilgrids(64)		≈250m
Soil	H2O capacity 15cm	Soilgrids(64)		≈250m
Soil	Sand content 15cm	Soilgrids(64)		≈250m
Precipitation	Aridity index	CGIAR (47)	AI value	1km
Precipitation	Annual precipitation	CHELSA(68)	mm	30 arcsec (≈900m at equator)
Precipitation	Precipitation of coldest quarter	CHELSA(68)	mm	30 arcsec (≈900m at equator)
Precipitation	Precipitation of driest quarter	CHELSA(68)	mm	30 arcsec (≈900m at equator)
Precipitation	Precipitation of warmest quarter	CHELSA(68)	mm	30 arcsec (≈900m at equator)
Precipitation	Precipitation of wettest quarter	CHELSA(68)	mm	30 arcsec (≈900m at equator)
Precipitation	Precipitation seasonality	CHELSA(68)	mm	30 arcsec (≈900m at equator)
Precipitation	Growing season precipitation sum	CHELSA(68)	mm	30 arcsec (≈900m at equator)
Precipitation	Depth to water table annual mean	CHELSA(68)	mm	30 arcsec (≈900m at equator)
Temperature	Isothermality	CHELSA(68)	Unitless	30 arcsec (≈900m at equator)

Temperature	Mean diurnal range	CHELSA(68)	°C	30 arcsec (≈900m at equator)
Temperature	Mean temperature of coldest quarter	CHELSA	°C	30 arcsec (≈900m at equator)
Temperature	Mean temperature of coldest quarter	CHELSA	°C	30 arcsec (≈900m at equator)
Temperature	Mean temperature of coldest quarter	CHELSA	°C	30 arcsec (≈900m at equator)
Temperature	Mean temperature of coldest quarter	CHELSA	°C	30 arcsec (≈900m at equator)
Temperature	Temperature seasonality	CHELSA	°C	30 arcsec (≈900m at equator)
Temperature	Growing season length	CHELSA	Number of days	30 arcsec (≈900m at equator)
Temperature	Growing season temperature mean	CHELSA	°C	30 arcsec (≈900m at equator)

table S5. Results of Bayesian generalized mixed effect model, with estimates of posterior means, upper and lower credible intervals.

Life history trait	Env. variable	post.mean	lower-95% CI	upper-95% CI	eff.samp	p value MCMC	
Life exp. From 10 cm dbh	--	0.055	-0.030	0.134	1000.0	0.218	
Yrs to 20 cm dbh	--	0.160	0.082	0.256	1000.0	0.001	**
Yrs to 70th max size	--	0.106	0.022	0.193	1000.0	0.020	*
Max size	--	-0.273	-0.357	-0.191	1000.0	0.001	***
Life exp. From 10 cm dbh	Soil PCA	0.012	0.003	0.022	1115.9	0.016	*
Yrs to 20 cm dbh	Soil PCA	0.002	-0.007	0.011	1000.0	0.686	
Yrs to 70th max size	Soil PCA	0.004	-0.004	0.011	1000.0	0.316	
Max size	Soil PCA	0.004	0.000	0.008	1117.3	0.040	*
Life exp. From 10 cm dbh	Precipitation PCA	0.013	0.007	0.021	1000.0	0.001	**
Yrs to 20 cm dbh	Precipitation PCA	0.002	-0.005	0.007	1000.0	0.620	
Yrs to 70th max size	Precipitation PCA	0.002	-0.004	0.007	1000.0	0.544	
Max size	Precipitation PCA	0.002	-0.001	0.004	1000.0	0.196	
Life exp. From 10 cm dbh	Temperature PCA	-0.067	-0.082	-0.055	1000.0	0.001	***
Yrs to 20 cm dbh	Temperature PCA	-0.020	-0.032	-0.005	1000.0	0.002	**
Yrs to 70th max size	Temperature PCA	-0.018	-0.029	-0.007	1000.0	0.002	**
Max size	Temperature PCA	-0.003	-0.009	0.002	1000.0	0.200	

Signif. codes: 0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

table S6. Phylogenetic variance-covariance of the Bayesian generalized mixed effect model, with the genetic and residual correlations for each life history trait and Pagel's lambda.

Phenotypic correlations [variance-covariance of standardized traits]

	Life exp. From 10 cm dbh	Yrs to 20 cm dbh	yrs to 70th max size	Max size
Life exp. From 10 cm dbh	1	0.18	0.32	0.34
Yrs to 20 cm dbh	0.18	1	0.61	-0.04
Yrs to 70th max size	0.32	0.61	1	0.41
Max size	0.34	-0.04	0.41	1

Genetic variance-covariance

	Life exp. From 10 cm dbh	Yrs to 20 cm dbh	yrs to 70th max size	Max size
Life exp. From 10 cm dbh	0.94	0.21	0.36	0.35
Yrs to 20 cm dbh	0.21	1.14	0.67	-0.05
Yrs to 70th max size	0.36	0.67	1.15	0.48
Max size	0.35	-0.05	0.48	1.09

Residual variance-covariance

	Life exp. From 10 cm dbh	Yrs to 20 cm dbh	yrs to 70th max size	Max size
Life exp. From 10 cm dbh	0.12	0.00	0.00	0.01
Yrs to 20 cm dbh	0.00	0.10	0.08	0.00
Yrs to 70th max size	0.00	0.08	0.07	0.00
Max size	0.01	0.00	0.00	0.02

Genetic correlations

	Life exp. From 10 cm dbh	Yrs to 20 cm dbh	yrs to 70th max size	Max size
Life exp. From 10 cm dbh	1	0.20	0.35	0.35
Yrs to 20 cm dbh	0.20	1	0.59	-0.05
Yrs to 70th max size	0.35	0.59	1	0.43
Max size	0.35	-0.05	0.43	1

Residual correlations

	Life exp. From 10 cm dbh	Yrs to 20 cm dbh	yrs to 70th max size	Max size
Life exp. From 10 cm dbh	1	-0.04	-0.01	0.28
Yrs to 20 cm dbh	-0.04	1	0.93	0.08
Yrs to 70th max size	-0.01	0.93	1	0.08
Max size	0.28	0.08	0.08	1

Pagel's lambda

	lambda	Lower CI	Upper CI
Life exp. From 10 cm dbh	0.89	0.88	0.90
Yrs to 20 cm dbh	0.92	0.92	0.93
Yrs to 70th max size	0.94	0.94	0.95
Max size	0.99	0.98	0.99

table S7. Linear model coefficients and summary statistics associated with Fig 4, including species richness and demographic trait diversity (**A**), mean annual temperature and demographic trait diversity (**B**), net primary productivity and demographic trait diversity table (**C**), and the combined effect of demographic trait diversity and mean annual temperature on net primary productivity (**D**).

Species richness on demo. diversity (Fig 4.A)

Term	Estimate	Std error	Statistic	P value
(Intercept)	-6.732	0.984	-6.840	<0.01
Species richness (log)	2.193	0.554	3.959	0.000
Species.richness^2 (log)	-0.146	0.073	-2.006	0.048

Adj $R^2 = 0.65$, $F_{2,82} = 79$, $p < 0.01$

Mean annual temp on demo diversity (Fig 4.B)

Term	Estimate	Std error	Statistic	P value
(Intercept)	-2.267	0.2376	-9.541	<0.01
Mean annual temp (scaled)	0.106	0.0139	7.593	<0.01

Adj $R^2 = 0.40$, $F_{1,83} = 58$, $p < 0.01$

NPP on demo diversity (Fig 4.C)

Term	Estimate	Std error	Statistic	P value
NPP (scaled and log)	0.708	0.077	9.182	<0.01

Adj $R^2 = 0.49$, $F_{1,84} = 84.32$, $p < 0.01$

Demographic diversity on NPP (Fig 4.D)

Term	Estimate	Std error	Statistic	P value
Demo. diversity (scaled and log)	0.178	0.0441	4.041	<0.01
Mean annual temp. (scaled and log)	0.827	0.044	18.777	<0.01

Adj $R^2 = 0.90$, $F_{2,83} = 394.9$, $p < 0.01$

The effect of demographic diversity on NPP, tropics

Term	Estimate	Std error	Statistic	P value
Temp (scaled)	0.308	0.152	2.030	0.051
Demo diversity (log and scaled)	0.412	0.152	2.716	0.011

Adj $R^2 = 0.26$, $F_{2,31} = 6.912$, $p = 0.003$

The effect of demographic diversity on NPP, extra-tropics

Term	Estimate	Std error	Statistic	P value
Temp (scaled)	0.790	0.068	11.611	<0.001
Demo diversity (log and scaled)	0.199	0.068	2.917	0.005

Adj $R^2 = 0.840$, $F_{2,50} = 136.6$, $p < 0.01$

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