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Article title: Beyond species means – the intraspecific contribution to global wood density variation

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A) Methods

Methods S1: Updating the first GWDD

Correcting inconsistencies

Entries in the first GWDD were updated to reflect structural changes in the GWDD v.2. In the case of large collections that had previously been transformed – through conversion factors or aggregation – or updated with new records since the publication of the first GWDD (Ilic et al., 2000; Langbour et al., 2019; Vieilledent et al., 2018), we reintegrated the entire data sets from scratch to ensure consistency. Where possible, this was done at the level of individual plants instead of species means. If published manuals were based on or overlapped with databases, but provided values for additional species from other sources (e.g., Détienne & Jacquet, 1983 and Langbour et al., 2019), we first included the raw values from the databases and then reincluded any non-matching taxa from the published literature to ensure continuity. All values were transformed with the new correction factors. Where re-integration would have been highly time-consuming or near-impossible (values from hard-to-access print-only manuals such as Desch, 1941, or previous compilations, such as Reyes et al., 1992), we inferred the source value by back-transforming entries with the original wood density conversion factor and reapplying a corrected factor. In this case, the taxon identifier from the original database was kept as *species_reference* and the column *backtransformed* is ticked. In a few cases, sources in the first GWDD could not be accessed anymore (Database of Brazilian Woods 2006, formerly: http://www.ibama.gov.br/lpf/madeira/default.htm) or have been overwritten in the meantime (ICRAF database, http://db.worldagroforestry.org/wd). Records exclusively attributed to these sources were removed (50 taxa in total, 1 lost genus, Table S2).

Database extension

In addition to updating the previous database, we searched the literature for new or previously overlooked studies and extracted values either manually or from supplementary files. To cover a wide range of trait values, we also wrote to authors of papers citing the original GWDD paper (Chave et al., 2009) and asked them whether they would be willing to participate in our effort, yielding more than 70 contributors (co-authors on this paper). While not a primary aim, we also received data for a range of wood density types outside of the scope of the first GWDD. For some tissue types (e.g., "bark" in *type_tissue*) and within-plant locations ("root" in *location_sample*), we included these values, as they are directly linked to intraspecific variation and form already part of some wood density assessments (e.g., bark is not always removed before estimating wood density). However, we decided not to include quantities such as green wood density (Niklas & Spatz, 2010) or dry mass fraction (Goodman et al., 2013), as there is no clear conversion to wood specific gravity. A complete list of literature references for wood density values can be found in Methods S2.

Methods S2: Literature references for wood density values

Below we provide all the sources of data for the GWDD v.2, and the number of records from these sources. Note that these records also include bark density measurements.

Source	N
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Methods S3: Converting air- and ovendry density to basic wood density

For air- and ovendry wood densities robust conversion factors to basic density can be derived (Vieilledent et al., 2018). The theory behind the conversion factors is as follows: wood is composed of a variable fraction of water, some of which is free to move in conduits (tracheids and vessels), and the rest is associated with other wood tissues including parenchyma and fibers. During drying, free water is gradually lost, until reaching the so-called fiber saturation point. The moisture at fiber saturation is quite variable across species from ca 10% to 50%, with a typical value of ~30% (Berry & Roderick, 2005; Vieilledent et al., 2018). Beyond this point, any further drying also shrinks the volume. If V_s is the volume of the sample at fiber saturation moisture S, and V_0 is the volume when the sample has lost all of its water, then the volumetric shrinkage, or retractability, is the percent loss in volume $R = (V_s - V_0)/V_s \times 100$, which varies from 5% to 25% across species (Vieilledent et al., 2018).

From these values, it is possible to derive a conversion formula between wood density at any moisture content w (D_w) and basic density (D_b):

$$D_b = \frac{1 - (R/100) \times (S - w)}{1 + w/100} \times D_w$$

This formula has been used together with the CIRAD wood technology database to derive robust conversion factors (Vieilledent et al., 2018). The CIRAD wood technology database is a collection of S, R, and D values for 3,832 individual trees with >10 samples per individual and measurements at four moisture contents w (from 18% to 0%). The data set allows the estimation of D_w at any w as well as an estimation of conversion factors to D_b by fitting regression models with intercepts forced through the origin. For the GWDD v.2, we calculated conversion factors for wood densities at four common moisture levels: 0.819 for airdry densities at w = 15%, 0.828 for airdry densities at w = 12%, 0.840 for airdry densities at w = 8%, and 0.868 for ovendry densities (or w = 0%).

Methods S4: Details on Bayesian modelling of wood density variation

We fitted linear mixed-effects either with a Bayesian framework in the *brms* R package (Bürkner, 2018) and the maximum-likelihood framework of *lme4* (Bates et al., 2015). We assume basic familiarity with mixed-effect model fitting in R (formulae provided in Table S3), and will only focus on details particular to the Bayesian context.

1/ Distributional model: Unlike *lme4*, *brms* allows to explicitly model the distributional parameter σ (i.e., the width of the residual distribution). We here use this to allow σ to vary across the same taxonomic groupings as the response variable (wood density). Given that variances are constrained to be positive and typically follow a lognormal distribution, we used the *brms* default of modelling σ on log-scales. In R's common random effects model notation, this can be simply expressed as $log(\sigma) \sim 1 + (1 \mid species)$ or $log(\sigma) \sim 1 + (1 \mid family / genus / species)$, but we note that in *brms*, the log-transformation is carried out automatically, so we redefine the distributional parameter as $\sigma^* = exp(\sigma)$ and write: $\sigma^* \sim 1 + (1 \mid species)$ or $\sigma^* \sim 1 + (1 \mid family / genus / species)$. A visual check of the assumption of lognormality is provided in Fig. S4.

2/ Prior specifications: Bayesian modelling requires the specification of priors, i.e. the provision of initial distributions for the parameters to be modelled. Since the data sets used in this study are large, exact prior choices have little influence on the resulting inference. Nevertheless, specification of weakly informative priors is recommended to constrain the initial parameter space and provide weak constraints on expected effect sizes (a form of regularization). Throughout all wood density models, we chose the following priors:

$$Intercept \sim \mathrm{N}(0.5, 0.25); lb = 0$$

$$Population\ level\ (fixed)\ effects \sim \mathrm{N}(0.0, 0.1)$$

$$Group\ level\ (random)\ effects \sim \mathrm{N}(0.1, 0.1); lb = 0$$

Here, *lb* stands for "lower bound". This means that we broadly expect the intercept for any wood density model to lie between 0 and 1.0, with fixed effects broadly constrained between -0.2 and 0.2, and random effects broadly constrained between 0 and 0.3 (all 95% intervals). Given that most wood density values lie between 0.3 and 0.8 and that we always standardize predictors (scaling and centering), effect sizes outside this range would be very large. Compare also to model results, where fixed effect sizes usually lie within a much more restricted [-0.05, 0.05] and never exceed [-0.1, 0.1]. In addition, we specify the following priors on the distributional parameter $\sigma = log(\sigma^*)$:

$$Intercept \sim \mathrm{N}(-3.0, 0.5)$$

$$Group\ level\ (random)\ effects \sim \mathrm{N}(0.5, 0.5); lb = 0$$

This corresponds to a realized σ^* = exp(-3.0) ~ 0.5, with an approximate range of [0.02, 0.14].

3/ Model fitting and checks: All *brms* models were fit with *adapt_delta* == 0.95 and *max_treedepth* == 10. We always ran 4 chains in parallel, with 2000 iterations (including 1000 for warmup) and checked against warnings about divergent transitions, effective sampling sizes (ESS), and the mixing of chains (R-hat <= 1.02). If ESS were low, we increased the total number of iterations up to 5000. Model fits were visually checked via the inbuilt pp_check() function (representative examples in Fig. S3).

Methods S5: Overview over R packages

For completeness, we here list all R packages used in the study. They include *terra* (Hijmans, 2023), *data.table* (Dowle & Srinivasan, 2023), *lme4* (Bates et al., 2015), *brms* (Bürkner, 2018), *WorldFlora* (Kindt, 2020), *ggplot2* (Wickham, 2016), *ggdist* (Kay, 2024), *patchwork* (Pedersen, 2024), *viridis* (Garnier et al., 2023), *sjPlot* (Lüdecke, 2021), *lmodel2* (Legendre, 2018), *rnaturalearth* (Massicotte & South, 2023), *rnaturalearthdata* (South, 2017), *corrplot* (Wei & Simko, 2021).

B) Tables

#	Field	Description
1	*id*	overall primary id of the record
2	*species*	species after spell-checking and resolution (WFO)
3	*group*	group after spell-checking and resolution (WFO)
4	*order*	order after spell-checking and resolution (WFO)
5	*family*	family after spell-checking and resolution (WFO)
6	*genus*	genus after spell-checking and resolution (WFO)
7	*epithet*	species epithet after spell-checking and resolution (WFO)
8	*epithet_infraspecific*	infraspecific epithet after spell-checking and resolution (WFO)
9	*authority*	taxonomic authority after spell-checking and resolution (WFO)
10	*status_taxonomic*	taxonomic status after spell-checking and resolution (WFO): "accepted", "unresolved", “unchecked”
11	*rank_taxonomic*	taxonomic rank after spell-checking and resolution (WFO): "genus", "species", "subspecies", "variety", "hybrid"
12	*source_taxonomic*	identifier after spell-checking and resolution (WFO)
13	*wsg*	wood specific gravity / basic wood density
14	*plant_agg*	is measurement aggregated over several individuals: 0 or 1, or NA if unclear
15	*plants_sampled*	number of individuals aggregated over: > 1, if *plant_agg* == 1, else 1 or NA
16	*location_sample*	the within-tree location of the sample: "root","bole","branch","twig", "shoot”, NA
17	*type_tissue*	the type of woody tissue sampled: "sapwood","heartwood","bark", "total (bark to pith)"
18	*region*	one of nine regions: "South America", "Central America and West Indies", "North America", "Asia", "South-East Asia", "Africa", "Indian Ocean", "Europe", "Oceania"
19	*country*	country of measurement
20	*site*	site of measurement, at various levels of precision
21-22	*longitude/latitude*	coordinates of the site of measurement
23	*type_forest*	type of forest, can contain locally specific types
24-26	*id_plant/age/dbh*	Individual plant-level information on IDs, age and diameter
27	*experiment*	is the study an experiment? if collected during an experiment 1, else 0
28	*experiment_design*	design of the study or experiment if applicable
29	*source_short*	the short name of the source of measurements
30	*source_long*	the full name of the source of measurements
31	*contributor*	the contributor of the data set
32	*id_dboriginal*	the id of the sample in the original database
33	*species_reference*	the taxon supplied to the GWDD v.2
34	*genus_reference*	the genus supplied to the GWDD v.2
35	*epithet_reference*	the epithet supplied to the GWDD v.2
36	*epithet_infraspecific_reference*	the infraspecific epithet supplied to the GWDD v.2
37	*species_reference_canonical*	the taxon supplied to the GWDD v.2., stripped of additional information such as taxonomic authorities
38	*value_reference*	the (untransformed) wood density supplied to the GWDD v.2
39	*quantity_reference*	the type of wood density that was measured: "Airdry SG/Density", "Ovendry SG/Density", "Basic SG/Density"
40	*moisture_airdry*	the moisture at which wood was considered airdry (%): 8, 12, 15 if airdry, else NA
41	*wsg_conversion*	the conversion factor to convert airdry or ovendry densities: 1.0 (Basic SG), 0.8676046 (Ovendry SG), 0.8404015 (8% SG), 0.8281316 (12% SG), 0.8194401 (15% SG)
42	*backtransformed*	is the value backconverted from the GWDD v.1? 0 or 1 (only applied to legacy data)
43	*type_sample*	the type of sample: "core", "disk"
44	*instrument*	the instrument used to obtain wood density
45	*temperature_drying*	the temperature at which samples have been dried

Table S1: Documentation of Global Wood Density Database (GWDD) v.2 columns. Given is the column ID, their name and a short description. “WFO” stands for WorldFloraOnline, which was used for taxonomic resolution. “SG” stands for “specific gravity”.

Binomial	*Resolved*	*N*
Acacia alleniana	Acacia alleniana	1
Acacia colei	Acacia colei	2
Acacia trinervata	Acacia trinervata	1
Acioa edulis	Acioa edulis	1
Aglaia hiernii	Aglaia hiernii	1
Albizia dinklagei	Albizia dinklagei	1
Albizia lebbekoides	Albizia lebbekoides	1
Alloxylon flammeum	Alloxylon flammeum	2
Anacardium tenuifolium	Anacardium tenuifolium	1
Aspidosperma decussatum	Aspidosperma decussatum	1
Atalaya australiana	Atalaya australiana	1
Borassus flabellifer	Borassus flabellifer	1
Breonia madagascariensis	Breonia madagascariensis	1
Bruguiera exaristata	Bruguiera exaristata	1
Calliandra calothyrsus	Calliandra houstoniana var. calothyrsus	1
Calliandra tweediei	Calliandra tweediei	1
Corymbia dallachiana	Corymbia dallachiana	4
Couepia robusta	Couepia robusta	1
Cullen australasicum	Cullen australasicum	**1**
Dicymbe corymbosa	Dicymbe corymbosa	1
Diospyros cayennensis	Diospyros cayennensis	1
Dipteryx ferrea	Dipteryx ferrea	1
Endiandra dielsiana	Endiandra dielsiana	1
Eucalyptus glomerosa	Eucalyptus glomerosa	1
Eucalyptus urophylla	Eucalyptus urophylla	2
Grewia crenata	Grewia prunifolia	1
Huertea cubensis	Huertea cubensis	1
Lacistema grandifolium	Lacistema grandifolium	1
Leucaena diversifolia	Leucaena diversifolia	1
Licania fanshawei	Licania fanshawei	1
Licania jimenezii	Licania jimenezii	1
Licania pallida	Licania pallida	1
Licania sparsipilis	Leptobalanus sparsipilis	2
Licaria rigida	Licaria rigida	2
Litsea breviumbellata	Litsea breviumbellata	1
Magnolia yoroconte	Magnolia yoroconte	1
Micrandra minor	Micrandra minor	1
Mischocarpus stipitatus	Mischocarpus stipitatus	3
Mouriri pseudogeminata	Mouriri pseudogeminata	1
Nectandra krugii	Nectandra krugii	1
Parashorea aptera	Parashorea aptera	1
Pinus hartwegii	Pinus hartwegii	1
Pittosporum angustifolium	Pittosporum angustifolium	2
Polyalthia asteriella	Monoon asteriellum	1
Pouteria izabalensis	Pouteria izabalensis	1
Pouteria oblanceolata	Pouteria oblanceolata	1
Pouteria obscura	Pouteria obscura	1
Pterocarpus osun	Pterocarpus osun	1
Rauvolfia paraensis	Rauvolfia paraensis	1
Rhodamnia glauca	Rhodamnia glauca	1

Table S2: Removed taxa in the Global Wood Density Database (GWDD) v.2. Shown are taxa from the GWDD v.1 whose references could not be verified and whose records are not available anymore in the GWDD v.2. We also provide their resolved names from World Flora Online (WFO) and their number of entries in the GWDD v.1. With one exception (Cullen australicum), the removal of the taxa did not result in the loss of the corresponding genus.

Model	Question	Data subset	Subsetting procedure	Model formula
M1	**Extent of intraspecific variation**	n = 79,488, $n_{species}$ = 10,780	full set of measurements from individual plants	wd ~ 1 + (1 | family / genus / species) + (1 | source)
M2		n = 79,488, $n_{species}$ = 10,780	full set of measurements from individual plants	wd ~ 1 + (1 | family / genus / species)
M3		n = 49,991, $n_{species}$ = 2735	higher quality (>= 3 individuals per species, >= 3 species per genus, >= 3 genera per family)	wd ~ 1 + (1 | family / genus / species) + (1 | source)
M4		n = 49,991, $n_{species}$ = 2735	higher quality (>= 3 individuals per species, >= 3 species per genus, >= 3 genera per family)	wd ~ 1 + (1 | family / genus / species)
M5	**Partitioning of intraspecific variance**	n = 19,246, $n_{species}$ = 147	minimum quality (>= 2 sites per species, >= 2 individuals for one site, >= 2 records for one individual)	wd ~ 1 + (1 | species / site / id_plant) + (1 | source)
M6		n = 19,246, $n_{species}$ = 147	minimum quality (>= 2 sites per species, >= 2 individuals for one site, >= 2 records for one individual)	wd ~ 1 + (1 | species / site / id_plant)
M7		n = 2,494, $n_{species}$ = 35	higher quality (>= 3 sites per species, >= 3 individuals for one site, >= 3 records for one individual)	wd ~ 1 + (1 | species / site / id_plant) + (1 | source)
M8		n = 2,494, $n_{species}$ = 35	higher quality (>= 3 sites per species, >= 3 individuals for one site, >= 3 records for one individual)	wd ~ 1 + (1 | species / site / id_plant)
M9	**Within-plant gradients**	n = 679, $n_{species}$ = 150	species with >= 1 measurement each from heartwood and sapwood	wd ~ 1 + sapwood + (1 + sapwood | species) + (1 | source)
M10		n = 48,494, $n_{species}$ = 2,018	species with >= 1 measurement each from branch and trunk	wd ~ 1 + branch + (1 + branch | species) + (1 | source)
M11		$n_{species}$ = 150	species with >= 1 measurement each from heartwood and sapwood; species means	$wd_{sapwood}$ ~ $wd_{heartwood}$ (MA regression)
M12		$n_{species}$ = 2,018	species with >= 1 measurement each from branch and trunk; species means	wd_{branch} ~ wd_{trunk} (MA regression)
M13		$n_{species}$ = 523	species with >= 1 measurement each from branch sapwood and trunk sapwood; species means	wd_{branch} ~ wd_{trunk} (MA regression)
M14		$n_{species}$ = 189	species with 5 randomly drawn measurements from both branch and trunk; species means	wd_{branch} ~ wd_{trunk} (MA regression)
M15		n = 3,527, $n_{species}$ = 145	Individual plants with 1 randomly drawn measurement from both branch and trunk	wd_{branch} ~ wd_{trunk} (MA regression)
M16	**Environmental predictors of intraspecific variation**	n = 41,893, $n_{species}$ = 2,160	species with >= 2 distinct locations	wd ~ 1 + $env1km_{species}$ + $env1km_{intrasp}$ + (1 + $env1km_{intrasp}$ | species) + (1 | source)
M17		n = 41,893, $n_{species}$ = 2,160	species with >= 2 distinct locations	wd ~ 1 + $env5km_{species}$ + $env5km_{intrasp}$ + (1 + $env5km_{intrasp}$ | species) + (1 | source)
M18		n = 30,128, $n_{species}$ = 692	species with >= 2 distinct locations + wide intraspecific predictor range (one predictor in top 10% of ranges)	wd ~ 1 + $env1km_{species}$ + $env1km_{intrasp}$ + (1 + $env1km_{intrasp}$ | species) + (1 | source)
M19		n = 30,128, $n_{species}$ = 692	species with >= 2 distinct locations + wide intraspecific predictor range (one predictor in top 10% of ranges)	wd ~ 1 + $env5km_{species}$ + $env5km_{intrasp}$ + (1 + $env5km_{intrasp}$ | species) + (1 | source)
M20	**Environmental predictors (tropical / extratropical)**	n = 8,783, $n_{species}$ = 700	species with >= 3 distinct locations in the tropics	wd ~ 1 + $env1km_{species}$ + $env1km_{intrasp}$ + (1 + $env1km_{intrasp}$ | species) + (1 | source)
M21		n = 8,783, $n_{species}$ = 700	species with >= 3 distinct locations in the tropics	wd ~ 1 + $env5km_{species}$ + $env5km_{intrasp}$ + (1 + $env5km_{intrasp}$ | species) + (1 | source)
M22		n = 26,437, $n_{species}$ = 247	species with >= 3 distinct locations outside the tropics	wd ~ 1 + $env1km_{species}$ + $env1km_{intrasp}$ + (1 + $env1km_{intrasp}$ | species) + (1 | source)
M23		n = 26,437, $n_{species}$ = 247	species with >= 3 distinct locations outside the tropics	wd ~ 1 + $env5km_{species}$ + $env5km_{intrasp}$ + (1 + $env5km_{intrasp}$ | species) + (1 | source)
M24	**Environmental predictors (gymnosperms)**	n = 12,089, $n_{species}$ = 59	species with >= 2 distinct locations; gymnosperms only	wd ~ 1 + $env1km_{species}$ + $env1km_{intrasp}$ + (1 + $env1km_{intrasp}$ | species) + (1 | source)
M25		n = 12,089, $n_{species}$ = 59	species with >= 2 distinct locations; gymnosperms only	wd ~ 1 + $env5km_{species}$ + $env5km_{intrasp}$ + (1 + $env5km_{intrasp}$ | species) + (1 | source)
M26	**Predictivity**	variable	full GWDD v.2, but tested on $n_{species}$ = 1,667 (records from >= 5 sources)	wd ~ 1 + (1 | family / genus / species) + (1 | source / site)
M27		variable	full GWDD v.2, but tested on $n_{species}$ = 318 (species with >= 3 sites, one site with >= 4 records)	wd ~ 1 + branch + (1 + branch | family / genus / species) + (1 | source / site)

Table S3: Overview over models and data subsets. This is a quick reference for combinations of data subsets and models used in this study, the questions they address, and the subsetting procedure. Except for models M11-M15, which were fitted with Major Axis regression ("MA regression"), model formulas are provided in the mixed-effects model notation employed by the R packages *lme4* (Bates et al., 2015) and *brms* (Bürkner, 2018) and fitted with both approaches. In the latter, we explicitly modelled the distributional parameter $\sigma^* = \exp(\sigma)$, where σ is the root of residual variance, as σ^* ~ 1 + (1 | species) or σ^* ~ 1 + (1 | family / genus / species), in line with random effects used for the response variable *wd*. The predictor *env1km* is a shorthand for six environmental and edaphic predictors from CHELSA (Brun et al., 2022; Karger et al., 2017) and *soilgrids* at 1km resolution (Hengl et al., 2017), *env5km* for the equivalents from TerraClimate (Abatzoglou et al., 2018) and *soilgrids* (5 km). All environmental and edaphic predictors were split into species means (subscript “species”) and within-species deviations from species means (subscript “intrasp”).

brms/STAN	**M1: Full dataset (incl. source effect)**		**M2: Full dataset (no source effect)**		**M3: High quality subset (incl. source effect)**		**M4: High quality subset (no source effect)**	
Wood density (g cm^{-3})	*Estimate*	*CI*	*Estimate*	*CI*	*Estimate*	*CI*	*Estimate*	*CI*
(Intercept)	0.557	[0.540; 0.575]	0.554	[0.538; 0.569]	0.579	[0.554; 0.605]	0.575	[0.552; 0.599]
Random effects	*Estimate*	*(%Var)*	*Estimate*	*(%Var)*	*Estimate*	*(%Var)*	*Estimate*	*(%Var)*
family	0.098	(30%)	0.098	(32%)	0.067	(17%)	0.065	(17%)
family:genus	0.097	(30%)	0.098	(32%)	0.092	(33%)	0.094	(36%)
family:genus:species	0.074	(17%)	0.077	(20%)	0.077	(23%)	0.079	(26%)
source	0.049	(8%)			0.049	(9%)		
residual (σ)	0.068	(15%)	0.071	(17%)	0.068	(18%)	0.071	(21%)
log(σ)	*Estimate*	*CI*	*Estimate*	*CI*	*Estimate*	*CI*	*Estimate*	*CI*
(Intercept)	-2.796	[-2.830; -2.764]	-2.786	[-2.818; -2.753]	-2.740	[-2.794; -2.686]	-2.727	[-2.780; -2.679]
Random effects	*Estimate*	*(%Var)*	*Estimate*	*(%Var)*	*Estimate*	*(%Var)*	*Estimate*	*(%Var)*
family	0.128	(9%)	0.122	(8%)	0.119	(8%)	0.114	(7%)
family:genus	0.173	(16%)	0.167	(15%)	0.194	(20%)	0.189	(19%)
family:genus:species	0.372	(75%)	0.375	(77%)	0.367	(72%)	0.367	(73%)
Sampling size (N)								
family	249		249		40		40	
family:genus	2576		2576		367		367	
family:genus:species	10780		10780		2735		2735	
source	293				265			
total	79488		79488		49991		49991	

Table S4: Variance components of wood density across the taxonomic hierarchy (brms). Shown are the results of four different random effects models (varying intercept models) fitted with the *brms* R package and the STAN software (Bürkner, 2018; Carpenter et al., 2017). The default model (M1) is fitted to the full set of measurements from individual plants and includes nested random effects for taxonomic groupings (species-level variation nested within genera, genus-level variation nested within families), as well as a crossed random effect for study methodology ("source"). Shown are also a simpler model (M2, no random effect for methodology) and the same two models fitted to a subset of records with higher quality (>= 3 records per species, >= 3 species per genus, >= 3 genera per family, M3 and M4). Throughout, the spread of residuals, σ, is itself modelled as varying between species with a nested random effects structure on log-scales (species within genera, genera within families). For simplicity, we also provide the residual variance on untransformed scales (σ = root of variance of residuals, where residuals are calculated as posterior means). The percentage of total variance explained is provided in brackets next to each variance component (random effects + residual variance). Point estimates are posterior means, intervals 95% credibility intervals, abbreviated as CIs.

lme4	**M1: Full dataset (incl. source effect)**		**M2: Full dataset (no source effect)**		**M3: High quality subset (incl. source effect)**		**M4: High quality subset (no source effect)**	
Wood density (g cm^{-3})	*Estimate*	*CI*	*Estimate*	*CI*	*Estimate*	*CI*	*Estimate*	*CI*
(Intercept)	0.561	[0.544; 0.577]	0.555	[0.540; 0.570]	0.582	[0.557; 0.606]	0.576	[0.553; 0.599]
Random effects	*Estimate*	*(%Var)*	*Estimate*	*(%Var)*	*Estimate*	*(%Var)*	*Estimate*	*(%Var)*
family	0.096	(29%)	0.096	(30%)	0.063	(16%)	0.062	(16%)
family:genus	0.095	(29%)	0.096	(30%)	0.092	(33%)	0.093	(36%)
family:genus:species	0.079	(20%)	0.080	(21%)	0.079	(24%)	0.080	(26%)
source	0.046	(7%)			0.046	(8%)		
residual (σ)	0.071	(16%)	0.074	(18%)	0.069	(19%)	0.073	(22%)
Sampling size (N)								
family	249		249		40		40	
family:genus	2576		2576		367		367	
family:genus:species	10780		10780		2735		2735	
source	293				265			
total	79488		79488		49991		49991	

Table S5: Variance components of wood density across the taxonomic hierarchy (lme4). Same as Table S4, but using reduced maximum likelihood modelling instead of a Bayesian approach (Bates et al., 2015) and not explicitly modelling the residual distribution. Intervals are 95% confidence intervals (Wald method).

brms/STAN	**M5: Minimum quality (incl. source effect)**		**M6: Minimum quality (no source effect)**		**M7: High quality (incl. source effect)**		**M8: High quality (no source effect)**	
Wood density (g cm^{-3})	*Estimate*	*CI*	*Estimate*	*CI*	*Estimate*	*CI*	*Estimate*	*CI*
(Intercept)	0.560	[0.542; 0.578]	0.564	[0.547; 0.582]	0.571	[0.524; 0.615]	0.575	[0.536; 0.610]
Random effects	*Estimate*	*(%Var)*	*Estimate*	*(%Var)*	*Estimate*	*(%Var)*	*Estimate*	*(%Var)*
species	0.098	(72%)	0.101	(78%)	0.100	(58%)	0.104	(70%)
species:site	0.025	(5%)	0.032	(8%)	0.035	(7%)	0.042	(11%)
species:site:idplant	0.017	(2%)	0.017	(2%)	0.028	(5%)	0.028	(5%)
source	0.035	(9%)			0.057	(19%)		
residual	0.040	(12%)	0.040	(12%)	0.045	(12%)	0.045	(13%)
log(σ)	*Estimate*	*CI*	*Estimate*	*CI*	*Estimate*	*CI*	*Estimate*	*CI*
(Intercept)	-3.015	[-3.116; -2.916]	-3.029	[-3.127; -2.929]	-3.049	[-3.233; -2.870]	-3.040	[-3.223; -2.859]
Random effects	*Estimate*		*Estimate*		*Estimate*		*Estimate*	
species	0.588		0.588		0.531		0.538	
Sampling size (N)								
source	95				20			
species	147		147		35		35	
species:site	1270		1270		233		233	
species:site:idplant	14373		14373		1052		1052	
total	19246		19246		2494		2494	

Table S6: Variance components of wood density within species (brms). Shown are the results of four different random effects models fitted with *brms*/STAN (Bates et al., 2015; Carpenter et al., 2017), in order to partition within-species variance. The default model (M5) is fitted to a GWDD v.2 subset with minimum quality requirements (only species with >= 2 sites, at least one site with >= 2 plants, at least one plant with >= 2 records) and includes nested random effects (plant-level variation nested within sites, site-level variation nested within species), as well as a crossed random effect for study methodology ("source"). In addition, a simpler model is presented (M6, no random effect for methodology) and the same two models fitted to a higher quality subset (species with >= 3 sites, at least one site with >= 3 plants, at least one plant with >= 3 records, M7 and M8). As described in Table S3, σ is modelled on log-scales, but residual variance is calculated on the original scales. The percentage of total variance explained is provided in brackets next to each variance component. Point estimates are posterior means, intervals 95% credibility intervals.

lme4	**M5: Minimum quality (incl. source effect)**		**M6: Minimum quality (no source effect)**		**M7: High quality (incl. source effect)**		**M8: High quality (no source effect)**	
Wood density (g cm^{-3})	*Estimate*	*CI*	*Estimate*	*CI*	*Estimate*	*CI*	*Estimate*	*CI*
(Intercept)	0.560	[0.541; 0.579]	0.565	[0.549; 0.581]	0.573	[0.530; 0.615]	0.575	[0.541; 0.608]
Random effects	*Estimate*	*(%Var)*	*Estimate*	*(%Var)*	*Estimate*	*(%Var)*	*Estimate*	*(%Var)*
species	0.094	(64%)	0.097	(68%)	0.092	(50%)	0.096	(58%)
species:site	0.045	(15%)	0.050	(18%)	0.050	(15%)	0.060	(23%)
species:site:idplant	0.018	(2%)	0.018	(2%)	0.028	(5%)	0.028	(5%)
source	0.031	(7%)			0.054	(17%)		
residual	0.041	(12%)	0.041	(12%)	0.047	(13%)	0.047	(14%)
Sampling size (N)								
source	95				20			
species	147		147		35		35	
species:site	1270		1270		233		233	
species:site:idplant	14373		14373		1052		1052	
total	19246		19246		2494		2494	

Table S7: Variance components of wood density within species (lme4). Same as Table S6, but using reduced maximum likelihood modelling instead of a Bayesian approach (Bates et al., 2015) and not explicitly modelling the residual distribution. Intervals are 95% confidence intervals (Wald method).

	M9: Sapwood (brms)		**M9: Sapwood (lme4)**		**M10: Branchwood (brms)**		**M10: Branchwood (lme4)**	
Wood density (g cm^{-3})	*Estimate*	*CI*	*Estimate*	*CI*	*Estimate*	*CI*	*Estimate*	*CI*
(Intercept)	0.572	[0.533; 0.613]	0.575	[0.536; 0.613]	0.601	[0.593; 0.609]	0.603	[0.595; 0.611]
sapwood	-0.001	[-0.028; 0.025]	-0.003	[-0.030; 0.024]				
branch					-0.023	[-0.029; -0.017]	-0.027	[-0.033; -0.021]
Random effects	*Estimate*		*Estimate*		*Estimate*		*Estimate*	
species	0.174		0.174		0.137		0.139	
source	0.035		0.032		0.044		0.045	
sapwood	0.060		0.055					
branch					0.075		0.083	
residual	0.068		0.080		0.065		0.067	
log(σ**)**	*Estimate*	*CI*			*Estimate*	*CI*		
	-2.787	[-2.925; -2.655]			-2.714	[-2.738; -2.690]		
Random effects	*Estimate*				*Estimate*			
species	0.448				0.401			
Sampling size (N)								
source	15		15		529		529	
species	150		150		2018		2018	
total	679		679		48494		48494	

Table S8: Within-plant effects on wood density variation (brms + lme4). Shown are the results of two different mixed effects models (random intercept/random slope models) fitted either with *brms*/STAN software (Bürkner, 2018; Carpenter et al., 2017) or *lme4* (Bates et al., 2015) to explore within-plant variation in wood density. In M9, we model wood density as varying from heartwood to sapwood via a fixed effect for heartwood-sapwood (sapwood == 0 vs. sapwood == 1) as well as random intercepts and slopes at species level and a crossed random effect for study methodology ("source"). M10 has the same model structure, but with a fixed effect and random slopes for the trunkwood-branchwood distinction (branch == 0 vs. branch == 1). In the Bayesian models (*brms*), we also allow the spread of residuals (σ) to vary on log-scales across species. Intervals are 95% credibility/confidence intervals (Wald method for ML estimates).

Model		*Estimate*	*CI*
M11: Sapwood-Heartwood	Intercept	0.160	[0.106; 0.210]
	Slope	0.673	[0.589; 0.764]
			r = 0.78, $n_{species}$ = 150
M12: Branchwood-Trunkwood	Intercept	0.123	[0.100; 0.145]
	Slope	0.757	[0.721; 0.795]
			r = 0.67, $n_{species}$ = 2018
M13: Branchwood-Trunkwood (sapwood only)	Intercept	0.062	[0.020; 0.102]
	Slope	0.871	[0.808; 0.938]
			r = 0.76, $n_{species}$ = 523
M14: Branchwood-Trunkwood (high quality subset)	Intercept	0.070	[0.006; 0.128]
	Slope	0.861	[0.761; 0.972]
			r = 0.76, $n_{species}$ = 189
M15: Branchwood-Trunkwood (individual plants)	Intercept	0.014	[0.004; 0.025]
	Slope	0.988	[0.969; 1.009]
			r = 0.85, n = 3,527, $n_{species}$ = 145

Table S9: Within-plant convergence in wood density (lmodel2). Shown are results from five Major Axis regression models, fitted with the *lmodel2* package in R (Legendre, 2018), to explore whether wood density converges towards sapwood and branchwood. Model M11 regresses mean sapwood densities of 150 species against their mean heartwood densities, Model M12 regresses mean branchwood densities of 2,018 species against their mean trunkwood densities. M13-15 are equivalent to M12, but M13 uses only sapwood measurements from branches and trunks, M14 a high-quality subset of measurements (>= 5 measurements of branches and >= 5 measurements of trunks), and M15 only measurements where both branch and trunk samples have been taken from the same plant, and regresses them at the individual plant instead of the species level. Intervals are parametric 95% confidence intervals.

brms/STAN	**M16: Full dataset CHELSA 1 km**		**M17: Full dataset TerraClimate 5 km**		**M18: High quality subset CHELSA 1 km**		**M19: High quality subset TerraClimate 5 km**	
Wood density (g cm^{-3})	*Estimate*	*CI*	*Estimate*	*CI*	*Estimate*	*CI*	*Estimate*	*CI*
(Intercept)	0.554	[0.544; 0.564]	0.559	[0.548; 0.569]	0.540	[0.526; 0.554]	0.546	[0.532; 0.559]
Temperature (intrasp)	0.012	[0.002; 0.022]	0.003	[-0.007; 0.013]	0.013	[0.001; 0.024]	0.004	[-0.007; 0.015]
Water deficit (intrasp)	0.010	[0.005; 0.015]	0.012	[0.006; 0.018]	0.008	[0.001; 0.014]	0.011	[0.005; 0.018]
Wind speed (intrasp)	-0.003	[-0.007; 0.000]	-0.006	[-0.011; -0.001]	-0.001	[-0.006; 0.003]	-0.003	[-0.008; 0.002]
Sand fraction. (intrasp)	0.003	[-0.002; 0.007]	-0.003	[-0.007; 0.002]	0.006	[0.002; 0.011]	0.004	[-0.001; 0.008]
Soil pH (intrasp)	-0.003	[-0.008; 0.002]	-0.005	[-0.010; -0.000]	-0.002	[-0.008; 0.003]	-0.005	[-0.010; 0.000]
Cat. ex. cap. (intrasp)	0.009	[0.004; 0.013]	0.001	[-0.004; 0.006]	0.003	[-0.002; 0.008]	-0.002	[-0.008; 0.004]
Temperature (species)	0.022	[0.009; 0.034]	0.013	[0.000; 0.025]	0.002	[-0.015; 0.019]	-0.005	[-0.024; 0.012]
Water deficit (species)	0.038	[0.027; 0.048]	0.036	[0.025; 0.047]	0.045	[0.027; 0.062]	0.042	[0.026; 0.058]
Wind speed (species)	-0.017	[-0.027; -0.007]	-0.013	[-0.022; -0.004]	-0.021	[-0.038; -0.003]	-0.016	[-0.032; -0.001]
Sand fraction. (species)	0.002	[-0.008; 0.012]	-0.000	[-0.010; 0.011]	-0.008	[-0.025; 0.010]	-0.008	[-0.025; 0.010]
Soil pH (species)	-0.013	[-0.024; -0.001]	-0.014	[-0.028; -0.001]	-0.010	[-0.029; 0.008]	-0.018	[-0.038; 0.002]
Cat. ex. cap. (species)	0.020	[0.008; 0.032]	0.001	[-0.010; 0.012]	0.012	[-0.005; 0.030]	-0.001	[-0.017; 0.016]
Random effects	*Estimate*		*Estimate*		*Estimate*		*Estimate*	
species	0.114		0.114		0.112		0.112	
source	0.051		0.051		0.053		0.052	
Temperature (intrasp)	0.058		0.061		0.060		0.059	
Water deficit (intrasp)	0.038		0.032		0.039		0.033	
Wind speed (intrasp)	0.019		0.025		0.022		0.025	
Sand fraction. (intrasp)	0.029		0.033		0.018		0.019	
Soil pH (intrasp)	0.035		0.030		0.029		0.024	
Cat. ex. cap. (intrasp)	0.024		0.031		0.021		0.032	
residual	0.062		0.062		0.054		0.055	
log(σ)	*Estimate*	*CI*	*Estimate*	*CI*	*Estimate*	*CI*	*Estimate*	*CI*
(Intercept)	-2.772	[-2.802; -2.743]	-2.766	[-2.796; -2.736]	-2.860	[-2.906; -2.814]	-2.854	[-2.902; -2.808]
Random effects	*Estimate*		*Estimate*		*Estimate*		*Estimate*	
species	0.497		0.500		0.463		0.468	

Sampling size (N)				
source	366	366	338	338
species	2160	2160	692	692
total	41879	41893	30128	30128

Table S10: Environmental predictors of wood density variation (brms). Shown are the results of four different mixed effects models (varying intercept/varying slope models) fitted with *brms*/STAN software (Bürkner, 2018; Carpenter et al., 2017) to explore environmental predictors of wood density variation within and across species. All models have the same structure, relying on three environmental predictors (annual means of temperature, water deficit, and wind speed) and three edaphic predictors (mean sand content, mean pH, mean cation exchange capacity). All six predictors are standardized (scaled) and split into species mean values (indicated by "species") and within-species deviations from the species means (indicated by "intrasp"). Species are allowed to vary both in their intercept and in their within-species effects (varying slopes). In addition, we include a crossed random effect for the measurement source/methodology, and allow the distributional parameter σ to vary across species. M16 and M17 are fitted to all species in the GWDD v.2 with wood density records from at least two distinct geographic locations (explicit coordinates), but differ in their environmental layers and scale of aggregation: M16 uses 1 km resolution data from CHELSA (Brun et al., 2022; Karger et al., 2017) and *soilgrids* predictions pre-aggregated at 1 km (Hengl et al., 2017). M17 uses ~4-5 km resolution data from TerraClimate (Abatzoglou et al., 2018) in conjunction with pre-aggregated 5 km *soilgrids* data. M18 and M19 use the same model structures, but restrict wood density records to species that display large within-species environmental or edaphic gradients, including only species for which the range of at least one environmental or edaphic predictor is in the top 10% of all species' ranges for that predictor. Point estimates are posterior means, intervals 95% credibility intervals. A visualization of effect sizes can be found in Figures S7-8.

lme4	**M16: Full dataset CHELSA 1 km**		**M17: Full dataset TerraClimate 5 km**		**M18: High quality subset CHELSA 1 km**		**M19: High quality subset TerraClimate 5 km**	
Wood density (g cm^{-3})	*Estimate*	*CI*	*Estimate*	*CI*	*Estimate*	*CI*	*Estimate*	*CI*
(Intercept)	0.555	[0.545; 0.565]	0.559	[0.548; 0.569]	0.540	[0.526; 0.554]	0.544	[0.530; 0.558]
Temperature (intrasp)	0.013	[0.002; 0.024]	0.001	[-0.009; 0.012]	0.014	[0.002; 0.026]	0.002	[-0.010; 0.014]
Water deficit (intrasp)	0.010	[0.004; 0.015]	0.014	[0.007; 0.021]	0.007	[0.000; 0.014]	0.012	[0.004; 0.021]
Wind speed (intrasp)	-0.003	[-0.007; 0.000]	-0.008	[-0.013; -0.004]	-0.002	[-0.007; 0.003]	-0.005	[-0.011; 0.001]
Sand fraction. (intrasp)	0.004	[-0.002; 0.009]	-0.004	[-0.010; 0.002]	0.010	[0.004; 0.016]	0.002	[-0.005; 0.009]
Soil pH (intrasp)	-0.005	[-0.011; 0.001]	-0.007	[-0.013; -0.001]	-0.001	[-0.007; 0.005]	-0.005	[-0.012; 0.001]
Cat. ex. cap. (intrasp)	0.012	[0.007; 0.017]	0.003	[-0.003; 0.009]	0.006	[0.001; 0.011]	-0.000	[-0.007; 0.006]
Temperature (species)	0.022	[0.010; 0.035]	0.013	[0.000; 0.025]	0.003	[-0.014; 0.020]	-0.005	[-0.023; 0.013]
Water deficit (species)	0.038	[0.027; 0.048]	0.035	[0.024; 0.046]	0.044	[0.026; 0.062]	0.042	[0.027; 0.058]
Wind speed (species)	-0.018	[-0.028; -0.009]	-0.015	[-0.023; -0.006]	-0.021	[-0.039; -0.004]	-0.016	[-0.031; -0.001]
Sand fraction. (species)	0.005	[-0.005; 0.016]	0.002	[-0.009; 0.013]	-0.004	[-0.021; 0.014]	-0.007	[-0.025; 0.011]
Soil pH (species)	-0.012	[-0.024; -0.000]	-0.013	[-0.026; 0.000]	-0.008	[-0.027; 0.010]	-0.016	[-0.036; 0.004]
Cat. ex. cap. (species)	0.022	[0.010; 0.033]	0.002	[-0.009; 0.014]	0.015	[-0.003; 0.032]	0.001	[-0.016; 0.018]
Random effects	*Estimate*		*Estimate*		*Estimate*		*Estimate*	
species	0.116		0.116		0.113		0.113	
source	0.048		0.048		0.053		0.053	
Temperature (intrasp)	0.067		0.068		0.063		0.064	
Water deficit (intrasp)	0.052		0.048		0.044		0.048	
Wind speed (intrasp)	0.020		0.026		0.028		0.028	
Sand fraction. (intrasp)	0.047		0.054		0.036		0.042	
Soil pH (intrasp)	0.051		0.045		0.034		0.039	
Cat. ex. cap. (intrasp)	0.027		0.038		0.024		0.037	
residual	0.063		0.064		0.055		0.055	
Sampling size (N)								
source	366		366		338		338	
species	2160		2160		692		692	
total	41879		41893		30128		30128	

Table S11: Environmental predictors of wood density variation (lme4). Same as Table S10, but using reduced maximum likelihood modelling instead of a Bayesian approach (Bates et al., 2015) and not explicitly modelling the residual distribution. Intervals are 95% confidence intervals (Wald method).

brms/STAN	**M20: Tropical species CHELSA 1 km**		**M21: Tropical species TerraClimate 5 km**		**M22: Extratropical species CHELSA 1 km**		**M23: Extratropical species TerraClimate 5 km**	
Wood density (g cm^{-3})	*Estimate*	*CI*	*Estimate*	*CI*	*Estimate*	*CI*	*Estimate*	*CI*
(Intercept)	0.528	[0.475; 0.582]	0.517	[0.467; 0.568]	0.569	[0.549; 0.588]	0.561	[0.540; 0.581]
Temperature (intrasp)	0.013	[-0.006; 0.032]	-0.000	[-0.019; 0.018]	0.016	[0.002; 0.030]	0.006	[-0.009; 0.021]
Water deficit (intrasp)	0.012	[0.004; 0.021]	0.021	[0.008; 0.034]	0.001	[-0.007; 0.009]	0.011	[0.003; 0.020]
Wind speed (intrasp)	-0.004	[-0.011; 0.003]	-0.021	[-0.031; -0.011]	0.002	[-0.003; 0.007]	0.004	[-0.001; 0.010]
Sand fraction. (intrasp)	0.004	[-0.005; 0.014]	-0.009	[-0.019; 0.001]	0.004	[0.001; 0.007]	0.002	[-0.001; 0.006]
Soil pH (intrasp)	-0.013	[-0.021; -0.004]	-0.012	[-0.023; -0.002]	0.001	[-0.004; 0.006]	-0.004	[-0.009; 0.001]
Cat. ex. cap. (intrasp)	0.019	[0.010; 0.029]	-0.003	[-0.014; 0.008]	0.001	[-0.004; 0.005]	-0.002	[-0.008; 0.003]
Temperature (species)	0.022	[-0.030; 0.072]	-0.010	[-0.056; 0.036]	0.043	[0.022; 0.064]	0.042	[0.020; 0.065]
Water deficit (species)	0.059	[0.038; 0.080]	0.078	[0.051; 0.104]	0.033	[0.009; 0.056]	0.027	[0.010; 0.045]
Wind speed (species)	-0.033	[-0.056; -0.010]	-0.049	[-0.068; -0.029]	0.001	[-0.018; 0.020]	0.015	[-0.004; 0.035]
Sand fraction. (species)	0.013	[-0.017; 0.042]	-0.009	[-0.039; 0.022]	-0.007	[-0.025; 0.011]	-0.013	[-0.031; 0.005]
Soil pH (species)	-0.031	[-0.055; -0.007]	-0.048	[-0.079; -0.017]	-0.015	[-0.041; 0.011]	-0.010	[-0.033; 0.013]
Cat. ex. cap. (species)	0.027	[-0.001; 0.056]	-0.021	[-0.051; 0.009]	0.008	[-0.009; 0.025]	0.003	[-0.014; 0.021]
Random effects	*Estimate*		*Estimate*		*Estimate*		*Estimate*	
species	0.122		0.121		0.088		0.087	
source	0.048		0.049		0.054		0.052	
Temperature (intrasp)	0.049		0.049		0.065		0.075	
Water deficit (intrasp)	0.038		0.044		0.037		0.034	
Wind speed (intrasp)	0.012		0.029		0.020		0.023	
Sand fraction. (intrasp)	0.044		0.051		0.010		0.011	
Soil pH (intrasp)	0.043		0.043		0.020		0.018	
Cat. ex. cap. (intrasp)	0.034		0.045		0.016		0.023	
residual	0.085		0.085		0.049		0.049	
log(σ)	*Estimate*	*CI*	*Estimate*	*CI*	*Estimate*	*CI*	*Estimate*	*CI*
(Intercept)	-2.603	[-2.645; -2.561]	-2.599	[-2.643; -2.557]	-3.130	[-3.195; -3.068]	-3.129	[-3.192; -3.065]
Random effects	*Estimate*		*Estimate*		*Estimate*		*Estimate*	
species	0.437		0.442		0.415		0.416	

Sampling size (N)				
source	140	140	253	253
species	700	700	247	247
total	8783	8783	26437	26439

Table S12: Environmental predictors of wood density variation, in and outside of tropics (brms). Same as Table S10, but splitting the original data set into tropical species (>= 3 occurrences in the GWDD v.2 between 23.5 N and 23.5 S) and extratropical species (>= 3 occurrences outside of 23.5 N and 23.5 S). Point estimates are posterior means, intervals 95% credibility intervals. A visualization of effect sizes can be found in Figures S9-10.

lme4	**M20: Tropical species CHELSA 1 km**		**M21: Tropical species TerraClimate 5 km**		**M22: Extratropical species CHELSA 1 km**		**M23: Extratropical species TerraClimate 5 km**	
Wood density (g cm^{-3})	*Estimate*	*CI*	*Estimate*	*CI*	*Estimate*	*CI*	*Estimate*	*CI*
(Intercept)	0.520	[0.466; 0.574]	0.515	[0.464; 0.567]	0.568	[0.549; 0.588]	0.560	[0.540; 0.580]
Temperature (intrasp)	0.022	[0.002; 0.042]	-0.003	[-0.022; 0.016]	0.017	[0.003; 0.030]	0.004	[-0.012; 0.019]
Water deficit (intrasp)	0.009	[0.001; 0.018]	0.020	[0.007; 0.033]	0.001	[-0.007; 0.009]	0.014	[0.006; 0.022]
Wind speed (intrasp)	-0.001	[-0.008; 0.006]	-0.017	[-0.027; -0.007]	0.002	[-0.002; 0.007]	0.005	[-0.001; 0.010]
Sand fraction. (intrasp)	0.005	[-0.005; 0.014]	-0.009	[-0.019; 0.001]	0.004	[0.000; 0.007]	0.002	[-0.001; 0.005]
Soil pH (intrasp)	-0.014	[-0.023; -0.006]	-0.015	[-0.026; -0.004]	0.002	[-0.003; 0.007]	-0.004	[-0.008; 0.000]
Cat. ex. cap. (intrasp)	0.021	[0.012; 0.030]	-0.002	[-0.013; 0.009]	0.001	[-0.003; 0.005]	-0.002	[-0.007; 0.004]
Temperature (species)	0.034	[-0.018; 0.085]	-0.008	[-0.055; 0.039]	0.043	[0.023; 0.063]	0.042	[0.020; 0.064]
Water deficit (species)	0.059	[0.037; 0.080]	0.079	[0.052; 0.106]	0.035	[0.011; 0.059]	0.028	[0.011; 0.045]
Wind speed (species)	-0.031	[-0.054; -0.007]	-0.049	[-0.068; -0.029]	0.001	[-0.018; 0.020]	0.015	[-0.004; 0.034]
Sand fraction. (species)	0.015	[-0.016; 0.045]	-0.007	[-0.037; 0.024]	-0.006	[-0.023; 0.011]	-0.012	[-0.030; 0.005]
Soil pH (species)	-0.033	[-0.057; -0.009]	-0.050	[-0.081; -0.019]	-0.016	[-0.042; 0.010]	-0.010	[-0.033; 0.012]
Cat. ex. cap. (species)	0.032	[0.003; 0.062]	-0.018	[-0.048; 0.012]	0.011	[-0.007; 0.029]	0.004	[-0.013; 0.022]
Random effects	*Estimate*		*Estimate*		*Estimate*		*Estimate*	
species	0.121		0.119		0.087		0.086	
source	0.045		0.047		0.053		0.051	
Temperature (intrasp)	0.030		0.029		0.059		0.074	
Water deficit (intrasp)	0.037		0.041		0.036		0.032	
Wind speed (intrasp)	0.013		0.020		0.019		0.020	
Sand fraction. (intrasp)	0.043		0.050		0.012		0.010	
Soil pH (intrasp)	0.037		0.037		0.018		0.014	
Cat. ex. cap. (intrasp)	0.011		0.031		0.014		0.023	
residual	0.092		0.093		0.050		0.050	
Sampling size (N)								
source	140		140		253		253	
species	700		700		247		247	
total	8783		8783		26437		26439	

Table S13: Environmental predictors of wood density variation, in and outside of tropics (lme4). Same as Table S12, but using reduced maximum likelihood modelling instead of a Bayesian approach (Bates et al., 2015) and not explicitly modelling the residual distribution. Intervals are 95% confidence intervals (Wald method).

	M24: Gymnosperms CHELSA 1 km (brms)		**M24: Gymnosperms CHELSA 1 km** (lme4)		**M25: Gymnosperms TerraClimate 5 km** (brms)		**M25: Gymnosperms TerraClimate 5 km** (lme4)	
Wood density (g cm^{-3})	*Estimate*	*CI*	*Estimate*	*CI*	*Estimate*	*CI*	*Estimate*	*CI*
(Intercept)	0.476	[0.452; 0.499]	0.477	[0.457; 0.497]	0.471	[0.447; 0.494]	0.469	[0.449; 0.489]
Temperature (intrasp)	0.021	[-0.008; 0.047]	0.035	[0.013; 0.057]	-0.001	[-0.042; 0.036]	-0.011	[-0.052; 0.030]
Water deficit (intrasp)	-0.008	[-0.025; 0.009]	-0.011	[-0.028; 0.005]	0.014	[-0.008; 0.036]	0.022	[0.005; 0.040]
Wind speed (intrasp)	0.010	[0.002; 0.021]	0.013	[0.004; 0.022]	0.006	[-0.005; 0.018]	0.006	[-0.004; 0.016]
Sand fraction. (intrasp)	0.000	[-0.007; 0.007]	-0.003	[-0.011; 0.004]	0.002	[-0.006; 0.009]	0.001	[-0.007; 0.008]
Soil pH (intrasp)	-0.010	[-0.022; 0.002]	-0.012	[-0.021; -0.003]	-0.015	[-0.027; -0.005]	-0.015	[-0.022; -0.007]
Cat. ex. cap. (intrasp)	0.005	[-0.005; 0.015]	0.003	[-0.006; 0.012]	0.002	[-0.007; 0.012]	0.003	[-0.007; 0.012]
Temperature (species)	0.004	[-0.019; 0.029]	-0.002	[-0.022; 0.019]	-0.006	[-0.032; 0.021]	-0.000	[-0.022; 0.021]
Water deficit (species)	0.034	[-0.001; 0.068]	0.041	[0.013; 0.068]	0.041	[0.008; 0.073]	0.036	[0.009; 0.064]
Wind speed (species)	-0.012	[-0.039; 0.015]	-0.016	[-0.038; 0.007]	-0.003	[-0.026; 0.020]	0.007	[-0.012; 0.027]
Sand fraction. (species)	-0.002	[-0.028; 0.023]	-0.015	[-0.031; 0.001]	0.005	[-0.018; 0.028]	0.004	[-0.014; 0.023]
Soil pH (species)	-0.005	[-0.035; 0.025]	-0.013	[-0.034; 0.009]	-0.006	[-0.037; 0.025]	-0.002	[-0.026; 0.022]
Cat. ex. cap. (species)	-0.001	[-0.027; 0.024]	-0.006	[-0.025; 0.014]	-0.010	[-0.035; 0.014]	-0.009	[-0.027; 0.010]
Random effects	*Estimate*		*Estimate*		*Estimate*		*Estimate*	
species	0.052		0.049		0.050		0.049	
source	0.053		0.054		0.052		0.052	
Temperature (intrasp)	0.051		0.046		0.087		0.106	
Water deficit (intrasp)	0.033		0.036		0.038		0.043	
Wind speed (intrasp)	0.016		0.023		0.018		0.022	
Sand fraction. (intrasp)	0.012		0.015		0.012		0.015	
Soil pH (intrasp)	0.020		0.021		0.017		0.012	
Cat. ex. cap. (intrasp)	0.015		0.020		0.014		0.019	
residual	0.050		0.050		0.050		0.051	
log(σ)	*Estimate*	*CI*			*Estimate*	*CI*		
(Intercept)	-3.041	[-3.166; -2.920]			-3.031	[-3.155; -2.905]		
Random effects	*Estimate*				*Estimate*			
species	0.417				0.424			

Sampling size (N)				
source	159	159	159	159
species	59	59	59	59
total	12089	12089	12089	12089

Table S14: Environmental predictors of wood density variation in gymnosperms (brms + lme4). Same as Tables S10-13, but with predictions only for gymnosperms. Shown are both models fits with the *brms* package and with *lme4*. Intervals are 95% credibility/confidence intervals (Wald method for ML estimates). Note how most effects are weak and overlap with 0. A visualization of effect sizes can be found in Figure S11.

brms/STAN	**M20: Tropical species CHELSA 1 km**		**M21: Tropical species TerraClimate 5 km**		**M22: Extratropical species CHELSA 1 km**		**M23: Extratropical species TerraClimate 5 km**	
Wood density (g cm^{-3})	*Estimate (original)*	*Estimate (rescaled)*	*Estimate (original)*	*Estimate (rescaled)*	*Estimate (original)*	*Estimate (rescaled)*	*Estimate (original)*	*Estimate (rescaled)*
Temperature (intrasp)	0.014	0.003	0.001	0.000	0.017	0.005	0.006	0.002
Water deficit (intrasp)	0.012	0.008	0.021	0.010	0.001	0.000	0.012	0.005
Wind speed (intrasp)	-0.003	-0.002	-0.020	-0.009	0.002	0.001	0.004	0.002
Sand fraction. (intrasp)	0.005	0.002	-0.008	-0.003	0.004	0.003	0.002	0.002
Soil pH (intrasp)	-0.012	-0.006	-0.012	-0.006	0.001	0.001	-0.004	-0.002
Cat. ex. cap. (intrasp)	0.019	0.008	-0.003	-0.001	0.001	0.001	-0.002	-0.001
Temperature (species)	0.030	0.033	-0.004	-0.005	0.045	0.041	0.045	0.041
Water deficit (species)	0.057	0.049	0.078	0.055	0.032	0.024	0.026	0.023
Wind speed (species)	-0.031	-0.029	-0.047	-0.053	0.003	0.002	0.016	0.011
Sand fraction. (species)	0.017	0.009	-0.005	-0.003	-0.006	-0.005	-0.012	-0.009
Soil pH (species)	-0.031	-0.024	-0.048	-0.037	-0.014	-0.012	-0.009	-0.007
Cat. ex. cap. (species)	0.031	0.020	-0.017	-0.011	0.009	0.008	0.004	0.004

Table S15: Rescaled environmental effect sizes, in and outside of tropics (brms). Same as fixed effects shown in Table S12, but extended to include separately rescaled estimates of within-species and among-species effects. Rescaling was carried out by calculating average within-species and among-species standard deviations for each predictor and then multiplying effect sizes with these standard deviations. The rescaled effect sizes thus correspond to the effect sizes one might observe across a species actual range.

Database	*Method*	*samples for prediction*	*RMSE* *(g cm^{-3})*	*R^2*	*$n_{species}$*
GWDD v.2	**Wood density means**	0 / genus	0.083	0.640	1557
		1	0.084	0.730	1667
		2	0.056	0.860	1667
	M26: Hierarchical model	0 / genus	0.071	0.710	1557
		1	0.053	0.840	1667
		2	0.043	0.900	1667
	M27: Hierarchical model branch & trunk	0 / genus	0.060	0.730	1557
		1	0.046	0.840	1667
		2	0.038	0.900	1667
GWDD v.1	**Wood density means**	0 / genus	0.098	0.620	1447
		1	0.095	0.740	1580
		2	0.069	0.840	1312

Table S16: Quality of wood density predictions at the species level. Shown is to what extent the wood density of 1,667 species (all well-sampled in the GWDD v.2, with records from >= 5 sources) can be estimated when only a limited number of wood density measurements are available (0, 1 or 2). The baseline approach is to estimate species-level wood density from simple wood density means, either at genus level (0 samples) or averaging across the provided 1-2 samples. Shown are also two alternative hierarchical modelling approaches: M26, which is a simple random effects model, with a nested taxonomic structure plus extra random effects for study and measurement location (cf. Table S3), as well as M27, which extends M26 with a fixed effect for the trunkwood-branchwood distinction. Both models were refitted three times for each species, using both the local species-specific samples (0, 1, 2) and the remainder of the GWDD v.2. To reduce the computational burden, we used only the *lme4* package. Summary statistics of predictive power are the mean absolute error (MAE, g cm^{-3}), root mean square error (RMSE, g cm^{-3}) and R^2, calculated with reference to estimates based on a full set of measurements (>= 5 sources). A comparison with the GWDD v.1 is provided for completeness, again taking the GWDD v.2 values as reference. We note that in some cases, species were either not available for prediction (i.e., not recorded in GWDD v.1), or were the sole species in their genus, which also removed them from predictions at genus level.

		RMSE (g cm^{-3})				***R^2***			
		Number of local samples				*Number of local samples*			
Model	***Extent***	0	1	2	3	0	1	2	3
Species means	Global	0.089	0.088	0.087	0.086	0.690	0.700	0.710	0.710
	Study	0.093	0.091	0.087	0.086	0.660	0.680	0.710	0.710
	Local		0.107	0.085	0.082		0.590	0.720	0.740
M26: Hierarchical model	Global	0.088	0.086	0.085	0.084	0.700	0.710	0.720	0.730
M27: Hierarchical model (branch & trunk)	Global	0.087	0.086	0.084	0.083	0.710	0.710	0.730	0.730

Table S17: Quality of wood density predictions at the individual plant level. Shown is the predictive power of the same models as in Table S16, but now applied to predict individual-level wood density and tested at well-sampled sites from well-sampled studies (only species and studies with >= 3 locations per study and >= 4 measurements per site, $n_{species}$ = 318). For each approach, we show how well it is able to predict an individual wood density measurement when 0, 1, 2, or 3 measurements from the same locality and the same study (identical measurement methodology) are available. The baseline is provided by simple species means, calculated in three ways: 1/ using a combination of the 0, 1, 2, or 3 local samples and all measurements from elsewhere in the GWDD v.2 (“Global”), 2/ using a combination of the 0, 1, 2, or 3 local samples and all samples measured as part of the same study (“Study”), or 3/ using only the 0, 1, 2, or 3 local samples (“Local”). This is compared to two hierarchical modelling approaches (M26, M27) that model wood density with a nested taxonomic hierarchy as well as crossed random effects for study methodology and study site, thus implicitly adjusting predictions for methodological biases and local wood density shifts. Note that, assuming that within-species wood density variation is distributed with sd = 0.068 g cm^{-3}, we would expect an RMSE = 0.096 g cm^{-3}, i.e., sqrt(2 * 0.068^2) when predicting a single tree’s wood density from another tree with no other knowledge about measurement location or the type of tissue sampled. The hierarchical models clearly outperform this expectation (RMSE = 0.086 g cm^{-3}).

C) Figures

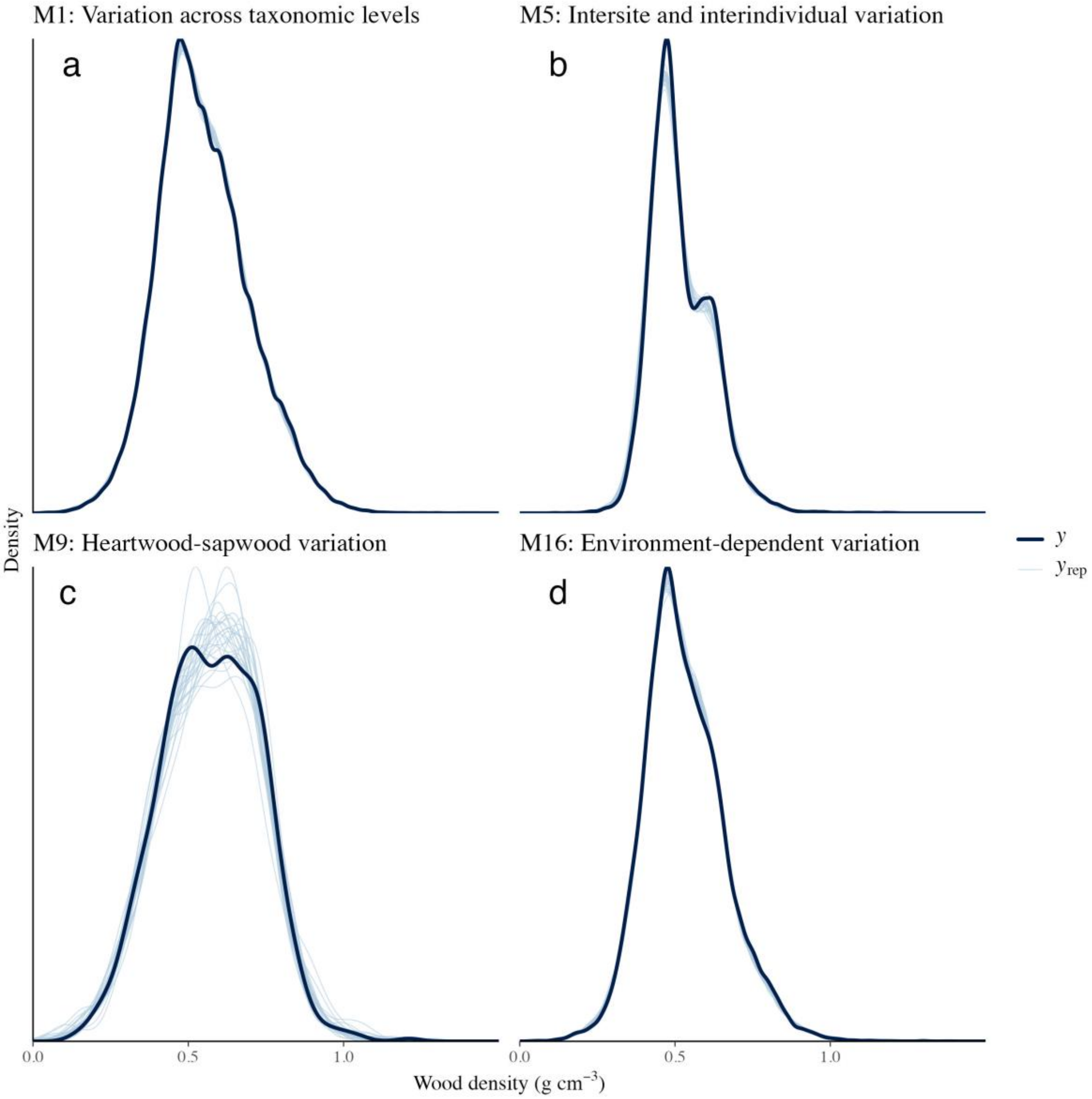


Fig. S1: Sample posterior predictive checks. Shown are posterior predictive checks for four of the models described in Table S3, using the default pp_check() function from the package *brms*. The black lines describe the distribution of wood density values for each of the Global Wood Density Database (GWDD) v.2 subsets used in models M1, M5, M9 and M16, the blue lines describe the modelled posterior densities from 10 random posterior draws. All model fits successfully reproduced the data distribution, with no deviations in models M1 and M16 (panels a, d), a negligible underestimation of the mode in model M5 (panel c) and some uncertainty, though no bias, in model M9 (panel c).

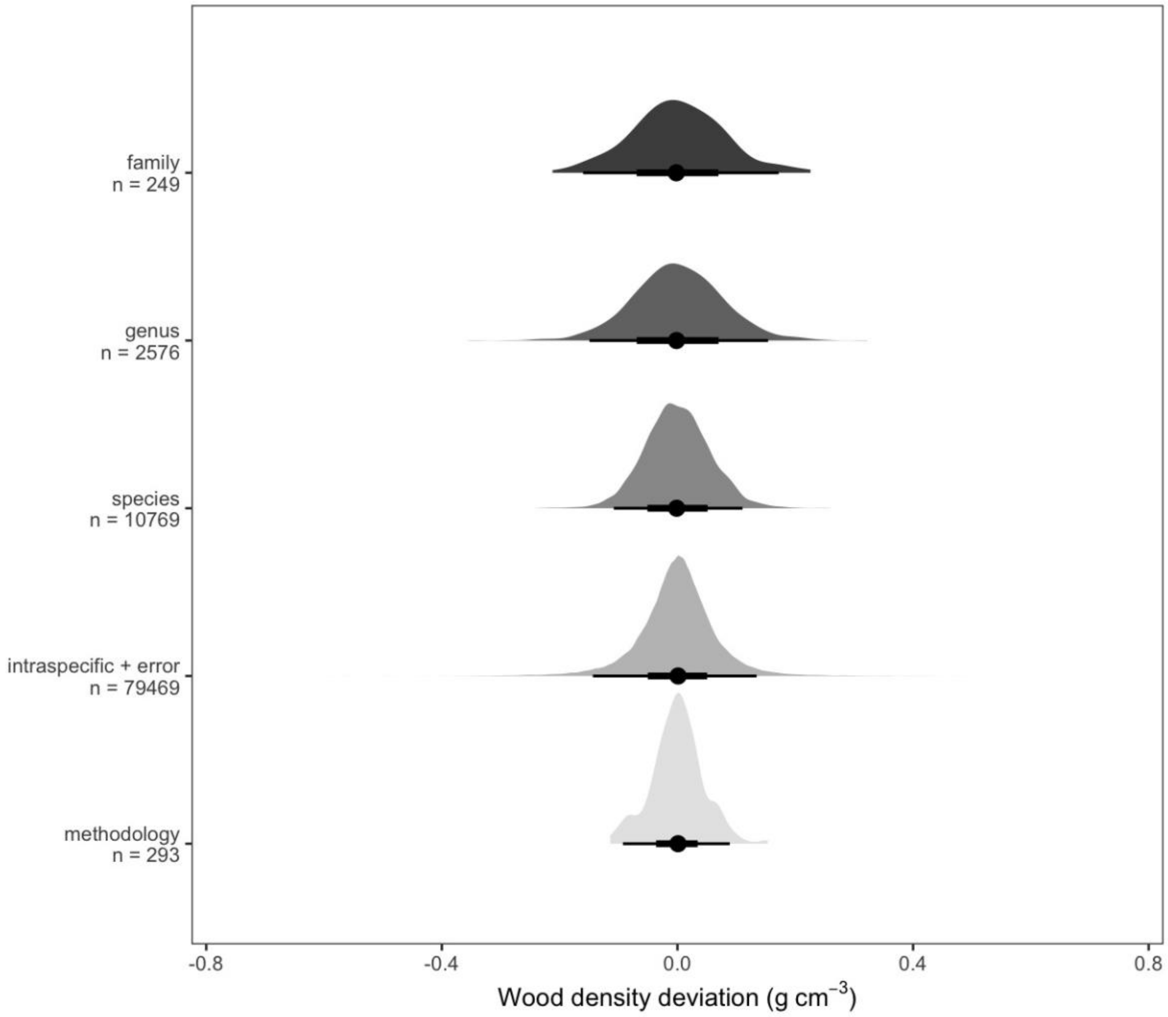


Fig. S2: Variance components estimated from a Bayesian hierarchical model. Shown are the different variance components as estimated from a Bayesian hierarchical model (M1 in Table S3). Shown are the nested random effects at family, genus and species level, as well as residual variation (intraspecific variation + error). We explicitly modelled residual variance to assess the consistency of intraspecific variation, and also included a crossed random effect for methodology (i.e., the study where values were obtained from). The figure shows that variation at family and genus level is much larger than species-level or intraspecific variation, and that these are again larger than methodological effects. Note that the residuals (intraspecific variation + error) are overdispersed compared to a normal distribution, with a large number of outliers. Throughout, black dots indicate the median effect size and black intervals quantile ranges (66% and 95%).

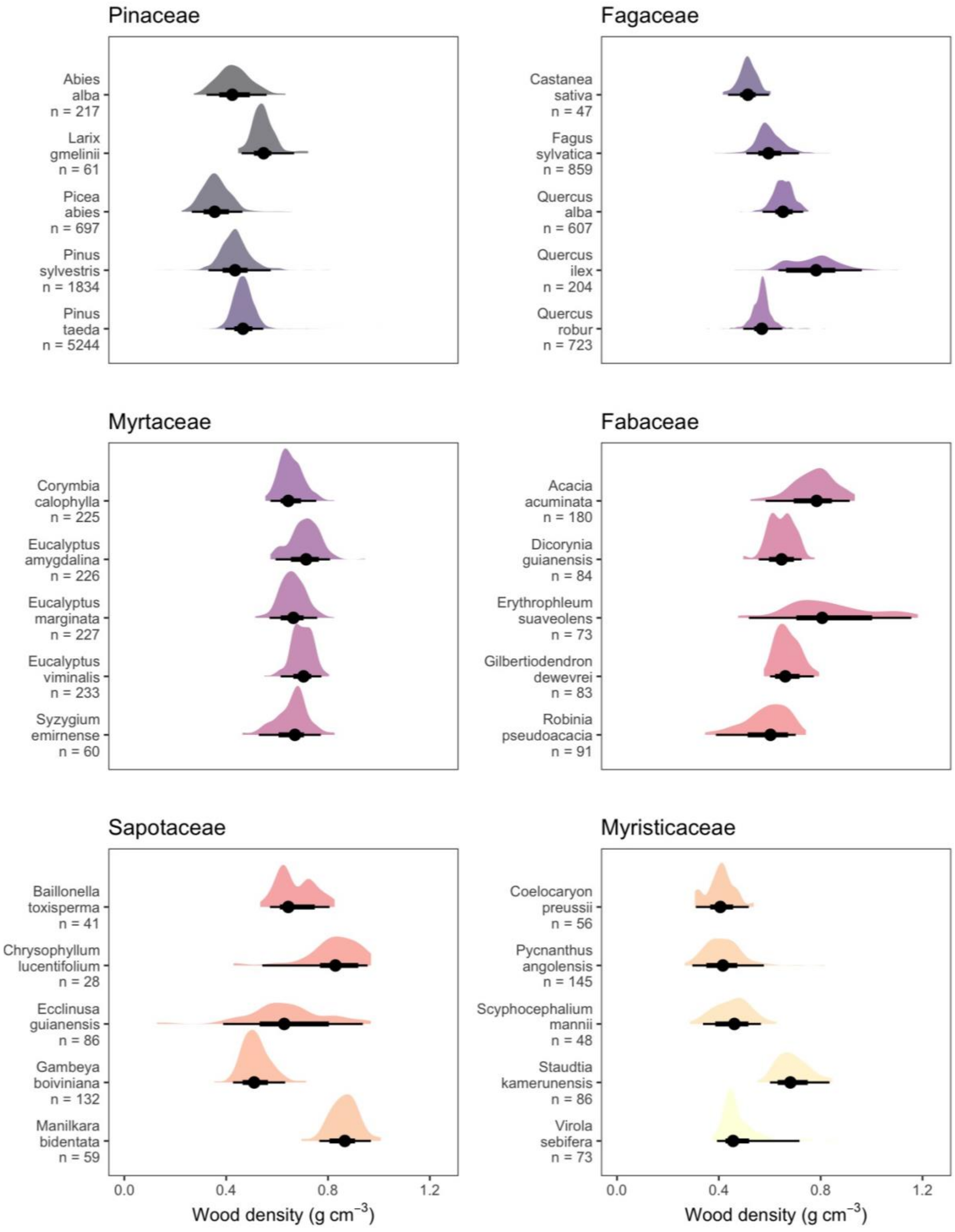


Fig. S3: Intraspecific variation in selected species from six plant families. Shown are estimated intraspecific wood density distributions for selected taxa, based on predictions from model M1 (Table S3). All values are based on wood density residuals, but have been corrected for methodological biases by subtracting study effects (cf. Fig. S2 and Table S4). Throughout, black dots indicate the median effect size and black intervals quantile ranges (66% and 95%). Sample size (n) is provided for each species.

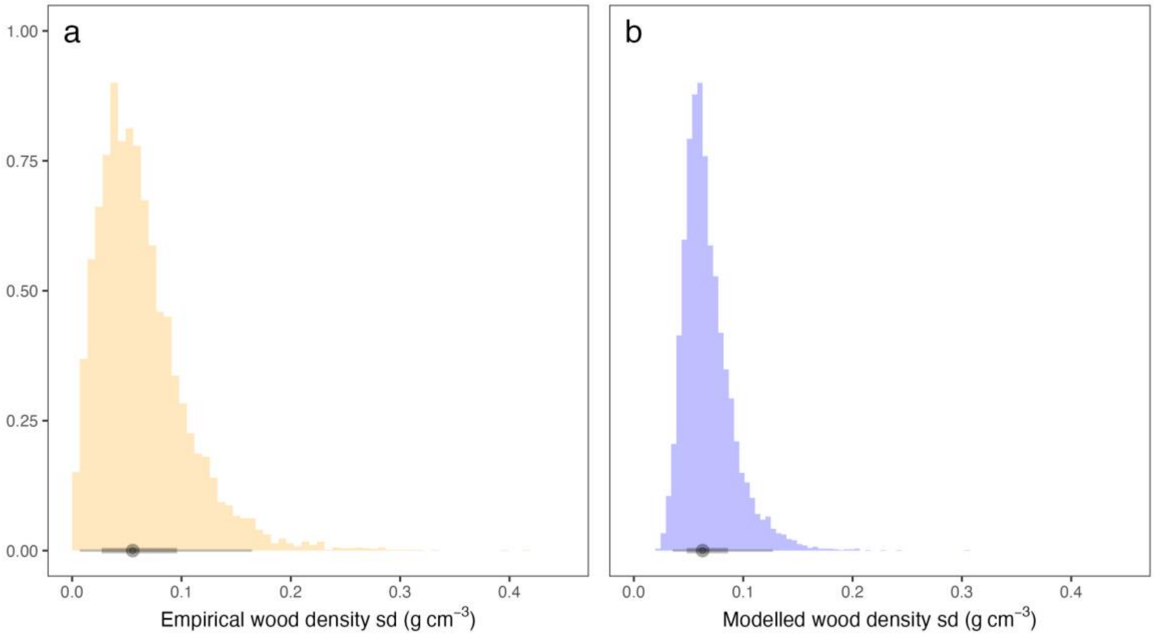


Fig. S4: Consistency of the extent of intraspecific variation across taxa. Shown is the distribution of empirical within-species standard deviations (sd) of wood density across all species with more than one plant-level record (a, $n_{species}$ = 6,361), as well as the distribution of inferred standard deviations (or σ) across the same species (b). The black dot indicates the median, the black intervals the corresponding quantile ranges (66% and 95%). Note that both follow approximately lognormal distributions, but the empirical standard deviations have a wider distribution. This is expected, as they include many species with low sample sizes (e.g. 2-3 measurements), which the modelled distribution corrects for.

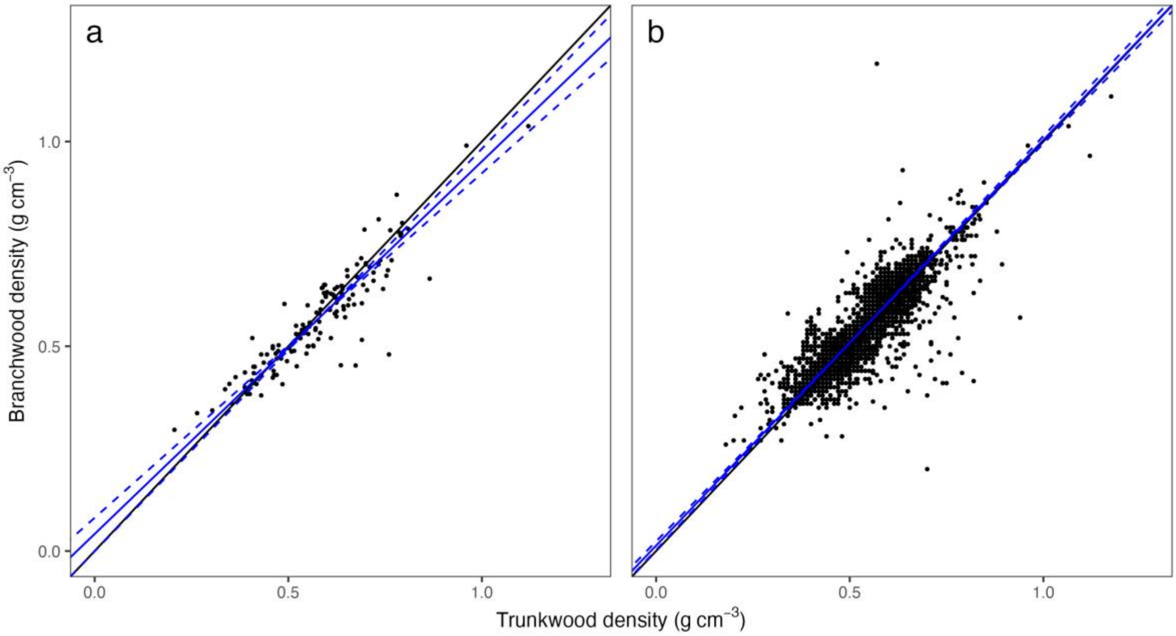


Fig. S5: Wood density variation between trunkwood and branchwood, high quality regressions. Shown is the same graph as in Fig. 3 (panels b and c), but for a subset of records where branch and trunk samples have been taken from the same individuals. Panel a) shows species mean values for both trunkwood and branchwood, panel b) shows each plant's mean trunkwood density and mean branchwood density. Blue lines are Major Axis regression lines, dashed lines the 95% CI. Note how the convergence observed in panel a) and in Fig. 3 disappears in panel b).

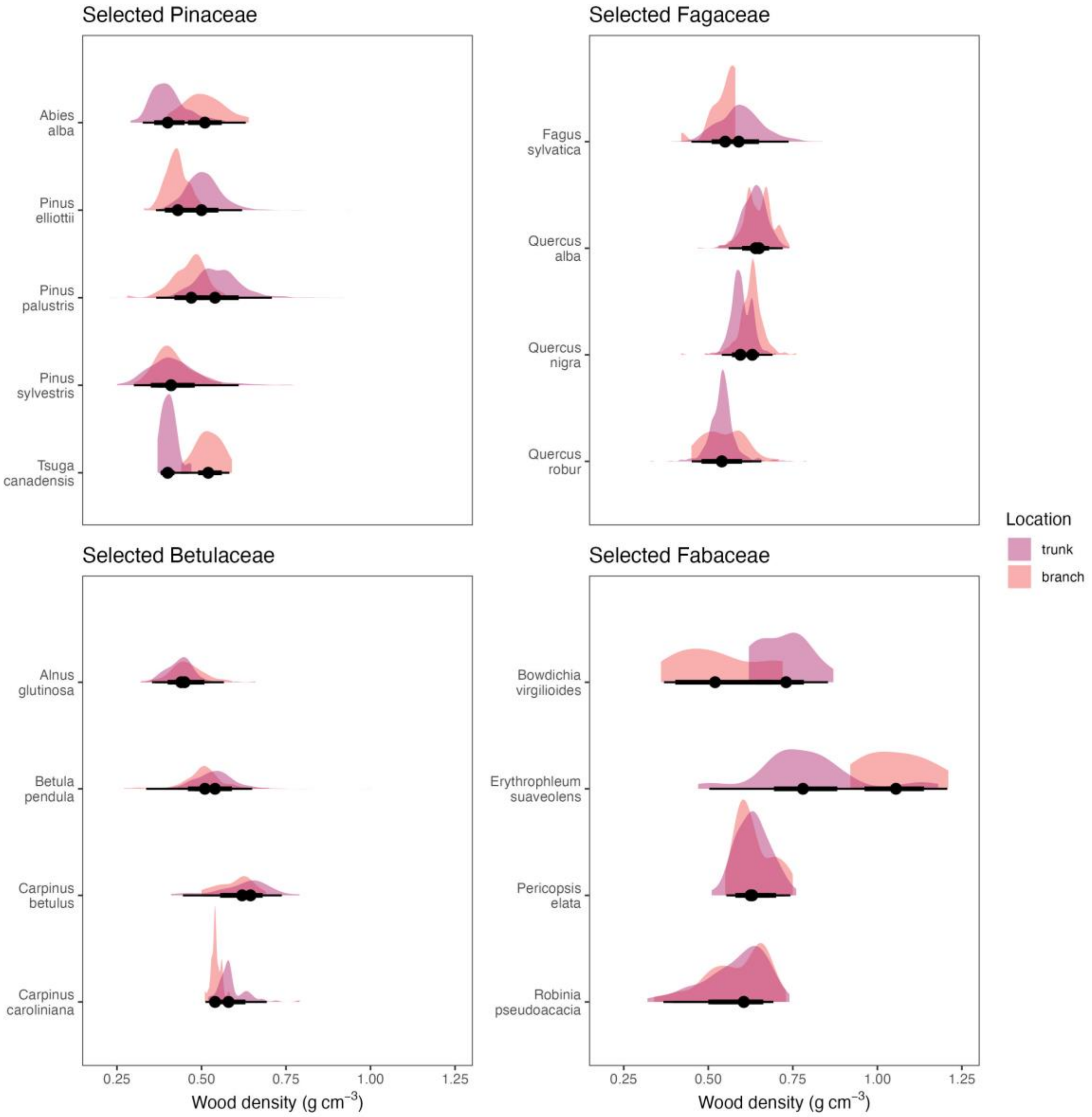


Fig. S6: Wood density variation in trunkwood and in branchwood in selected species. Shown are distributions of within-species variation in wood density for sample species from four families, split by within-tree location of samples (trunkwood or branchwood). Families and species were chosen to maximize sampling size. Black dots indicate the median effect size and black intervals quantile ranges (66% and 95%). Note how there is no clear clear convergence (i.e., branchwood distributions being closer to each other), nor a simple predictive pattern.

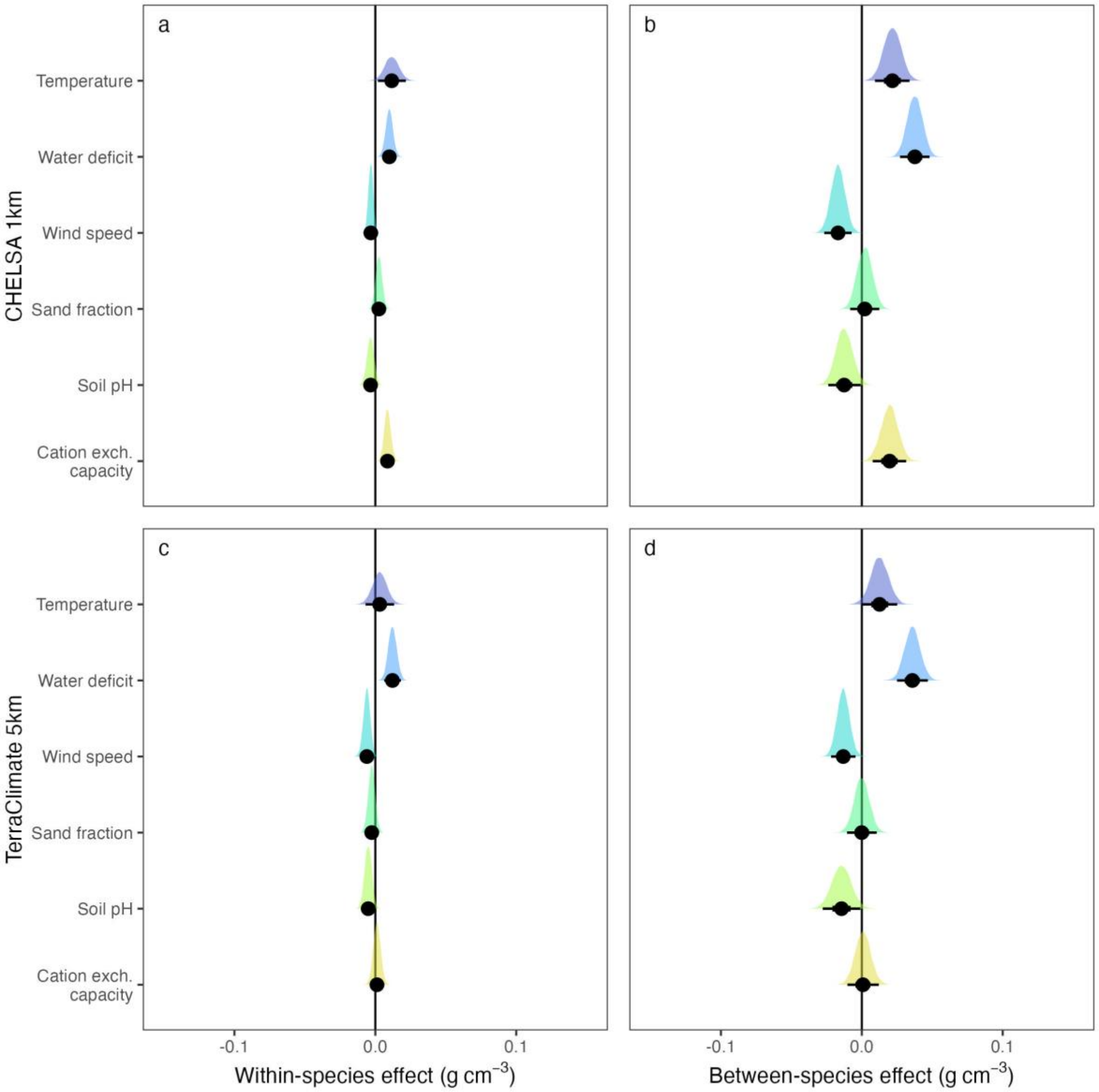


Fig. S7: Environmental and edaphic effects on wood density. Panels a) and b) are equivalent to panels a) and b) in Fig. 4 in the main text and show global within-species and between-species effects of environmental variables on wood density. Effects are derived from a Bayesian hierarchical model, with all predictors scaled by one standard deviation. Climatic variables were from CHELSA/BIOCIM+ (Karger et al., 2017; Brun et al., 2022), edaphic variables from *soilgrids* (Hengl et al., 2017). X-axis limits were chosen wider than in the main text for comparability with effect sizes in data subsets (cf. Fig. S9). Panels c) and d) are the equivalents of panels a) and b), but using the TerraClimate (Abatzoglou et al., 2018) climatology 1981-2010. Variables are mean annual temperature ("Temperature", in °C), climatic water deficit ("Water deficit", in mm), and mean wind speed ("Wind speed", m s^{-1}). The *soilgrids* layers are the same, but have been extracted at 5 km to match the 4-5 km resolution of TerraClimate. The corresponding model results can be found in Table S10. Throughout, black dots indicate the median effect size and black intervals quantile ranges (66% and 95%).

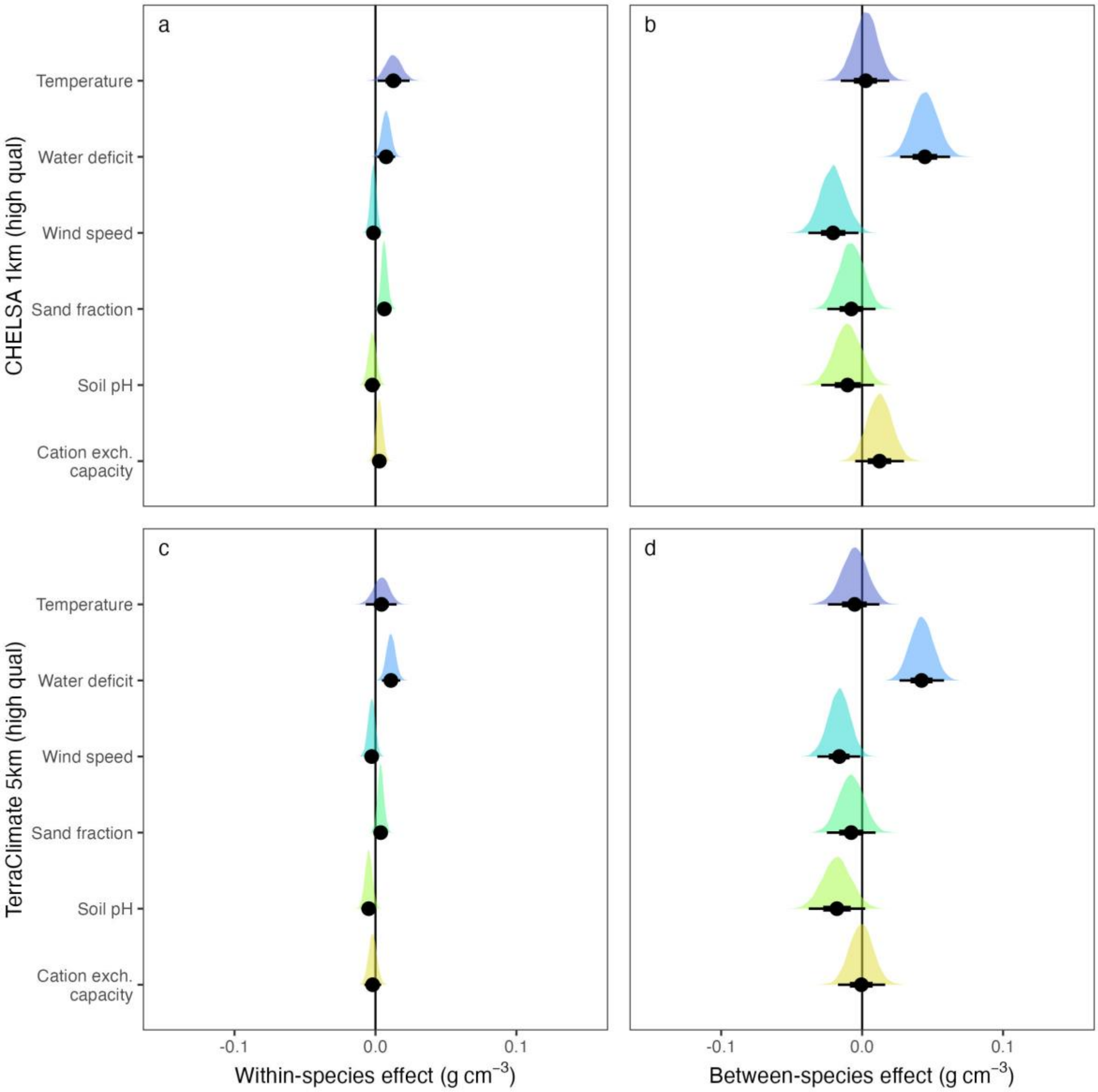


Fig. S8: Environmental and edaphic effects on wood density, high-quality subset. Same as Fig. S7, but for a higher-quality subset of the GWDD v.2 where each species varied strongly in at least environmental variable. This meant that a species was only included if the range of at least one of the environmental predictors was in the top 10% of ranges for that predictor among all other species. We note that this may slightly bias the data set towards the better-sampled higher latitude regions. The corresponding model results can be found in Table S10. Throughout, black dots indicate the median effect size and black intervals quantile ranges (66% and 95%).

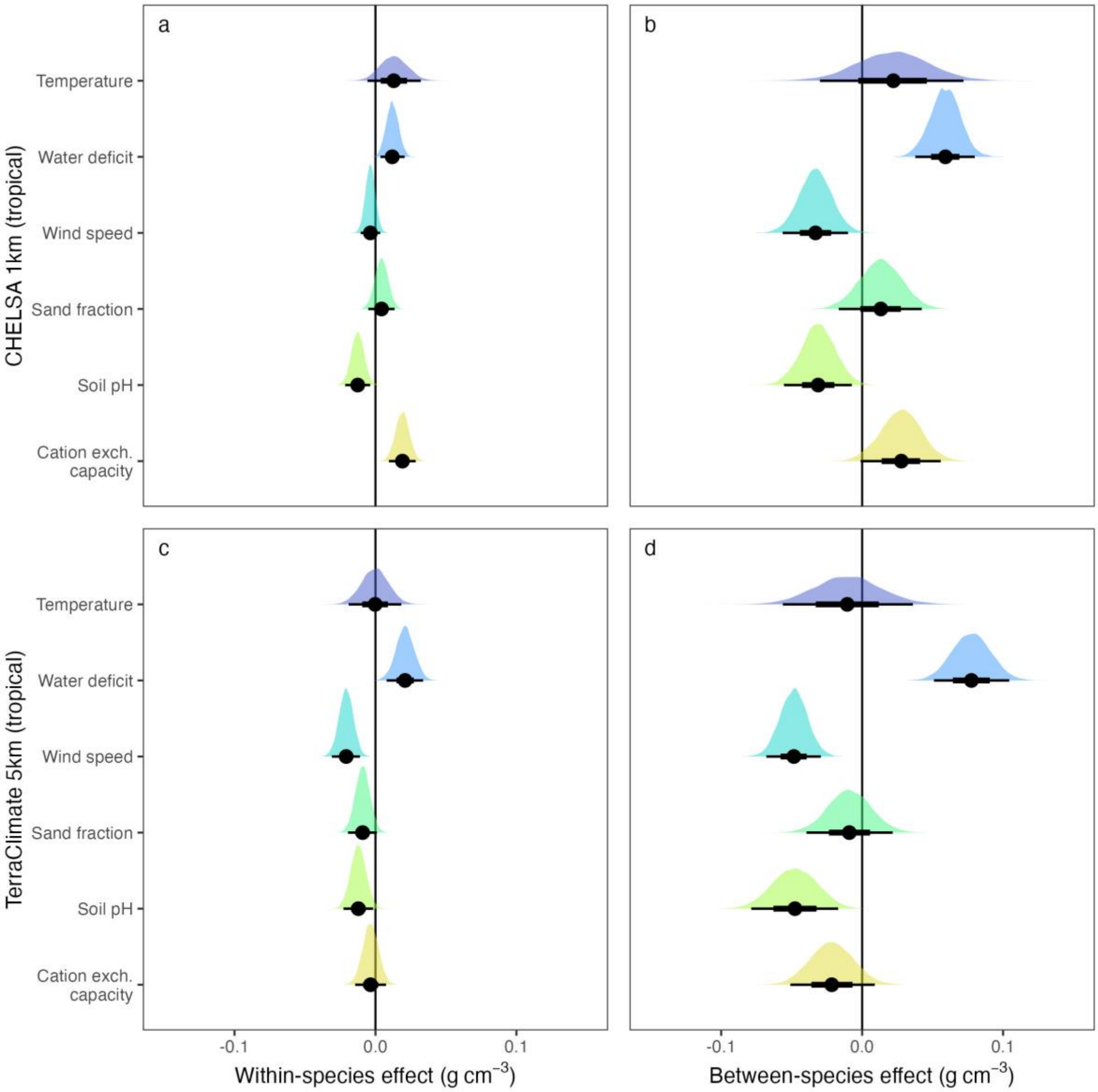


Fig. S9: Environmental and edaphic effects on wood density, within tropics. Same as Fig.S7-8, but for a subset of species with at least three locations in the tropics. Locations were defined as distinct 5 km grid cells. The corresponding model results can be found in Table S12. Throughout, black dots indicate the median effect size and black intervals quantile ranges (66% and 95%).

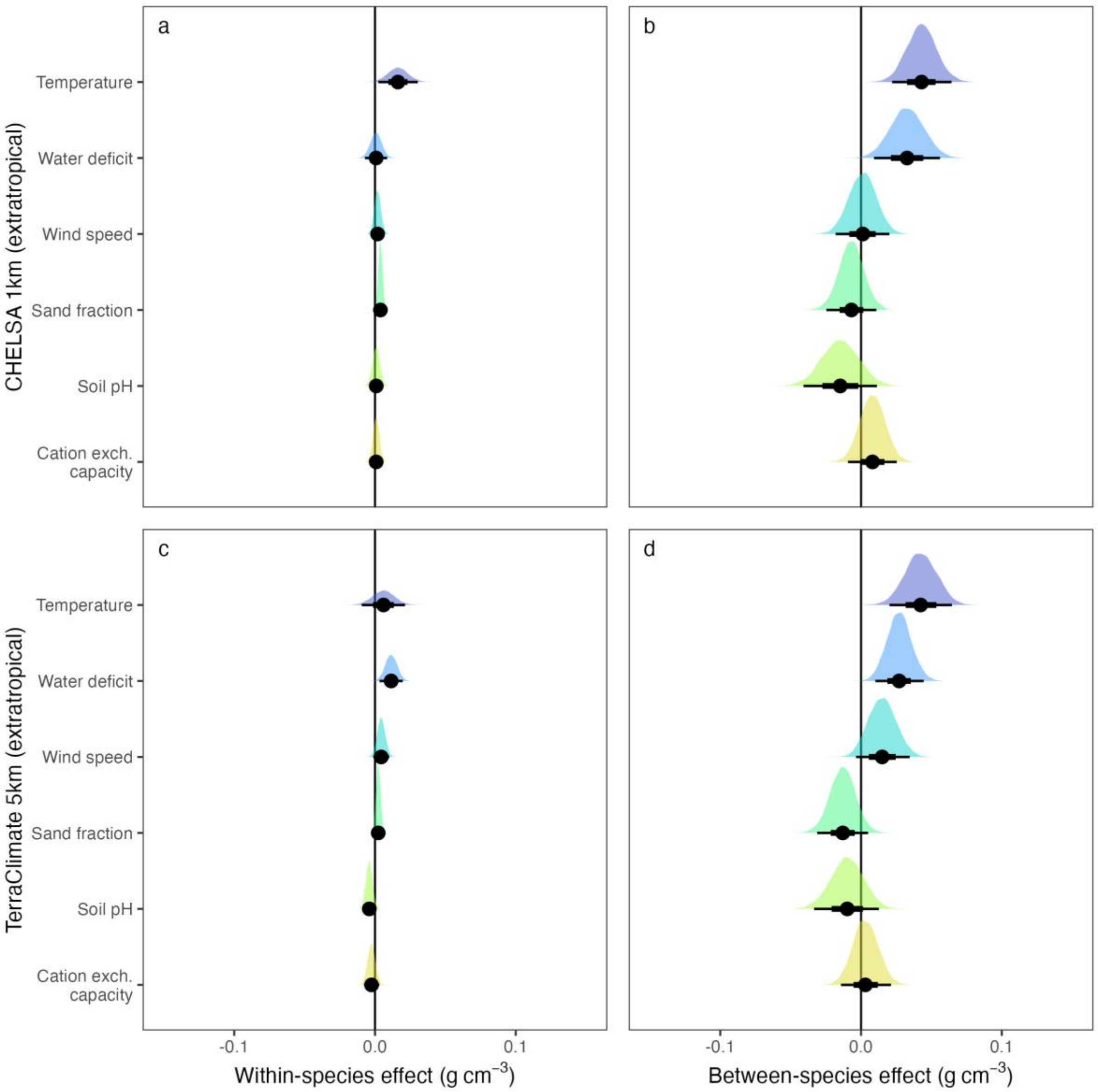


Fig. S10: Environmental and edaphic effects on wood density, outside of tropics. Same as Fig.S7-9, but for a subset of species with at least three locations outside of the tropics. Locations were defined as distinct 5 km grid cells. The corresponding model results can be found in Table S12. Throughout, black dots indicate the median effect size and black intervals quantile ranges (66% and 95%).

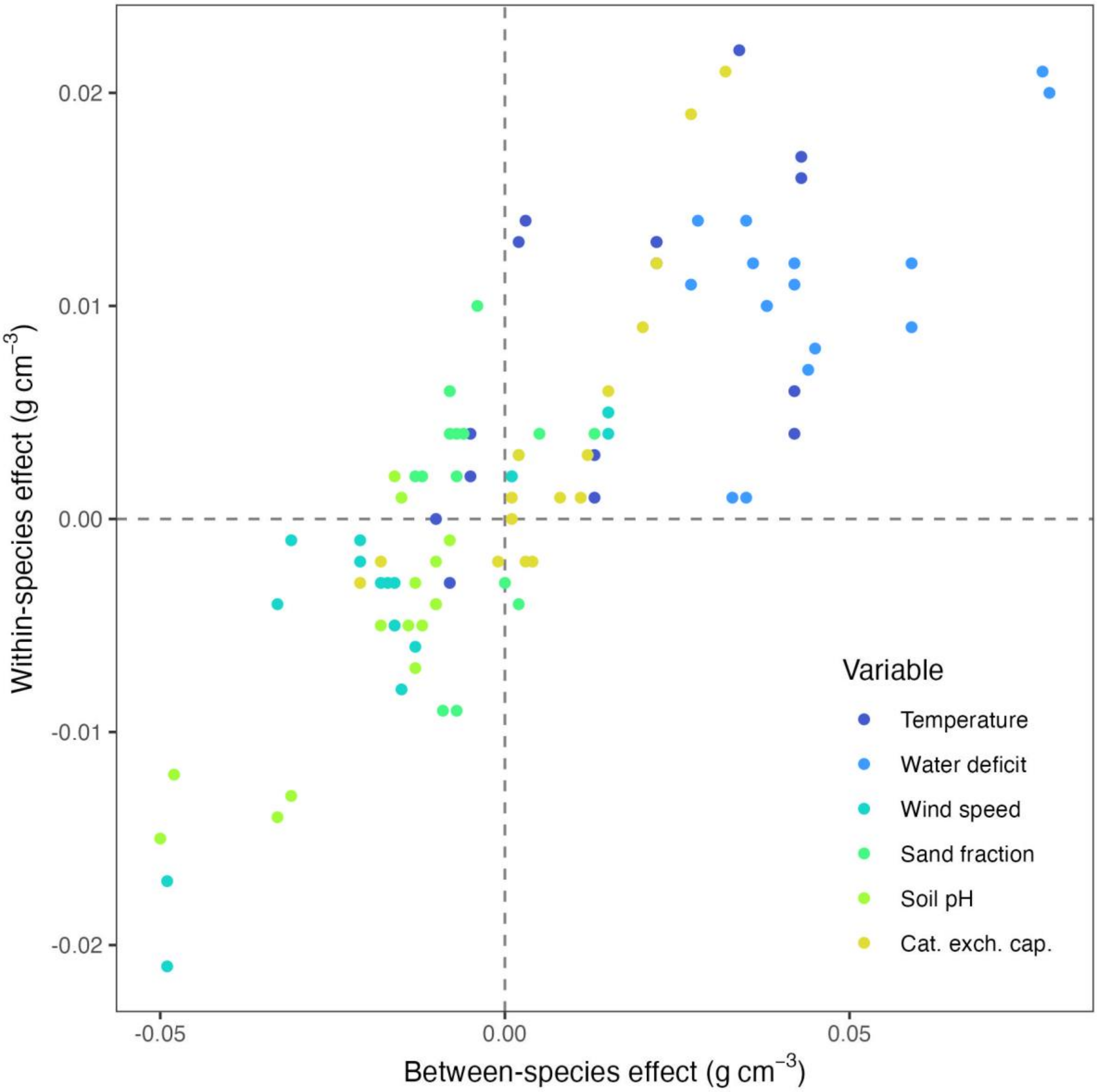


Fig. S11: Correlation between within-species effects and between-species effects. Shown are correlations between estimated within-species and between-species effects of environmental and edaphic predictors on wood density variation. Every point represents an estimated effect of one predictor from one of the 8 models we used (Table S3, Tables S10-13) and counting Bayesian and ML models separately (96 estimates overall). The overall correlation is r = 0.83. Note that this correlation between within-species and between-species effects is not due to correlation between environmental predictors within and across species, as these are decoupled by construction and also have strikingly different correlation structures (Fig. S17).

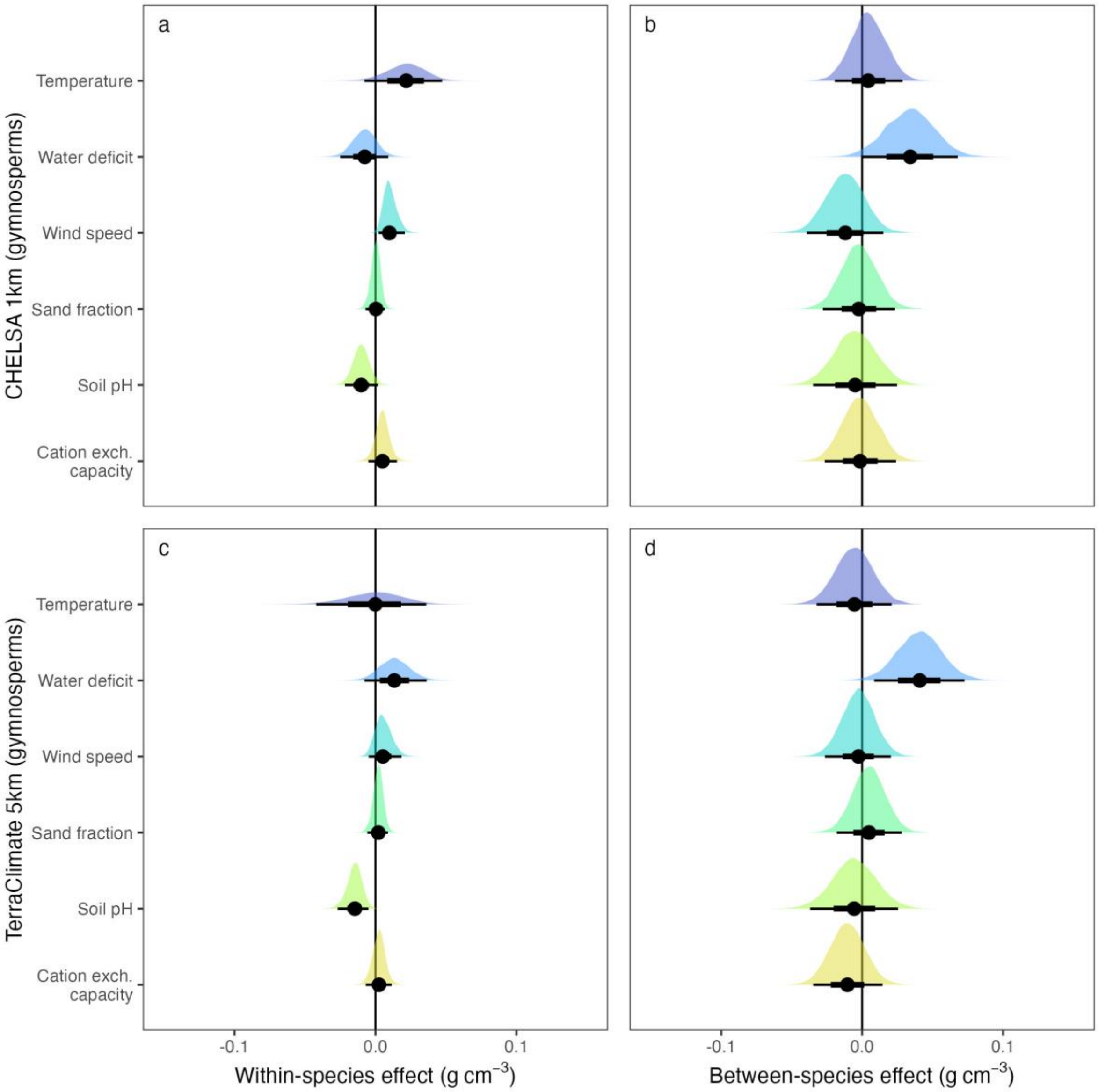


Fig. S12: Environmental and edaphic effects on wood density in gymnosperms. Same as Fig.S7-10, but for gymnosperms only. The corresponding model results can be found in Table S15. Throughout, black dots indicate the median effect size and black intervals quantile ranges (66% and 95%). Note how most effects are close to 0 or strongly overlap with 0.

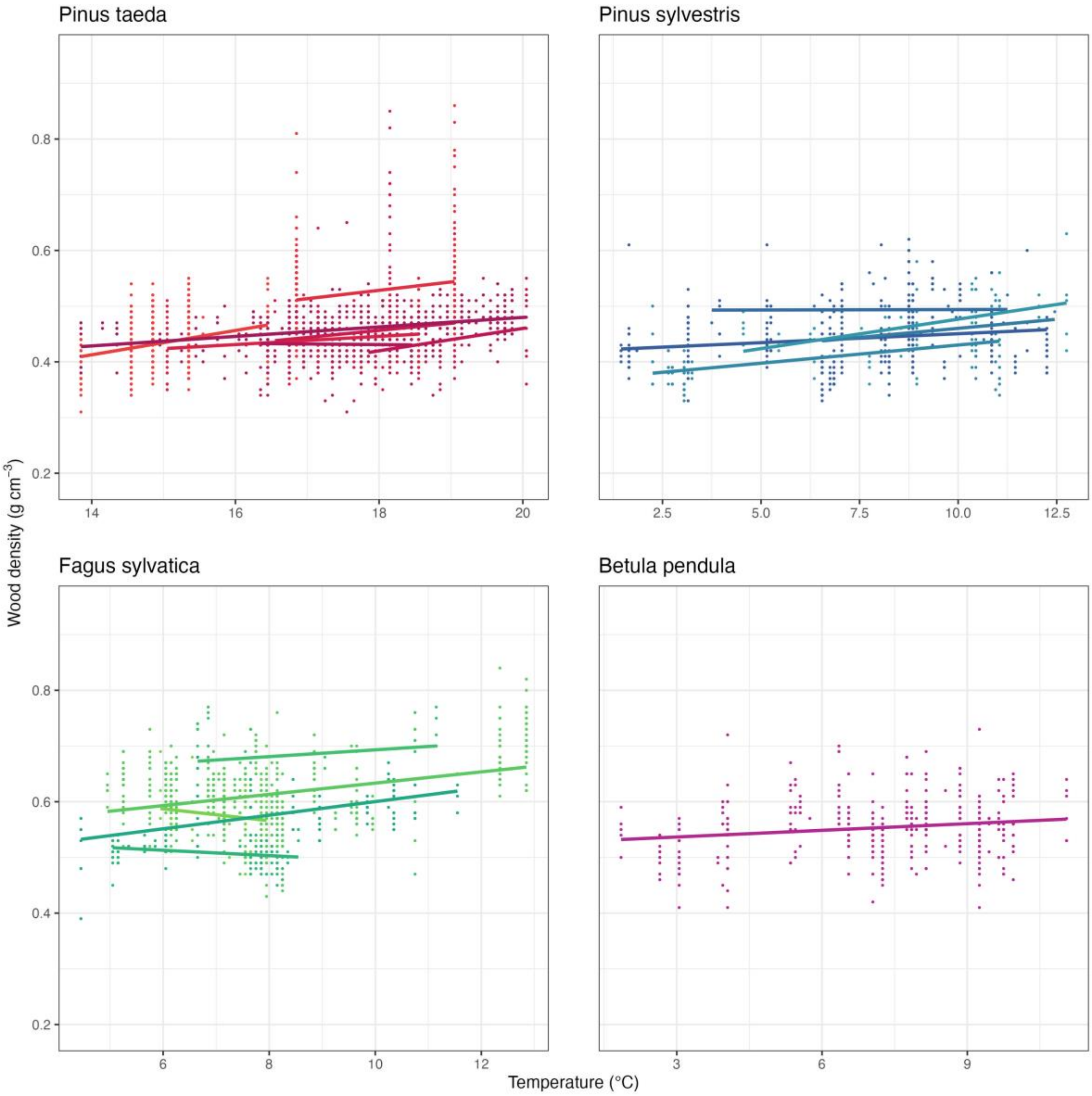


Fig. S13: Temperature effects on within-species wood density variation, examples. Shown are the within-species effects of temperature variation on wood density in four temperate species that cover large environmental gradients and are well-sampled (several studies or large sample sizes). Each line represents a different study and is fitted via simple OLS regression. Note how wood density increases slightly with temperature, but how this effect is overwhelmed by variation around the regression line and even differs between studies. Temperatures are based on the CHELSA/BIOCLIM+ data set (Karger et al., 2017; Brun et al., 2022).

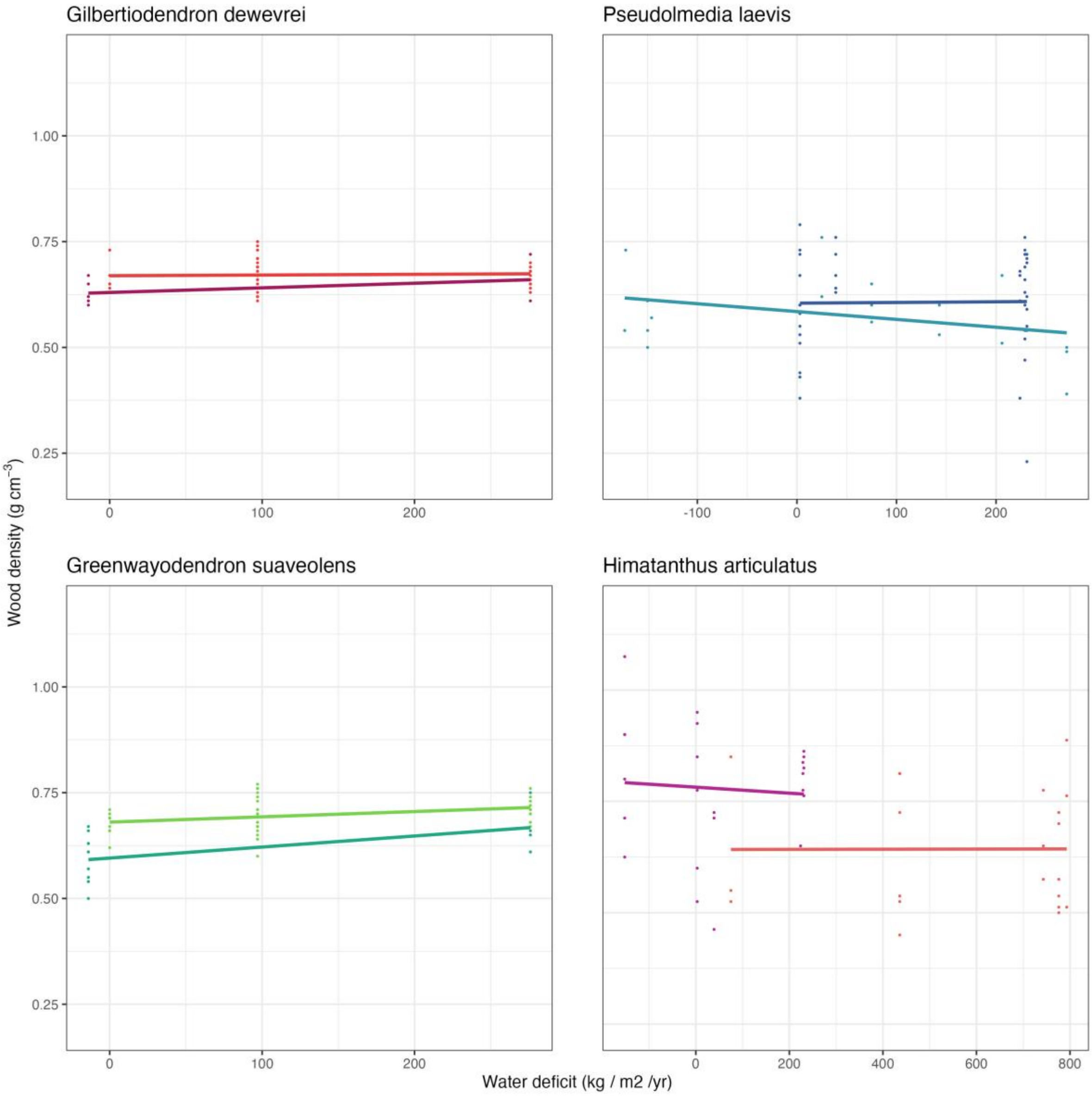


Fig. S14: Water deficit effects on within-species wood density variation, examples. Same as Fig. S11, but for water deficit. Shown are the within-species effects of water deficit on wood density in four tropical species that cover large environmental gradients and are well-sampled (two different studies for each). Each line represents a different study and is fitted via simple OLS regression. Note how there is no clear overall effect and how effect sizes are weak even across large gradients. Water deficits are based on the CHELSA/BIOCLIM+ data set (Karger et al., 2017; Brun et al., 2022).

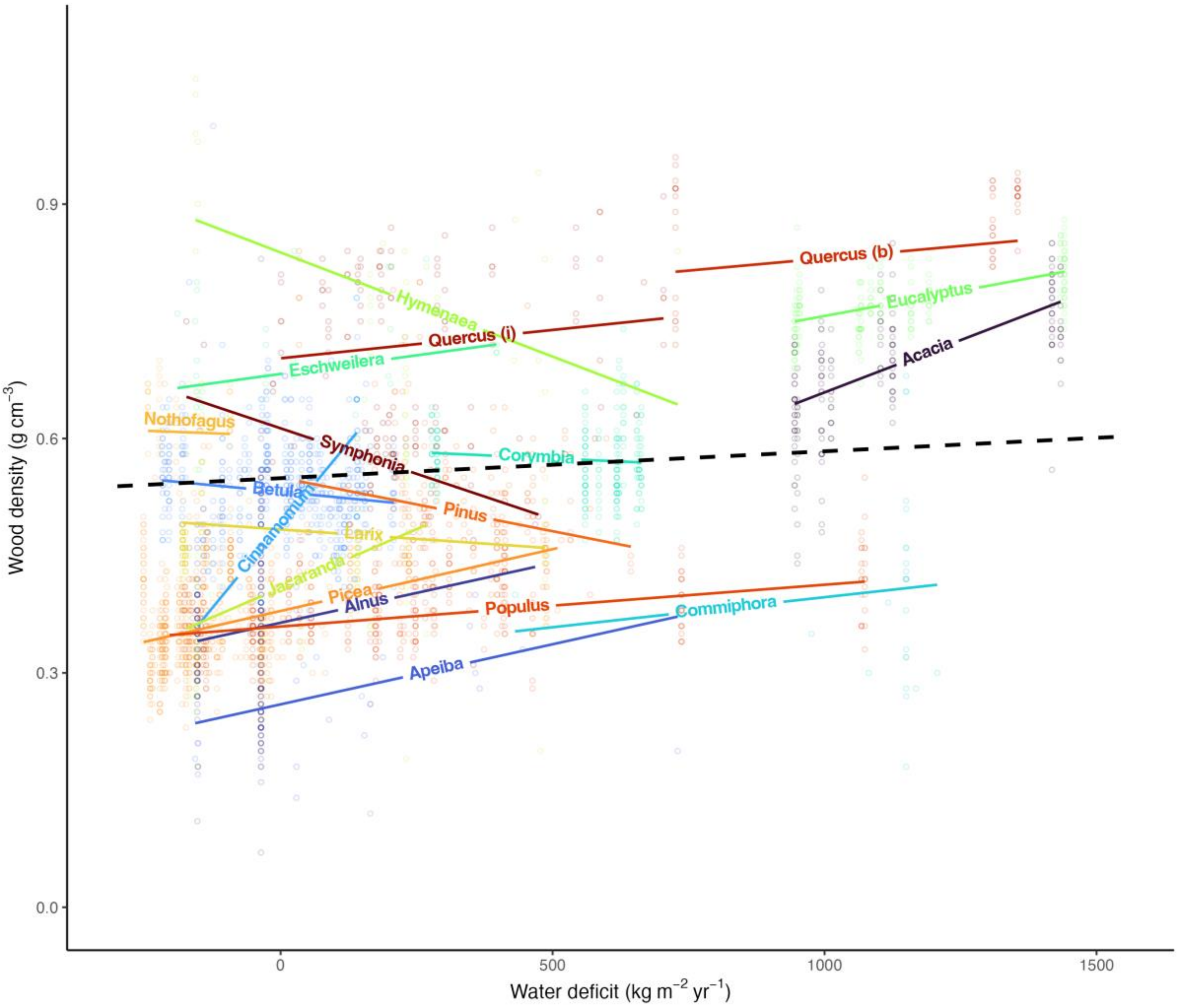


Fig. S15: Intraspecific effects of climatic water deficit on wood density. Enlarged panel from Fig. 4a in main text, with species labels superimposed on regression lines for improved accessibility. Shown are the mean intraspecific effect of climatic water deficit on wood density, as estimated from a hierarchical model (M16) and a large set of geolocated wood density records (dashed black slope, $n_{species}$ = 2,160) as well as species-specific slopes and raw data for 19 species that cover a wide geographic and wood density range (in colour, n = 3,224, > 20 samples per species).

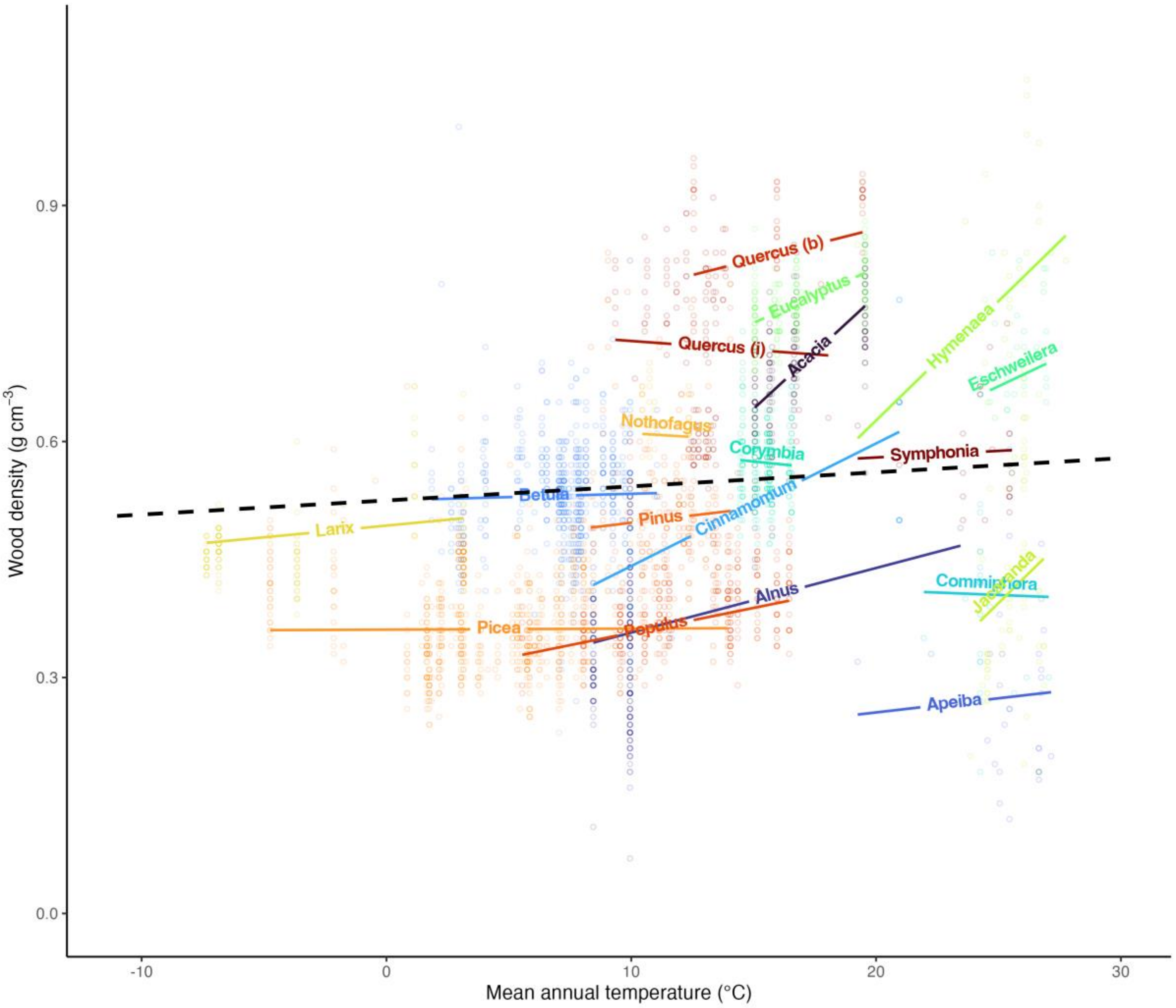
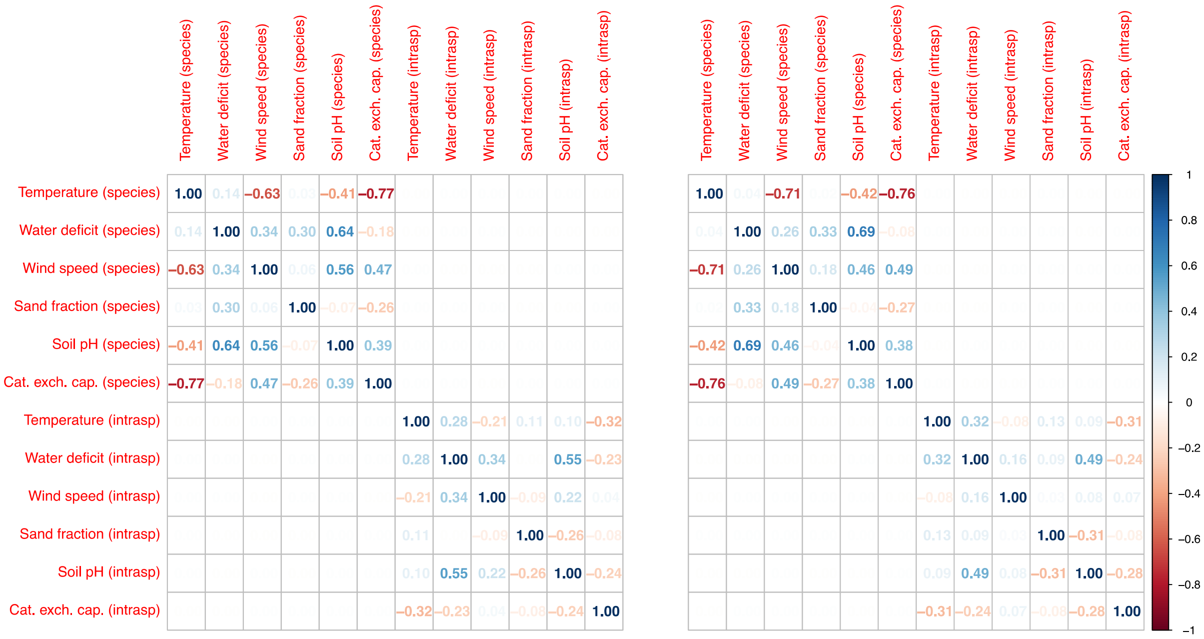


Fig. S16: Intraspecific effects of mean annual temperature on wood density. Enlarged panel from Fig. 4b in main text, with species labels superimposed on regression lines for improved accessibility. Shown are the mean intraspecific effect of mean annual temperature on wood density, as estimated from a hierarchical model (M16) and a large set of geolocated wood density records (dashed black slope, $n_{species}$ = 2,160), as well as species-specific slopes and raw data for 19 species that cover a wide geographic and wood density range (in colour, n = 3,224, > 20 samples per species).



CHELSA + soilgrids (1 km)

TerraClimate + soilgrids (5 km)

Fig. S17: Correlation between environmental and edaphic predictors. Shown are the correlations between environmental and edaphic predictors matched to the Global Wood Density Database (GWDD) v.2. All predictors are separated into species mean values, summarizing the typical environment a species experiences (“species” in brackets), and deviations from the species means at the individual level, i.e., indicating within-species environmental variation (“intrasp” in brackets). Correlation matrices are shown for both sets of predictors used throughout the study, i.e. the CHELSA climatologies 1981-2010 (Brun et al., 2022; Karger et al., 2017) in conjunction with 1 km gridded *soilgrids* layers (Hengl et al., 2017), as well as TerraClimate climatologies 1981-2010 (Abatzoglou et al., 2018) in conjunction with 5 km gridded *soilgrids* layers. Note that, by construction, species means are fully decorrelated from within-species deviations from the species means ($r < 0.01$), hence large parts of the correlation matrices appear empty. Also note that, at species level, temperature is correlated in excess of $|r| = 0.7$ with one variable (cation exchange capacity) and has an absolute correlation of ~0.7 with one other variable (wind speed). Since we are predominately interested in within-species effects and not in exactly partitioning out species-level effects, we include all three variables in the model. A high absolute correlation, but below 0.7, also exists between soil pH and water deficit.

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