

SI: Functional traits as predictors of vital rates across the life-cycle of tropical trees.

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S1 TEXT: COMPARISON OF RESULTS USING INVERSE MODELING

When multiple adult trees contribute seeds to a single location it becomes complicated to assign individual seeds to their respective sources. A now commonly used method pioneered by Ribbens et al (1994) to overcome this problem is inverse modeling (IM) of seed shadows (Clark et al, 1999; Muller-Landau et al, 2008). A seed shadow describes the distribution of seeds with distance from

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S1 TEXT: COMPARISON OF RESULTS USING INVERSE MODELING

their parent, and consists of two elements; (1) a component describing the fecundity of a tree, usually as a function of size and (2) a dispersal kernel describing the distribution of seeds as a function of distance from the source. The seed shadow is the product of these two elements (Clark et al., 1999).

Seed shadows from individual trees will overlap within a stand and the seed rain of these multiple sources can be viewed as a smoothed version of the individual shadows (Clark et al., 1999). This smoothed shadow can be expressed as the summed contributions of each individual seed shadow (hereafter the summed seed shadow SSS). The number of seeds in a certain quadrat is predicted by summing the densities the quadrat receives from each of the surrounding sources, as projected by each individual seed shadow. IM has been shown to be a promising estimate of dispersal distances, as it is not inherently biased to long or short distance dispersal (Jones and Muller-Landau, 2008; Muller-Landau et al, 2008). With IM the predicted seed density in a sample quadrat at location j is given by the summed seed shadow of all N trees at location j (SSS_j);

$$SSS_j = \alpha \cdot \sum_{i=1}^T F(p_i b_i | \beta) \cdot Q(r_{ij} | \mu, \sigma) \quad (1)$$

where SSS_j is the predicted seed number in trap j , which is the sum of seed contributions from T trees multiplied by trap size α ($0.5 m^2$). For each tree i , the seed shadow is a function of the fecundity F , and a two-dimensional dispersal kernel Q . Q depends on the distance r_{ij} between tree i and trap j , while F is a function of basal area b_i (calculated as $[dbh/2]^2\pi$) and seed production probabilities p_i (obtained from the reproductive census as described in the main text). Only females were included for dioecious species.

The parameters β , μ and σ were fitted per species. We tested four different dispersal kernels: the Exponential, 2dt (Clark et al., 1999), 2dt1k (which is the 2dt distribution with the degrees of freedom parameter set to 3) (Muller-Landau et al., 2008) and the Cauchy density distribution.

Off plot integration

Traps within 20 meter from the edge of the plot were excluded since they could be highly influenced by trees outside the plot (Muller-Landau et al., 2008). Data from the remaining 188 traps were used. We then estimated the contribution to the seed rain from unknown sources outside the mapped plot. Here it is assumed that the per unit area seed production off plot is uniform to that within the plot (see Muller-Landau et al., 2008, for details). The total expected seed count \hat{SSS}_j in trap j then becomes the sum of the expected contributions from trees inside the plot SSS_j and the expected contributions from trees outside the plot (immigrant seeds) \hat{I}_j to seed trap j .

$$\hat{SSS}_j = SSS_j + \hat{I}_j \quad (2)$$

S2 TABLES

Parameter estimation

Models were fit using maximum likelihood, assuming seed counts in traps were distributed according to a negative binomial distribution, with an additional clumping parameter k (Muller-Landau et al., 2008), as previous studies have shown that seed arrival tends to be clumped (Muller-Landau et al., 2008).

The results from the above described inverse modeling approach are compared to the alternative estimates (see maintext) in figure S2.

S2 TABLES

Table S1. Overview of species used in each analysis, ordered alphabetically. True indicates a species was included.

Species	Reproduction	Seed production	Seedling establishment	Seedling survival	Seedling growth	Tree survival	Tree growth
<i>Adelia triloba</i>	FALSE	FALSE	FALSE	FALSE	FALSE	TRUE	TRUE
<i>Alchornea costaricensi</i>	TRUE	TRUE	TRUE	TRUE	TRUE	TRUE	TRUE
<i>Alibertia edulis</i>	FALSE	FALSE	TRUE	TRUE	TRUE	TRUE	TRUE
<i>Allophylus psilospermus</i>	FALSE	FALSE	FALSE	FALSE	FALSE	TRUE	TRUE
<i>Alseis blackiana</i>	TRUE	TRUE	TRUE	TRUE	TRUE	TRUE	TRUE
<i>Anacardium excelsum</i>	FALSE	TRUE	FALSE	TRUE	TRUE	FALSE	FALSE
<i>Andira inermis</i>	FALSE	FALSE	FALSE	FALSE	FALSE	TRUE	TRUE
<i>Annona acuminata</i>	FALSE	FALSE	FALSE	TRUE	TRUE	TRUE	TRUE
<i>Annona spraguei</i>	FALSE	FALSE	FALSE	TRUE	TRUE	TRUE	TRUE
<i>Apeiba membranacea</i>	TRUE	FALSE	TRUE	TRUE	TRUE	TRUE	TRUE
<i>Apeiba tibourbou</i>	TRUE	FALSE	FALSE	FALSE	FALSE	FALSE	FALSE
<i>Aspidosperma spruceanum</i>	TRUE	FALSE	TRUE	TRUE	TRUE	TRUE	TRUE
<i>Astronium graveolens</i>	TRUE	TRUE	FALSE	FALSE	FALSE	TRUE	TRUE
<i>Beilschmiedia pendula</i>	TRUE	TRUE	TRUE	TRUE	TRUE	TRUE	TRUE
<i>Brosimum alicastrum</i>	TRUE	TRUE	TRUE	TRUE	TRUE	TRUE	TRUE
<i>Calophyllum longifolium</i>	FALSE	FALSE	TRUE	TRUE	TRUE	TRUE	TRUE
<i>Capparis frondosa</i>	FALSE	FALSE	TRUE	TRUE	TRUE	TRUE	TRUE
<i>Casearia aculeata</i>	TRUE	FALSE	FALSE	FALSE	FALSE	TRUE	TRUE
<i>Casearia arborea</i>	FALSE	FALSE	FALSE	FALSE	FALSE	TRUE	TRUE
<i>Cassipourea elliptica</i>	TRUE	FALSE	TRUE	TRUE	TRUE	TRUE	TRUE
<i>Cecropia insignis</i>	FALSE	FALSE	FALSE	FALSE	FALSE	FALSE	FALSE
<i>Chrysochlamy eclipses</i>	FALSE	FALSE	FALSE	FALSE	FALSE	TRUE	TRUE
<i>Chrysophyllum argenteum</i>	TRUE	TRUE	TRUE	TRUE	TRUE	TRUE	TRUE
<i>Chrysophyllum cainito</i>	TRUE	TRUE	TRUE	TRUE	TRUE	TRUE	TRUE
<i>Coccocloba coronata</i>	FALSE	FALSE	FALSE	FALSE	FALSE	TRUE	TRUE
<i>Coccocloba manzinellens</i>	FALSE	FALSE	FALSE	FALSE	FALSE	TRUE	TRUE
<i>Cordia alliodora</i>	TRUE	TRUE	TRUE	TRUE	TRUE	TRUE	TRUE
<i>Cordia bicolor</i>	TRUE	TRUE	TRUE	TRUE	TRUE	TRUE	TRUE
<i>Coussarea curvigemmia</i>	TRUE	TRUE	TRUE	TRUE	TRUE	TRUE	TRUE
<i>Cupania rufescens</i>	FALSE	FALSE	FALSE	FALSE	FALSE	TRUE	TRUE
<i>Cupania seemannii</i>	FALSE	FALSE	FALSE	FALSE	FALSE	TRUE	TRUE

Table S1. Overview of species used in each analysis, ordered alphabetically. True indicates a species was included.

Species	Reproduction	Seed production	Seedling establishment	Seedling survival	Seedling growth	Tree survival	Tree growth
<i>Dendropanax arboreus</i>	FALSE	FALSE	TRUE	FALSE	FALSE	FALSE	FALSE
<i>Desmopsis panamensis</i>	TRUE	TRUE	TRUE	TRUE	TRUE	TRUE	TRUE
<i>Dipteryx oleifera</i>	TRUE	TRUE	FALSE	TRUE	TRUE	FALSE	FALSE
<i>Drypetes standleyi</i>	FALSE	TRUE	TRUE	TRUE	TRUE	TRUE	TRUE
<i>Erythroxylum panamense</i>	FALSE	FALSE	FALSE	FALSE	FALSE	TRUE	TRUE
<i>Eugenia coloradoensi</i>	FALSE	FALSE	TRUE	TRUE	TRUE	TRUE	TRUE
<i>Eugenia galalonensis</i>	FALSE	FALSE	FALSE	TRUE	TRUE	TRUE	TRUE
<i>Eugenia nesiotica</i>	FALSE	FALSE	TRUE	TRUE	TRUE	TRUE	TRUE
<i>Eugenia oerstediana</i>	TRUE	TRUE	TRUE	TRUE	TRUE	TRUE	TRUE
<i>Faramea occidentalis</i>	TRUE	TRUE	TRUE	TRUE	TRUE	TRUE	TRUE
<i>Ficus insipida</i>	FALSE	FALSE	TRUE	FALSE	FALSE	FALSE	FALSE
<i>Garcinia intermedia</i>	TRUE	TRUE	TRUE	TRUE	TRUE	TRUE	TRUE
<i>Garcinia madruno</i>	FALSE	FALSE	FALSE	FALSE	FALSE	TRUE	TRUE
<i>Genipa americana</i>	FALSE	FALSE	TRUE	FALSE	FALSE	FALSE	FALSE
<i>Guapira standleyana</i>	FALSE	FALSE	TRUE	TRUE	TRUE	TRUE	TRUE
<i>Guarea guidonia</i>	TRUE	TRUE	TRUE	TRUE	TRUE	TRUE	TRUE
<i>Guatteria dumetorum</i>	TRUE	FALSE	TRUE	TRUE	TRUE	TRUE	TRUE
<i>Gustavia superba</i>	TRUE	TRUE	TRUE	TRUE	TRUE	TRUE	TRUE
<i>Hamelia axillaris</i>	FALSE	FALSE	FALSE	TRUE	TRUE	TRUE	TRUE
<i>Hampea appendiculat</i>	FALSE	FALSE	TRUE	TRUE	TRUE	TRUE	TRUE
<i>Hasseltia floribunda</i>	TRUE	FALSE	TRUE	FALSE	FALSE	TRUE	TRUE
<i>Heisteria acuminata</i>	FALSE	FALSE	TRUE	FALSE	FALSE	TRUE	TRUE
<i>Heisteria concinna</i>	TRUE	TRUE	TRUE	TRUE	TRUE	TRUE	TRUE
<i>Herrania purpurea</i>	FALSE	FALSE	FALSE	FALSE	FALSE	TRUE	TRUE
<i>Hirtella triandra</i>	TRUE	TRUE	TRUE	TRUE	TRUE	TRUE	TRUE
<i>Hybanthus prunifolius</i>	FALSE	FALSE	TRUE	TRUE	TRUE	TRUE	TRUE
<i>Hieronyma alchorneoides</i>	TRUE	TRUE	FALSE	FALSE	FALSE	TRUE	TRUE
<i>Inga goldmanii</i>	FALSE	FALSE	FALSE	FALSE	FALSE	TRUE	TRUE
<i>Inga marginata</i>	TRUE	TRUE	TRUE	TRUE	TRUE	TRUE	TRUE
<i>Inga nobilis</i>	FALSE	FALSE	FALSE	FALSE	FALSE	TRUE	TRUE
<i>Inga acuminata</i>	FALSE	FALSE	TRUE	TRUE	TRUE	TRUE	TRUE

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Table S1. Overview of species used in each analysis, ordered alphabetically. True indicates a species was included.

Species	Reproduction	Seed production	Seedling establishment	Seedling survival	Seedling growth	Tree survival	Tree growth
<i>Inga sapindoides</i>	FALSE	FALSE	FALSE	FALSE	FALSE	TRUE	TRUE
<i>Inga thibaudiana</i>	FALSE	FALSE	FALSE	TRUE	TRUE	TRUE	TRUE
<i>Inga umbellifera</i>	FALSE	FALSE	FALSE	TRUE	TRUE	TRUE	TRUE
<i>Jacaranda copaia</i>	TRUE	FALSE	TRUE	FALSE	FALSE	TRUE	TRUE
<i>Lacistema aggregatum</i>	FALSE	FALSE	FALSE	TRUE	TRUE	TRUE	TRUE
<i>Lacistema panamensis</i>	FALSE	FALSE	TRUE	TRUE	TRUE	TRUE	TRUE
<i>Laetia thamnia</i>	TRUE	FALSE	FALSE	FALSE	FALSE	TRUE	TRUE
<i>Licania hypoleuca</i>	FALSE	FALSE	FALSE	FALSE	FALSE	TRUE	TRUE
<i>Licania platypus</i>	FALSE	FALSE	FALSE	FALSE	FALSE	TRUE	TRUE
<i>Lonchocarpus heptaphyllus</i>	TRUE	FALSE	TRUE	TRUE	TRUE	TRUE	TRUE
<i>Luehea seemannii</i>	TRUE	TRUE	TRUE	TRUE	TRUE	TRUE	TRUE
<i>Mosannona garwoodii</i>	TRUE	FALSE	FALSE	FALSE	FALSE	TRUE	TRUE
<i>Maquira guianensis</i>	FALSE	FALSE	FALSE	FALSE	FALSE	TRUE	TRUE
<i>Mouriri myrtilloides</i>	TRUE	TRUE	TRUE	TRUE	TRUE	TRUE	TRUE
<i>Nectandra cissiflora</i>	FALSE	FALSE	FALSE	FALSE	FALSE	TRUE	TRUE
<i>Ocotea cernua</i>	FALSE	FALSE	FALSE	TRUE	TRUE	TRUE	TRUE
<i>Ocotea puberula</i>	FALSE	FALSE	TRUE	TRUE	TRUE	TRUE	TRUE
<i>Trophis caucana</i>	FALSE	FALSE	FALSE	TRUE	TRUE	TRUE	TRUE
<i>Ormosia coccinea</i>	FALSE	FALSE	FALSE	FALSE	FALSE	TRUE	TRUE
<i>Ormosia macrocalyx</i>	FALSE	FALSE	FALSE	FALSE	FALSE	TRUE	TRUE
<i>Ouratea lucens</i>	FALSE	FALSE	TRUE	TRUE	TRUE	TRUE	TRUE
<i>Palicourea guianensis</i>	FALSE	FALSE	TRUE	TRUE	TRUE	TRUE	TRUE
<i>Pentagonia macrophylla</i>	FALSE	FALSE	FALSE	FALSE	FALSE	TRUE	TRUE
<i>Perebea xanthochyma</i>	FALSE	FALSE	FALSE	FALSE	FALSE	TRUE	TRUE
<i>Cinnamomum triplinerve</i>	FALSE	FALSE	TRUE	TRUE	TRUE	FALSE	FALSE
<i>Picramnia latifolia</i>	FALSE	FALSE	TRUE	TRUE	TRUE	TRUE	TRUE
<i>Platymiscium pinnatum</i>	FALSE	FALSE	FALSE	TRUE	TRUE	TRUE	TRUE
<i>Platypodium elegans</i>	TRUE	FALSE	FALSE	FALSE	FALSE	TRUE	TRUE
<i>Poulsenia armata</i>	TRUE	FALSE	TRUE	FALSE	FALSE	TRUE	TRUE
<i>Pourouma bicolor</i>	FALSE	FALSE	FALSE	FALSE	FALSE	TRUE	TRUE
<i>Pouteria reticulata</i>	TRUE	TRUE	TRUE	TRUE	TRUE	TRUE	TRUE

Table S1. Overview of species used in each analysis, ordered alphabetically. True indicates a species was included.

Species	Reproduction	Seed production	Seedling establishment	Seedling survival	Seedling growth	Tree survival	Tree growth
<i>Prioria copaifera</i>	TRUE	TRUE	FALSE	TRUE	TRUE	TRUE	TRUE
<i>Protium panamense</i>	TRUE	FALSE	FALSE	TRUE	TRUE	TRUE	TRUE
<i>Protium tenuifolium</i>	TRUE	TRUE	TRUE	TRUE	TRUE	TRUE	TRUE
<i>Pseudobombax septenatum</i>	TRUE	FALSE	FALSE	FALSE	FALSE	FALSE	FALSE
<i>Psychotria acuminata</i>	FALSE	FALSE	TRUE	TRUE	TRUE	FALSE	FALSE
<i>Psychotria deflexa</i>	FALSE	FALSE	FALSE	TRUE	TRUE	FALSE	FALSE
<i>Psychotria horizontalis</i>	FALSE	FALSE	TRUE	TRUE	TRUE	TRUE	TRUE
<i>Psychotria marginata</i>	FALSE	FALSE	TRUE	TRUE	TRUE	TRUE	TRUE
<i>Psychotria racemosa</i>	FALSE	FALSE	TRUE	TRUE	TRUE	FALSE	FALSE
<i>Pterocarpus rohrii</i>	TRUE	FALSE	FALSE	FALSE	FALSE	TRUE	TRUE
<i>Quararibea asterolepis</i>	TRUE	TRUE	TRUE	TRUE	TRUE	TRUE	TRUE
<i>Quassia amara</i>	FALSE	FALSE	FALSE	FALSE	FALSE	TRUE	TRUE
<i>Randia armata</i>	TRUE	TRUE	TRUE	TRUE	TRUE	TRUE	TRUE
<i>Simarouba amara</i>	TRUE	TRUE	TRUE	TRUE	TRUE	TRUE	TRUE
<i>Sloanea terniflora</i>	TRUE	FALSE	FALSE	FALSE	FALSE	TRUE	TRUE
<i>Sorocea affinis</i>	FALSE	FALSE	TRUE	TRUE	TRUE	TRUE	TRUE
<i>Spondias mombin</i>	FALSE	FALSE	FALSE	FALSE	FALSE	TRUE	TRUE
<i>Spondias radlkoferi</i>	FALSE	FALSE	FALSE	TRUE	TRUE	TRUE	TRUE
<i>Sterculia apetala</i>	FALSE	FALSE	FALSE	TRUE	TRUE	FALSE	FALSE
<i>Stylogyne turbacensis</i>	FALSE	FALSE	FALSE	TRUE	TRUE	TRUE	TRUE
<i>Swartzia simplex</i>	FALSE	FALSE	FALSE	TRUE	TRUE	FALSE	FALSE
<i>Symphonia globulifera</i>	FALSE	FALSE	FALSE	FALSE	FALSE	TRUE	TRUE
<i>Tabebuia guayacan</i>	FALSE	FALSE	TRUE	FALSE	FALSE	FALSE	FALSE
<i>Tabebuia rosea</i>	TRUE	TRUE	TRUE	TRUE	TRUE	TRUE	TRUE
<i>Tabernaemont arborea</i>	TRUE	FALSE	TRUE	TRUE	TRUE	TRUE	TRUE
<i>Tachigali versicolor</i>	FALSE	FALSE	FALSE	TRUE	TRUE	TRUE	TRUE
<i>Talisia nervosa</i>	TRUE	FALSE	FALSE	FALSE	FALSE	TRUE	TRUE
<i>Talisia princeps</i>	FALSE	FALSE	FALSE	TRUE	TRUE	TRUE	TRUE
<i>Terminalia amazonia</i>	TRUE	TRUE	FALSE	FALSE	FALSE	FALSE	FALSE
<i>Terminalia oblonga</i>	TRUE	FALSE	FALSE	FALSE	FALSE	FALSE	FALSE
<i>Tetragastris panamensis</i>	TRUE	TRUE	TRUE	TRUE	TRUE	TRUE	TRUE

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Table S1. Overview of species used in each analysis, ordered alphabetically. True indicates a species was included.

Species	Reproduction	Seed production	Seedling establishment	Seedling survival	Seedling growth	Tree survival	Tree growth
<i>Thevetia ahouai</i>	FALSE	FALSE	FALSE	FALSE	FALSE	TRUE	TRUE
<i>Trattinnickia aspera</i>	TRUE	TRUE	FALSE	FALSE	FALSE	FALSE	FALSE
<i>Trichilia pallida</i>	TRUE	TRUE	TRUE	FALSE	FALSE	TRUE	TRUE
<i>Trichilia tuberculata</i>	TRUE	TRUE	TRUE	TRUE	TRUE	TRUE	TRUE
<i>Triplaris cumingiana</i>	TRUE	TRUE	TRUE	FALSE	FALSE	TRUE	TRUE
<i>Turpinia occidentalis</i>	FALSE	FALSE	FALSE	FALSE	FALSE	TRUE	TRUE
<i>Unonopsis pittieri</i>	TRUE	FALSE	TRUE	TRUE	TRUE	TRUE	TRUE
<i>Virola sebifera</i>	TRUE	FALSE	TRUE	TRUE	TRUE	TRUE	TRUE
<i>Virola surinamensis</i>	FALSE	FALSE	FALSE	FALSE	FALSE	TRUE	TRUE
<i>Vochysia ferruginea</i>	TRUE	FALSE	TRUE	FALSE	FALSE	FALSE	FALSE
<i>Xylopia macrantha</i>	TRUE	FALSE	FALSE	TRUE	TRUE	TRUE	TRUE
<i>Zanthoxylum panamense</i>	FALSE	FALSE	TRUE	TRUE	TRUE	TRUE	TRUE

S2 TABLES

Table S2. All evaluated forms of the models for demographic rates (Y) that are potentially size-dependent. The variable Y refers to seedling growth, seedling survival, tree growth, tree survival, or tree reproduction. The variable size refers to seedling height, tree dbh (when Y is tree reproduction or survival) or tree basal area (when Y is tree growth). The variables wd, sm, lma and d_{max} refer to wood density, seed mass, leaf mass per area and maximum dbh, respectively. Random effects are for species (1 | species) and individual (1 | tag).

	formula
1	$Y \sim 1 + (1 species) + (1>tag)$
2	$Y \sim size + (1 species) + (1>tag)$
3	$Y \sim size + lma + (1 species) + (1>tag)$
4	$Y \sim size * lma + (1 species) + (1>tag)$
5	$Y \sim size + sm + (1 species) + (1>tag)$
6	$Y \sim size + sm + lma + (1 species) + (1>tag)$
7	$Y \sim size + sm + size * lma + (1 species) + (1>tag)$
8	$Y \sim size * sm + (1 species) + (1>tag)$
9	$Y \sim size * sm + lma + (1 species) + (1>tag)$
10	$Y \sim size * sm + size * lma + (1 species) + (1>tag)$
11	$Y \sim size + wd + (1 species) + (1>tag)$
12	$Y \sim size + wd + lma + (1 species) + (1>tag)$
13	$Y \sim size + wd + size * lma + (1 species) + (1>tag)$
14	$Y \sim size + wd + sm + (1 species) + (1>tag)$
15	$Y \sim size + wd + sm + lma + (1 species) + (1>tag)$
16	$Y \sim size + wd + sm + size * lma + (1 species) + (1>tag)$
17	$Y \sim size + wd + size * sm + (1 species) + (1>tag)$
18	$Y \sim size + wd + size * sm + lma + (1 species) + (1>tag)$
19	$Y \sim size + wd + size * sm + size * lma + (1 species) + (1>tag)$
20	$Y \sim size * wd + (1 species) + (1>tag)$
21	$Y \sim size * wd + lma + (1 species) + (1>tag)$
22	$Y \sim size * wd + size * lma + (1 species) + (1>tag)$
23	$Y \sim size * wd + sm + (1 species) + (1>tag)$
24	$Y \sim size * wd + sm + lma + (1 species) + (1>tag)$
25	$Y \sim size * wd + sm + size * lma + (1 species) + (1>tag)$
26	$Y \sim size * wd + size * sm + (1 species) + (1>tag)$
27	$Y \sim size * wd + size * sm + size * lma + (1 species) + (1>tag)$
28	$Y \sim size * wd + size * sm + size * lma + (1 species) + (1>tag)$
29	$Y \sim size + dmax + (1 species) + (1>tag)$
30	$Y \sim size + lma + dmax + (1 species) + (1>tag)$
31	$Y \sim size * lma + dmax + (1 species) + (1>tag)$
32	$Y \sim size + sm + dmax + (1 species) + (1>tag)$
33	$Y \sim size + sm + lma + dmax + (1 species) + (1>tag)$
34	$Y \sim size + sm + size * lma + dmax + (1 species) + (1>tag)$
35	$Y \sim size * sm + dmax + (1 species) + (1>tag)$
36	$Y \sim size * sm + lma + dmax + (1 species) + (1>tag)$
37	$Y \sim size * sm + size * lma + dmax + (1 species) + (1>tag)$
38	$Y \sim size + wd + dmax + (1 species) + (1>tag)$
39	$Y \sim size + wd + lma + dmax + (1 species) + (1>tag)$
40	$Y \sim size + wd + size * lma + dmax + (1 species) + (1>tag)$
41	$Y \sim size + wd + sm + dmax + (1 species) + (1>tag)$
42	$Y \sim size + wd + sm + lma + dmax + (1 species) + (1>tag)$
43	$Y \sim size + wd + sm + size * lma + dmax + (1 species) + (1>tag)$
44	$Y \sim size + wd + size * sm + dmax + (1 species) + (1>tag)$
45	$Y \sim size + wd + size * sm + lma + dmax + (1 species) + (1>tag)$
46	$Y \sim size + wd + size * sm + size * lma + dmax + (1 species) + (1>tag)$
47	$Y \sim size * wd + dmax + (1 species) + (1>tag)$
48	$Y \sim size * wd + lma + dmax + (1 species) + (1>tag)$
49	$Y \sim size * wd + size * lma + dmax + (1 species) + (1>tag)$
50	$Y \sim size * wd + sm + dmax + (1 species) + (1>tag)$
51	$Y \sim size * wd + sm + lma + dmax + (1 species) + (1>tag)$
52	$Y \sim size * wd + sm + size * lma + dmax + (1 species) + (1>tag)$
53	$Y \sim size * wd + size * sm + dmax + (1 species) + (1>tag)$
54	$Y \sim size * wd + size * sm + lma + dmax + (1 species) + (1>tag)$
55	$Y \sim size * wd + size * sm + size * lma + dmax + (1 species) + (1>tag)$
56	$Y \sim size * dmax + (1 species) + (1>tag)$
57	$Y \sim size + lma + size * dmax + (1 species) + (1>tag)$
58	$Y \sim size * lma + size * dmax + (1 species) + (1>tag)$
59	$Y \sim size + sm + size * dmax + (1 species) + (1>tag)$
60	$Y \sim size + sm + lma + size * dmax + (1 species) + (1>tag)$
61	$Y \sim size + sm + size * lma + size * dmax + (1 species) + (1>tag)$
62	$Y \sim size * sm + size * dmax + (1 species) + (1>tag)$
63	$Y \sim size * sm + lma + size * dmax + (1 species) + (1>tag)$
64	$Y \sim size * sm + size * lma + size * dmax + (1 species) + (1>tag)$
65	$Y \sim size + wd + size * dmax + (1 species) + (1>tag)$
66	$Y \sim size + wd + lma + size * dmax + (1 species) + (1>tag)$
67	$Y \sim size + wd + size * lma + size * dmax + (1 species) + (1>tag)$
68	$Y \sim size + wd + sm + size * dmax + (1 species) + (1>tag)$
69	$Y \sim size + wd + sm + lma + size * dmax + (1 species) + (1>tag)$
70	$Y \sim size + wd + sm + size * lma + size * dmax + (1 species) + (1>tag)$
71	$Y \sim size + wd + size * sm + size * dmax + (1 species) + (1>tag)$
72	$Y \sim size + wd + size * sm + lma + size * dmax + (1 species) + (1>tag)$
73	$Y \sim size + wd + size * sm + size * lma + size * dmax + (1 species) + (1>tag)$
74	$Y \sim size * wd + size * dmax + (1 species) + (1>tag)$
75	$Y \sim size * wd + lma + size * dmax + (1 species) + (1>tag)$
76	$Y \sim size * wd + size * lma + size * dmax + (1 species) + (1>tag)$
77	$Y \sim size * wd + sm + size * dmax + (1 species) + (1>tag)$
78	$Y \sim size * wd + sm + lma + size * dmax + (1 species) + (1>tag)$
79	$Y \sim size * wd + sm + size * lma + size * dmax + (1 species) + (1>tag)$
80	$Y \sim size * wd + size * sm + size * dmax + (1 species) + (1>tag)$
81	$Y \sim size * wd + size * sm + lma + size * dmax + (1 species) + (1>tag)$
82	$Y \sim size * wd + size * sm + size * lma + size * dmax + (1 species) + (1>tag)$

Table S3. All evaluated model forms, model weights, and ΔAIC values for the seed production analysis (f_{seeds}).

formulas	weight	ΔAIC
$fec \sim sm + dmax + lma$	0.212	0.000
$fec \sim sm + dmax + wd$	0.203	0.091
$fec \sim sm + lma$	0.178	0.354
$fec \sim sm + dmax$	0.120	1.144
$fec \sim sm + wd$	0.087	1.778
$fec \sim sm + dmax + wd + lma$	0.084	1.859
$fec \sim sm + lma + wd$	0.072	2.166
$fec \sim sm$	0.043	3.211
$fec \sim lma$	0.001	11.975
$fec \sim lma + wd$	0.000	12.628
$fec \sim wd$	0.000	13.034
$fec \sim dmax + wd$	0.000	13.535
$fec \sim dmax + lma$	0.000	13.779
$fec \sim dmax + lma + wd$	0.000	14.241
$fec \sim 1$	0.000	19.228
$fec \sim dmax$	0.000	20.645

Table S4. All evaluated model forms, model weights, and ΔAIC values for the seedling establishment analysis.

formulas	weight	ΔAIC
$qlogis(p) \sim sm + dmax$	0.484	0.000
$qlogis(p) \sim sm + dmax + wd$	0.246	1.356
$qlogis(p) \sim sm + dmax + lma$	0.178	1.999
$qlogis(p) \sim sm + dmax + wd + lma$	0.093	3.303
$qlogis(p) \sim dmax + wd$	0.000	31.452
$qlogis(p) \sim dmax + lma + wd$	0.000	33.443
$qlogis(p) \sim dmax$	0.000	34.448
$qlogis(p) \sim dmax + lma$	0.000	35.980
$qlogis(p) \sim sm + wd$	0.000	39.262
$qlogis(p) \sim sm + lma$	0.000	39.317
$qlogis(p) \sim sm + lma + wd$	0.000	39.588
$qlogis(p) \sim sm$	0.000	40.278
$log(p) \sim 1$	0.000	47.684
$qlogis(p) \sim wd$	0.000	48.810
$qlogis(p) \sim lma + wd$	0.000	49.492
$qlogis(p) \sim lma$	0.000	51.928

Table S5. Evaluated model forms, model weights, and ΔAIC values for the seedling growth analysis, for the top 30 models (out of 82). A full list of model forms can be found in table S2.

formulas	weight	ΔAIC
$growth \sim height * wd + height * sm + lma + dmax + (1 species) + (1>tag)$	0.599	0.000
$growth \sim height * wd + height * sm + lma + (1 species) + (1>tag)$	0.166	2.567
$growth \sim height * wd + height * sm + dmax + (1 species) + (1>tag)$	0.143	2.870
$growth \sim height * wd + height * sm + (1 species) + (1>tag)$	0.041	5.368
$growth \sim height * wd + height * sm + height * lma + dmax + (1 species) + (1>tag)$	0.021	6.727
$growth \sim height * wd + height * sm + height * lma + height * dmax + (1 species) + (1>tag)$	0.020	6.752
$growth \sim height * wd + height * sm + height * lma + (1 species) + (1>tag)$	0.006	9.293
$growth \sim height * wd + height * sm + lma + height * dmax + (1 species) + (1>tag)$	0.004	10.255
$growth \sim height * wd + height * sm + height * dmax + (1 species) + (1>tag)$	0.001	13.125
$growth \sim height + wd + height * sm + lma + dmax + (1 species) + (1>tag)$	0.000	16.569
$growth \sim height + wd + height * sm + lma + (1 species) + (1>tag)$	0.000	19.128
$growth \sim height + wd + height * sm + dmax + (1 species) + (1>tag)$	0.000	19.429
$growth \sim height + wd + height * sm + (1 species) + (1>tag)$	0.000	21.918
$growth \sim height + wd + height * sm + lma + height * dmax + (1 species) + (1>tag)$	0.000	22.950
$growth \sim height * sm + lma + dmax + (1 species) + (1>tag)$	0.000	24.422
$growth \sim height + wd + height * sm + height * dmax + (1 species) + (1>tag)$	0.000	25.810
$growth \sim height * sm + lma + (1 species) + (1>tag)$	0.000	27.096
$growth \sim height * sm + dmax + (1 species) + (1>tag)$	0.000	27.599
$growth \sim height * sm + (1 species) + (1>tag)$	0.000	30.311
$growth \sim height * sm + lma + height * dmax + (1 species) + (1>tag)$	0.000	30.802
$growth \sim height + wd + height * sm + height * lma + dmax + (1 species) + (1>tag)$	0.000	31.209
$growth \sim height + wd + height * sm + height * lma + (1 species) + (1>tag)$	0.000	33.768
$growth \sim height * sm + height * dmax + (1 species) + (1>tag)$	0.000	33.972
$growth \sim height + wd + height * sm + height * lma + height * dmax + (1 species) + (1>tag)$	0.000	34.538
$growth \sim height * sm + height * lma + dmax + (1 species) + (1>tag)$	0.000	39.062
$growth \sim height * sm + height * lma + (1 species) + (1>tag)$	0.000	41.735
$growth \sim height * sm + height * lma + height * dmax + (1 species) + (1>tag)$	0.000	42.380
$growth \sim height * wd + sm + height * lma + dmax + (1 species) + (1>tag)$	0.000	61.905
$growth \sim height * wd + sm + height * lma + (1 species) + (1>tag)$	0.000	64.478
$growth \sim height * wd + sm + lma + dmax + (1 species) + (1>tag)$	0.000	65.205

Table S6. Evaluated model forms, model weights, and ΔAIC values for the seedling survival analysis, for the top 30 models (out of 82). A full list of model forms can be found in table S2.

formulas	weight	ΔAIC
<i>survive</i> ~ <i>height</i> * <i>wd</i> + <i>height</i> * <i>sm</i> + <i>height</i> * <i>dmax</i> + <i>height</i> * <i>lma</i> + (1 <i>species</i>) + (1 <i>tag</i>)	1.000	0.000
<i>survive</i> ~ <i>height</i> * <i>wd</i> + <i>height</i> * <i>sm</i> + <i>height</i> * <i>dmax</i> + (1 <i>species</i>) + (1 <i>tag</i>)	0.000	81.243
<i>survive</i> ~ <i>height</i> * <i>wd</i> + <i>height</i> * <i>sm</i> + <i>height</i> * <i>dmax</i> + <i>lma</i> + (1 <i>species</i>) + (1 <i>tag</i>)	0.000	83.232
<i>survive</i> ~ <i>height</i> + <i>wd</i> + <i>height</i> * <i>sm</i> + <i>height</i> * <i>lma</i> + <i>dmax</i> + (1 <i>species</i>) + (1 <i>tag</i>)	0.000	114.721
<i>survive</i> ~ <i>height</i> + <i>wd</i> + <i>height</i> * <i>sm</i> + <i>height</i> * <i>lma</i> + (1 <i>species</i>) + (1 <i>tag</i>)	0.000	120.806
<i>survive</i> ~ <i>height</i> + <i>wd</i> + <i>height</i> * <i>lma</i> + <i>height</i> * <i>dmax</i> + (1 <i>species</i>) + (1 <i>tag</i>)	0.000	205.165
<i>survive</i> ~ <i>height</i> * <i>wd</i> + <i>height</i> * <i>lma</i> + <i>height</i> * <i>dmax</i> + (1 <i>species</i>) + (1 <i>tag</i>)	0.000	206.284
<i>survive</i> ~ <i>height</i> + <i>wd</i> + <i>sm</i> + <i>height</i> * <i>lma</i> + <i>height</i> * <i>dmax</i> + (1 <i>species</i>) + (1 <i>tag</i>)	0.000	207.109
<i>survive</i> ~ <i>height</i> * <i>wd</i> + <i>sm</i> + <i>height</i> * <i>lma</i> + <i>height</i> * <i>dmax</i> + (1 <i>species</i>) + (1 <i>tag</i>)	0.000	208.230
<i>survive</i> ~ <i>height</i> + <i>sm</i> + <i>height</i> * <i>lma</i> + <i>height</i> * <i>dmax</i> + (1 <i>species</i>) + (1 <i>tag</i>)	0.000	231.883
<i>survive</i> ~ <i>height</i> * <i>wd</i> + (1 <i>species</i>) + <i>height</i> * <i>dmax</i> + (1 <i>tag</i>)	0.000	279.614
<i>survive</i> ~ <i>height</i> * <i>wd</i> + <i>sm</i> + <i>height</i> * <i>dmax</i> + (1 <i>species</i>) + (1 <i>tag</i>)	0.000	281.542
<i>survive</i> ~ <i>height</i> * <i>wd</i> + <i>lma</i> + <i>height</i> * <i>dmax</i> + (1 <i>species</i>) + (1 <i>tag</i>)	0.000	281.589
<i>survive</i> ~ <i>height</i> * <i>wd</i> + <i>sm</i> + <i>lma</i> + <i>height</i> * <i>dmax</i> + (1 <i>species</i>) + (1 <i>tag</i>)	0.000	283.529
<i>survive</i> ~ <i>height</i> + <i>lma</i> + <i>height</i> * <i>dmax</i> + (1 <i>species</i>) + (1 <i>tag</i>)	0.000	314.015
<i>survive</i> ~ <i>height</i> + <i>wd</i> + <i>height</i> * <i>lma</i> + <i>dmax</i> + (1 <i>species</i>) + (1 <i>tag</i>)	0.000	517.184
<i>survive</i> ~ <i>height</i> + <i>wd</i> + <i>sm</i> + <i>height</i> * <i>lma</i> + <i>dmax</i> + (1 <i>species</i>) + (1 <i>tag</i>)	0.000	519.107
<i>survive</i> ~ <i>height</i> + <i>wd</i> + <i>height</i> * <i>lma</i> + (1 <i>species</i>) + (1 <i>tag</i>)	0.000	525.973
<i>survive</i> ~ <i>height</i> + <i>wd</i> + <i>sm</i> + <i>height</i> * <i>lma</i> + (1 <i>species</i>) + (1 <i>tag</i>)	0.000	526.077
<i>survive</i> ~ <i>height</i> * <i>wd</i> + <i>lma</i> + (1 <i>species</i>) + (1 <i>tag</i>)	0.000	526.516
<i>survive</i> ~ <i>height</i> * <i>lma</i> + <i>dmax</i> + (1 <i>species</i>) + (1 <i>tag</i>)	0.000	542.056
<i>survive</i> ~ <i>height</i> + <i>sm</i> + <i>height</i> * <i>lma</i> + <i>dmax</i> + (1 <i>species</i>) + (1 <i>tag</i>)	0.000	543.147
<i>survive</i> ~ <i>height</i> + <i>lma</i> + (1 <i>species</i>) + (1 <i>tag</i>)	0.000	549.065
<i>survive</i> ~ <i>height</i> * <i>lma</i> + (1 <i>species</i>) + (1 <i>tag</i>)	0.000	549.670
<i>survive</i> ~ <i>height</i> + <i>sm</i> + <i>height</i> * <i>lma</i> + (1 <i>species</i>) + (1 <i>tag</i>)	0.000	551.647
<i>survive</i> ~ 1 + (1 <i>species</i>) + (1 <i>tag</i>)	0.000	2721.140
<i>survive</i> ~ <i>height</i> + <i>wd</i> + <i>height</i> * <i>sm</i> + <i>height</i> * <i>lma</i> + <i>height</i> * <i>dmax</i> + (1 <i>species</i>) + (1 <i>tag</i>)	0.000	4640.336
<i>survive</i> ~ <i>height</i> + <i>wd</i> + <i>height</i> * <i>sm</i> + <i>lma</i> + <i>height</i> * <i>dmax</i> + (1 <i>species</i>) + (1 <i>tag</i>)	0.000	4752.207
<i>survive</i> ~ <i>height</i> + <i>wd</i> + <i>height</i> * <i>sm</i> + <i>height</i> * <i>dmax</i> + (1 <i>species</i>) + (1 <i>tag</i>)	0.000	4763.285
<i>survive</i> ~ <i>height</i> + <i>wd</i> + <i>height</i> * <i>sm</i> + <i>lma</i> + <i>dmax</i> + (1 <i>species</i>) + (1 <i>tag</i>)	0.000	4820.751

Table S7. Evaluated model forms, model weights, and ΔAIC values for the tree growth analysis, for the top 30 models (out of 82). A full list of model forms can be found in table S2. The variable BA refers to basal area (mm^2).

formulas	weight	ΔAIC
$growth \sim (BA) * wd + (BA) * sm + (BA) * lma + BA * dmax + (1 species) + (1>tag)$	1.000	0.000
$growth \sim (BA) * wd + (BA) * sm + lma + BA * dmax + (1 species) + (1>tag)$	0.000	722.011
$growth \sim (BA) * wd + (BA) * sm + BA * dmax + (1 species) + (1>tag)$	0.000	727.452
$growth \sim (BA) * wd + (BA) * sm + (BA) * lma + dmax + (1 species) + (1>tag)$	0.000	1434.112
$growth \sim (BA) * wd + (BA) * sm + (BA) * lma + (1 species) + (1>tag)$	0.000	1455.667
$growth \sim (BA) * wd + sm + (BA) * lma + BA * dmax + (1 species) + (1>tag)$	0.000	1732.065
$growth \sim (BA) * wd + (BA) * lma + BA * dmax + (1 species) + (1>tag)$	0.000	1745.412
$growth \sim (BA) * wd + (BA) * sm + (BA) * lma + BA * dmax + (1 species) + (1>tag)$	0.000	1809.328
$growth \sim (BA) * sm + (BA) * lma + BA * dmax + (1 species) + (1>tag)$	0.000	1857.663
$growth \sim (BA) * wd + sm + lma + BA * dmax + (1 species) + (1>tag)$	0.000	2075.792
$growth \sim (BA) * wd + sm + BA * dmax + (1 species) + (1>tag)$	0.000	2080.841
$growth \sim (BA) * wd + lma + BA * dmax + (1 species) + (1>tag)$	0.000	2088.759
$growth \sim (BA) * wd + BA * dmax + (1 species) + (1>tag)$	0.000	2094.665
$growth \sim (BA) * wd + (BA) * sm + lma + BA * dmax + (1 species) + (1>tag)$	0.000	2680.176
$growth \sim (BA) * wd + (BA) * sm + BA * dmax + (1 species) + (1>tag)$	0.000	2685.318
$growth \sim (BA) * sm + lma + BA * dmax + (1 species) + (1>tag)$	0.000	2730.689
$growth \sim (BA) * sm + BA * dmax + (1 species) + (1>tag)$	0.000	2736.455
$growth \sim (BA) * wd + (BA) * sm + lma + dmax + (1 species) + (1>tag)$	0.000	2785.345
$growth \sim (BA) * wd + (BA) * sm + dmax + (1 species) + (1>tag)$	0.000	2791.423
$growth \sim (BA) * wd + (BA) * sm + lma + (1 species) + (1>tag)$	0.000	2807.186
$growth \sim (BA) * wd + (BA) * sm + (1 species) + (1>tag)$	0.000	2812.767
$growth \sim (BA) * wd + sm + (BA) * lma + BA * dmax + (1 species) + (1>tag)$	0.000	3643.162
$growth \sim (BA) * wd + (BA) * lma + BA * dmax + (1 species) + (1>tag)$	0.000	3656.590
$growth \sim (BA) * sm + (BA) * lma + BA * dmax + (1 species) + (1>tag)$	0.000	3689.670
$growth \sim (BA) * lma + BA * dmax + (1 species) + (1>tag)$	0.000	3707.314
$growth \sim (BA) * wd + sm + lma + BA * dmax + (1 species) + (1>tag)$	0.000	4086.731
$growth \sim (BA) * wd + sm + BA * dmax + (1 species) + (1>tag)$	0.000	4091.493
$growth \sim (BA) * wd + lma + BA * dmax + (1 species) + (1>tag)$	0.000	4099.658
$growth \sim (BA) * wd + BA * dmax + (1 species) + (1>tag)$	0.000	4105.179
$growth \sim (BA) * sm + lma + BA * dmax + (1 species) + (1>tag)$	0.000	4135.374

Table S8. Evaluated model forms, model weights, and ΔAIC values for the tree survival analysis, for the top 30 models (out of 82). A full list of model forms can be found in table S2.

formulas	weight	ΔAIC
$surv \sim dbh * wd + dbh * sm + dbh * lma + dbh * dmax + (1 species) + (1>tag)$	0.997	0.000
$surv \sim dbh * wd + dbh * sm + lma + dbh * dmax + (1 species) + (1>tag)$	0.003	11.965
$surv \sim dbh + wd + dbh * sm + dbh * lma + dbh * dmax + (1 species) + (1>tag)$	0.000	75.464
$surv \sim dbh + wd + dbh * sm + lma + dbh * dmax + (1 species) + (1>tag)$	0.000	83.261
$surv \sim dbh * wd + sm + dbh * lma + dbh * dmax + (1 species) + (1>tag)$	0.000	155.016
$surv \sim dbh * wd + sm + lma + dbh * dmax + (1 species) + (1>tag)$	0.000	167.228
$surv \sim dbh + wd + sm + dbh * lma + dbh * dmax + (1 species) + (1>tag)$	0.000	274.457
$surv \sim dbh + wd + sm + lma + dbh * dmax + (1 species) + (1>tag)$	0.000	279.971
$surv \sim dbh * wd + dbh * sm + dbh * dmax + (1 species) + (1>tag)$	0.000	606.679
$surv \sim dbh + wd + dbh * sm + dbh * dmax + (1 species) + (1>tag)$	0.000	685.003
$surv \sim dbh * wd + sm + dbh * dmax + (1 species) + (1>tag)$	0.000	771.537
$surv \sim dbh + wd + sm + dbh * dmax + (1 species) + (1>tag)$	0.000	898.364
$surv \sim dbh * wd + dbh * sm + lma + (1 species) + (1>tag)$	0.000	1003.192
$surv \sim dbh * wd + dbh * sm + dbh * lma + (1 species) + (1>tag)$	0.000	1003.911
$surv \sim dbh * wd + dbh * sm + lma + dmax + (1 species) + (1>tag)$	0.000	1004.600
$surv \sim dbh * wd + dbh * sm + dbh * lma + dmax + (1 species) + (1>tag)$	0.000	1005.322
$surv \sim dbh * wd + sm + lma + (1 species) + (1>tag)$	0.000	1140.664
$surv \sim dbh * wd + sm + dbh * lma + (1 species) + (1>tag)$	0.000	1140.977
$surv \sim dbh * wd + sm + lma + dmax + (1 species) + (1>tag)$	0.000	1142.302
$surv \sim dbh * wd + sm + dbh * lma + dmax + (1 species) + (1>tag)$	0.000	1142.616
$surv \sim dbh + wd + dbh * sm + dbh * lma + (1 species) + (1>tag)$	0.000	1198.664
$surv \sim dbh + wd + dbh * sm + dbh * lma + dmax + (1 species) + (1>tag)$	0.000	1200.094
$surv \sim dbh + wd + dbh * sm + lma + (1 species) + (1>tag)$	0.000	1216.958
$surv \sim dbh + wd + dbh * sm + lma + dmax + (1 species) + (1>tag)$	0.000	1218.383
$surv \sim dbh + wd + sm + dbh * lma + (1 species) + (1>tag)$	0.000	1366.128
$surv \sim dbh + wd + sm + dbh * lma + dmax + (1 species) + (1>tag)$	0.000	1367.800
$surv \sim dbh + wd + sm + lma + (1 species) + (1>tag)$	0.000	1385.911
$surv \sim dbh + wd + sm + lma + dmax + (1 species) + (1>tag)$	0.000	1387.589
$surv \sim dbh * wd + dbh * sm + (1 species) + (1>tag)$	0.000	1589.261
$surv \sim dbh * wd + dbh * sm + dmax + (1 species) + (1>tag)$	0.000	1590.885

Table S9. Evaluated model forms, model weights, and ΔAIC values for the reproduction analysis, for the top 30 models (out of 82). A full list of model forms can be found in table S2.

formulas	weight	ΔAIC
$repr \sim dbh * sm + dbh * dmax + lma + (1 species) + (1>tag)$	0.232	0.000
$repr \sim dbh * sm + dbh * dmax + dbh * lma + (1 species) + (1>tag)$	0.158	0.775
$repr \sim dbh * wd + dbh * sm + dbh * lma + dbh * dmax + (1 species) + (1>tag)$	0.149	0.895
$repr \sim dbh + wd + dbh * sm + dbh * dmax + lma + (1 species) + (1>tag)$	0.104	1.601
$repr \sim dbh * wd + dbh * sm + lma + dbh * dmax + (1 species) + (1>tag)$	0.097	1.741
$repr \sim dbh * sm + dbh * dmax + (1 species) + (1>tag)$	0.077	2.222
$repr \sim dbh + wd + dbh * sm + dbh * dmax + dbh * lma + (1 species) + (1>tag)$	0.071	2.361
$repr \sim dbh + wd + dbh * sm + dbh * dmax + (1 species) + (1>tag)$	0.055	2.878
$repr \sim dbh * wd + dbh * sm + dbh * dmax + (1 species) + (1>tag)$	0.055	2.885
$repr \sim dbh * lma + dbh * dmax + (1 species) + (1>tag)$	0.000	13.651
$repr \sim dbh * dmax + lma + (1 species) + (1>tag)$	0.000	13.751
$repr \sim dbh + wd + dbh * lma + dbh * dmax + (1 species) + (1>tag)$	0.000	15.238
$repr \sim dbh + wd + lma + dbh * dmax + (1 species) + (1>tag)$	0.000	15.352
$repr \sim dbh + sm + dbh * lma + dbh * dmax + (1 species) + (1>tag)$	0.000	15.601
$repr \sim dbh + sm + lma + dbh * dmax + (1 species) + (1>tag)$	0.000	15.680
$repr \sim dbh * wd + dbh * lma + dbh * dmax + (1 species) + (1>tag)$	0.000	16.003
$repr \sim dbh * dmax + (1 species) + (1>tag)$	0.000	16.543
$repr \sim dbh * wd + lma + dbh * dmax + (1 species) + (1>tag)$	0.000	17.059
$repr \sim dbh + wd + dbh * dmax + (1 species) + (1>tag)$	0.000	17.228
$repr \sim dbh + wd + sm + dbh * lma + dbh * dmax + (1 species) + (1>tag)$	0.000	17.231
$repr \sim dbh + wd + sm + lma + dbh * dmax + (1 species) + (1>tag)$	0.000	17.335
$repr \sim dbh * wd + sm + dbh * lma + dbh * dmax + (1 species) + (1>tag)$	0.000	17.999
$repr \sim dbh + sm + dbh * dmax + (1 species) + (1>tag)$	0.000	18.538
$repr \sim dbh * wd + dbh * dmax + (1 species) + (1>tag)$	0.000	18.896
$repr \sim dbh * wd + sm + lma + dbh * dmax + (1 species) + (1>tag)$	0.000	19.044
$repr \sim dbh + wd + sm + dbh * dmax + (1 species) + (1>tag)$	0.000	19.204
$repr \sim dbh * wd + sm + dbh * dmax + (1 species) + (1>tag)$	0.000	20.871
$repr \sim dbh * wd + dbh * sm + dbh * lma + dmax + (1 species) + (1>tag)$	0.000	260.580
$repr \sim dbh + wd + dbh * sm + dmax + dbh * lma + (1 species) + (1>tag)$	0.000	263.641
$repr \sim dbh * wd + dbh * sm + lma + dmax + (1 species) + (1>tag)$	0.000	264.562

S2 TABLES

Table S10. R^2 values for average models including only single traits for seed production and seedling establishment.

	dmax	lma	sm	wd
Fecundity	0.01	0.04	0.63	0.00
Establishment	0.20	0.05	0.33	0.10

Table S11. R^2 values at different sizes for average models including only single traits for seedlings. Dmax, LMA, SM and WD represent adult stature, leaf mass per area, seed mass and wood density.

Size (mm hght)	Dmax		LMA		SM		WD	
	Growth	Survival	Growth	Survival	Growth	Survival	Growth	Survival
200	0.283	0.283	0.002	0.022	0.103	0.053	0.151	0.219
260	0.261	0.261	0.002	0.032	0.114	0.036	0.14	0.263
320	0.234	0.234	0.003	0.041	0.104	0.021	0.142	0.305
380	0.126	0.126	0	0.018	0.086	0.002	0.173	0.357
440	0.1	0.1	0.001	0.017	0.081	0.01	0.174	0.385
500	0.08	0.08	0.002	0.016	0.074	0.021	0.168	0.405
560	0.063	0.063	0.003	0.014	0.066	0.036	0.161	0.418
620	0.064	0.064	0.005	0.015	0.058	0.042	0.152	0.42
680	0.054	0.054	0.008	0.014	0.037	0.06	0.141	0.42
740	0.041	0.041	0.01	0.012	0.031	0.074	0.124	0.431
800	0.04	0.04	0.009	0.01	0.026	0.082	0.116	0.429
860	0.032	0.032	0.008	0.008	0.019	0.092	0.101	0.423
920	0.027	0.027	0.01	0.008	0.012	0.1	0.086	0.42
980	0.028	0.028	0.011	0.02	0.008	0.094	0.068	0.408
1040	0.025	0.025	0.015	0.019	0.004	0.105	0.06	0.4
1100	0.024	0.024	0.007	0.015	0.008	0.11	0.067	0.407
1160	0.022	0.022	0.011	0.016	0.006	0.109	0.042	0.4
1220	0.019	0.019	0.004	0.015	0.005	0.104	0.027	0.393
1280	0.021	0.021	0.008	0.019	0.004	0.097	0.039	0.392
1340	0.03	0.03	0.003	0.011	0.003	0.087	0.009	0.451
1400	0.028	0.028	0.001	0.019	0.002	0.081	0.001	0.508
1460	0.032	0.032	0.011	0.021	0.011	0.068	0.004	0.502
1490	0.036	0.036	0.01	0.022	0.013	0.061	0.01	0.495

Table S12. R^2 values at different sizes from average models for growth, survival and reproduction including only single traits for trees (>1cm dbh). Dmax, LMA, SM and WD represent adult stature, leaf mass per area, seed mass and wood density.

Size (mm dbh)	Dmax				LMA				SM				WD			
	Growth	Survival	Repr.	Survival	Repr.	Survival	Repr.									
10	0.1108	0.0172	0.4429	0.0258	3e-04	0.4525	0.0564	0.1666	0.0269	0.3446	0.2765	0.3842				
40	0.1187	0.0062	0.4429	0.0091	4e-04	0.4525	0.0863	0.0938	0.0269	0.3596	0.2609	0.3842				
70	0.0701	0.0344	0.5423	0.0206	0.0068	0.3898	0.0799	0.0544	0.0035	0.4181	0.2547	0.1874				
100	0.0012	6e-04	0.5808	0.0257	0.0191	0.433	0.0532	0.0411	0.003	0.4112	0.2253	0.426				
130	0.025	0.0024	0.3845	0.0196	0.0214	0.1971	0.0208	0.0143	1e-04	0.371	0.193	0.1509				
160	0.0139	0.0164	0.3976	0.0046	0.018	0.0618	0.0184	0.0048	0.0095	0.2693	0.1712	0.0534				
190	0.0035	0.1314	0.2418	0.011	0.008	0.0423	0.0343	7e-04	7e-04	0.2859	0.1176	0.0175				
220	0.0096	0.1105	0.195	8e-04	0.0028	0.0611	0.0812	0.0048	0.0082	0.3293	0.0922	0.0028				
250	0.0418	0.2496	0.2374	0.0216	0.0025	0.0693	0.0716	1e-04	0.009	0.2707	0.0922	0.0046				

S3 FIGURES

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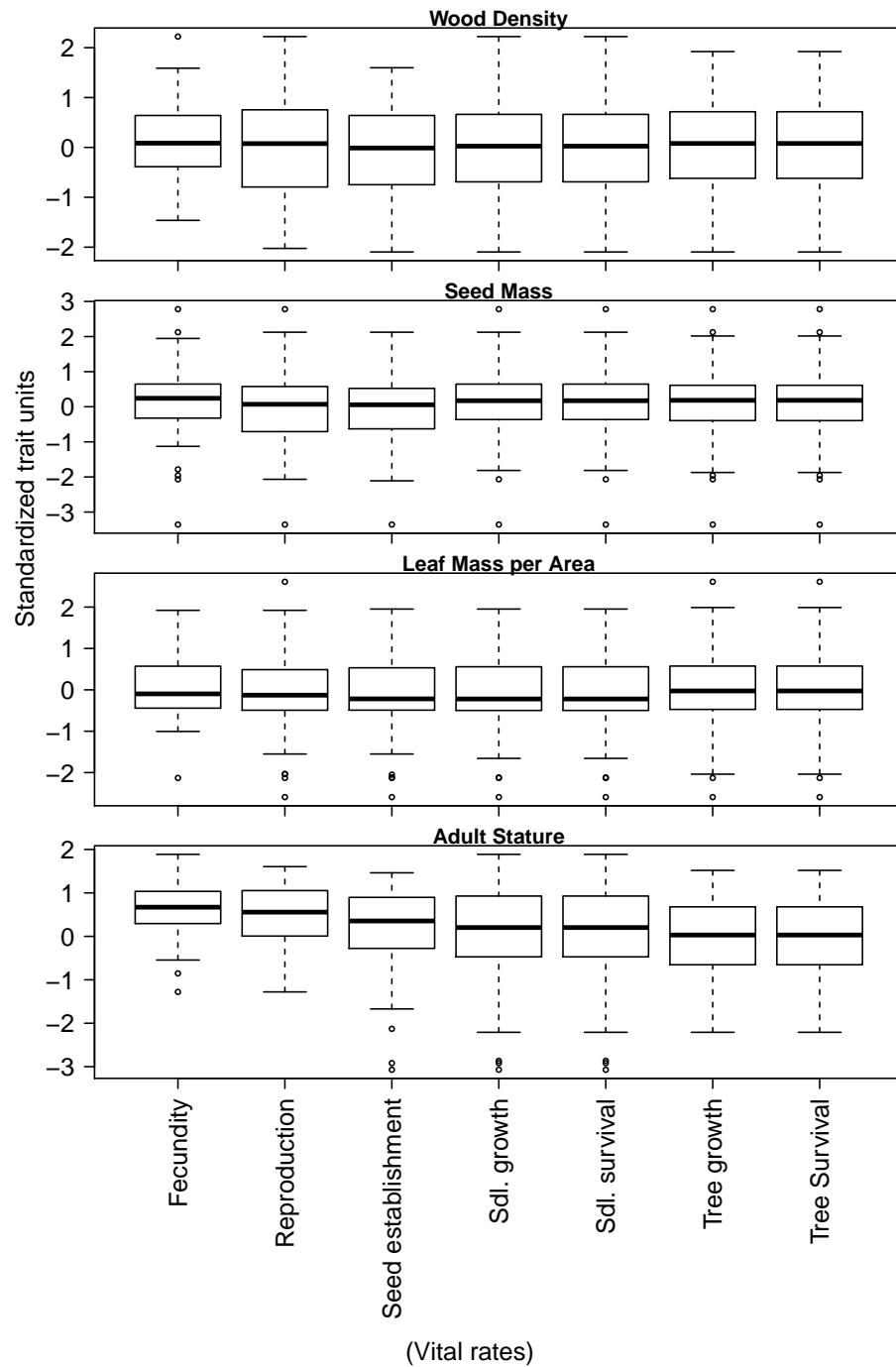


Figure S1. Boxplots showing the distribution of trait values (in standardized units) for each vital rate analysis. Each box plot within a panel corresponds to the distribution of trait values for the species used within that specific analysis.

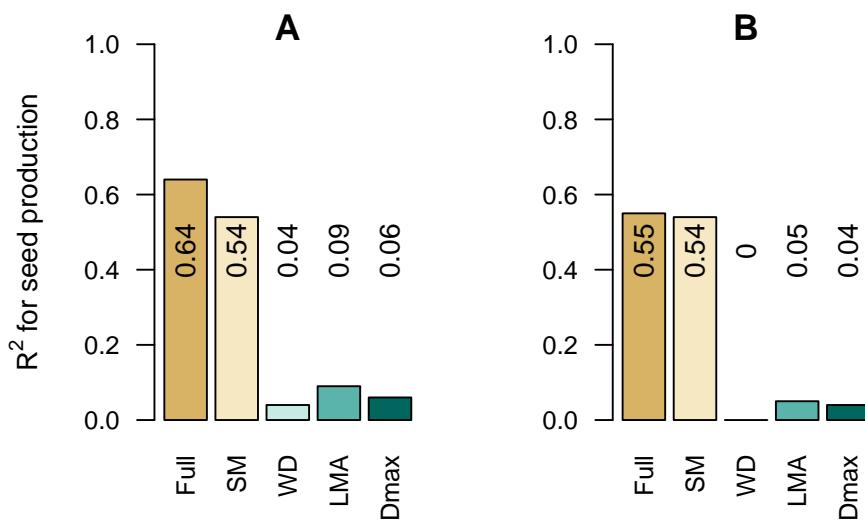


Figure S2. R^2 values for interspecific variation in seed production from averaged models for a single trait and for the full averaged model for all four traits, compared between seed production estimates obtained through inverse modeling (A, 18 species) or by estimating seed production per unit basal area as described in the main text (B, 38 species).

S3 FIGURES

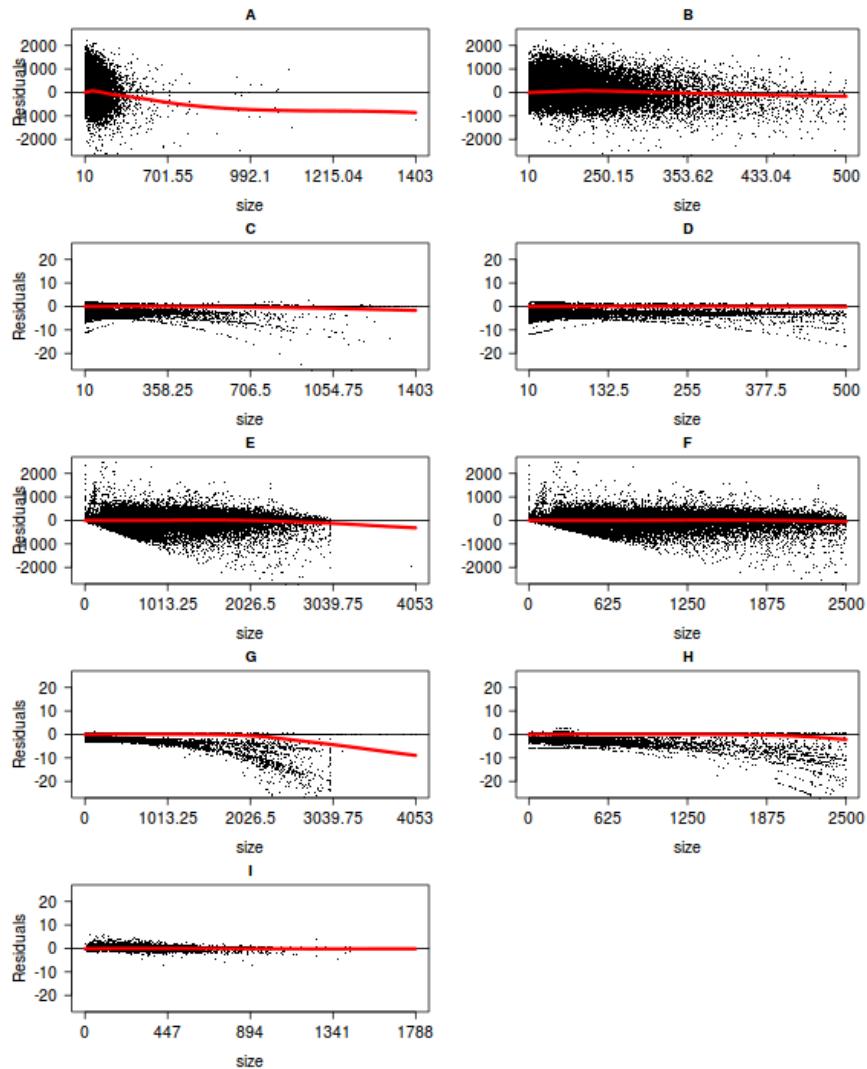
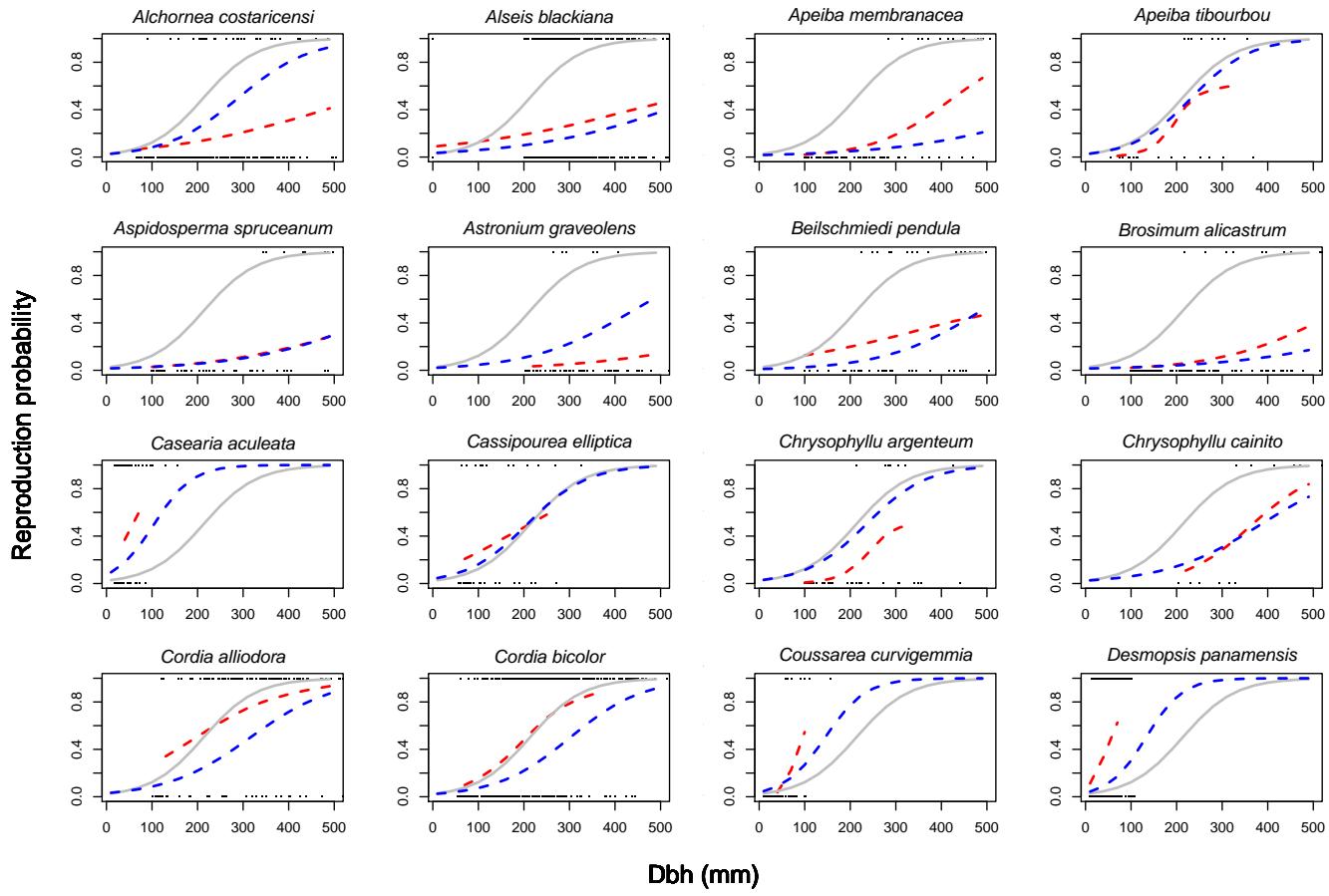


Figure S3. Plots of residuals of the full averaged model against size for tree growth (A,B), tree survival (C,D), seedling growth (E,F), seedling survival (G,H), and reproduction (I). Black dots indicate residual values from each model-averaged mixed-effect model (predicted - observed), while the red line is the moving average. The first column (A,C,E,G,I) shows residuals for models fit to the full datasets, while the second column (B,D,F,H) shows residuals for models fit to datasets truncated above at 500 mm diameter (B,D) or 2500 mm height (F, H) to avoid non-linearities with size.



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Figure S4. Observed and fitted proportion of individuals that are reproductive as a function of tree diameter (mm) for each species. Black dots show observations, red dashed lines show species-specific moving averages (from a Generalized Additive Model using a loess smoother), blue dashed lines show the fitted trait based average model, and grey lines show a fitted model based only on size (not on traits, thus identical for all species).

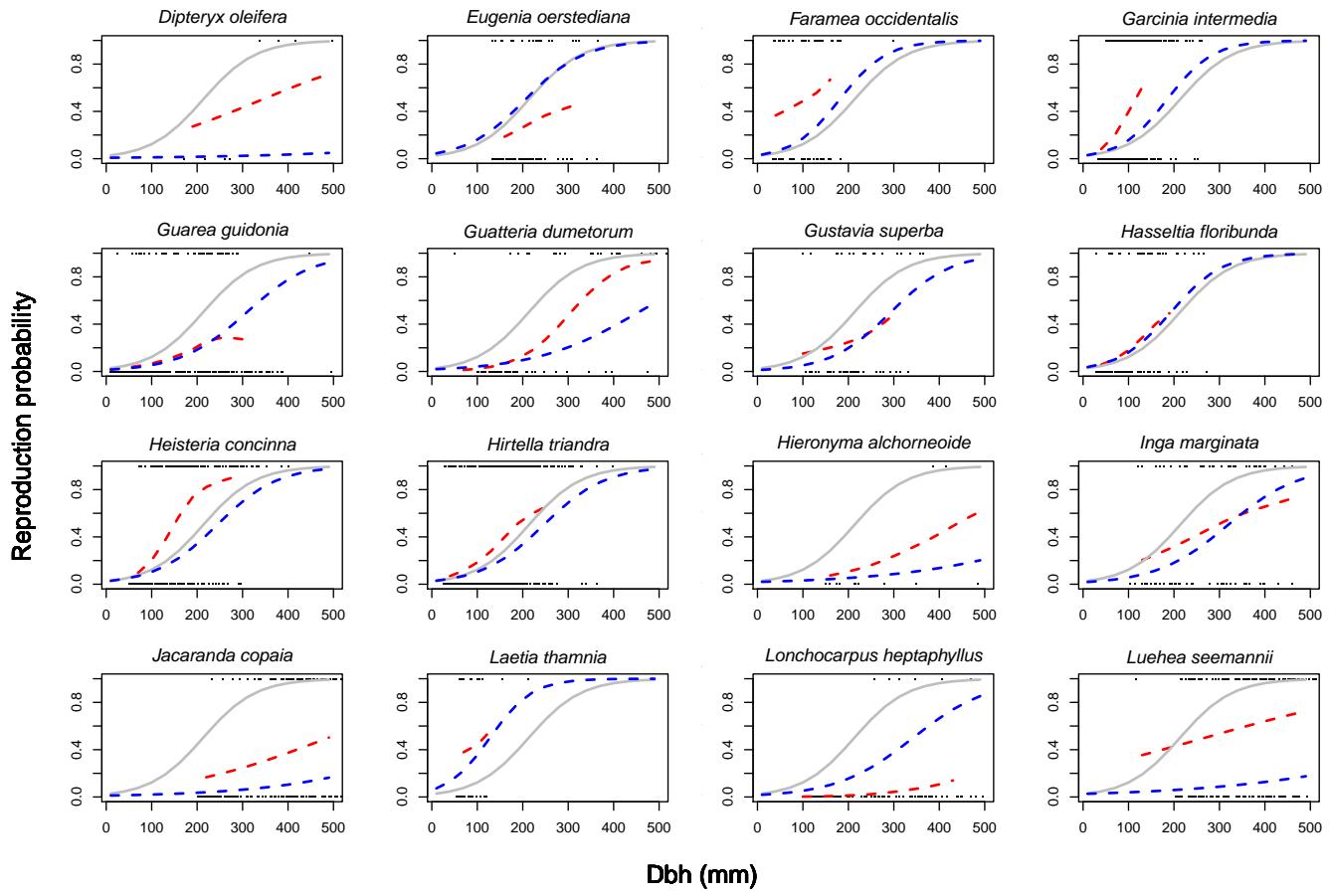


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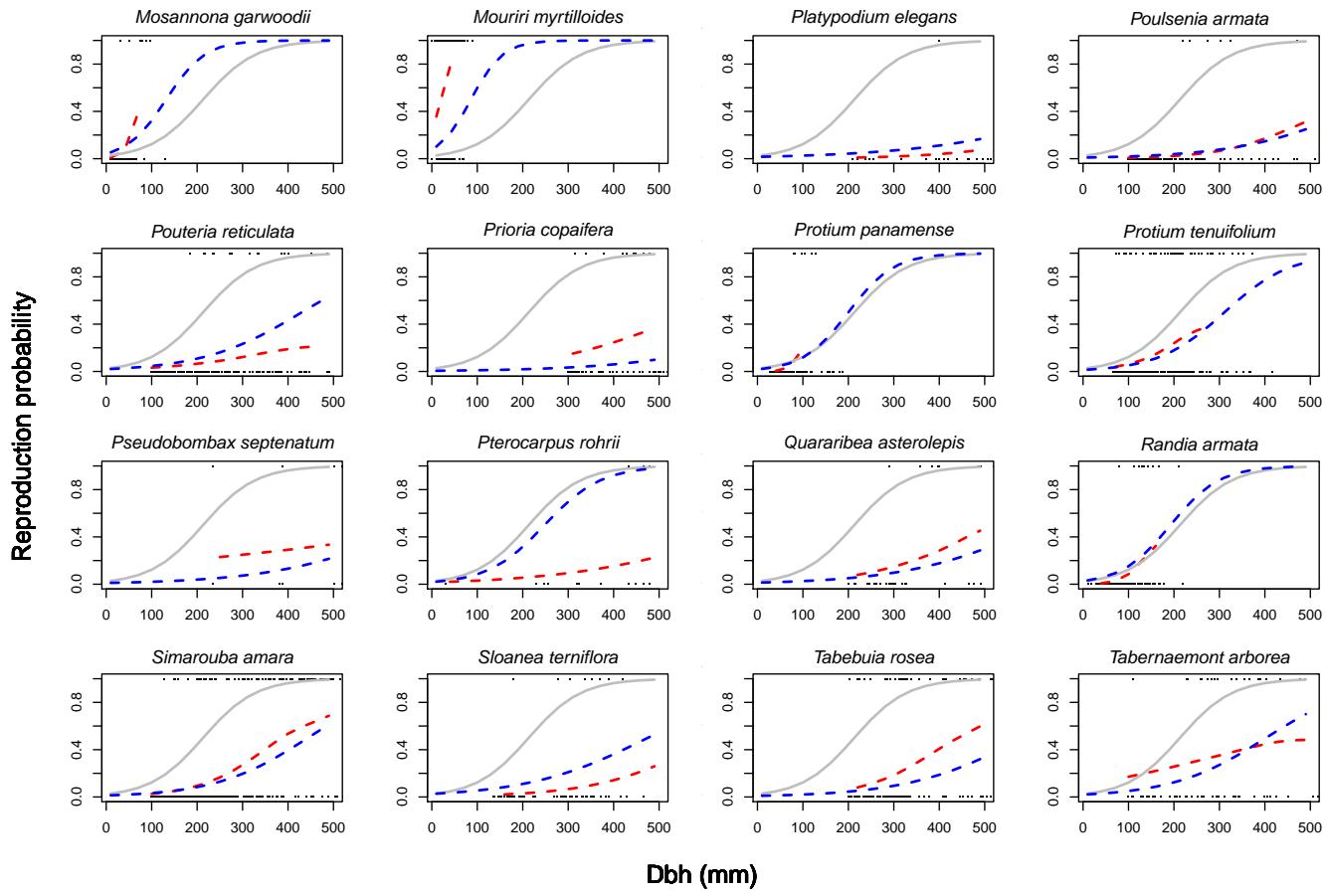


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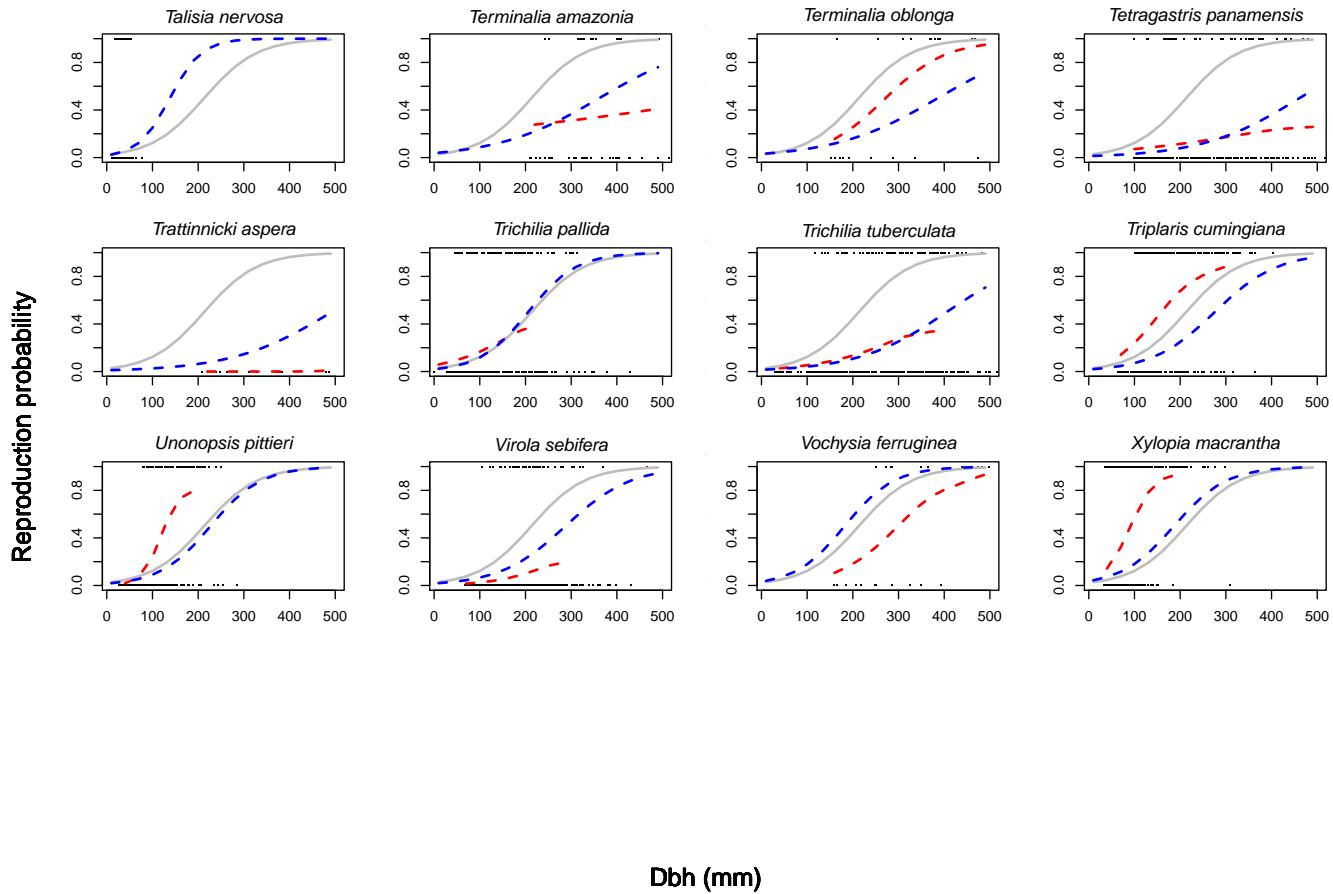


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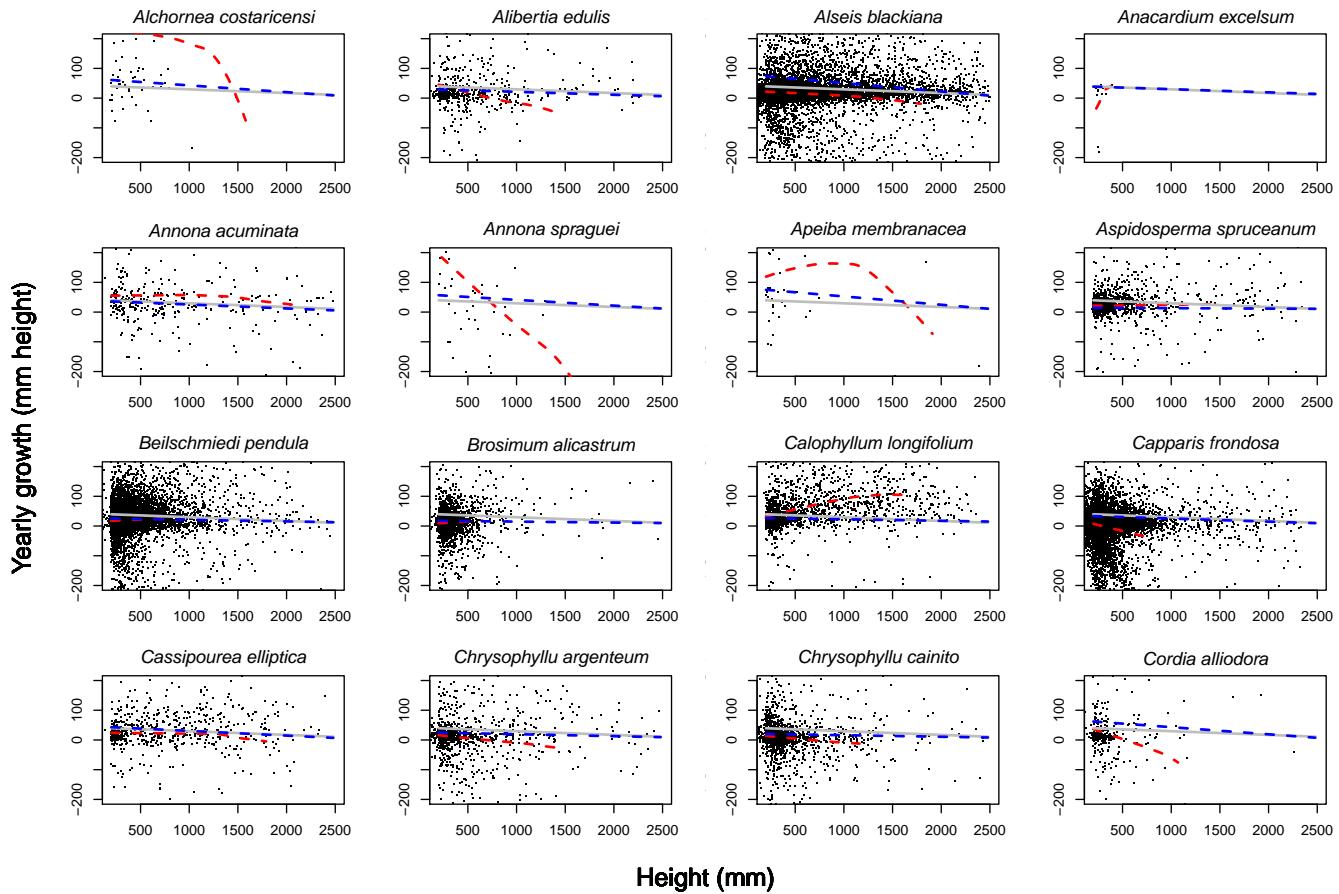


Figure S5. Observed and predicted annual seedling height growth (mm/yr) as a function of initial height (mm). Black dots show observations, red dashed lines show species-specific moving averages (from a Generalized Additive Model using a loess smoother), blue dashed lines show the fitted trait based average model, and grey lines show a fitted model based only on size (not on traits, thus identical for all species).

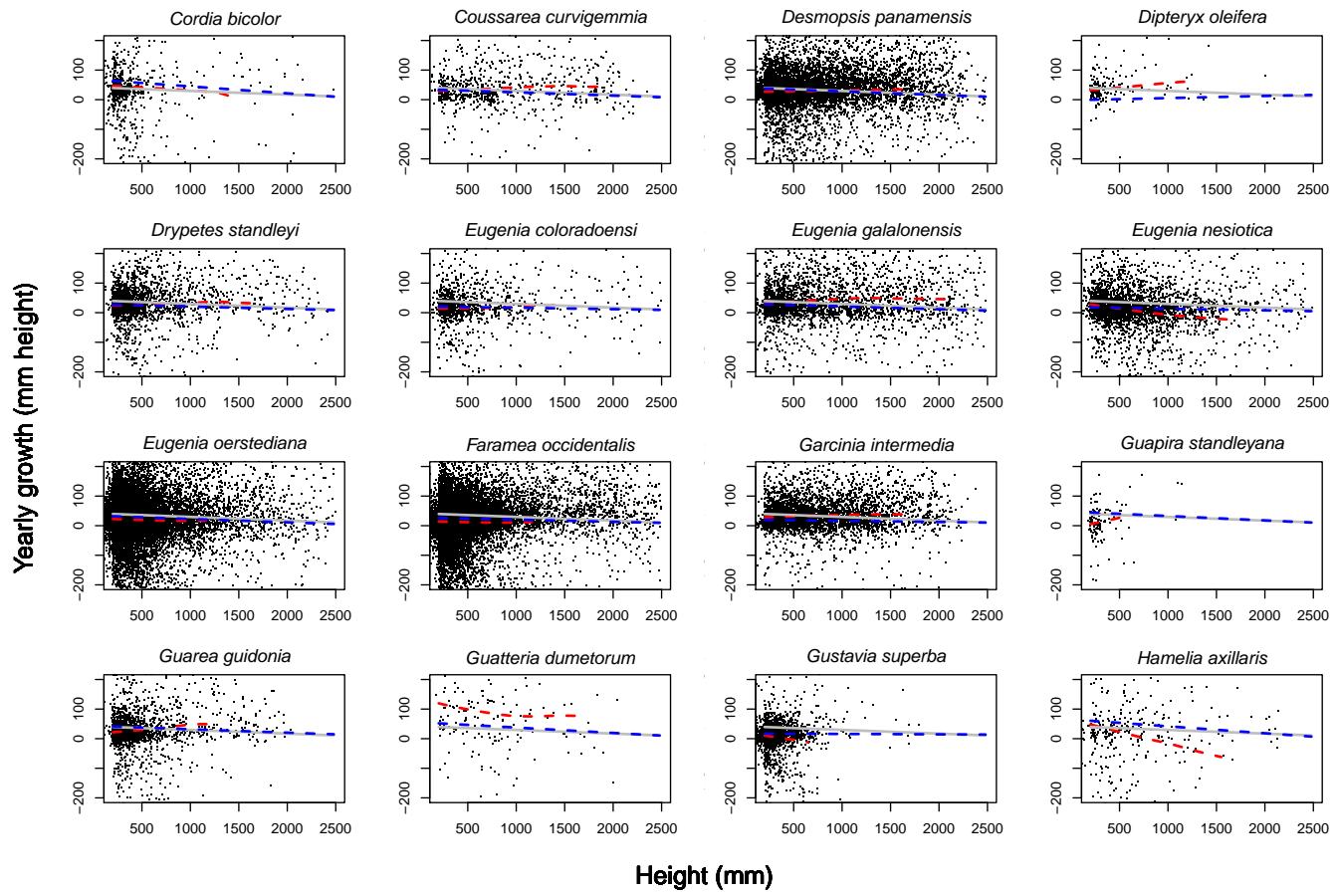


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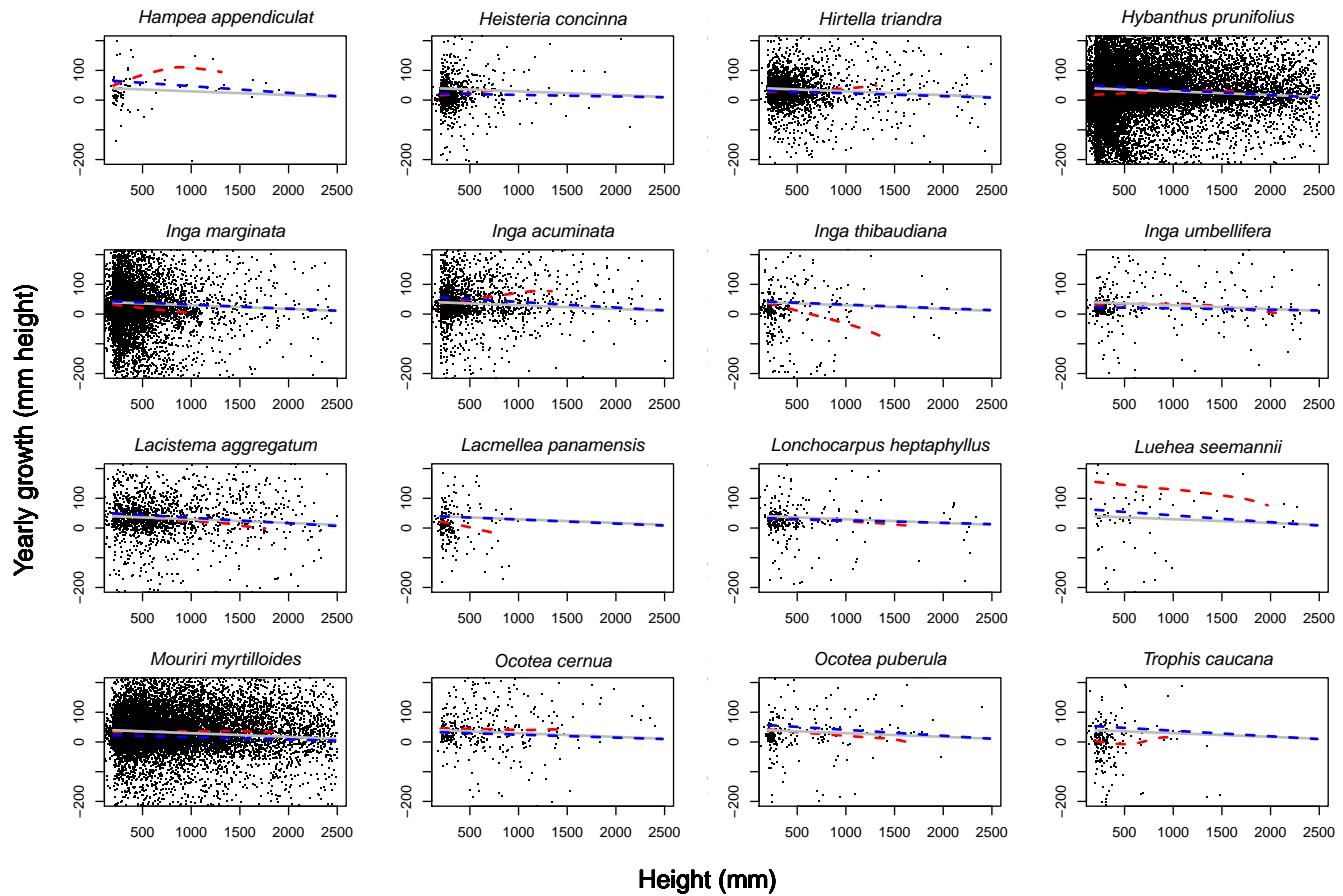


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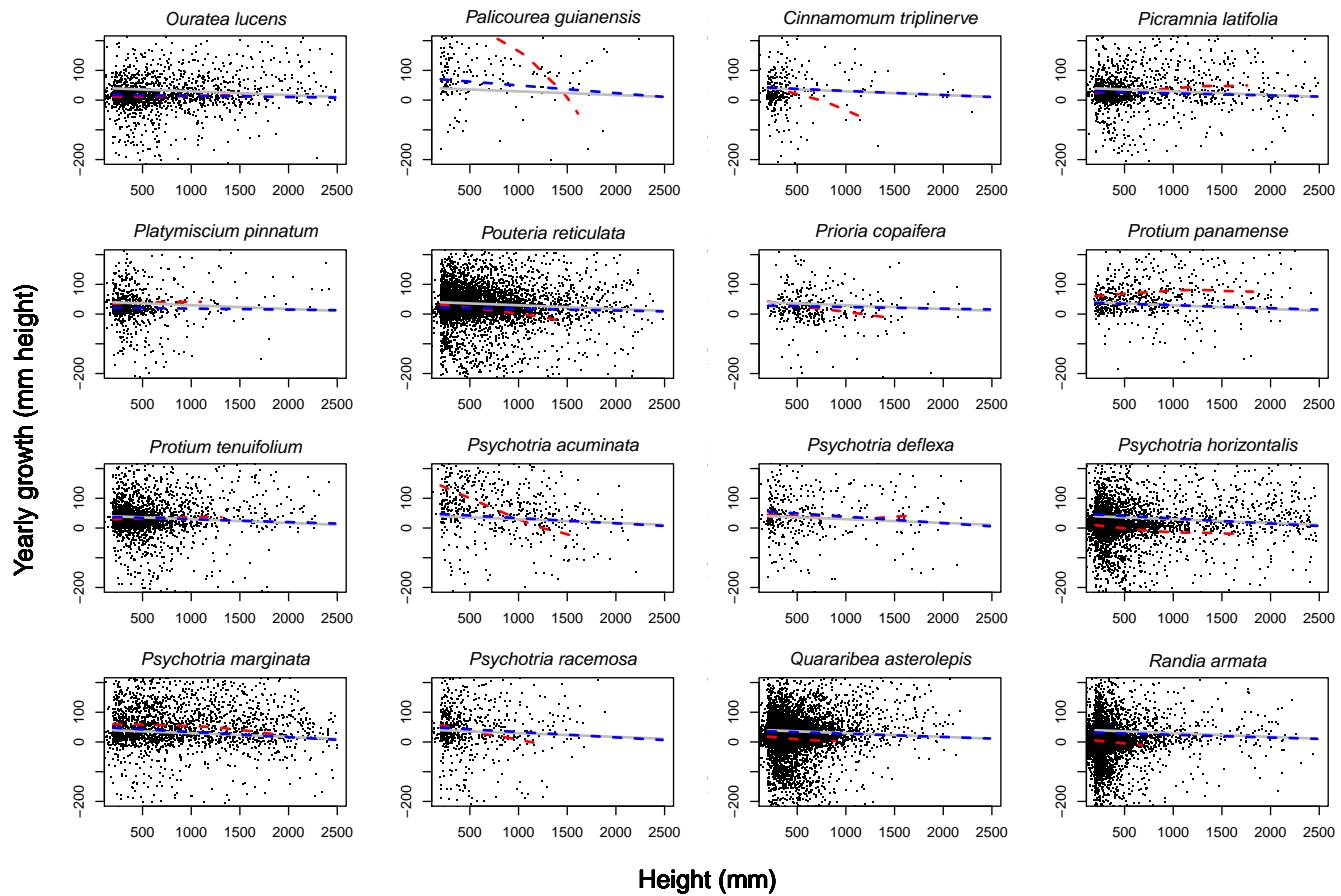


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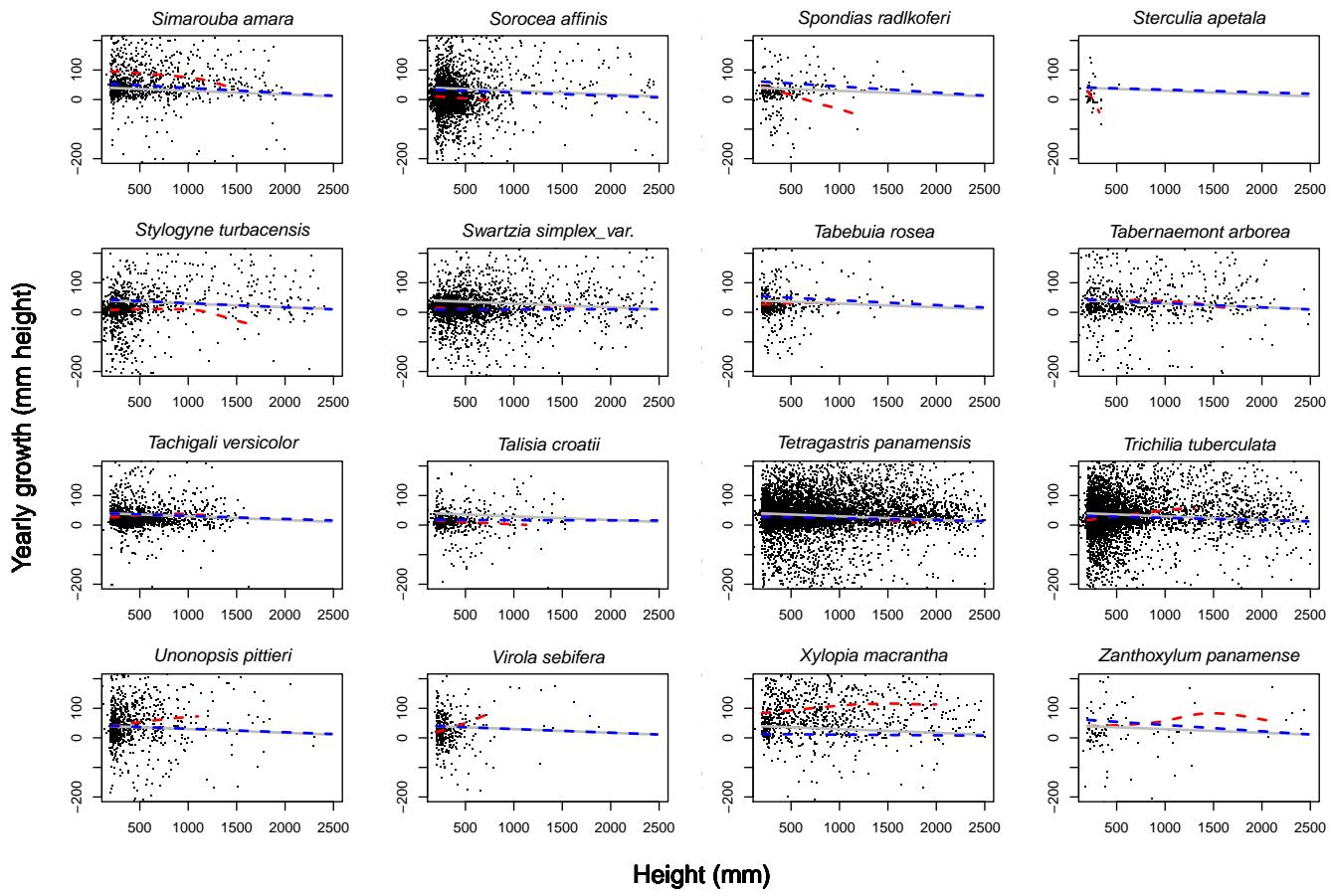
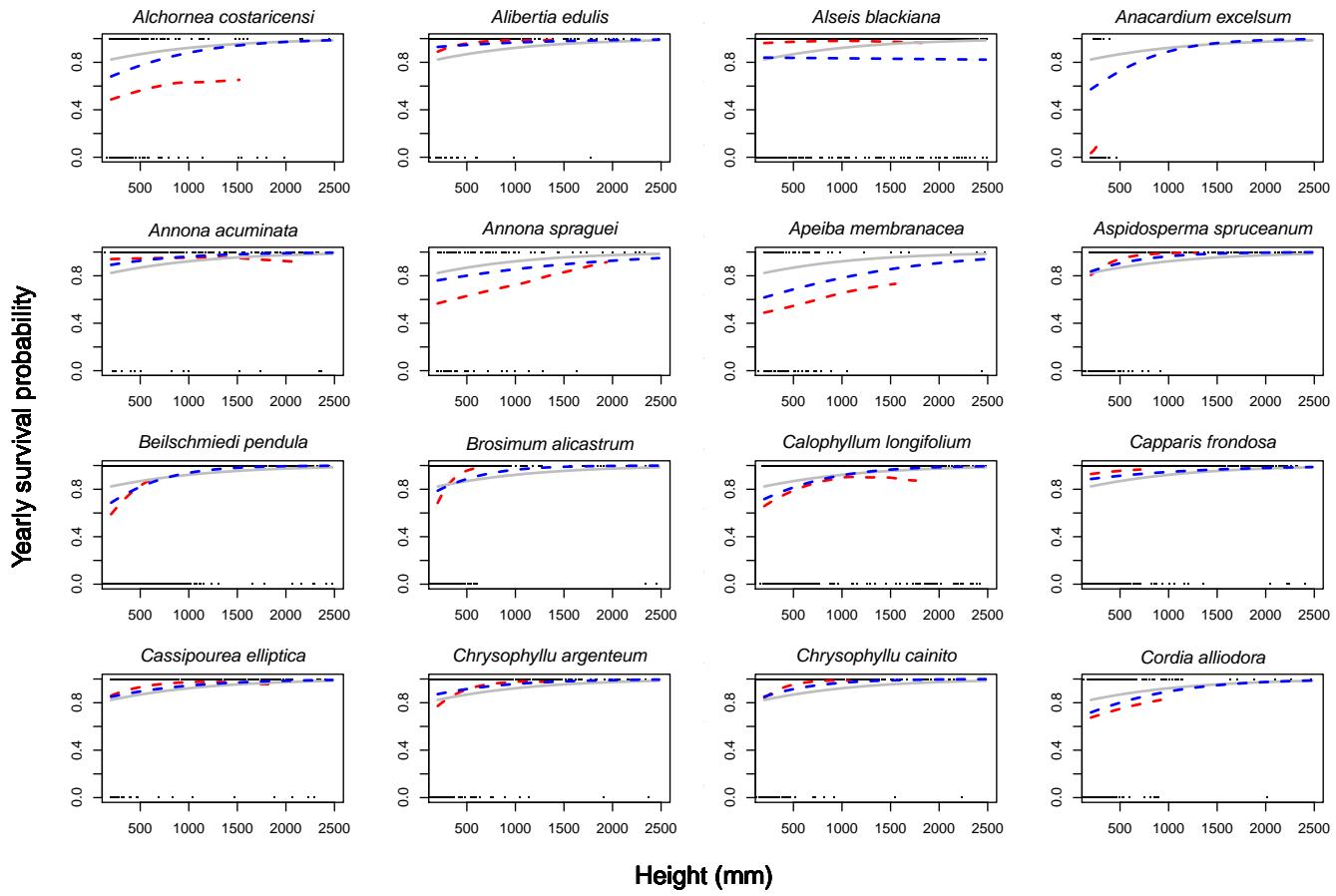


Figure S5. Continued.



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Figure S6. Observed and predicted annual seedling survival as a function of initial height (mm). Black dots show observations, red dashed lines show species-specific moving averages (from a Generalized Additive Model using a loess smoother), blue dashed lines show the fitted trait based average model, and grey lines show a fitted model based only on size (not on traits, thus identical for all species).

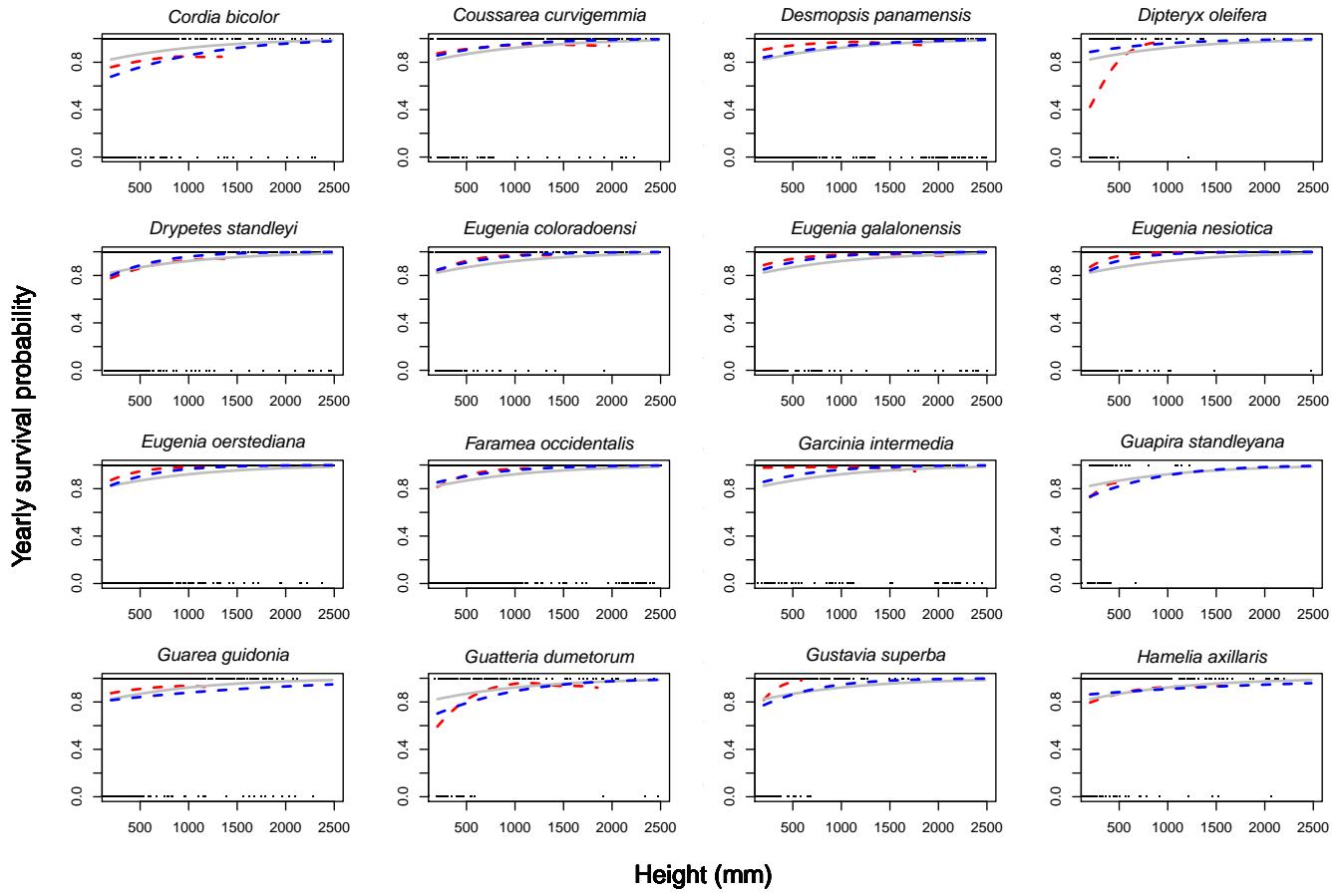


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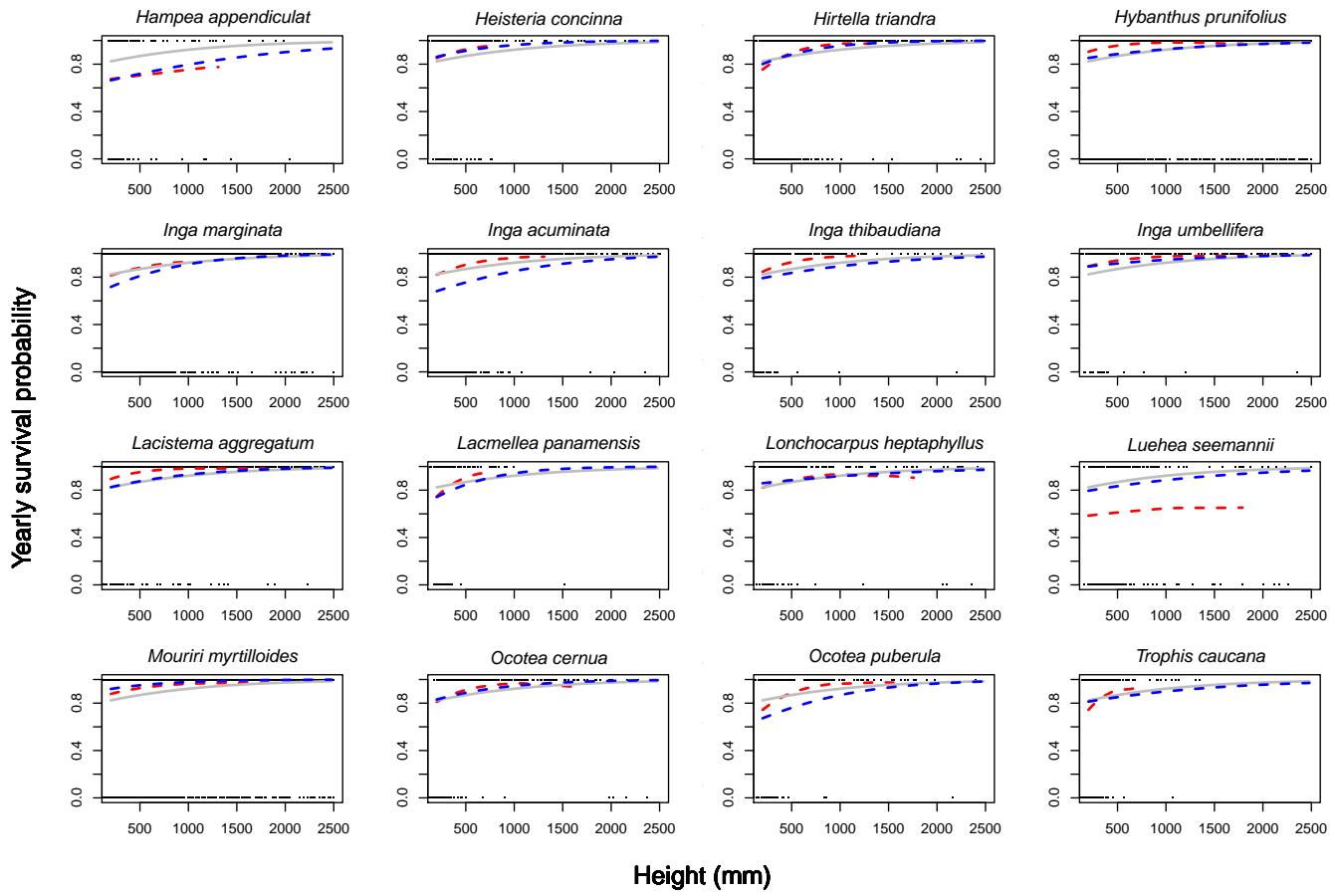


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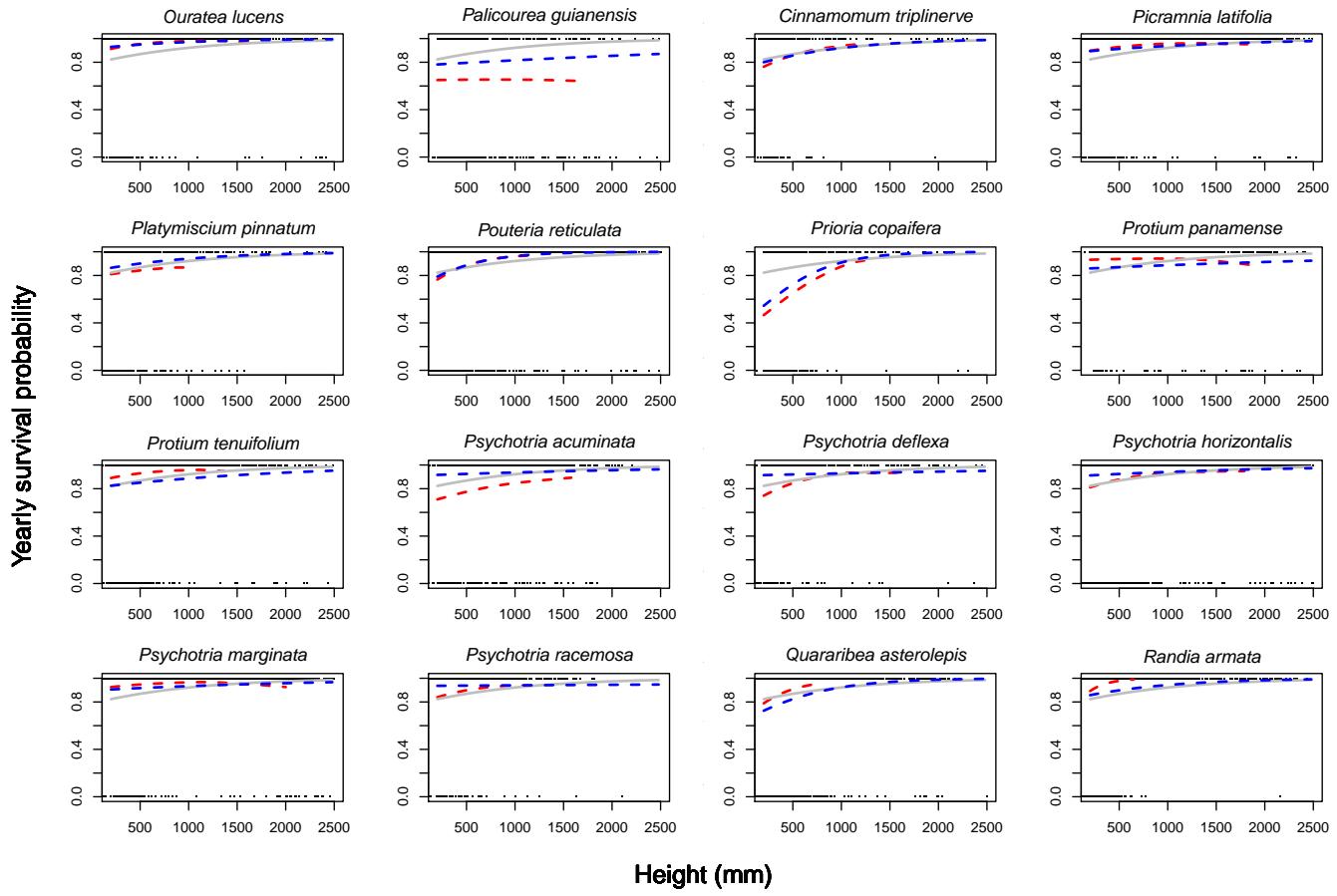


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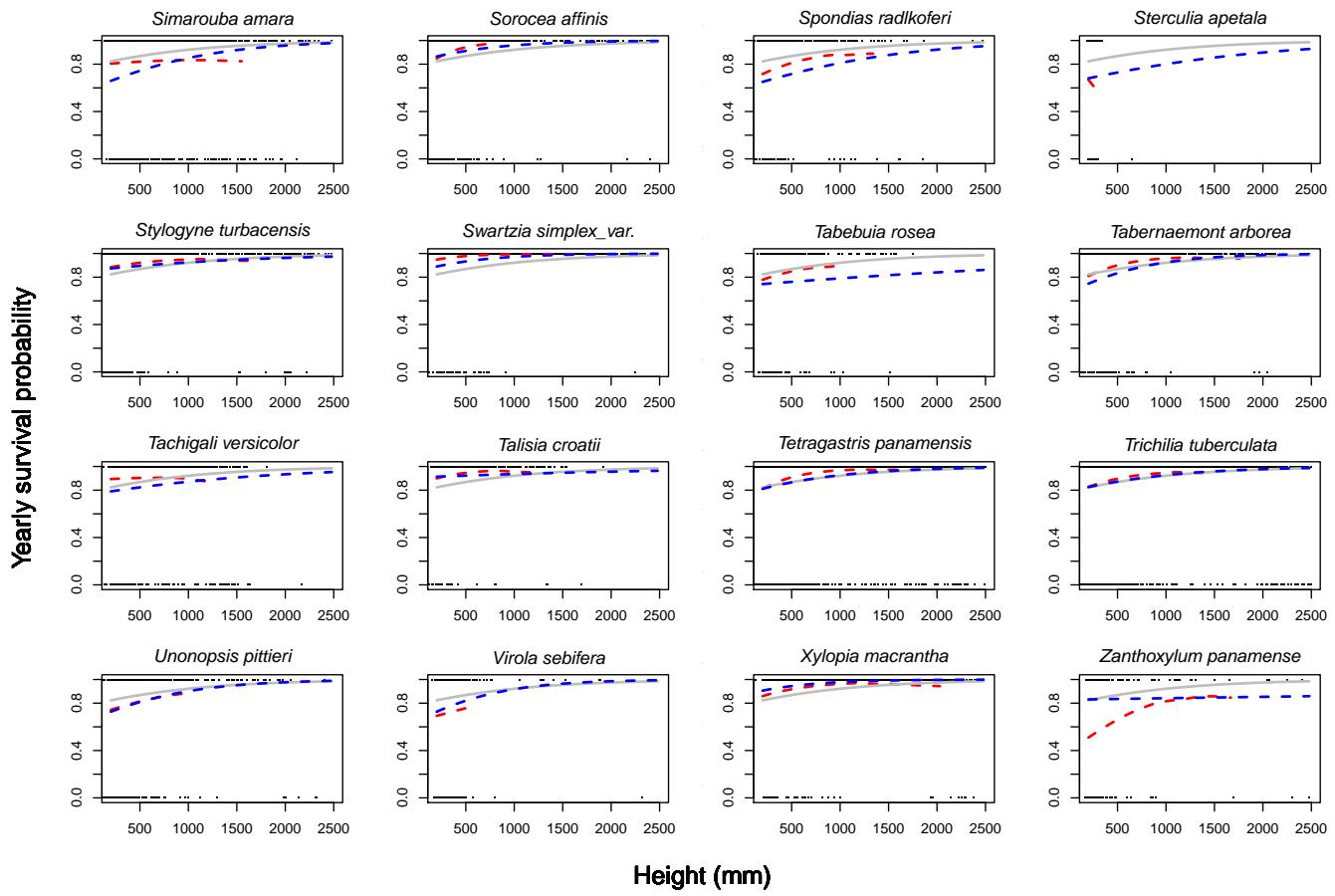


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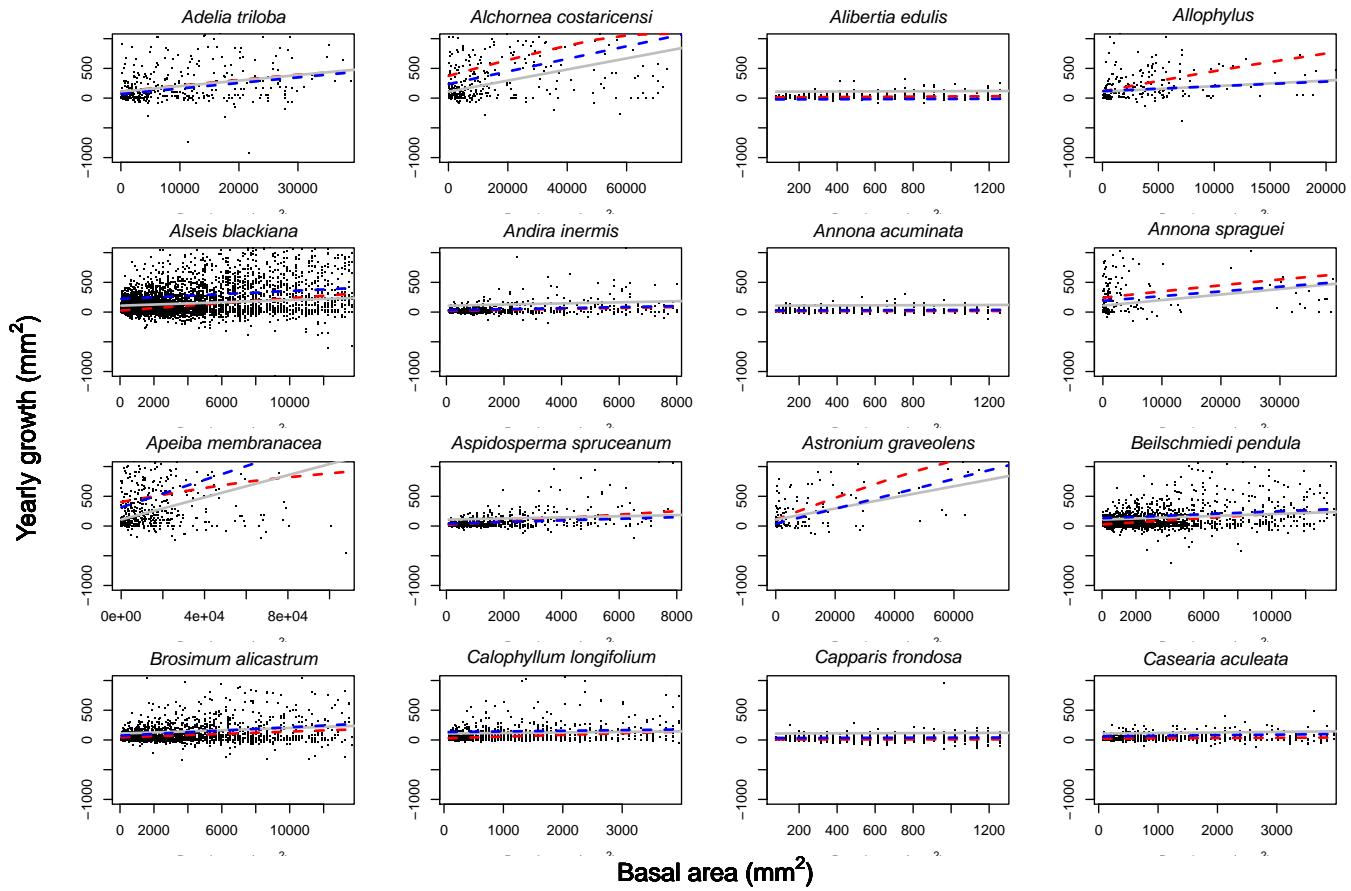


Figure S7. Observed and predicted annual tree growth (mm^2 basal area/yr) as a function of initial size (mm^2 basal area). Black dots show observations, red dashed lines show species-specific moving averages (from a Generalized Additive Model using a loess smoother), blue dashed lines show the fitted trait based average model, and grey lines show a fitted model based only on size (not on traits, thus identical for all species).

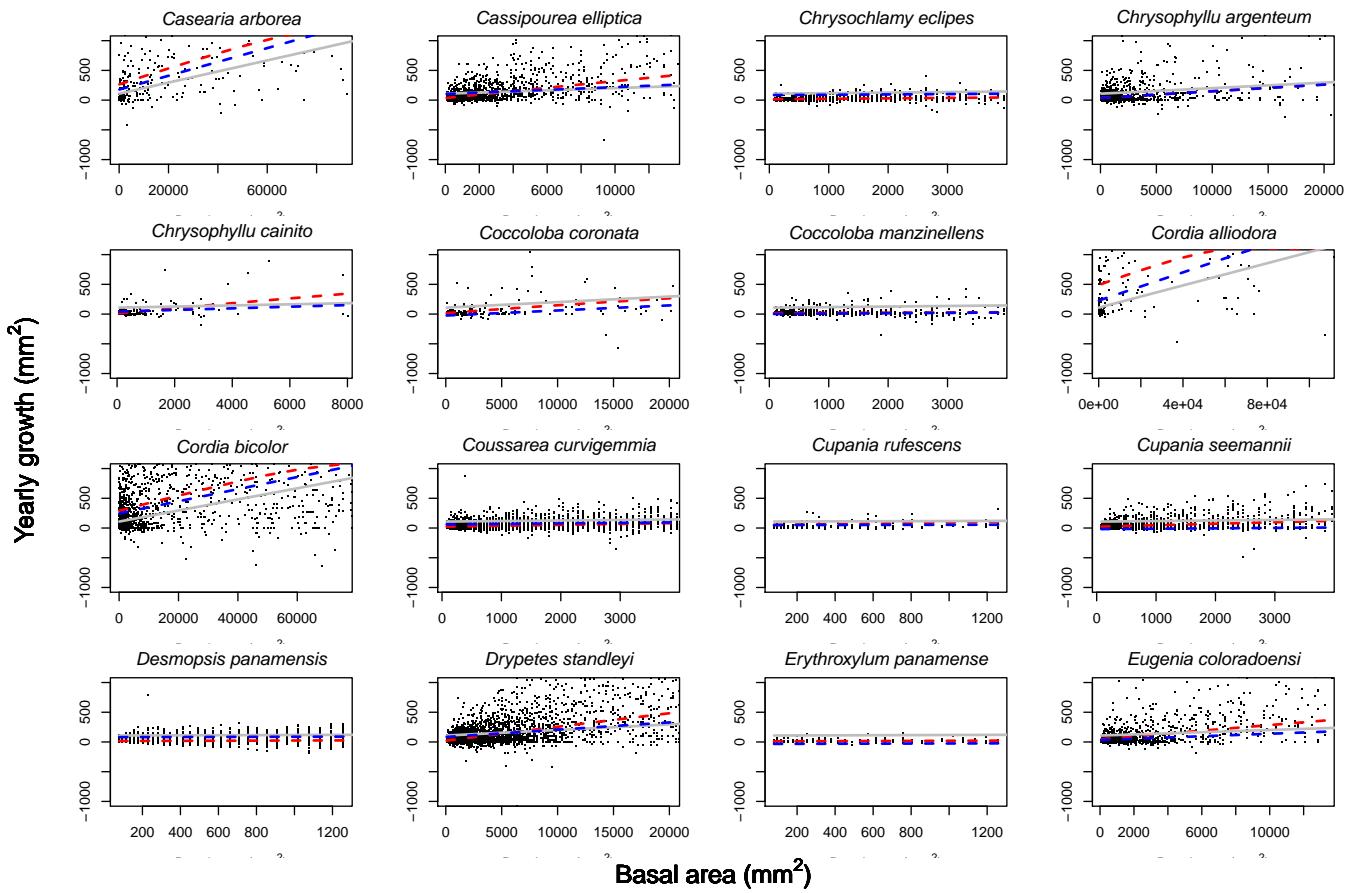


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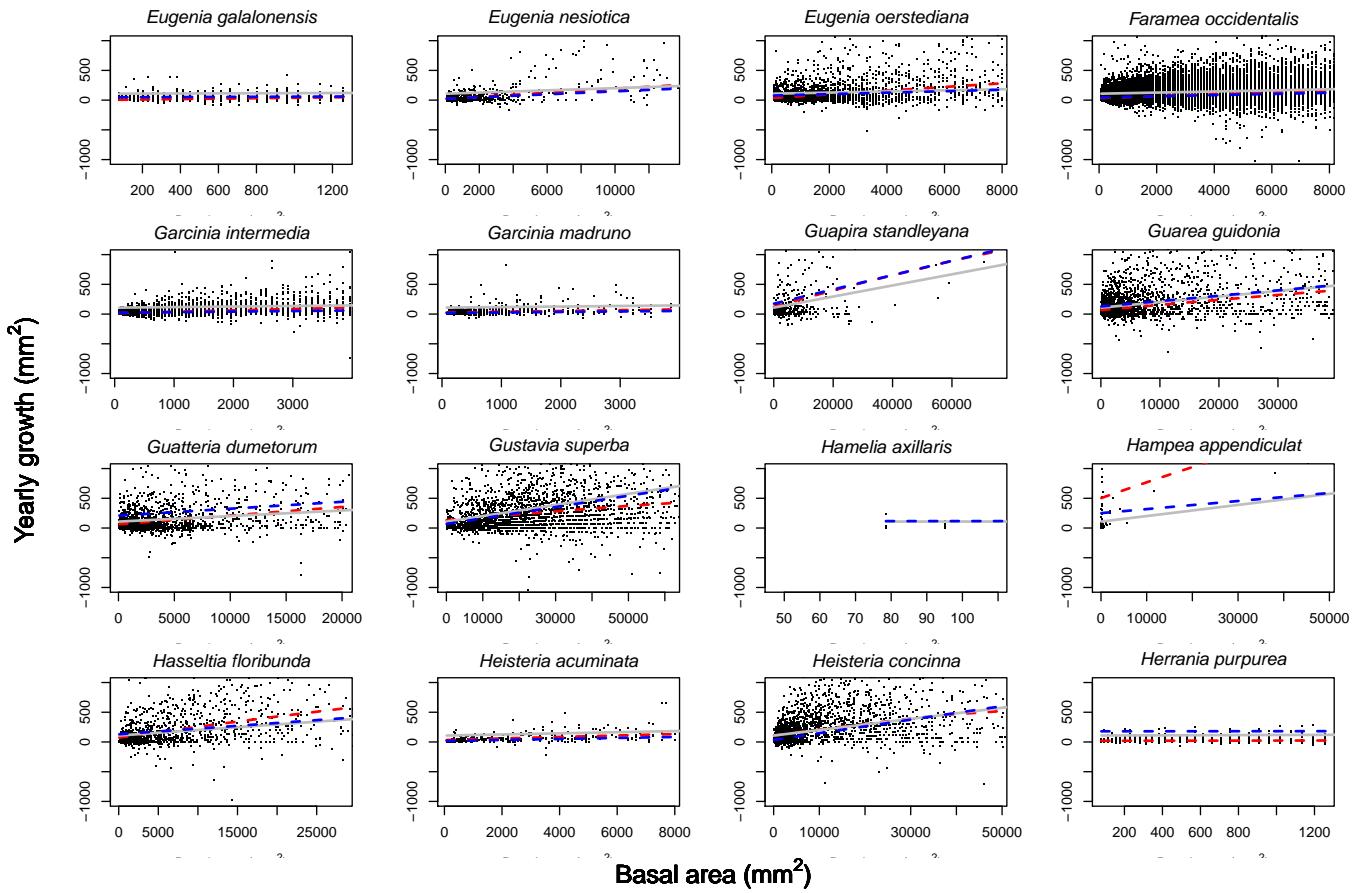


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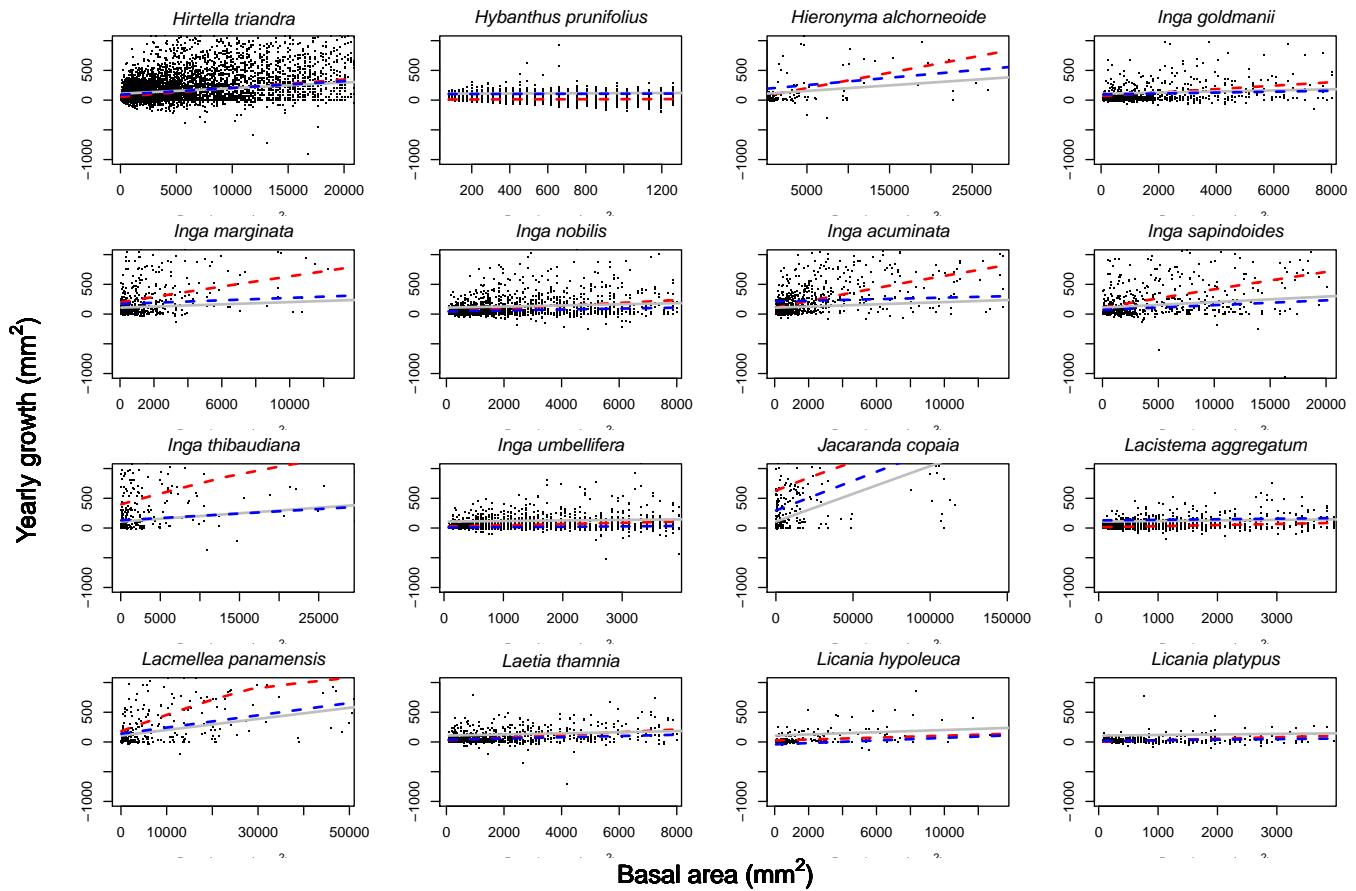


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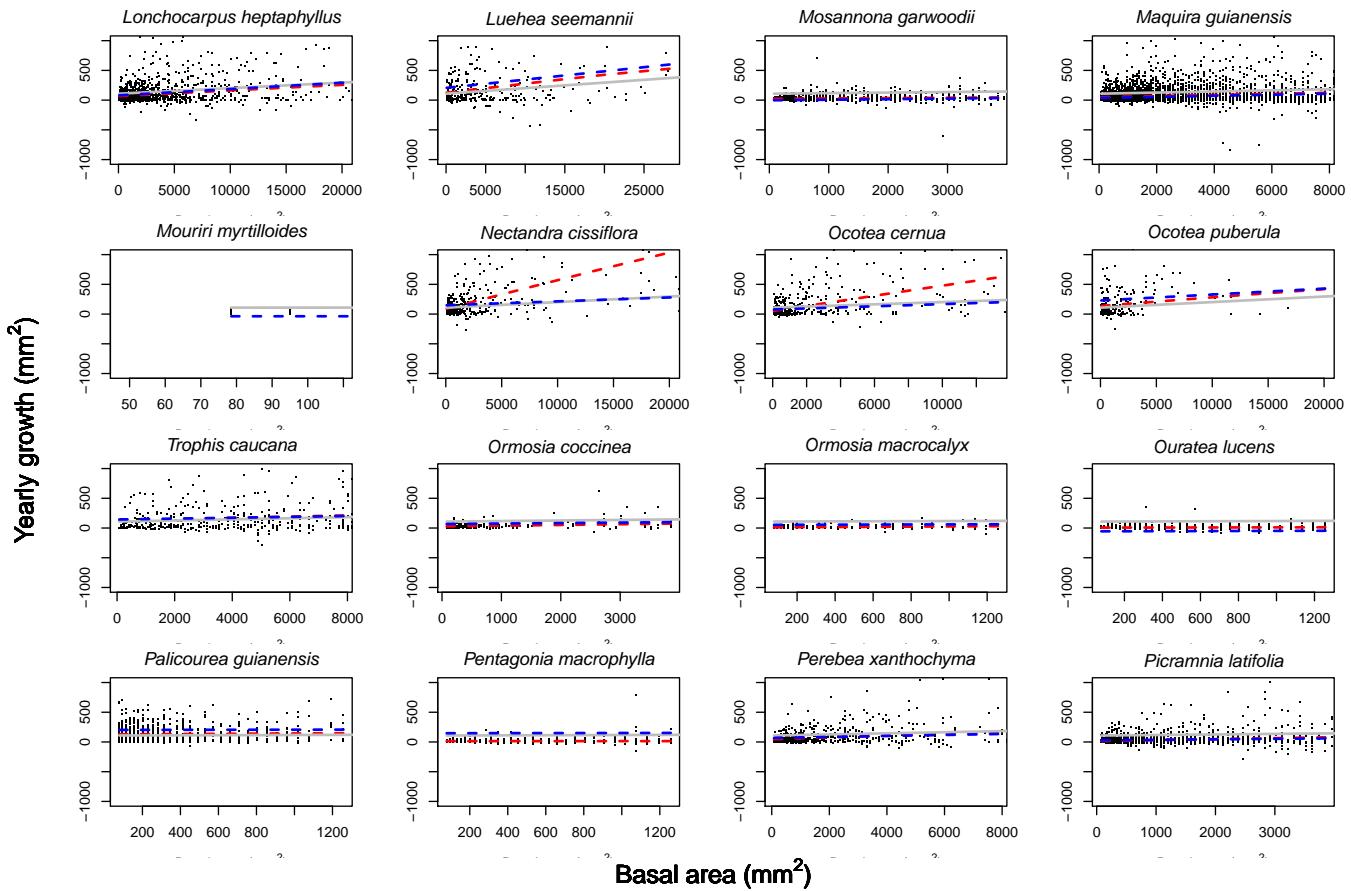


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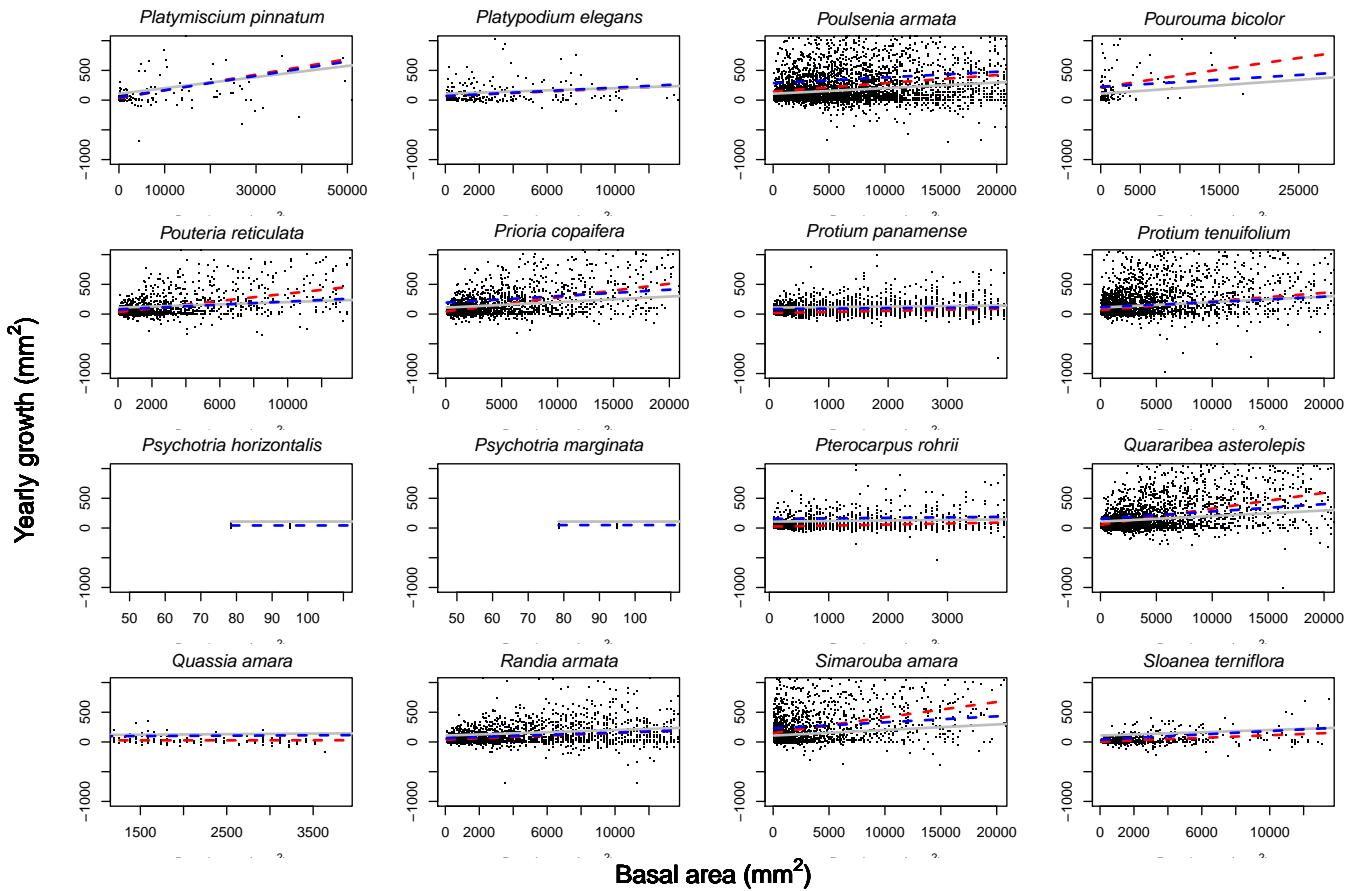


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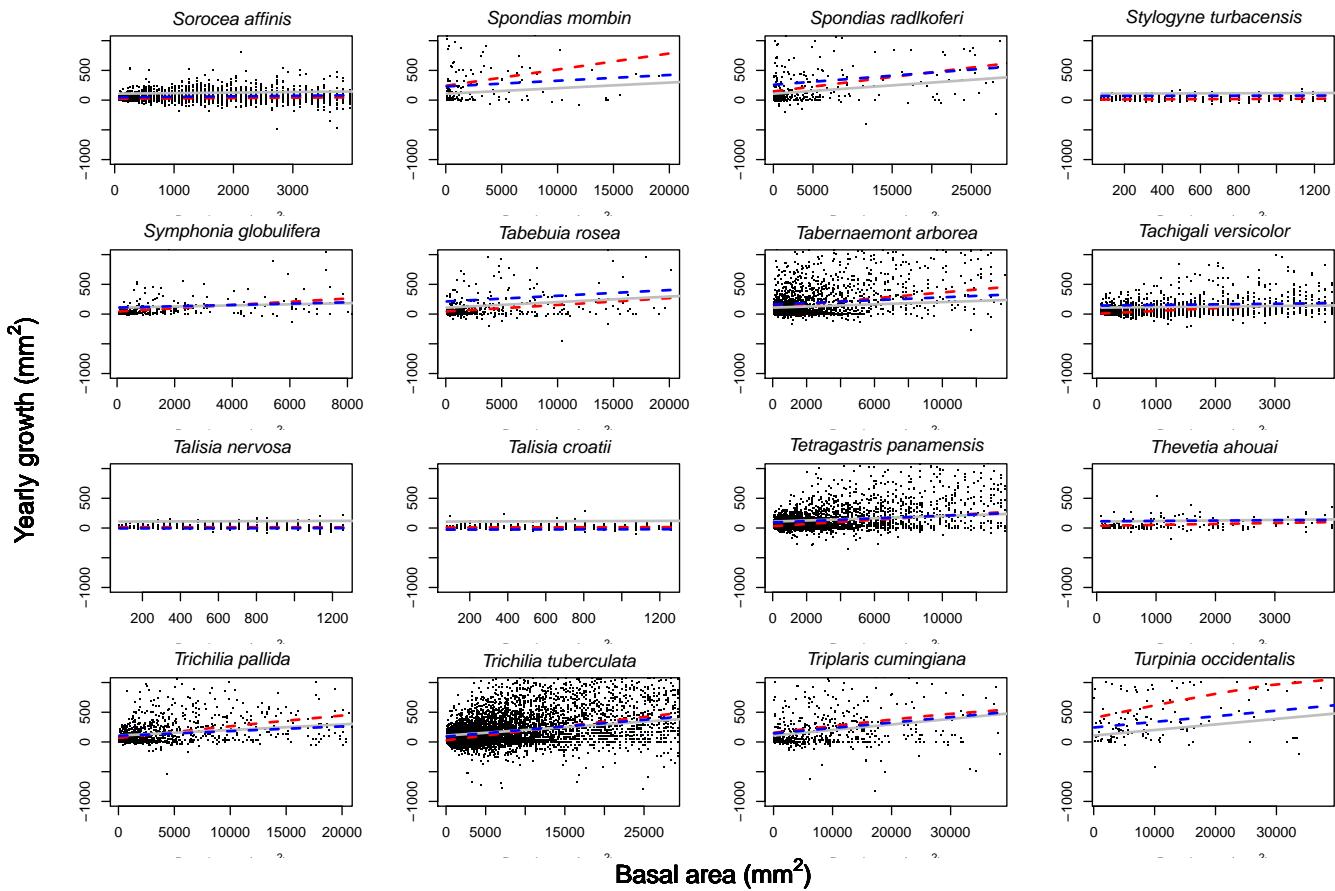


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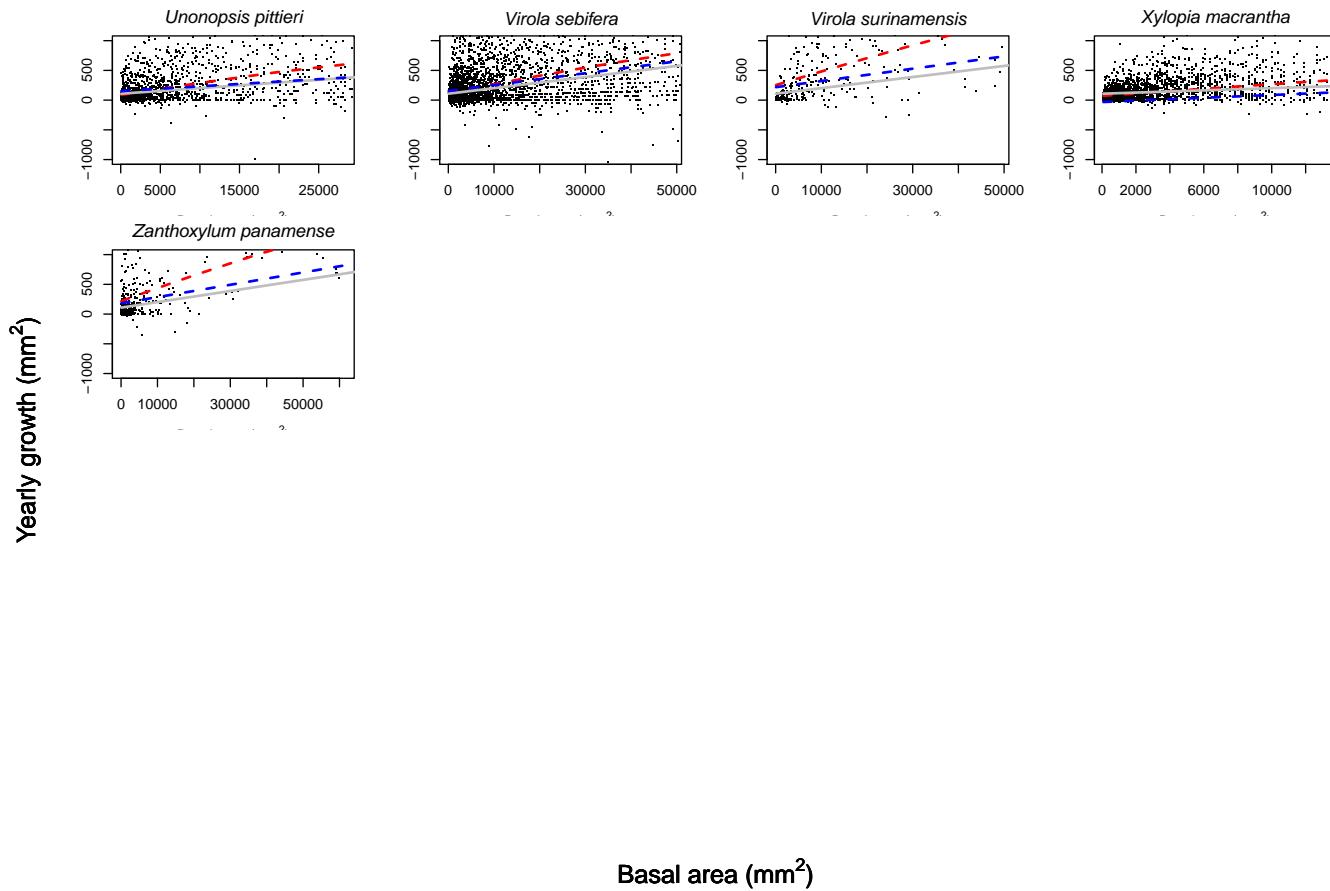
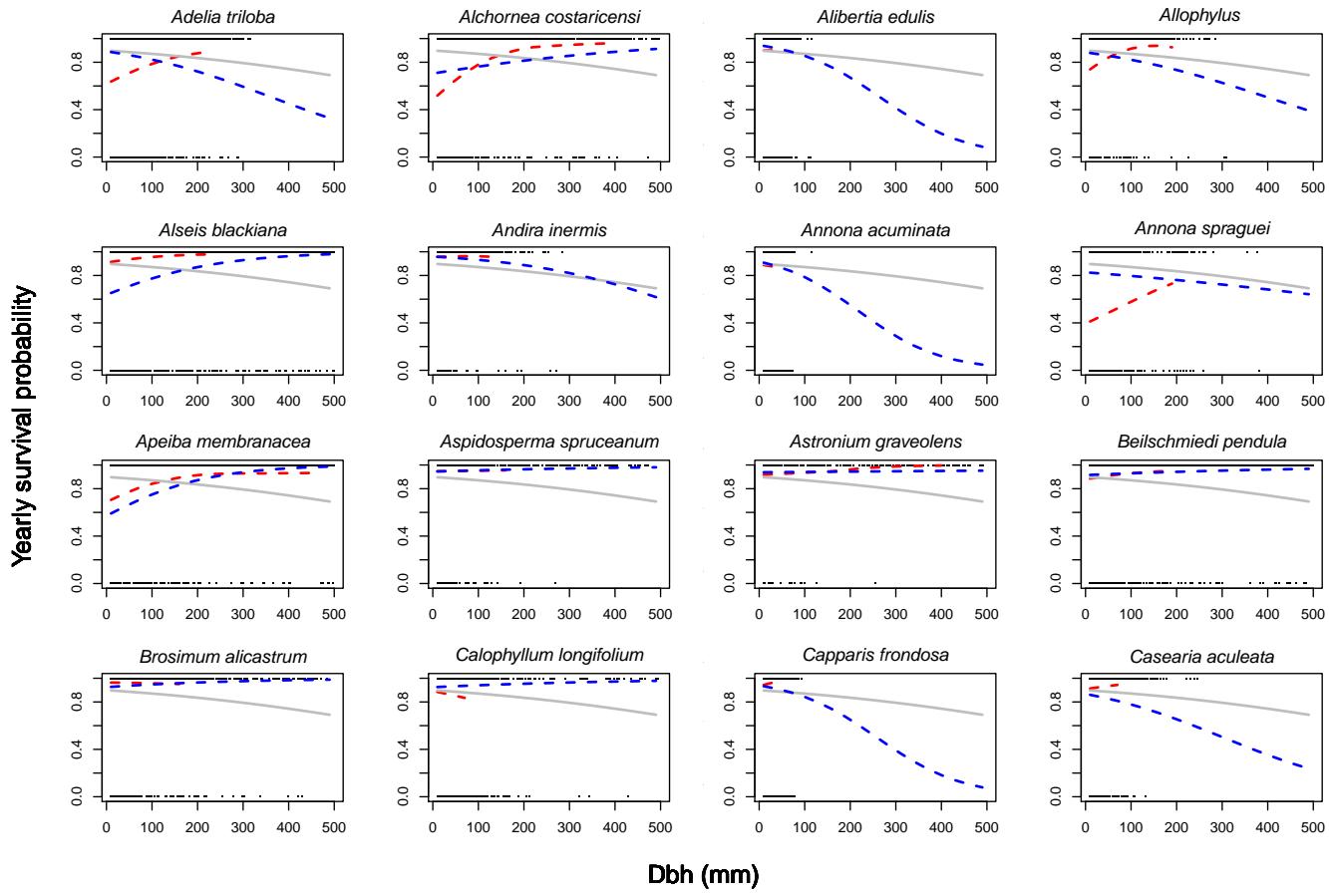


Figure S7. Continued.



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Figure S8. Observed and predicted annual tree survival as a function of initial dbh (mm). Black dots show observations, red dashed lines show species-specific moving averages (from a Generalized Additive Model using a loess smoother), blue dashed lines show the fitted trait based average model, and grey lines show a fitted model based only on size (not on traits, thus identical for all species).

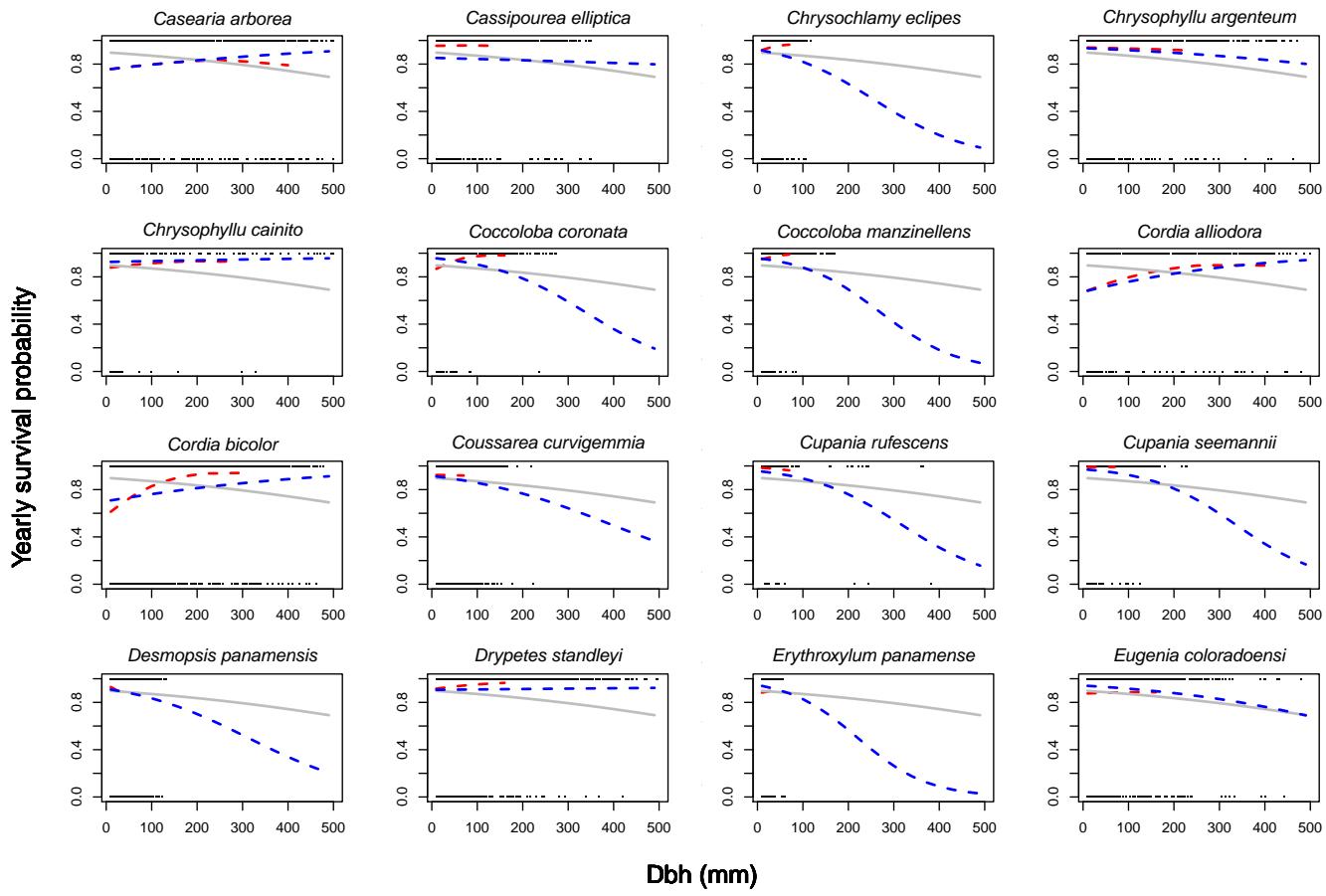


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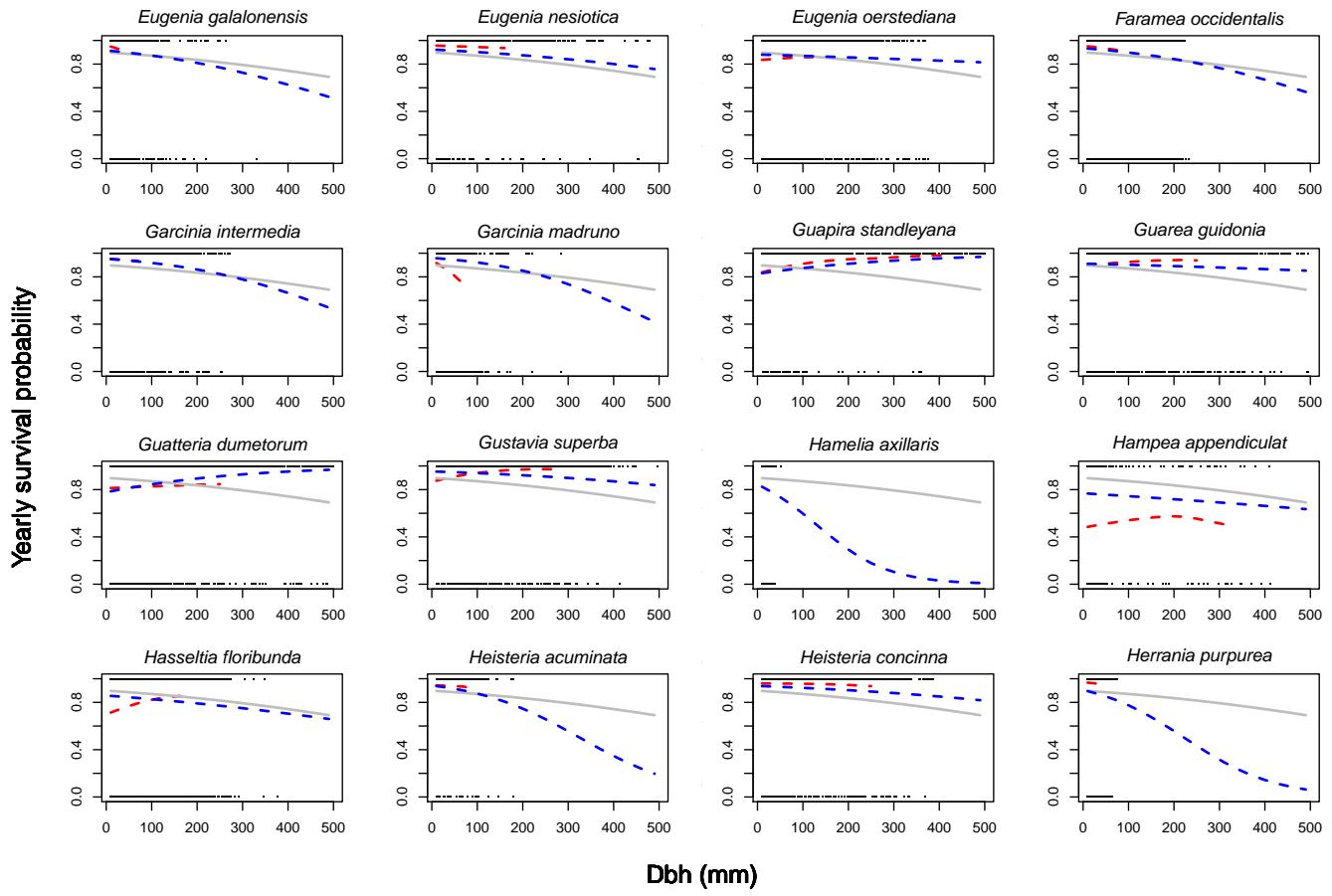


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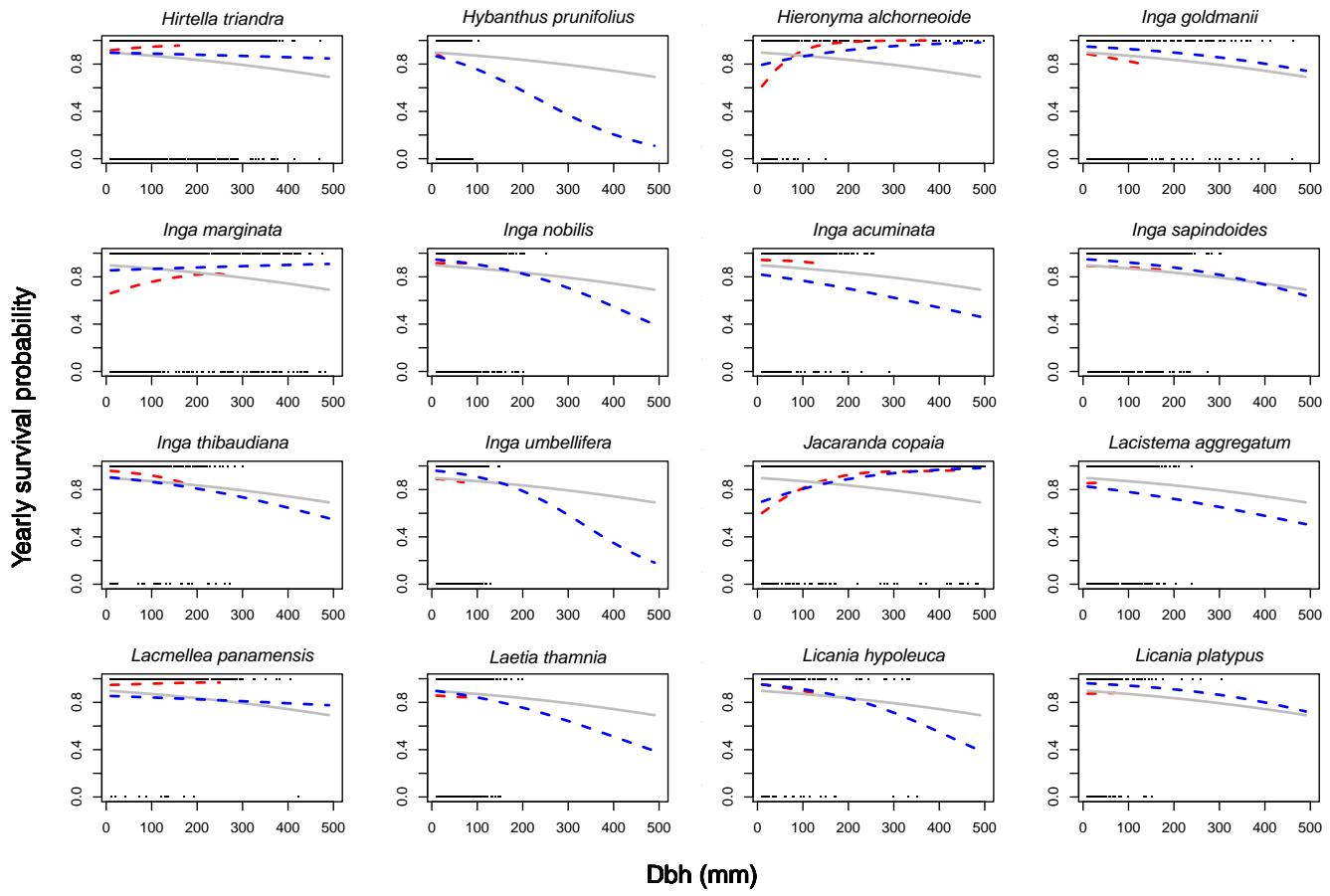


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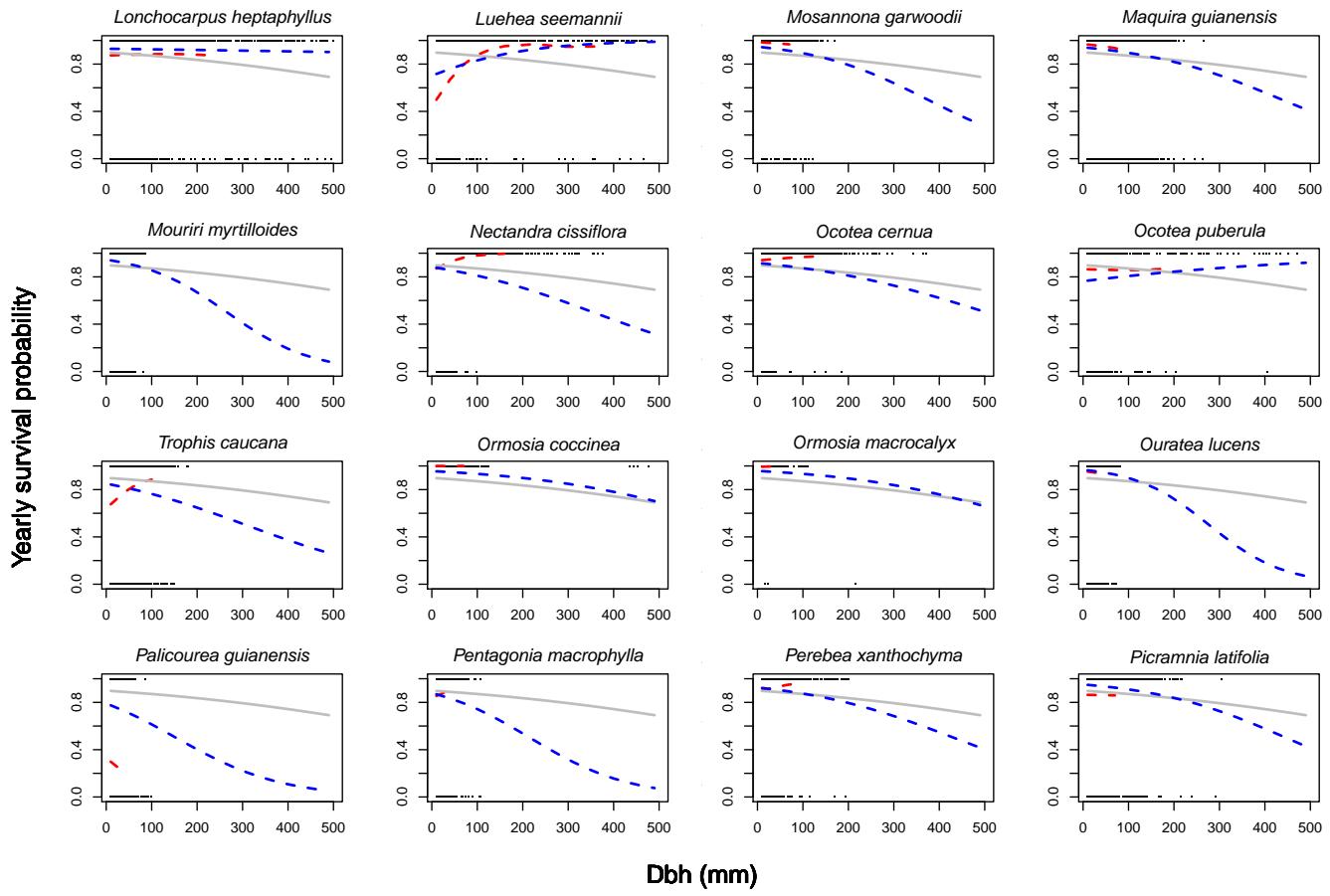


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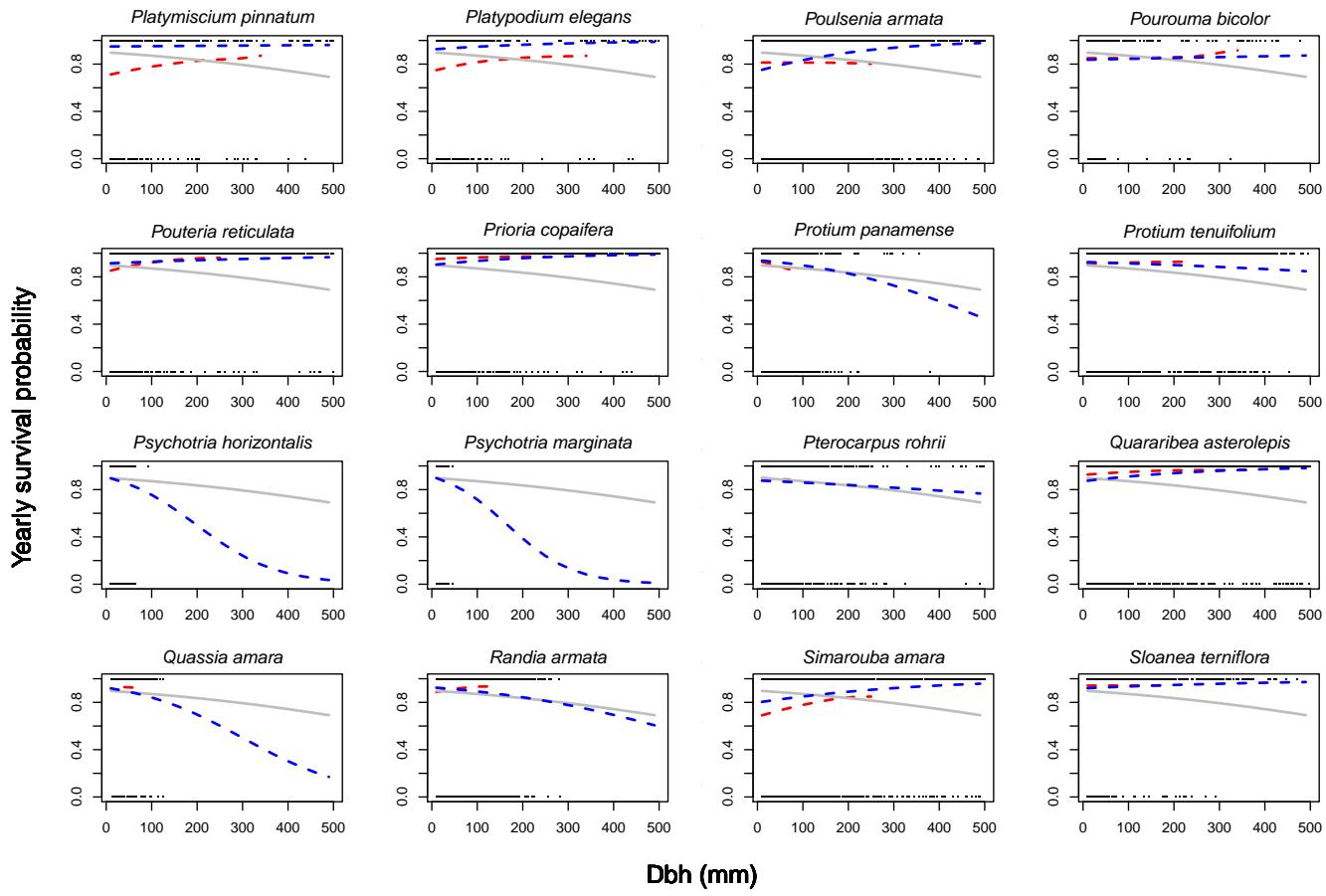


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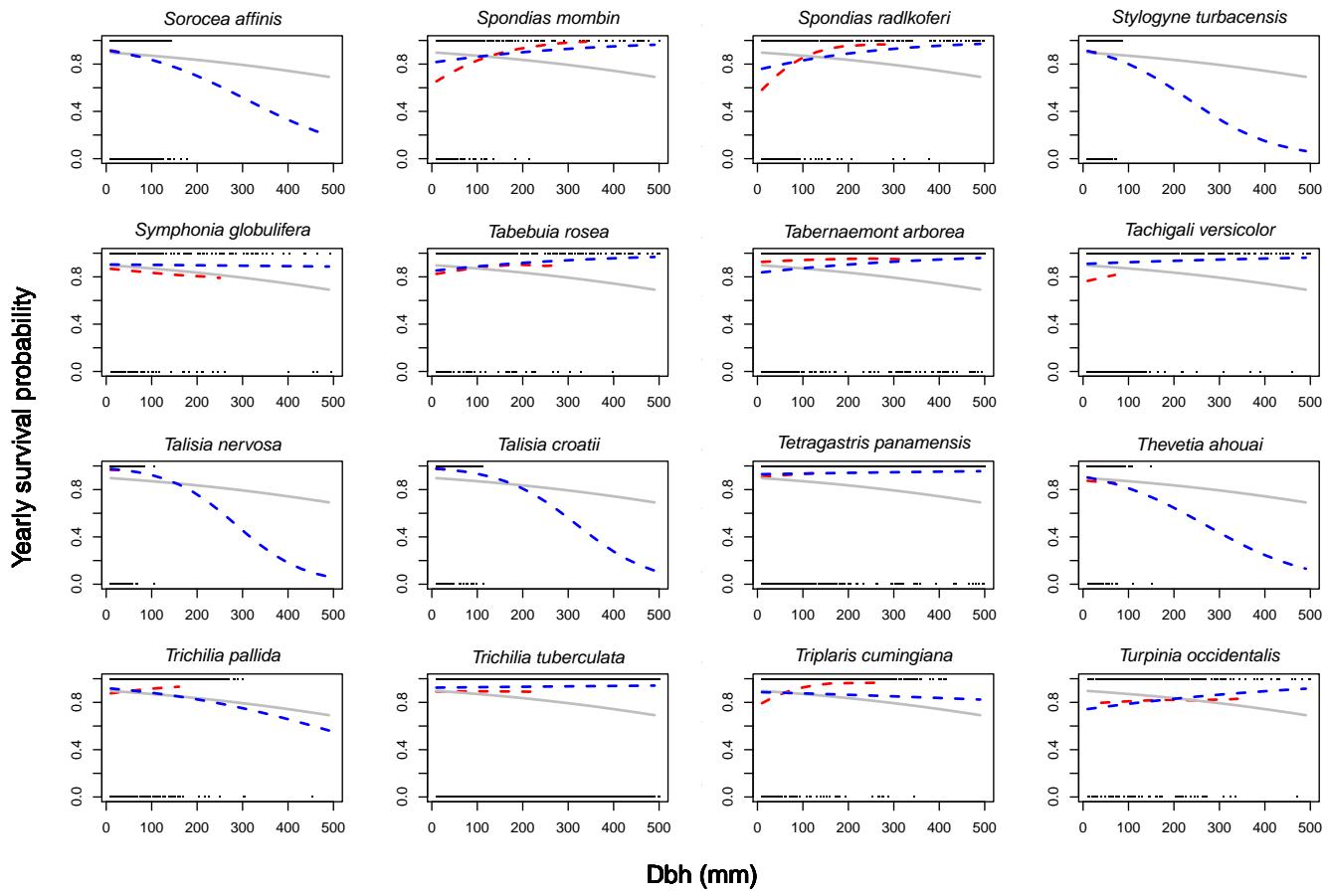


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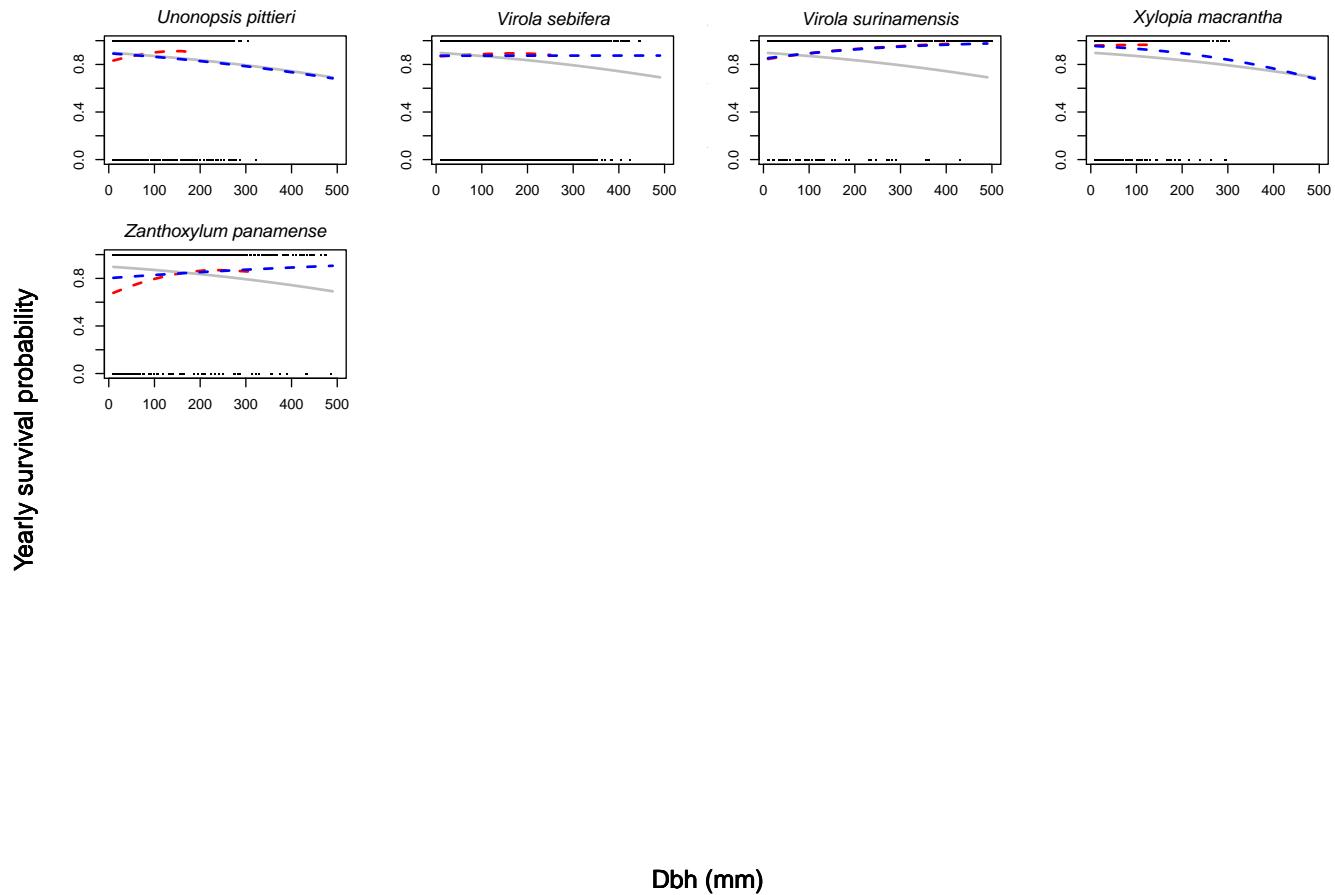


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S3 FIGURES

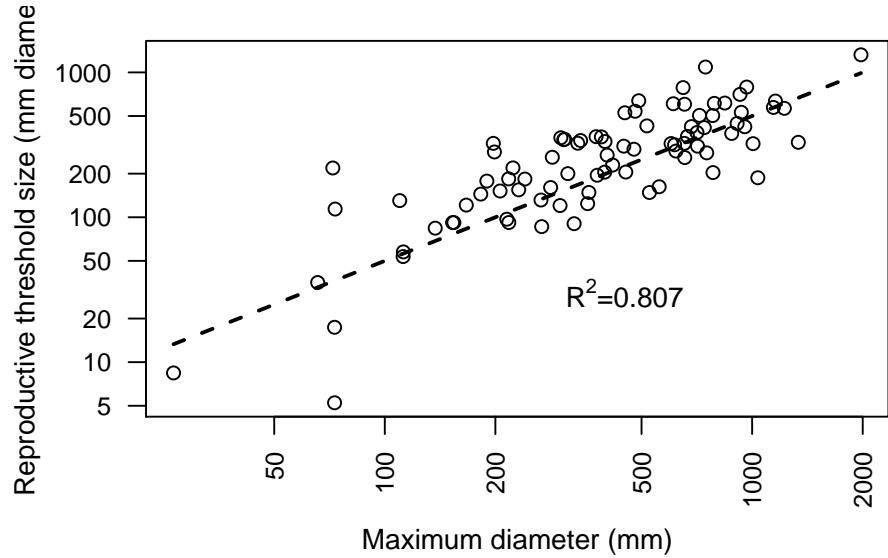
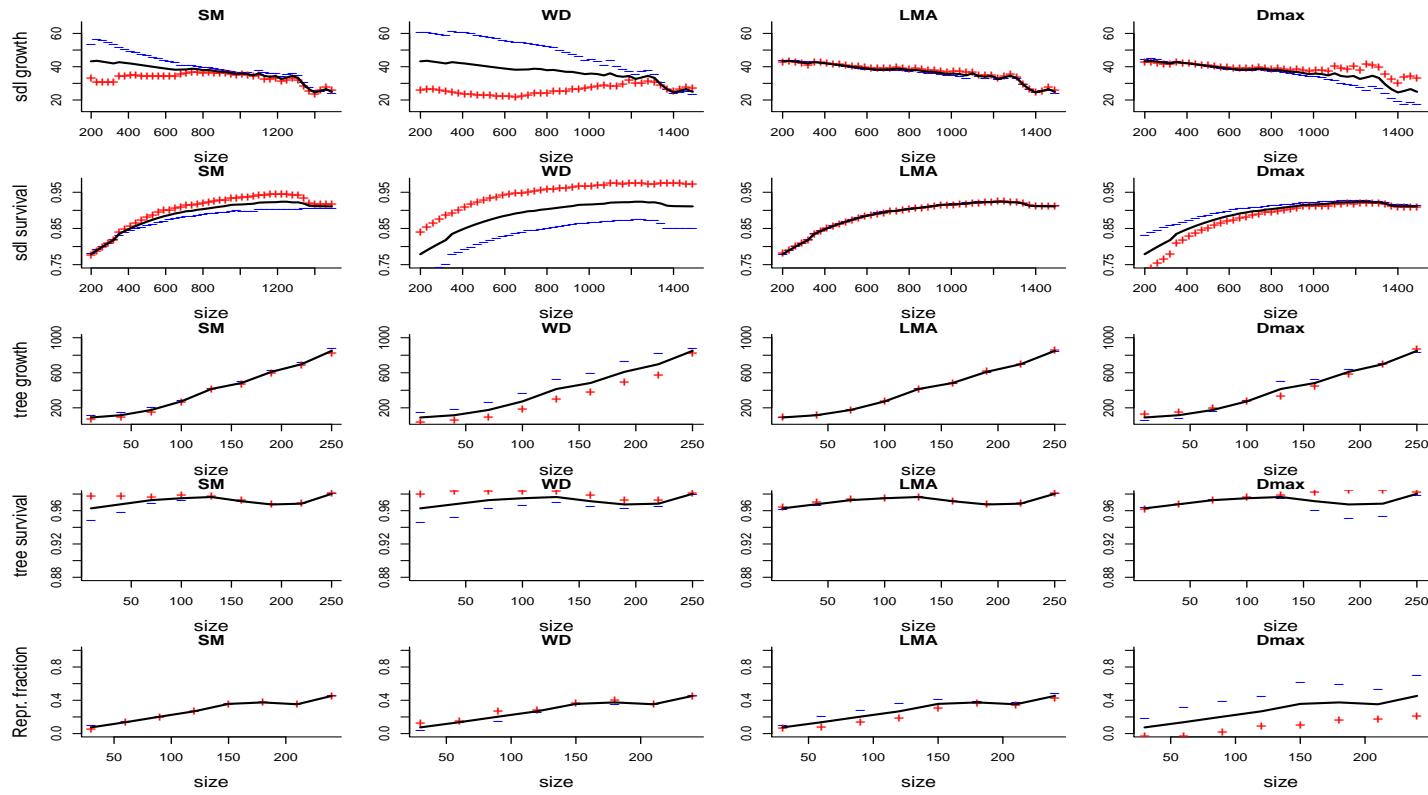
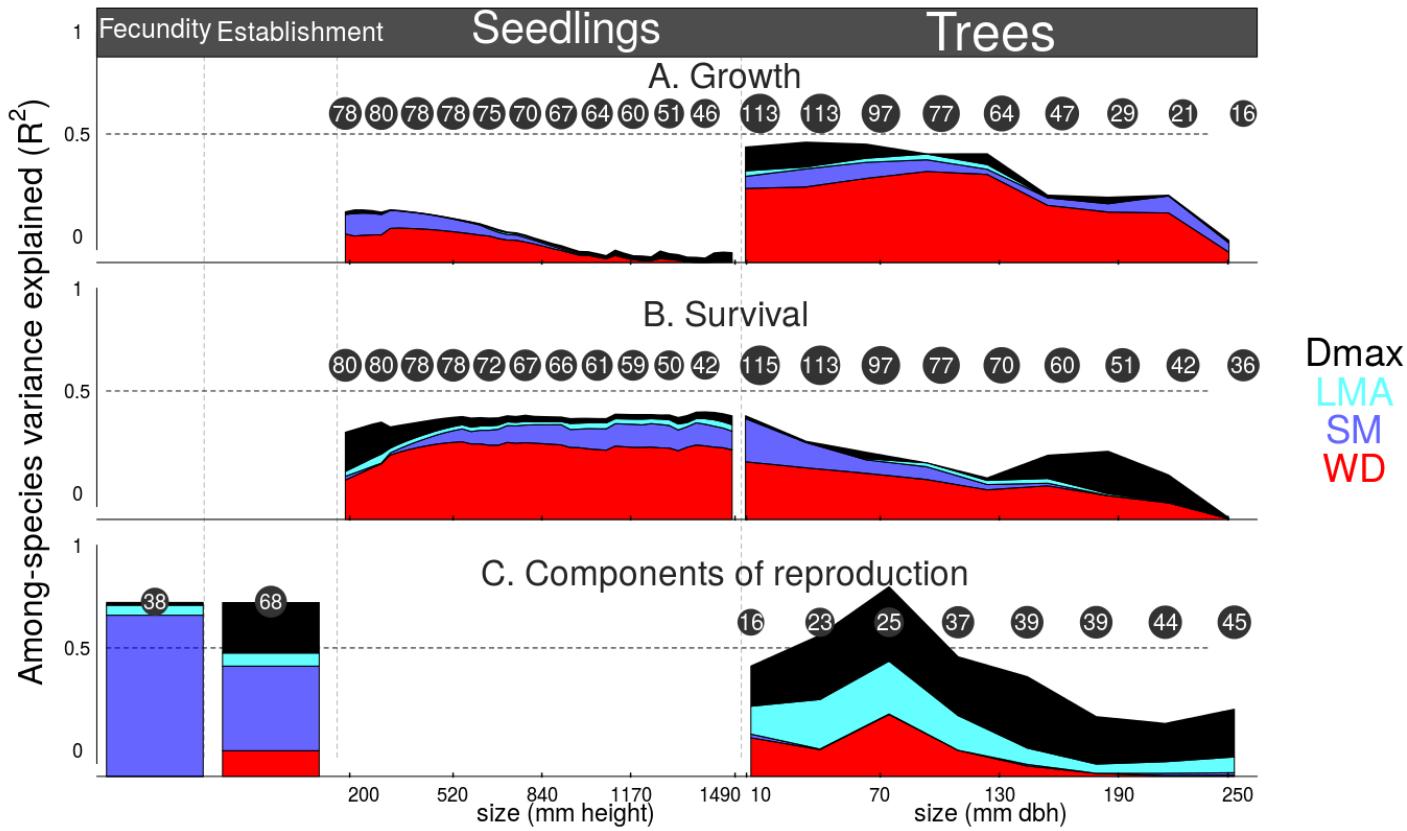


Figure S9. Relationship between species' maximum observed tree diameter (D_{max}) and the onset of reproduction (50 percent quantile of reproduction; R_{50}). The dashed line indicates the relationship $R_{50} = 0.5D_{max}$.



S5

Figure S10. Separate Analyses at Every Size. Fitted effects of each trait (columns) on size-dependent vital rates (rows), as in Figure 2, but based on separate models for each size (the robustness analysis). The black lines present the vital rate-size relationships with all traits set to their mean values (with the corresponding predictions from the hierarchical model in grey). The blue and red lines present the same relationships with one trait set to its mean plus or minus one standard deviation, respectively, and the two remaining traits set to their mean values (with exception of D_{max} , see below). The trait whose value varies among the blue, black and red lines is named at the top of each column. Actual mean values and standard deviations for each trait are given in table 1. An important difference from figure 3 is that for this analysis here, small statured species drop out at larger sizes and thus a different subset of species are used at each size (mean D_{max} increases); in contrast, the result in figure 3 based on the hierarchical model simply shows the main effects as fitted across sizes. The size ranges of the axis differ from Fig. 2 also because species drop out with increasing size, and we limited the analysis include at least 15 species.



9G

Figure S11. Separate Analyses at Every Size. Among-species variance explained by traits (as measured by R^2 values) throughout the life-cycle of tree species from Barro Colorado Island, as in Figure 3, but based on separate models for each size (the robustness analysis). The rows show results for (top to bottom) size-dependent growth, size-dependent survival, and vital rates associated with reproduction. The R^2 value at the upper edge of the stacked colors represents the proportion of the total variation among species explained by traits, as reflected in the averaged model when species-specific values for that vital rate are regressed on all four traits (i.e. including traits Dmax, LMA, SM and WD) and model averaging is applied, where the observed values for each species are based on species-specific GAMs. The relative importance of different traits is indicated by the relative height of each color band as a proportion of the total, with height scaled to the R^2 values for averaged models including only one trait (i.e. including only Dmax, LMA, SM or WD). The number of species included in the analyses depends on size; for reference, species numbers are shown in solid circles above each graph at fixed intervals, with their diameters proportional to log species number.

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