Supplementary Information for

The maleness of larger angiosperm flowers

Gustavo Brant Paterno, Carina Lima Silveira, Johannes Kollmann, Mark Westoby, Carlos Roberto Fonseca

Corresponding authors:
Gustavo Brant Paterno
e-mail: paternogbc@gmail.com

Carlos Roberto Fonseca
e-mail: fonseca.crsd@gmail.com

This PDF file includes:

> Supplementary text
> Figures S1 to S26
> Tables S1 to S8
> Dataset S1
> SI References

Supplementary text

1. The dataset: taxonomic and phylogenetic coverage

In total, we compiled a comprehensive dataset with flower biomass allocation measurements for 307 plant species occurring in four different continents, including a diverse range of angiosperm lineages (75 families and 32 orders) (Fig. S1-S3, see Dataset S1 for the complete species list). The great majority of the species included in this study (87%) are primary data, from our own field sampling. The most species-rich orders were Lamiales, Fabales, Myrtales, Ericales, and Malpighiales, while the largest families in the study were Fabaceae, Lamiaceae, Ericaceae, Brassicaceae, and Malvaceae (Fig. S1-S3).

2. Absolute and relative flower biomass allocation

Flower biomass varied five orders of magnitude across angiosperm lineages (between 0.000083 g and 0.72 g, Fig S4) with an average of 0.016 g ($\pm$ 0.58 SD) and with 50% of the species with their flower mass ranging 2–10 mg (Fig. S5A). Flower biomass of male organs (i.e., androecium), female organs (i.e., gynoecium), petals (i.e., corolla), and sepals (i.e., calix) also showed large variation across species (Fig. S5). The relative investment of biomass into different flower organs showed wide variation across species and between flower components (Fig. S6). Across species, flowers invest most of their biomass into petals (41% $\pm$ 15% SD). Petals are also the flower component that varies more among species, ranging 2–89% of the relative biomass allocation. Additionally, species also show relatively high percentage of biomass invested in sepals (24 $\pm$ 12% SD), and less investment into the female (19 $\pm$ 10%) and male organs (16 $\pm$ 11%) (Fig. S6, Table S1). Details about flower biomass allocation for the ten species with the heaviest and lightest flowers are reported in Table S2.

3. Sensitivity analyses for SMA and phySMA

We submitted the flower allometries performed by SMA and phySMA to several sensitivity analyses. Together, the results described below strongly support a robust pattern where flowers have higher scaling slopes for the male in comparison to the female organs ($\beta_{male} > \beta_{female}$) and for petals in comparison to sepals ($\beta_{petals} > \beta_{sepals}$) (Table S3) across the angiosperms, regardless of multiple causes of uncertainty sources (1).

3.1 Sampling effort: species number and composition

The estimated slopes with reduced datasets were very similar to the slope estimated with the full dataset for the male organs, female organs, petals, and sepals, even after removing up to 50% of the species for both Standardized Major Axis (SMA) and Phylogenetic Standardized Major Axis (phySMA) regressions (Fig. S7-S8). For SMA, even after removing 50% of species, the mean average estimated slopes for the male organs ($\beta_{male} = 1.107 \pm 0.027$), female organs ($\beta_{female} = 1.033 \pm 0.026$), petals ($\beta_{petals} = 1.103 \pm 0.018$), and sepals ($\beta_{sepals} = 1.030 \pm 0.023$) were very similar to the values estimated with the full dataset (see Fig. 2, Table S3 and regression lines in Fig. S7). For phySMA, the mean simulated estimates were also very similar to the values estimated with the full dataset, except for the petals. For petals, mean simulated slopes tend to be underestimated for species removal higher than 30%, but still showing a positive allometry (Fig. S8). Therefore, results from resampling show that estimated slopes for the male organs, female organs, petals, and sepals were highly robust to large variation in sample size and species set, supporting the generality of the allometric patterns.

3.2 Taxonomic influence

Estimated SMA and phySMA slopes were mostly robust to the removal of the five most species-rich families (Fig. S9) and orders (Fig. S10) from the dataset. Estimated slopes for the male organs remained statistically higher than one ($\beta_{male} > 1$) after removing the top families and orders from the analysis (Table S4-S5, Fig. S9-S10). For the female organs, estimated slopes after removing the top families and orders remained statistically isometric ($\beta_{female} = 1$), except for the removal of the Malvaceae family in the SMA regression, where the estimated slope was higher than one ($CI_{95\%}$: 1.003–1.103; Table S5-S6). Estimated slopes for the petals also remained statistically higher than one ($\beta_{petals} > 1$) after removing the top families and orders from the analysis (Table S5, Fig. S9-S10). For sepals, the estimated slopes after removing most top families and orders remained statistically isometric ($\beta_{sepals} = 1$), with the exceptions of removing Malvaceae (phySMA, negative allometry) and Lamiales (SMA, positive allometry) (Table S5-S6, Fig. S9-S10). These results demonstrate that the main allometric patterns reported are only marginally affected by the major clades included in the study.

3.3 Phylogenetic uncertainty

To account for phylogenetic uncertainty we fitted all phySMA regression models across 300 alternative phylogenetic trees. In accordance with the main results, estimated slopes for the male organs remained statistically higher than one ($\beta_{male} > 1$) in 98% of the fitted models (Fig. S11) while, for the female organs, estimated slopes remained statistically isometric ($\beta_{female} = 1$) in 98% of the fitted models. For petals, all slopes remained statistically higher than one ($\beta_{petals} > 1$) while sepals remained statistically isometric or below one in 100% of the cases (Fig S11). Additionally, we also fitted each

4

phySMA regression using the lambda transformation to optimize branch lengths. Lambda value was set by maximum likelihood. Results for phySMA using Brownian model or lambda transformation, however, are equivalent. Estimated lambda values ranged between 0.46 and 0.66 across models. These results confirm that the estimated slopes for male, female, petals, and sepals were highly robust independently of the phylogenetic uncertainty and evolutionary model considered for the error structure.

3.4 Species variation in showiness strategy

Many plant species have showy sepals and stamens which contribute to pollination attraction while, in others, the perianth whorls can be very similar in appearance (tepals). Besides, in some species small flowers are grouped in inflorescences for pollinator attraction. To account for potential influence of these groups, we re-analyzed all SMA and phySMA regressions after the exclusion of species with showy stamens, showy sepals, with inflorescence, and tepals. The classification of species into these groups was based on species descriptions in floras, flower illustrations, and pictures of the species' flowers. In support of our main results, despite some variation in the estimated SMA and phySMA slopes (Fig. S12, Table S6), after the removal of species with showy stamens, showy sepals, inflorescence, and tepals, all estimated slopes for male and petals remained statistically higher than one ($\beta_{male} > 1$, $\beta_{petals} > 1$) while estimated slopes for the female organs and sepals remained statistically isometric ($\beta_{female} = 1$, $\beta_{sepals} = 1$) (Fig. S12). These results indicate that the allometric patterns here described are robust to interspecific variation in showiness strategy.

3.5 Outlying species

The allometric regressions explained a great amount of the variation in the biomass of flower components across the angiosperms; nonetheless, some species deviate from the expected SMA regressions lines (Fig. S13). The allometric patterns, however, remained the same after the removal of outlying species from the dataset. Estimated slopes for the male organs and petals remained statistically higher than one ($\beta_{male} = 1.10$, $P_{\beta=1} = 0.00001$, $\beta_{petals} = 1.09$, $P_{\beta=1} < 0.00001$) while estimated slopes for the female organs and sepals remained statistically non-different than one (isometric) ($\beta_{female} = 1.03$, $P_{\beta=1} = 0.14448$, $\beta_{sepals} = 1.01$, $P_{\beta=1} < 0.42335$).

4. Allometric scaling controlling for axis independence

To account for the potential bias related to allometric regressions between two or more parts in respect to a whole (axis non-independence), all allometric regressions were re-analyzed using flower component in the y-axis and total flower biomass minus the flower component in the x-axis. The results demonstrate that the allometric patterns reported in this study are consistent and were not generated by bias due to axis non-independence in both standardized major axis regressions (SMA) and phylogenetic standardized major axis regressions (phySMA) (see Fig. S14-15 for details).

5. Common slope test for phySMA regressions

We used a permutation approach to test the difference in slope between the male (β_{male}) and the female organs (β_{female}), and between petals (β_{petals}) and sepals (β_{sepals}) for phylogenetic standardized reduced major axis regressions (phySMA). The difference in phySMA slopes between flower organs was tested with a null distribution generated from

10,000 permutations (shuffling the raw data). In each permutation, flower data were swapped at random between the organs being compared, and the difference in estimated slopes between phySMA regression was used to generate a null distribution of slope differences. The observed slope difference was then compared with the null distribution. In support of our predictions, results from the permutation test show that the phySMA slope of the male organs is statistically higher than the slope of the females organ while the slope of petals is statistically higher than the slope of sepals (Fig. S16).

6. Allometric scaling between flower organs

Results from standardized major axis regressions (SMA) between primary sexual organs (male plus female) against flower biomass support a statistically isometric relationship (Fig. S17A), while those for secondary sexual organs (petals plus sepals) against flower biomass show positive allometry (Fig. S17B). Primary sexual organs against secondary sexual organs show isometry (Fig. S17C). Within flower organs, the female organs and sepals both scale with a slope below one against petals, while male scales isometrically against petals and the female organs scales isometrically against sepals (Fig. S18).

7. Predicted biomass allocation

We used ordinary least squares allometric regression models to predict the relative allocation of biomass into the four flower components (male organs, female organs, petals, and sepals) along the flower biomass gradient. This method is the preferable line-fitting method for prediction purposes (reviewed in Ref. 2). We first generated the predicted values of biomass for each flower component along different flower biomass values using the slope and intercept from regressions to estimate the

predicted flower component biomass. Then, we used these values to calculate the relative allocation of biomass into each of the four flower components along the flower biomass gradient. This analysis was also performed using the phylogenetic generalized least squares regression models (PGLS).

Due to attenuation bias and statistical issues related to ordinary least squares regression models between parts against wholes, the sum of the biomass of the four flower components predicted from each allometric model tends to be biased. Therefore, the sum of predicted relative allocation for each flower component will not sum to one. Predicted flower biomass can be both underestimated or overestimated along the flower biomass gradient. To account for this issue, we initially estimated the bias, expressed in biomass (g), for flower biomass x (B_x) as:

$$B_x = x - \sum P_{ix}$$

where ΣP_{ix} is the sum of the predicted biomass of each flower component i for flower biomass x (P_{ix}). Then, we calculated unbiased estimates for each flower component by redistributing the estimated bias proportionally to the predicted relative biomass allocation of each flower component. This approach ensures that the sum of the predicted biomass for each flower component equals the total flower biomass. The unbiased estimate (U) of a given flower component i for flower biomass x (U_{ix}) was calculated as:

$$U_{ix} = P_{ix} + \left(\frac{P_{ix}}{\sum P_{ix}} \right) B_x$$

Our results show that both ordinary least squares and phylogenetic generalized least squares show some degree of bias, underestimating or overestimating the predicted relative allocation of flower components along the flower biomass gradient (Fig. S19A–B). In both cases, the estimated bias was a u-shaped function of the flower biomass, while bias from ordinary least squares models were much less variable along the biomass gradient and tends to underestimate flower biomass in 11% on average. Meanwhile, phylogenetic generalized least squares models had a more accentuated non-linear pattern in which the predicted biomass is overestimated at both ends of the flower biomass gradient and underestimated at intermediary flower biomass values (Fig. S19A–B). Estimated bias from PGLS models ranged between +12% and -10% of the expected flower biomass. In both cases, estimated bias was corrected through the application of the correction described above (Fig. S19D–E).

The predicted relative allocation of biomass into the four flower components revealed a clear pattern in which the percentage of biomass invested in the male organs and petals increased, while female organs and sepals decreased along the flower biomass gradient (Fig. S20). Due to steeper allometric slope estimates from the PGLS models, the predicted increase and decrease of flower relative allocation into flower components were much stronger in PGLS compared with OLS. Nonetheless, despite differences between OLS and PGLS predictions, the general pattern remained the same for both approaches, with biased and unbiased estimates, where male organs and petals tended to increase together, while female organs and sepals relative allocation decreased along the flower biomass gradient (Fig. S20).

8. Sensitivity analysis for OLS and PGLS

To account for several types of uncertainties in biomass prediction from OLS and PGLS allometric regressions, we repeated the same set of sensitivity analyses described above (section 3) for all OLS and PGLS allometric regressions: (i) sensitivity to sampling effort: species number and composition (Fig. S21-S22), (ii) sensitivity to taxonomic influence (Fig. S23-S24), (iii) sensitivity to phylogenetic uncertainty (Fig. S25), and (iv) sensitivity to species variation in flower showiness (Fig S26). Consistent with our main results, the OLS and PGLS allometric regressions were also very robust to different types of uncertainties in the dataset, taxonomic influence, phylogenetic uncertainty, and variation in flower showiness (see Figs. S21-S26). In comparison with SMA and phySMA line-fits, OLS and PGLS regressions show similar outcomes (see Table S7).
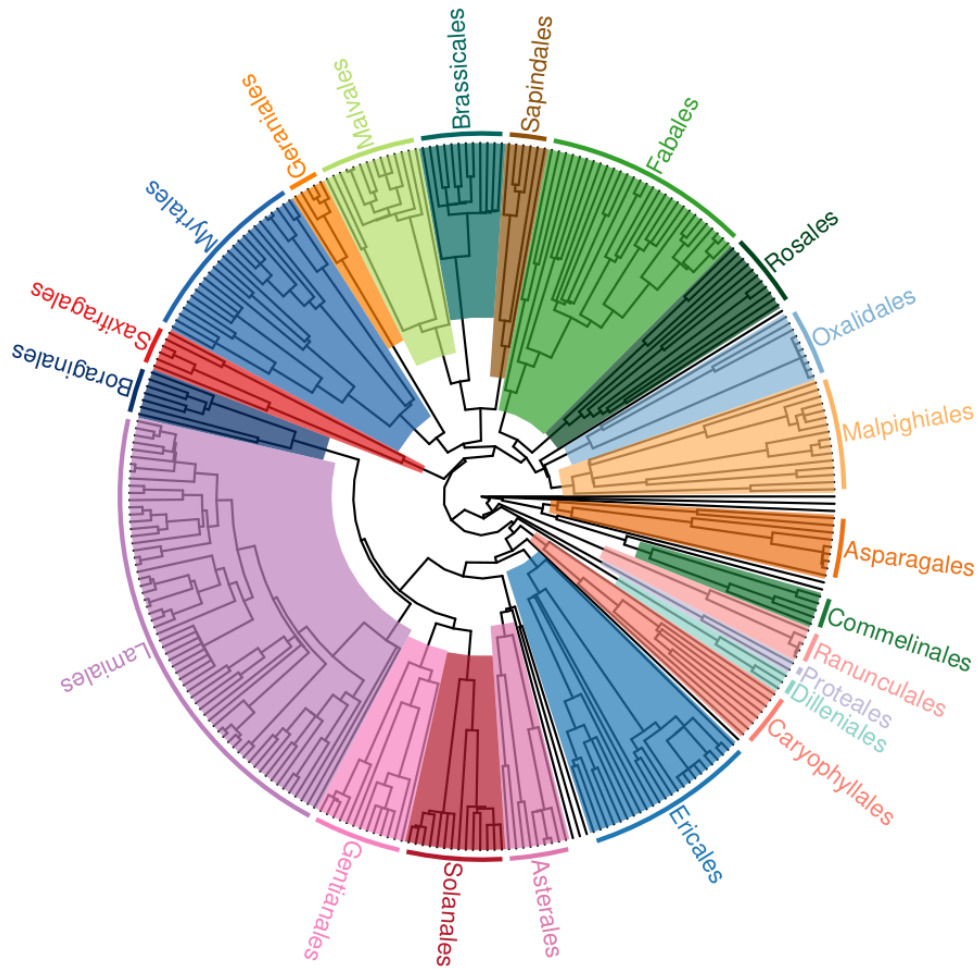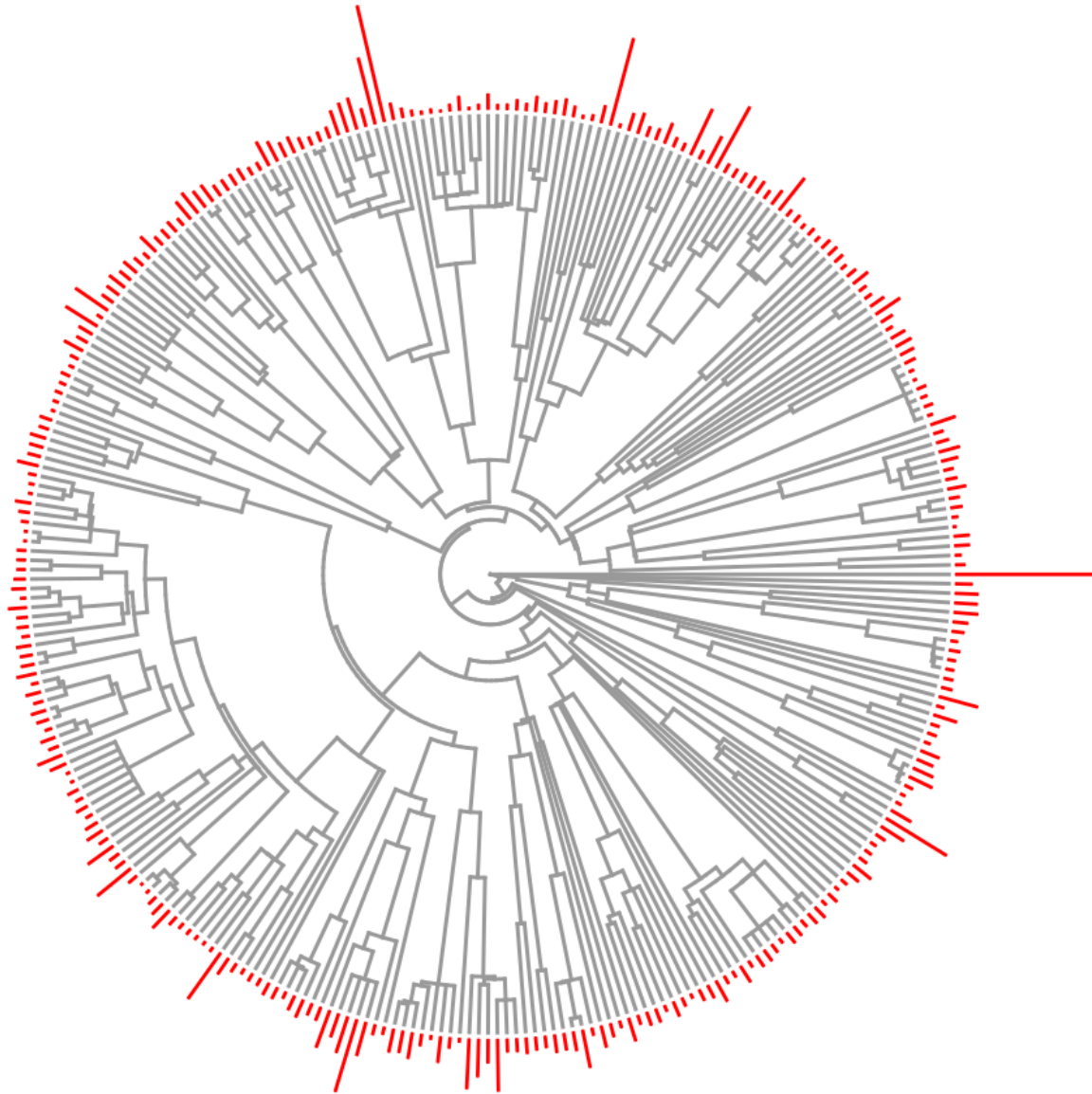
Fig. S1. Phylogeny of the 307 Angiosperm species included in this study. The tree was pruned from the most comprehensive dated phylogeny for the angiosperms (3). Taxonomic orders of Angiosperms with more than two species were highlighted in different colors.
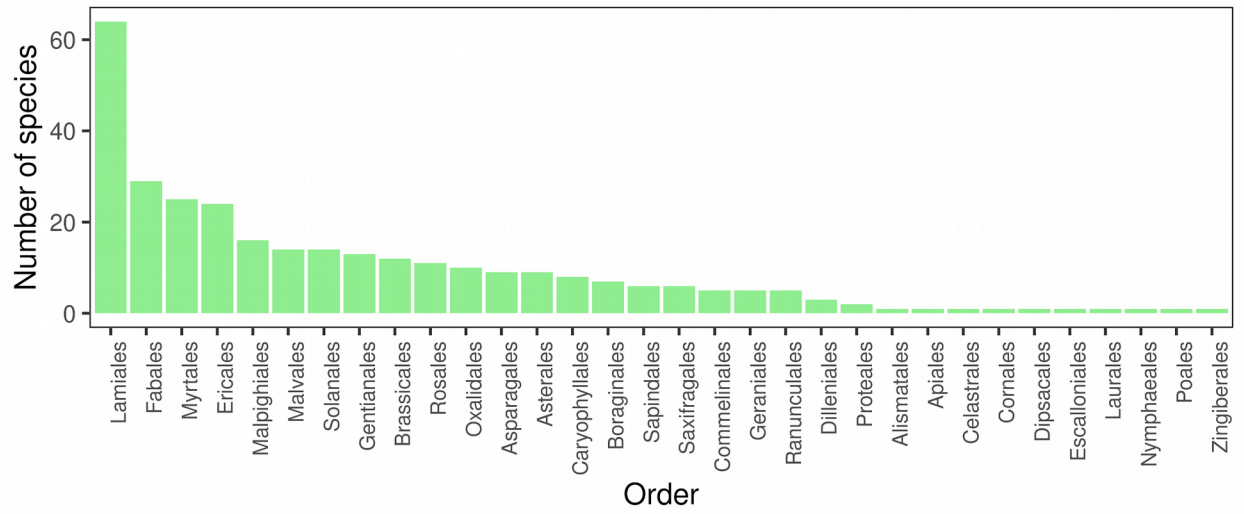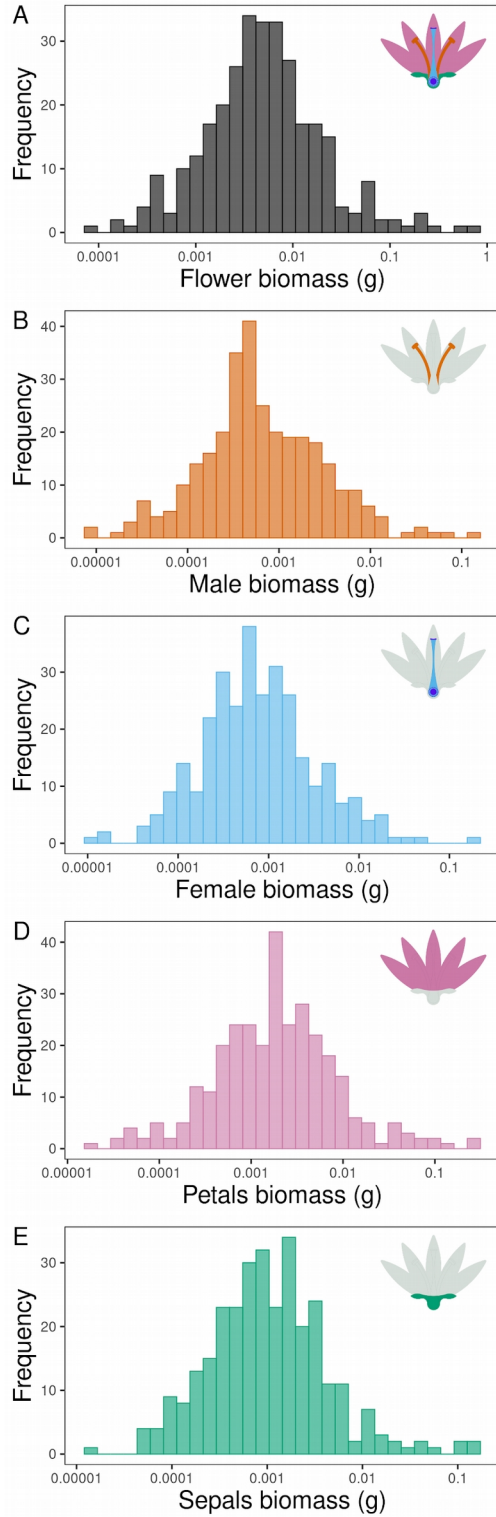
Fig. S2. Number of species in the 32 angiosperm orders included in the study (N = 307 study species).
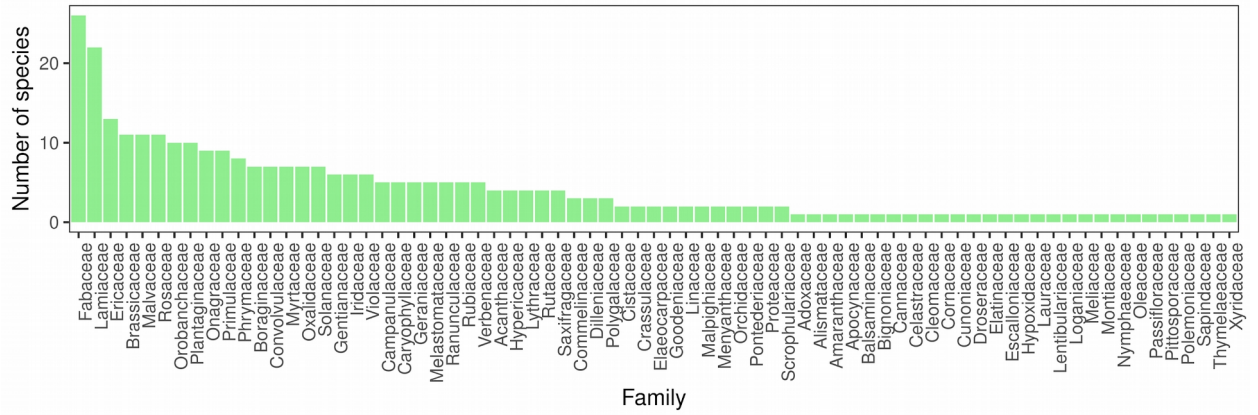
Fig. S3. Number of species in the 75 angiosperm families included in the study (N = 307 study species).

Fig. S4. Phylogeny of the 307 angiosperm species included in this study, with their respective flower biomass (square-root transformed) represented on the red bars.

Fig. S5. Distribution of flower biomass and their four components across the 307 angiosperm species included in this study. (A) flower biomass, (B) male organs biomass, (C) female organs biomass, (D) petals biomass, and (E) sepals biomass.
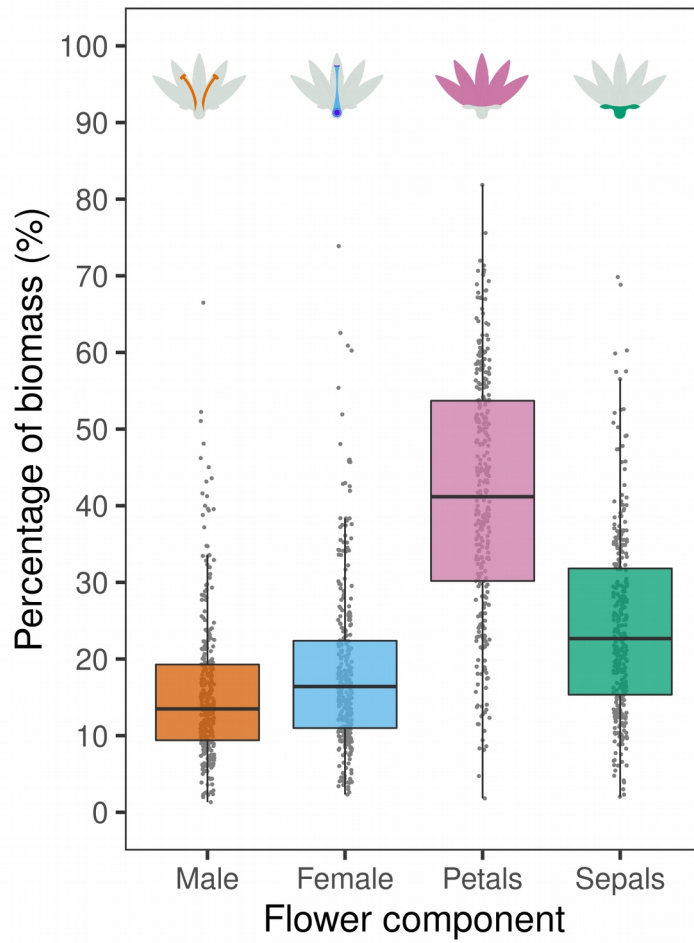
Fig. S6. Relative biomass allocation into different flower organs: male organs (androecium), female organs (gynoecium), petals (corolla), sepals (calyx). Relative allocation is given in percentage of total flower biomass estimated for 307 angiosperm species.
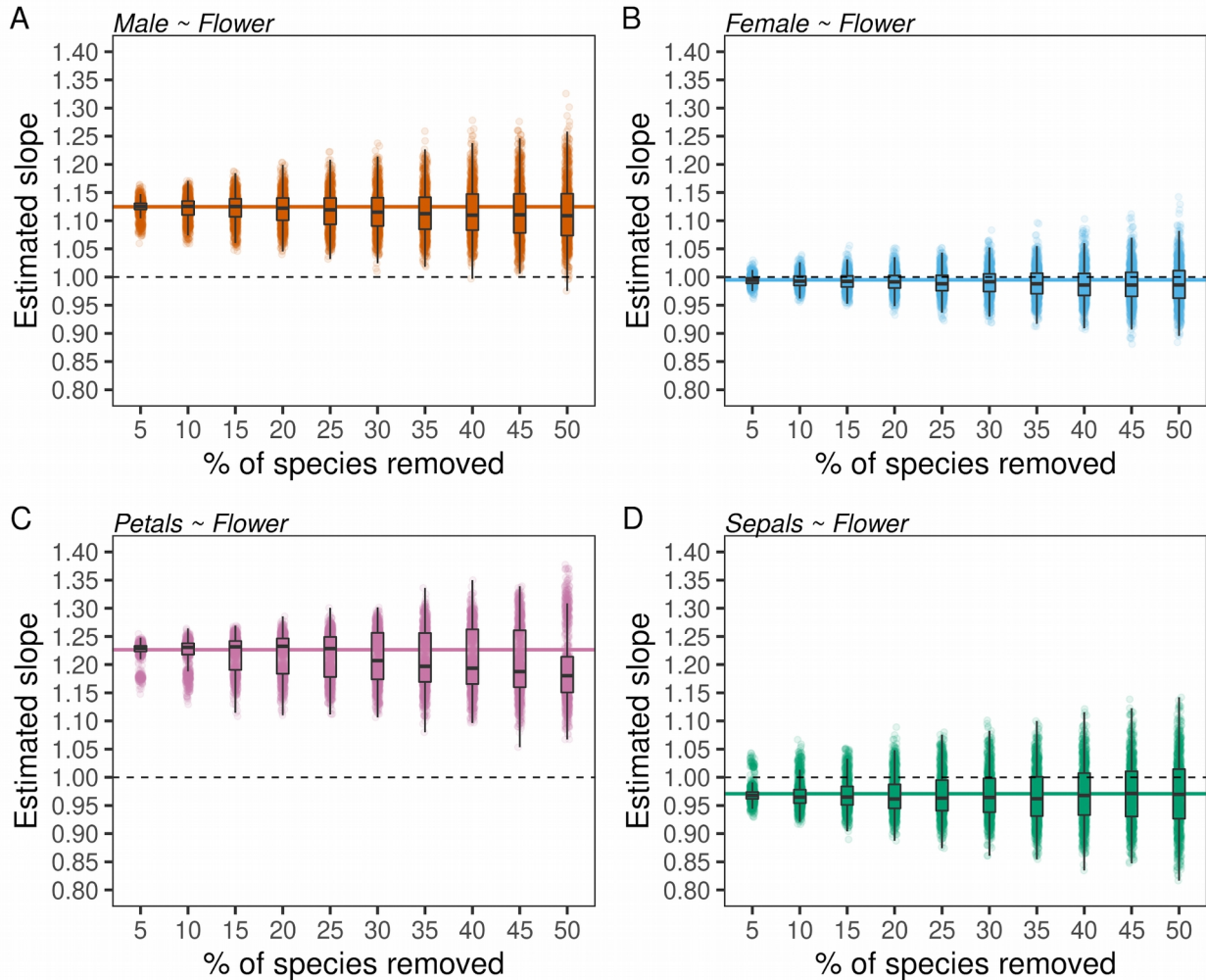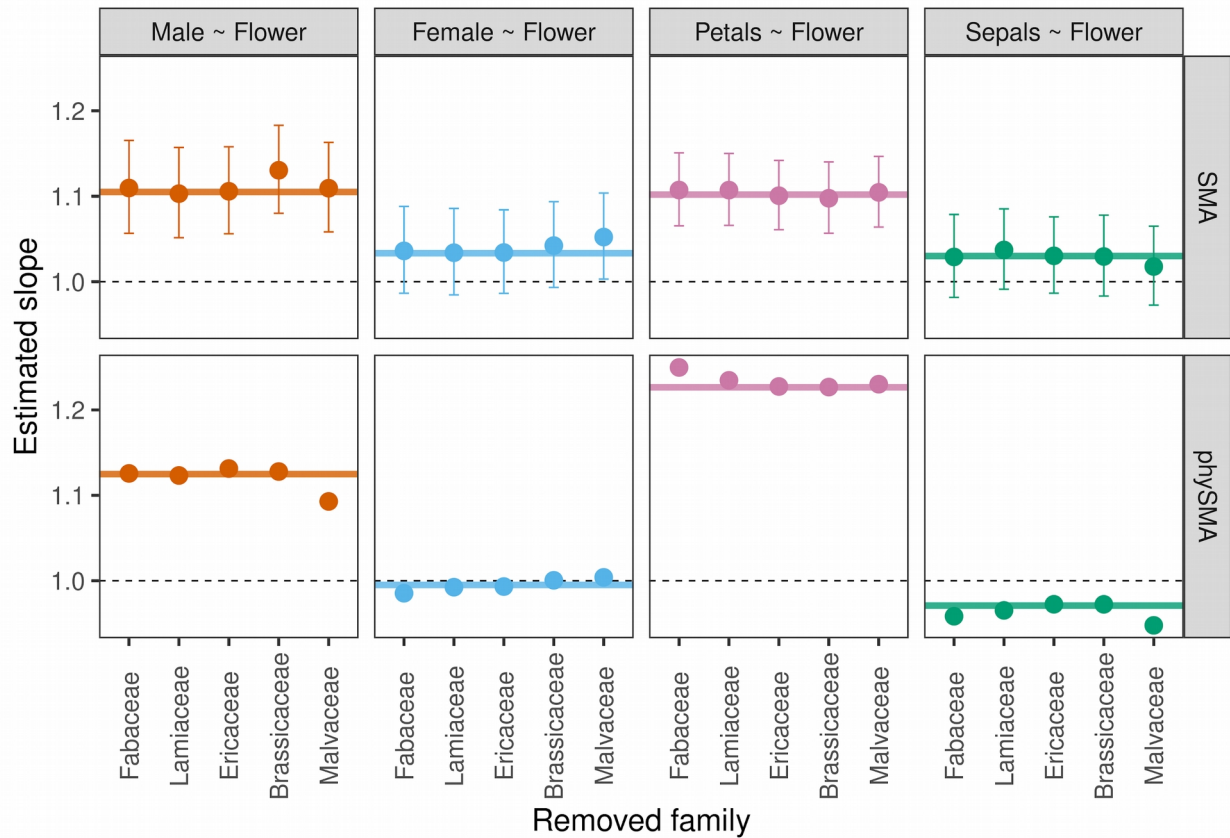
Sensitivity analysis - Sampling uncertainty (SMA)
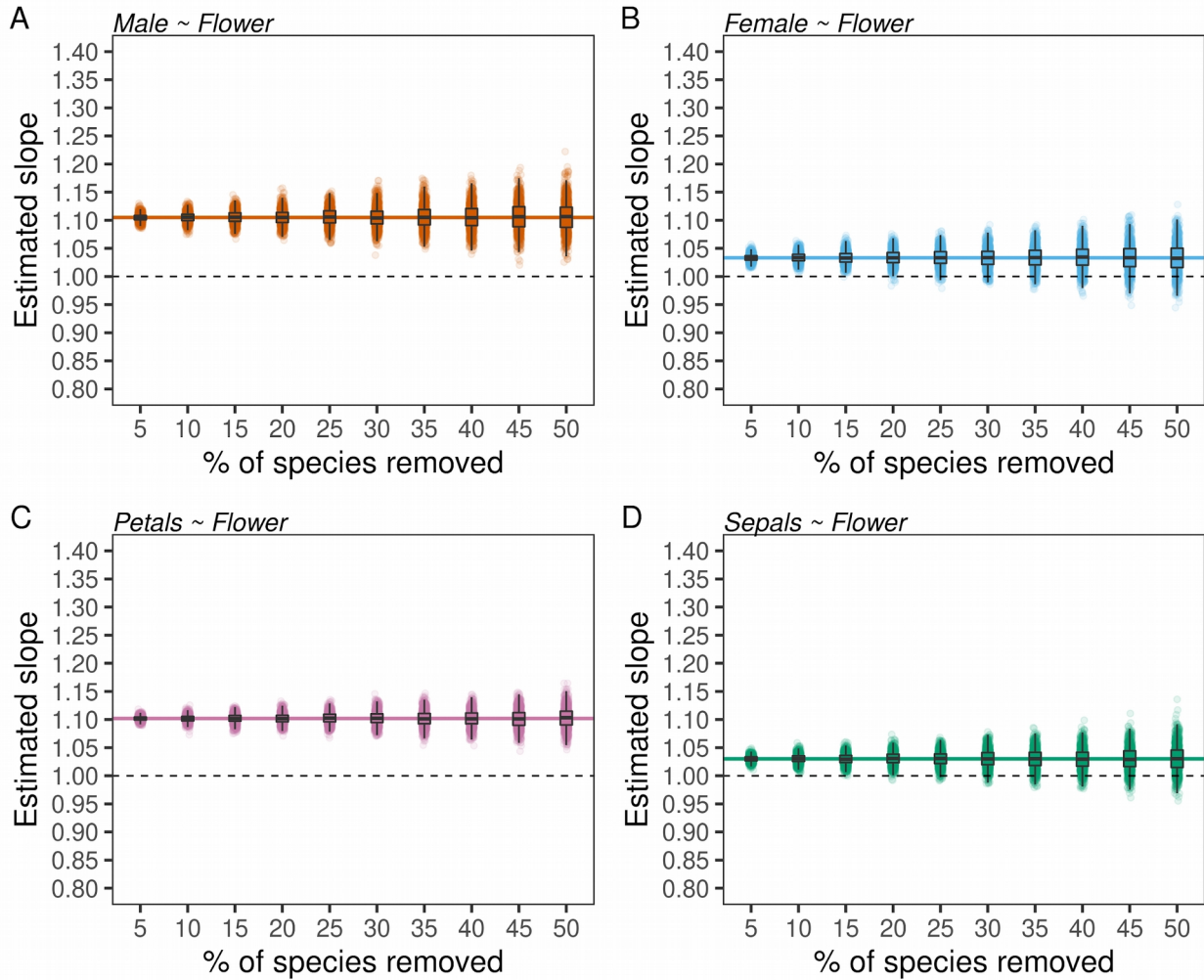
Fig. S7. Sensitivity analyses of the sampling effort on the slopes (β) of the relationships between the biomass of the four flower components against flower biomass as estimated by standardized major axis regressions (SMA). Simulations were performed with random subsets where 5% to 50% of the species were removed (N = 1000 trials). The continuous colored horizontal lines represent the estimated slopes based on the complete dataset (N = 307 species). The broken lines represent the isometric hypothesis (β = 1). Colored dots show the estimated slopes of individual trials. The boxplots represent the data variation for each treatment level.
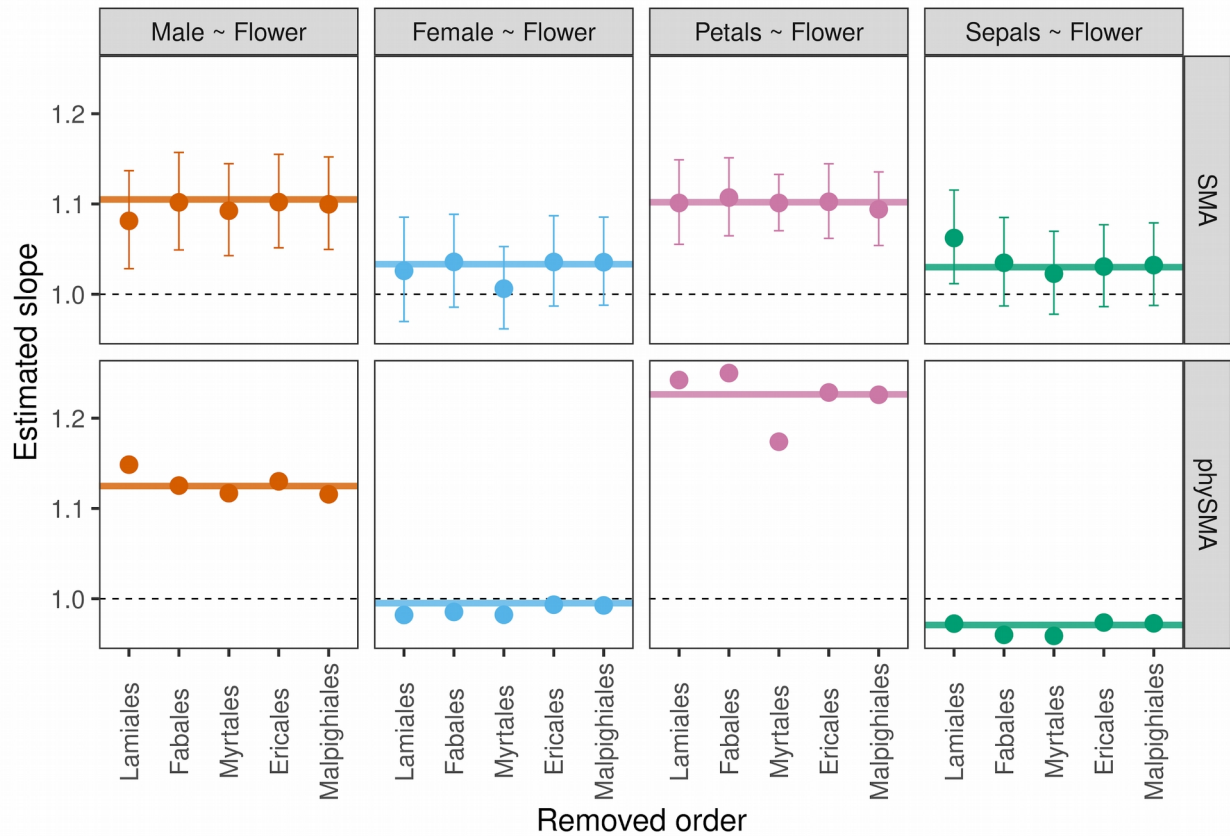
Fig. S8. Sensitivity analyses of the sampling effort on the slopes (β) of the relationships between the biomass of the four flower components against flower biomass as estimated by phylogenetic standardized major axis regressions (phySMA). Simulations were performed with random subsets where 5% to 50% of the species were removed (N = 1000 trials). The continuous colored horizontal lines represent the estimated slopes based on the complete dataset (N = 307 species). The broken lines represent the isometric hypothesis (β = 1). Colored dots show the estimated slopes of individual trials. The boxplots represent the data variation for each treatment level.
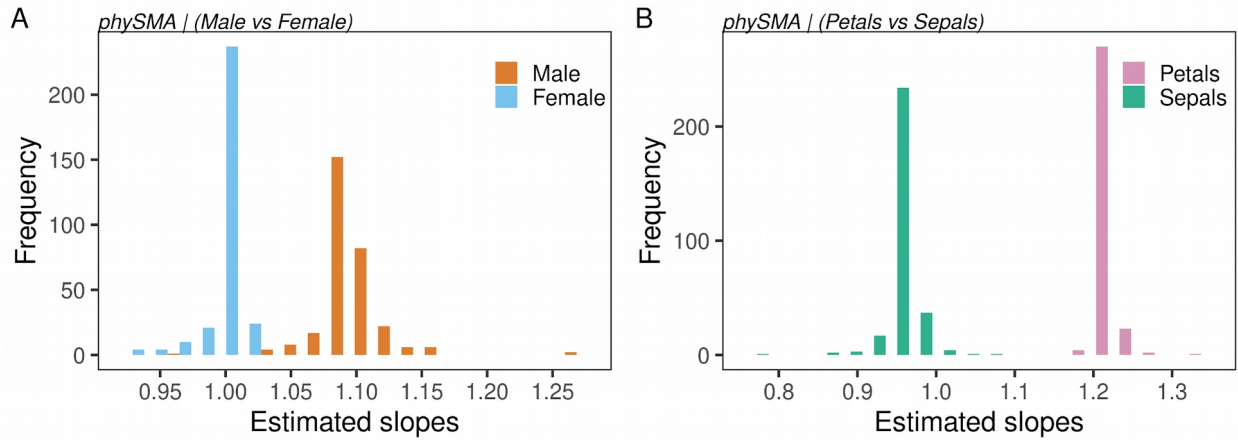
Fig. S9. Sensitivity analyses of potentially influential families (i.e., species-rich) on the slopes (β) of the relationships between the biomass of the four flower components against flower biomass as estimated by standardized major axis regressions (SMA, top row) and phylogenetic major axis regressions (phySMA, bottom row). Simulations were performed by subtracting the potentially influential families from the full dataset. The continuous colored horizontal lines represent the estimated slopes based on the complete dataset (N = 307 species). The broken lines represent the isometric hypothesis (β = 1). Colored dots show the estimated slopes of each simulation. The error bars represent the 95% confidence intervals for SMA regressions.
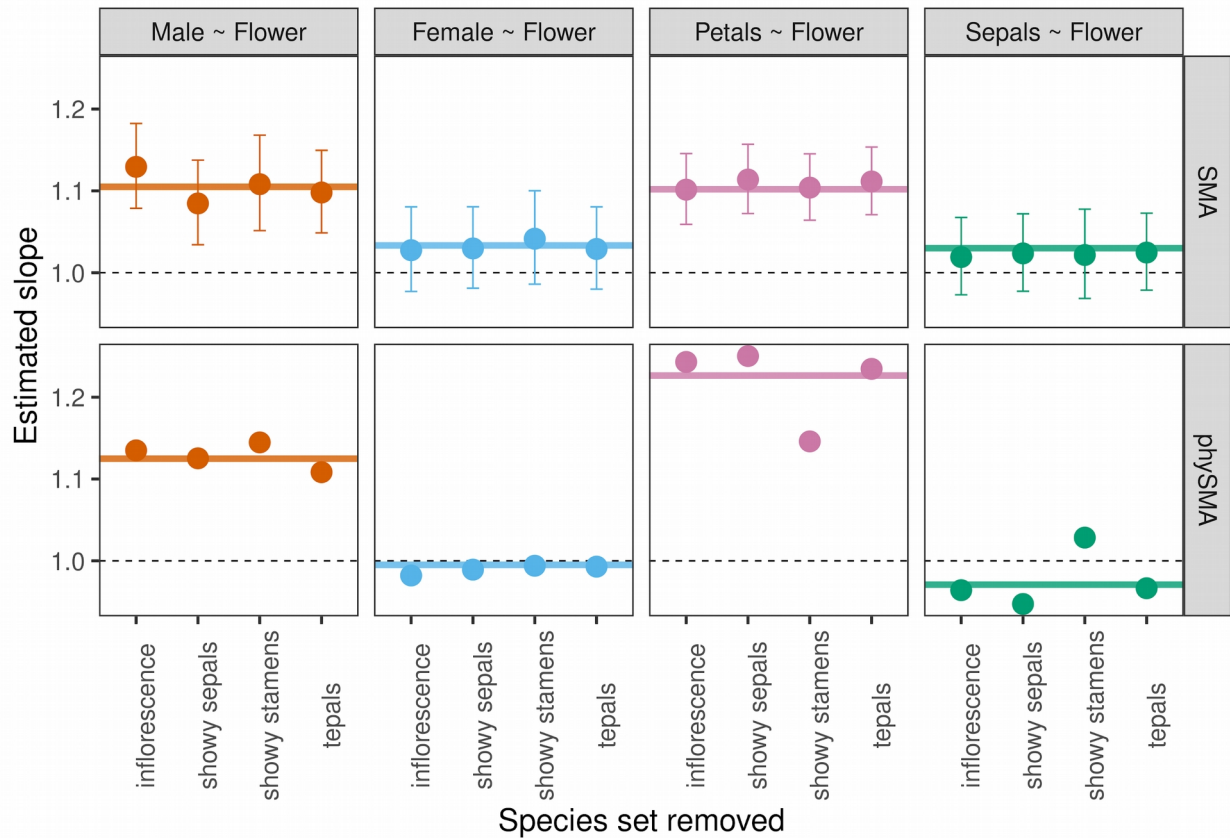
Fig. S10. Sensitivity analyses of potentially influential orders (i.e., speciose) on the slopes (β) of the relationships between the biomass of the four flower components against flower biomass as estimated by standardized major axis regressions (SMA, top row) and phylogenetic major axis regressions (phySMA, bottom row). Simulations were performed by subtracting the potentially influential orders from the full dataset. The continuous colored horizontal lines represent the estimated slopes based on the complete dataset (N = 307 species). The broken lines represent the isometric hypothesis (β = 1). Colored dots show the estimated slopes of each simulation. The error bars represent the 95% confidence intervals for SMA regressions.

Fig. S11. Sensitivity analyses of phylogenetic uncertainty on the slopes (β) of the relationships between the biomass of the four flower components against flower biomass as estimated by phylogenetic major axis regressions (phySMA). Simulations were performed by considering 300 alternative phylogenetic hypotheses. (A) The frequency distribution of slopes for male and female organs. (B) The distribution of slopes for petals and sepals.
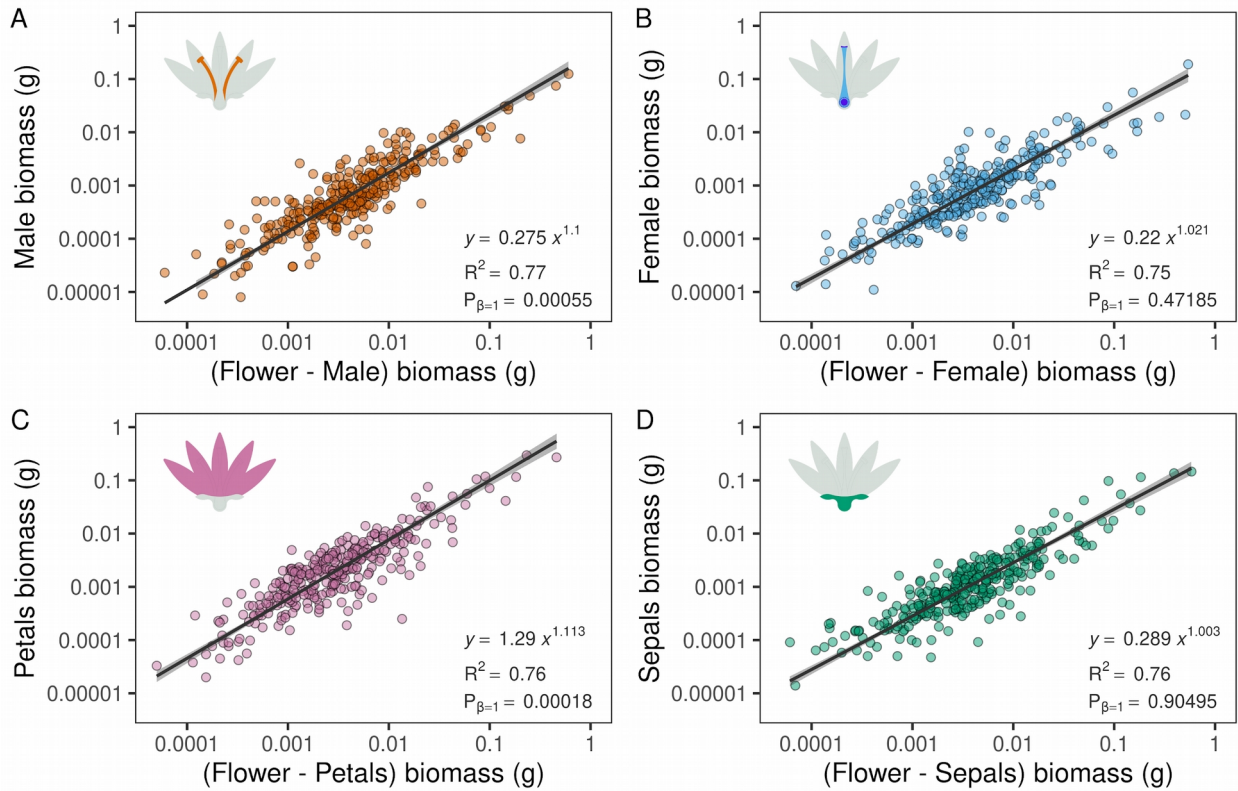
Fig. S12. Sensitivity analyses of different showiness strategies on the slopes (β) of the relationships between the biomass of the four flower components against flower biomass as estimated by standardized major axis regressions (SMA, top row) and phylogenetic major axis regressions (phySMA, bottom row). The showiness categories were (i) inflorescence - species with flowers particularly clustered together in the branch, (ii) showy sepals - species with flowers containing particularly colorful or enlarged sepals, (iii) showy stamens - species with flowers containing particularly colorful or enlarged stamens, and (iv) tepals - species with flowers containing relatively undifferentiated petals and sepals. Simulations were performed by subtracting the species with particular showiness strategy from the full dataset. The continuous colored horizontal lines represent the estimated slopes based on the complete dataset (N = 307 species). The broken lines represent the isometric hypothesis (β = 1). Colored dots show the estimated slopes of each simulation. The error bars represent the 95% confidence intervals.
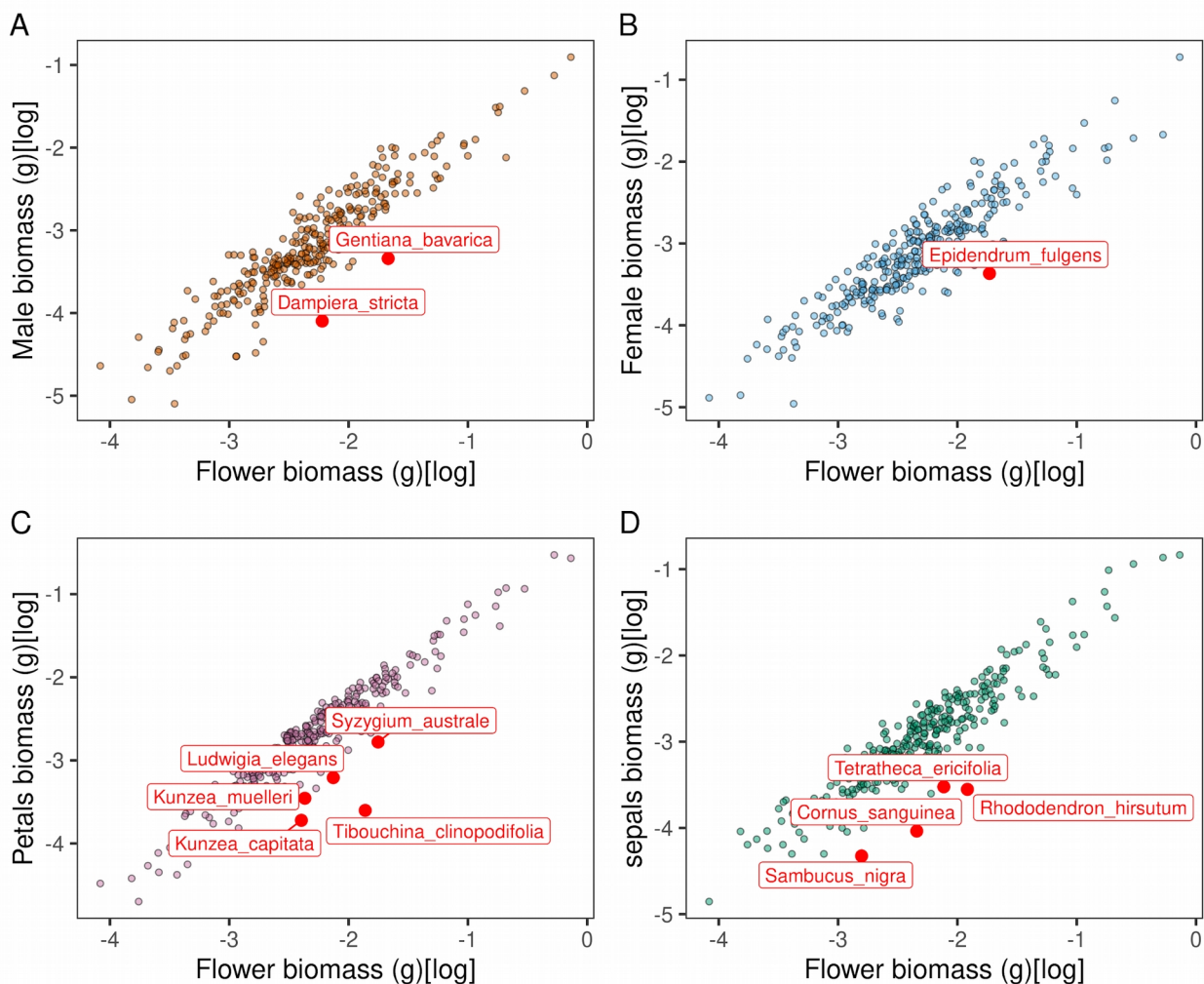
Fig. S13. Relationship between the biomass of the four flower components and flower biomass (both in log-scale) for 307 angiosperm species, with special attention to outlier species identified in standardized major axis regressions (SMA). (A) Male organs, (B) Female organs, (C) Petals, and (D) Sepals. Outlier species were recognized by their standardized residuals larger than three, The large red dots represent the outlier species (and their respective Latin names are provided).

Fig. S14. Across-species flower allometries of 307 Angiosperm species controlling for axis non-independence. Standardized major axis relationship between flower component on the y axis and total flower biomass minus the flower component on the x-axis for (A) male organs, (B) female organs, (C) petals, and (D) sepals. All axes are log10-transformed. The black lines are standardized major axis regressions and the gray shadow their 95% confidence interval. Allometric equations ($Y = \alpha X^\beta$) and R^2 are provided. $P_{\beta=1}$ indicates the probability of rejecting the isometric hypothesis ($\beta = 1$).

phySMA allometries controlling for axis non-independence (Y ~ (X - Y))

A

Male biomass (g) vs (Flower - Male) biomass (g)

$y = 0.358\ x^{1.124}$
$R^2 = 0.72$
$P_{\beta=1} = 0.00013$

B

Female biomass (g) vs (Flower - Female) biomass (g)

$y = 0.164\ x^{0.964}$
$R^2 = 0.72$
$P_{\beta=1} = 0.23263$

C

Petals biomass (g) vs (Flower - Petals) biomass (g)

$y = 3.373\ x^{1.312}$
$R^2 = 0.72$
$P_{\beta=1} = 0.000001$

D

Sepals biomass (g) vs (Flower - Sepals) biomass (g)

$y = 0.163\ x^{0.905}$
$R^2 = 0.61$
$P_{\beta=1} = 0.0054$
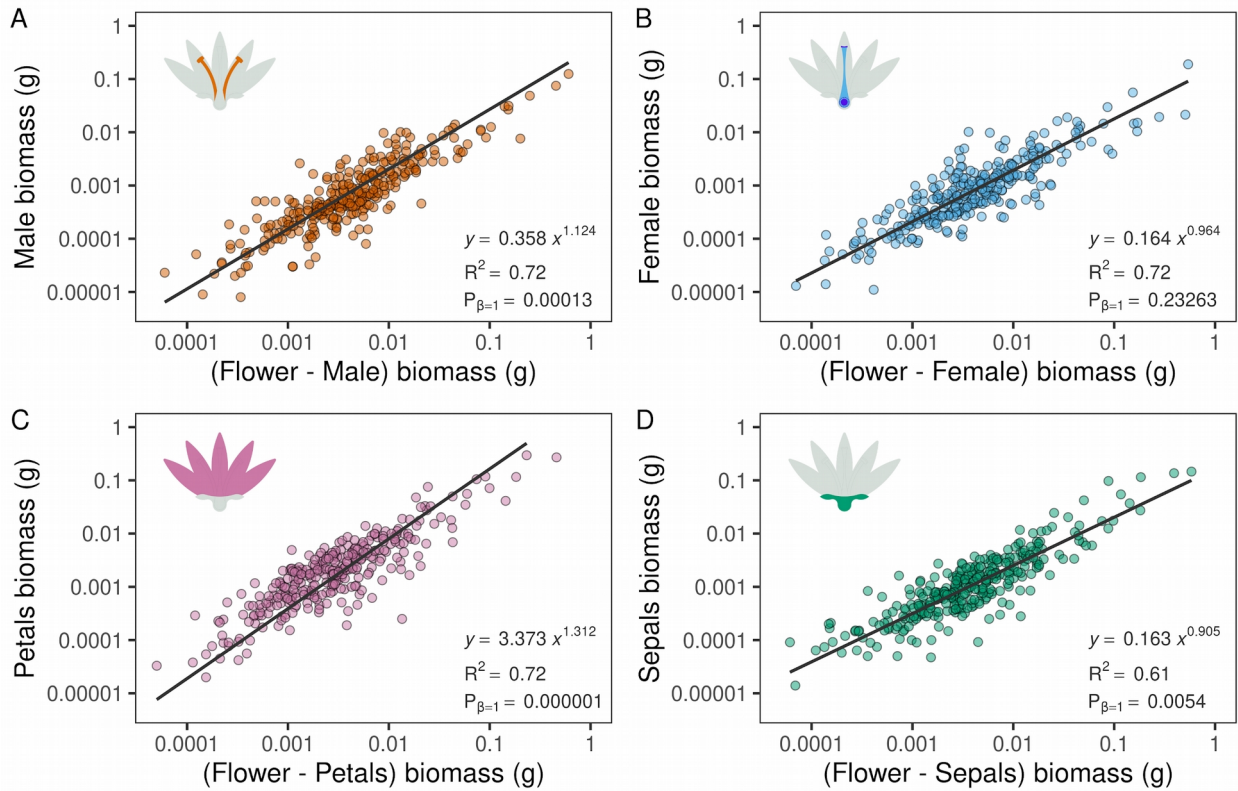
**Fig. S15.** Across-species flower allometries of 307 Angiosperm species controlling for axis non-independence. Phylogenetic standardized major axis relationship between flower component on the y axis and total flower biomass minus the flower component on the x-axis for (A) male organs, (B) female organs, (C) petals, and (D) sepals. All axes are log10-transformed. The black lines are standardized major axis regressions and the gray shadow their 95% confidence interval. Allometric equations ($Y = \alpha X^{\beta}$) and R^2 are provided. $P_{\beta=1}$ indicates the probability of rejecting the isometric hypothesis ($\beta = 1$).
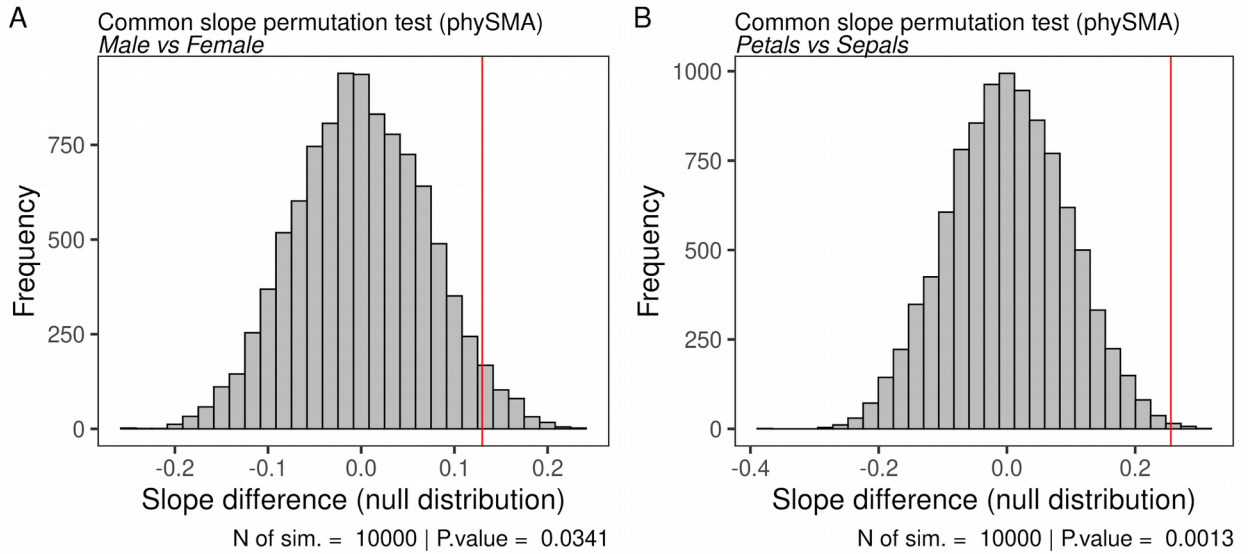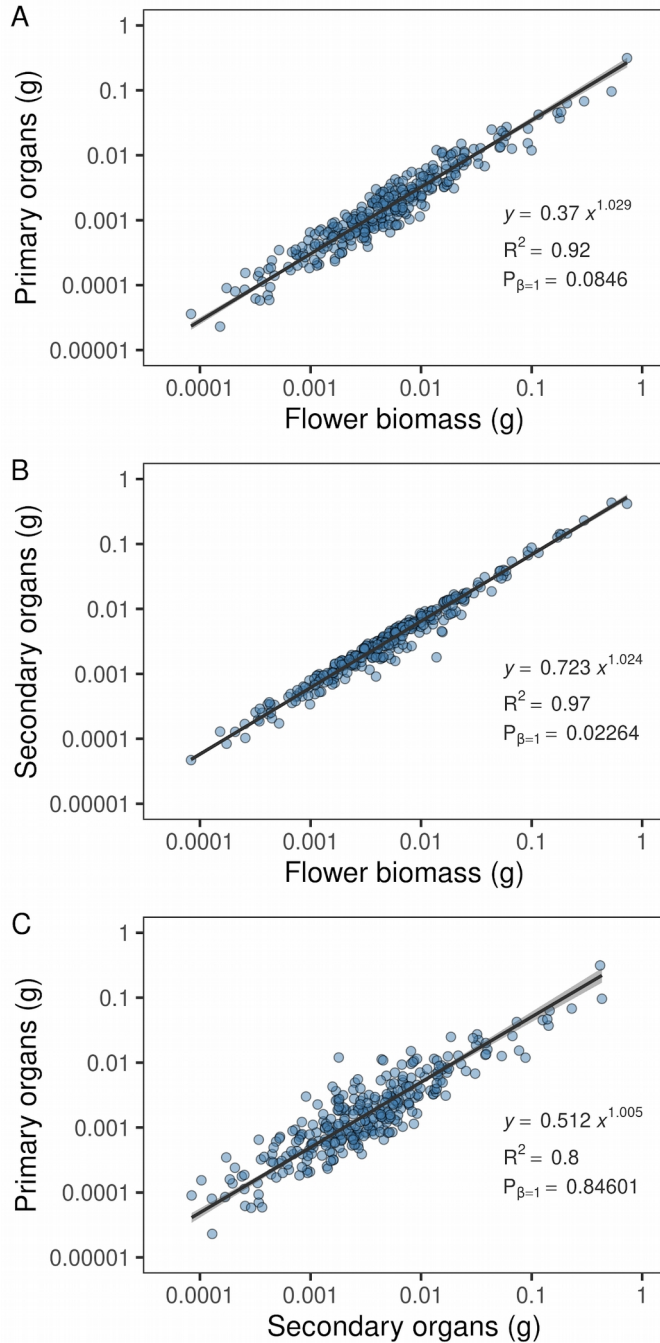
Fig. S16. Common slope permutation test for phylogenetic standardized major axis regressions (phySMA) for (A) male (β_{male}) compared to the female organs (β_{female}), and (B) for petals (β_{petals}) compared to sepals (β_{sepals}). Histogramas show the null distribution of the difference in phySMA slopes between flower organs for 10.000 simulations. The vertical red line indicates the observed difference in slope between male and female organs (A) and between petals and sepals. P.value indicates the probability of rejecting the null hypothesis (slope difference = 0).

A

$y = 0.37\ x^{1.029}$
$R^2 = 0.92$
$P_{\beta=1} = 0.0846$

Primary organs (g)

Flower biomass (g)

B

$y = 0.723\ x^{1.024}$
$R^2 = 0.97$
$P_{\beta=1} = 0.02264$

Secondary organs (g)

Flower biomass (g)

C

$y = 0.512\ x^{1.005}$
$R^2 = 0.8$
$P_{\beta=1} = 0.84601$

Primary organs (g)

Secondary organs (g)

Fig. S17. Across-species allometries across 307 Angiosperm flowers. Relationship between the biomass allocation for (A) primary sexual organs (male plus female), (B) secondary sexual organs (petals plus sepals) and (C) primary sexual organs against secondary sexual organs. All axes are log10-transformed. The black lines are standardized major axis regressions and the gray shadow their 95% confidence interval. Allometric equations ($Y = \alpha X^{\beta}$) and R^2 are provided. $P_{\beta=1}$ indicates the probability of rejecting the isometric hypothesis ($\beta = 1$).
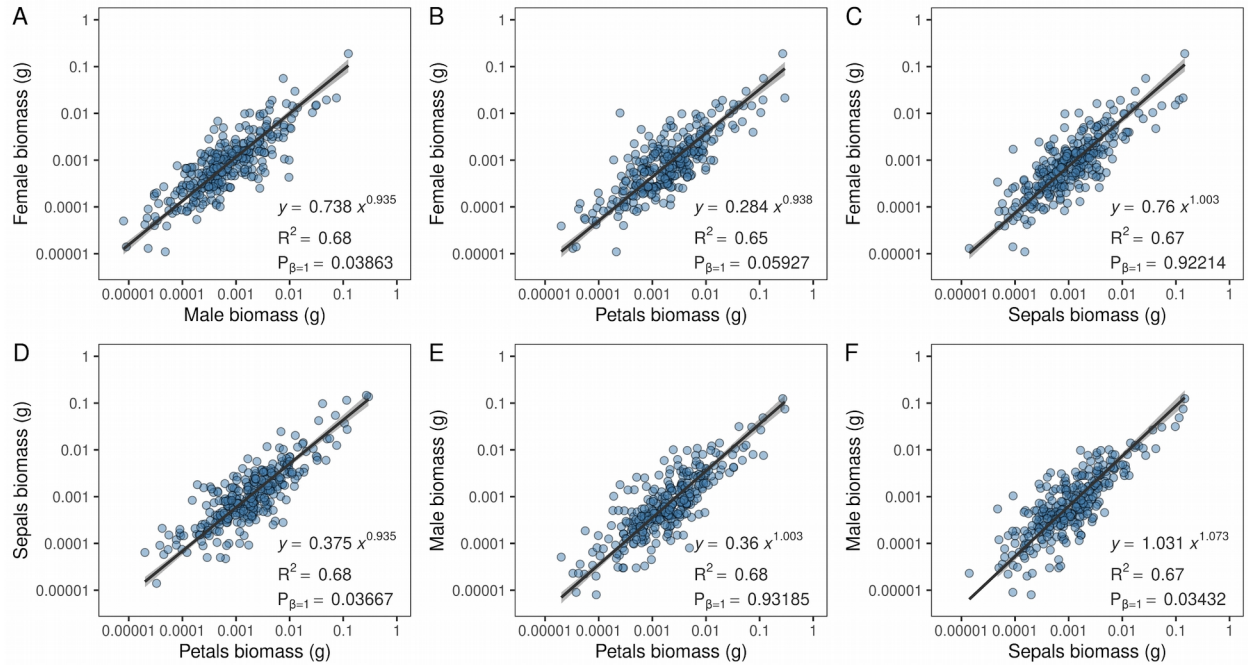
Fig. S18. Across-species allometries across 307 Angiosperm flowers. Relationship between the biomass allocation for (A) female against male organs, (B) female organs against petals, (C) female organs against sepals, (D) sepals against petals, (E) male organs against petals, and (F) male organs against sepals. All axes are log10-transformed. The black lines are standardized major axis regressions and the gray shadow their 95% confidence interval. Allometric equations ($Y = \alpha X^{\beta}$) and R^2 are provided. $P_{\beta=1}$ indicates the probability of rejecting the isometric hypothesis ($\beta = 1$).
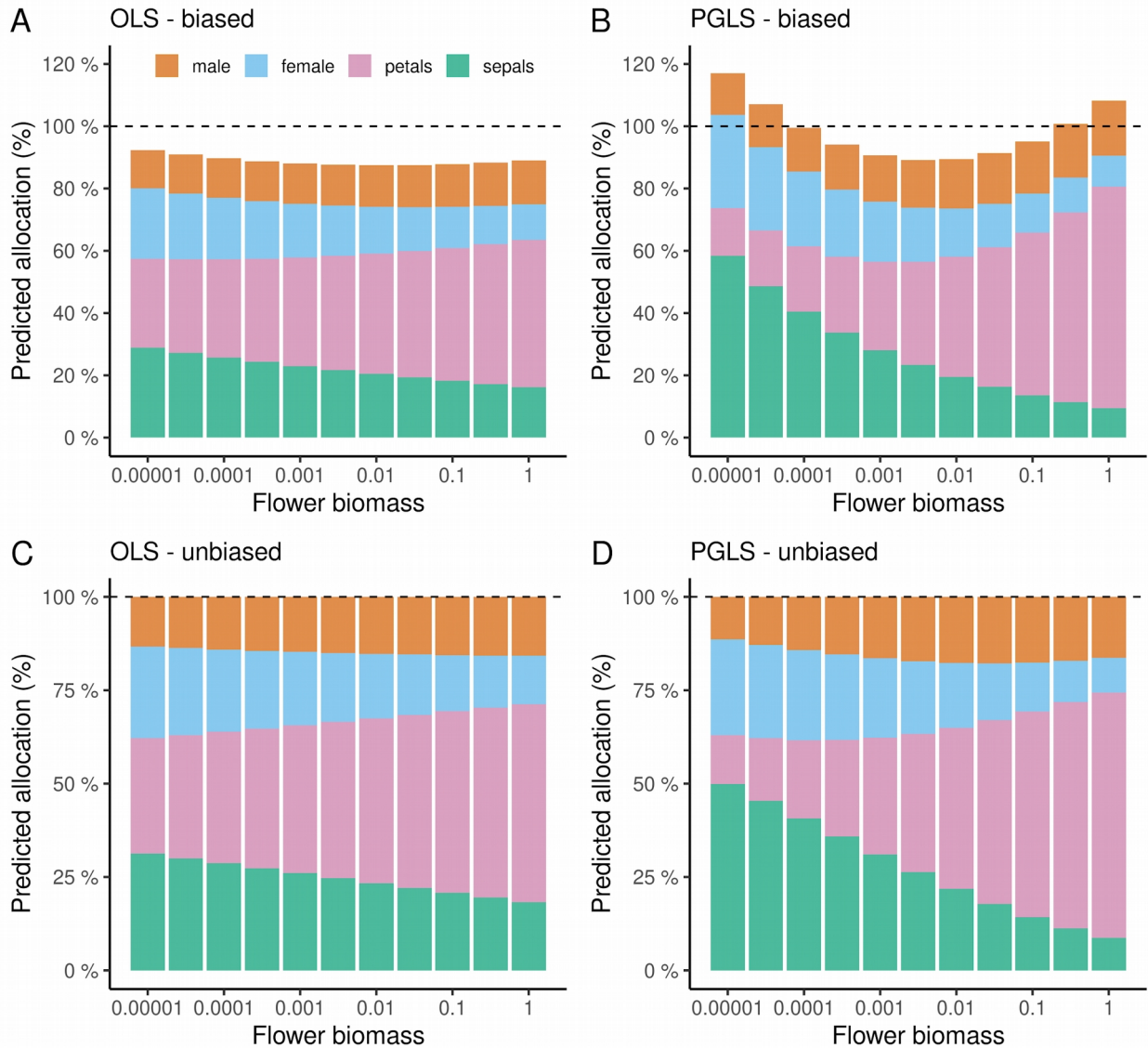
Fig. S19. Predicted relative allocation into four flower components along a flower biomass gradient for (A) ordinary least squares (biased), (B) phylogenetic generalized least squares (biased), (C) ordinary least squares (unbiased), and (D) phylogenetic generalized least squares (unbiased). Unbiased estimates were calculated following equations described above.
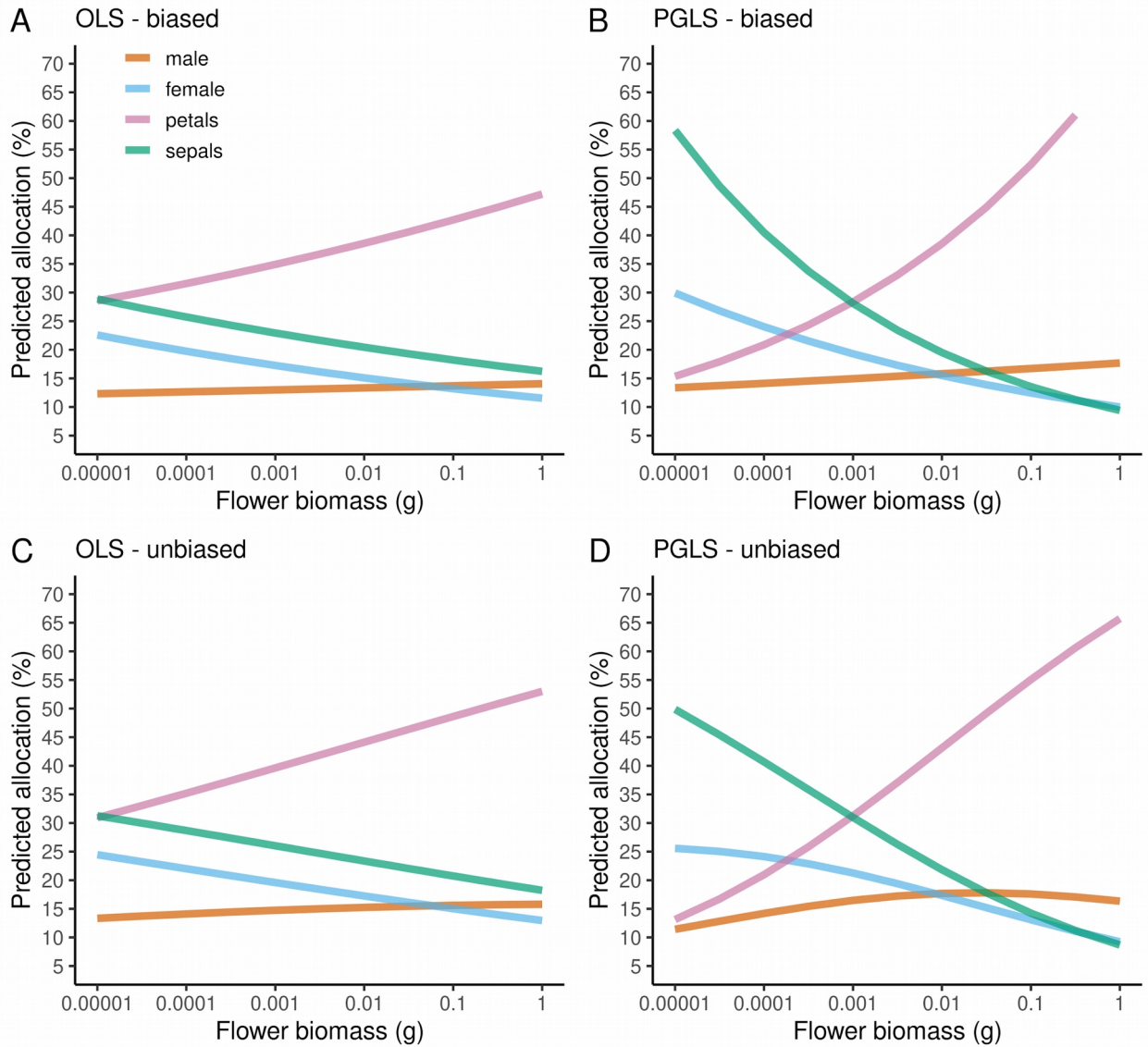
Fig. S20. Predicted relative biomass allocation in primary and secondary sexual organs along the flower biomass gradient. The curves are biased and unbiased-estimates according to (A) OLS allometric models, (B) PGLS allometric models, (C) OLS allometric models (unbiased), and (D) PGLS allometric models (unbiased). Unbiased relative allocation was calculated following equations described above.
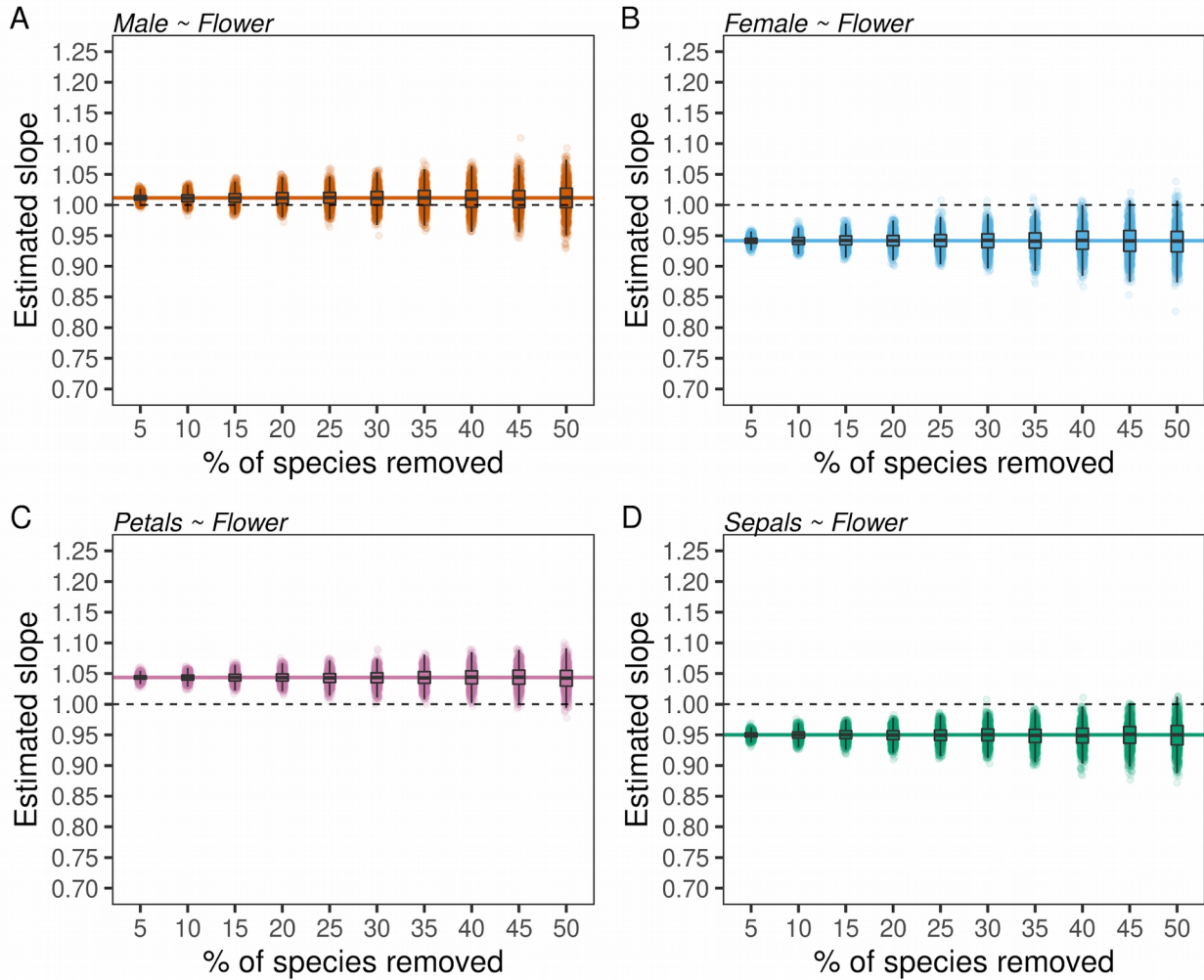
Fig. S21. Sensitivity analyses of the sampling effort on the slopes (β) of the relationships between the biomass of the four flower components against flower biomass as estimated by ordinary least square (OLS). Simulations were performed with random subsets where 5% to 50% of the species were removed (N = 1000 trials). The continuous colored horizontal lines represent the estimated slopes based on the complete dataset (N = 307 species). The broken lines represent the isometric hypothesis (β = 1). Colored dots show the estimated slopes of individual trials. The boxplots represent the data variation for each treatment level.

Sensitivity analysis - Sampling uncertainty (PGLS)
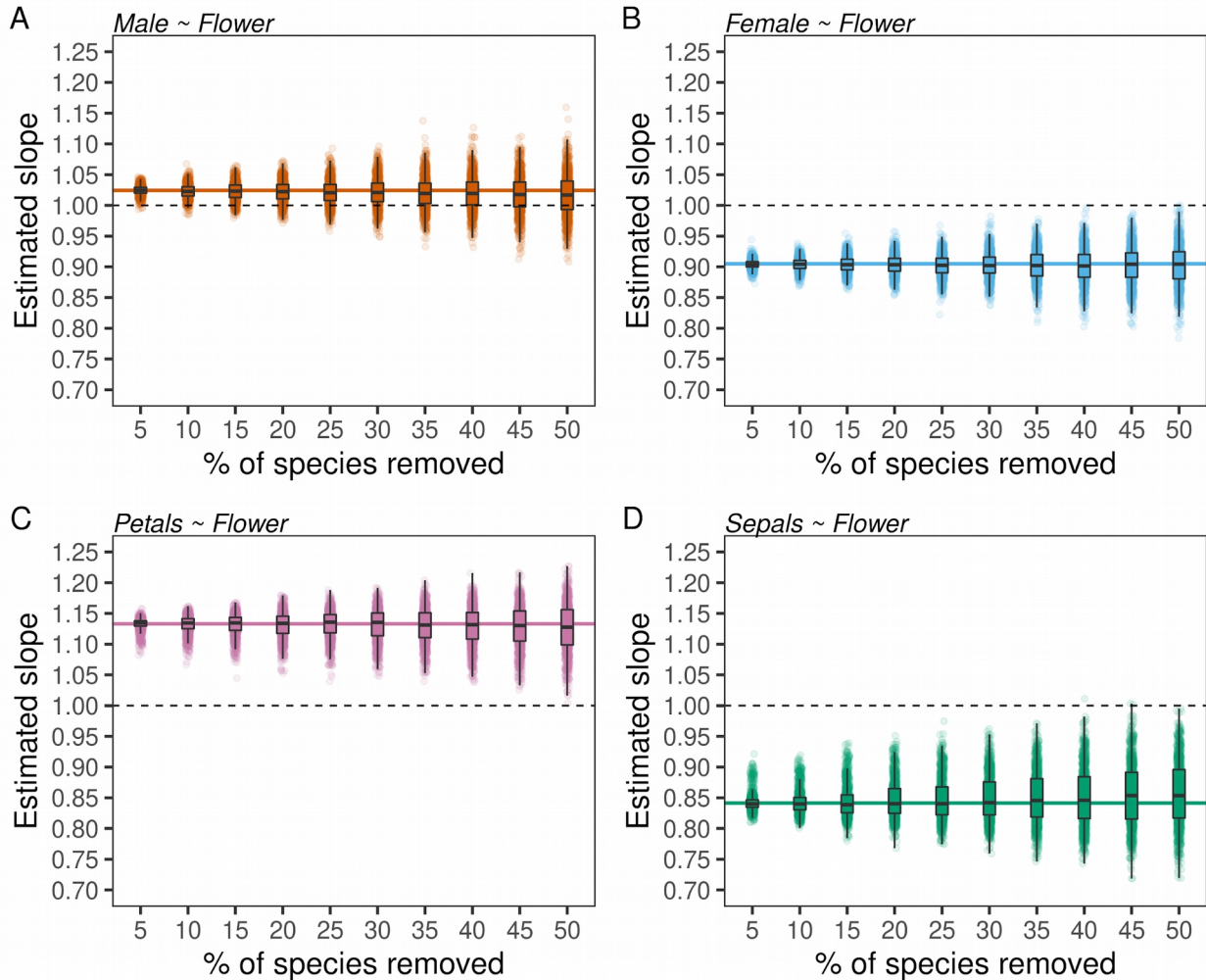
Fig. S22. Sensitivity analyses of the sampling effort on the slopes (β) of the relationships between the biomass of the four flower components against flower biomass as estimated by phylogenetic generalized least squares (PGLS). Simulations were performed with random subsets where 5% to 50% of the species were removed (N = 1000 trials). The continuous colored horizontal lines represent the estimated slopes based on the complete dataset (N = 307 species). The broken lines represent the isometric hypothesis (β = 1). Colored dots show the estimated slopes of individual trials. The boxplots represent the data variation for each treatment level.

Fig. S23. Sensitivity analyses of potentially influential families (i.e., speciose) on the slopes (β) of the relationships between the biomass of the four flower components against flower biomass as estimated by ordinary least squares (OLS, top row) and phylogenetic generalized least squares (PGLS, bottom row). Simulations were performed by subtracting the potentially influential orders from the full dataset. The continuous colored horizontal lines represent the estimated slopes based on the complete dataset (N = 307 species). The broken lines represent the isometric hypothesis (β = 1). Colored dots show the estimated slopes of each simulation. The error bars represent the 95% confidence intervals.

Fig. S24. Sensitivity analyses of potentially influential orders (i.e., speciose) on the slopes (β) of the relationships between the biomass of the four flower components against flower biomass as estimated by ordinary least squares (OLS, top row) and phylogenetic generalized least squares (PGLS, bottom row). Simulations were performed by subtracting the potentially influential orders from the full dataset. The continuous colored horizontal lines represent the estimated slopes based on the complete dataset (N = 307 species). The broken lines represent the isometric hypothesis (β = 1). Colored dots show the estimated slopes of each simulation. The error bars represent the 95% confidence intervals.

Fig. S25. Sensitivity analyses of phylogenetic uncertainty on the slopes (β) of the relationships between the biomass of the four flower components against flower biomass as estimated by phylogenetic generalized least squares regressions (PGLS). Simulations were performed by considering 300 alternative phylogenetic hypotheses. (A) The frequency distribution of slopes for male and female organs. (B) The distribution of slopes for petals and sepals.
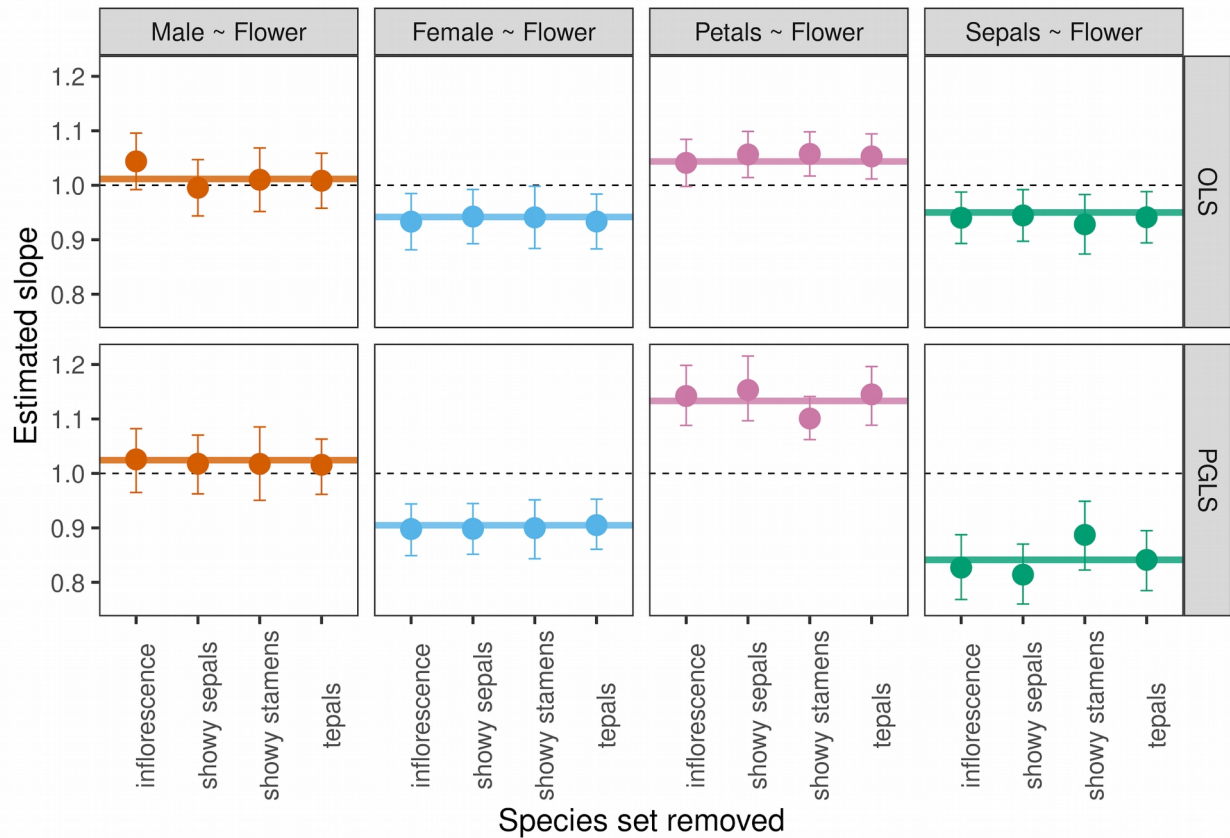
Fig. S26. Sensitivity analyses of different showiness strategies on the slopes (β) of the relationships between the biomass of the four flower components against flower biomass as estimated by ordinary least squares (OLS, top row) and phylogenetic generalized least squares (PGLS, bottom row). The showiness categories were (A) inflorescence - species with flowers particularly clustered together in the branch, (B) showy sepals - species with flowers containing particularly colorful or enlarged sepals, (C) showy stamens - species with flowers containing particularly colorful or enlarged stamens, and (D) tepals - species with flowers containing relatively undifferentiated petals and sepals. Simulations were performed by subtracting the species with particular showiness strategy from the full dataset. The continuous colored horizontal lines represent the estimated slopes based on the complete dataset (N = 307 species). The broken lines represent the isometric hypothesis (β = 1). Colored dots show the estimated slopes of each simulation. The error bars represent the 95% confidence intervals.

Table S1. Relative biomass allocation of four flower components across 307 angiosperm species. The components are male organs (androecium), female organs (gynoecium), petals (corolla), and sepals (calyx). Mean relative allocation is provided as a percentage of the total flower biomass. The standard deviation (SD), and the minimum (min) and maximal (max) values are provided.

Flower component	Mean (%)	SD	min	max
Male	15.8	9.8	1.3	66.5
Female	18.6	11.1	2.3	73.9
Petals	41.3	15.8	1.8	81.9
Sepals	24.3	12	2	69.8

Table S2. Flower traits for the ten species with the heaviest and lightest flower biomass across 307 angiosperm study species. Rank shows species in descending order from the 10 heaviest flowers (rank between 1-10) to the 10 lightest flowers (rank between 307-298).

Rank	Species	Flower (g)	Androecium (g)	Gynoecium (g)	Petals (g)	Sepals (g)	maleness
1	*Nymphaea alba*	0.7296800	0.1244300	0.1888900	0.2701900	0.1461700	0.66
2	*Ceiba speciosa*	0.5284100	0.0747100	0.0213300	0.2959900	0.1363800	3.50
3	*Bauhinia forficata*	0.2986100	0.0485500	0.0193400	0.1158200	0.1149000	2.51
4	*Gentiana pannonica*	0.2088533	0.0076000	0.0557167	0.1182367	0.0273000	0.14
5	*Hibbertia scandens*	0.1850714	0.0314143	0.0151000	0.0412000	0.0973571	2.08
6	*Erythrina crista-galli*	0.1793600	0.0266500	0.0103900	0.1052700	0.0370500	2.56
7	*Hibiscus diversifolius*	0.1711300	0.0305400	0.0145300	0.0714700	0.0545900	2.10
8	*Digitalis purpurea*	0.1155500	0.0125500	0.0296500	0.0558900	0.0174600	0.42
9	*Ipomoea purpurea*	0.0998500	0.0079600	0.0039500	0.0754700	0.0124700	2.02
10	*Gompholobium latifolium*	0.0927900	0.0112100	0.0144900	0.0499300	0.0171600	0.77
307	*Lepidium virginicum*	0.0000830	0.0000230	0.0000130	0.0000330	0.0000140	1.77
306	*Verbena bracteata*	0.0001520	0.0000090	0.0000140	0.0000380	0.0000910	0.64
305	*Capsella bursa-pastoris*	0.0001740	0.0000510	0.0000390	0.0000200	0.0000640	1.31
304	*Lycopus virginicus*	0.0002080	0.0000220	0.0000580	0.0000540	0.0000740	0.38
303	*Lycopus americanus*	0.0002540	0.0000340	0.0000510	0.0000770	0.0000920	0.67
302	*Elatine alsinastrum*	0.0002570	0.0000360	0.0001180	0.0000450	0.0000580	0.31
301	*Polygala sanguinea*	0.0003180	0.0000200	0.0000420	0.0000890	0.0001670	0.48
300	*Oxalis corniculata*	0.0003350	0.0000650	0.0000730	0.0000770	0.0001200	0.89
299	*Hornungia alpina*	0.0003450	0.0000770	0.0000820	0.0001220	0.0000640	0.94
298	*Mimulus micranthus*	0.0003480	0.0000080	0.0000500	0.0000900	0.0002000	0.16

Table S3. Standardized major axis (SMA) and phylogenetic standardized major axis (phySMA) allometric regressions of the four flower components in relation to flower biomass. R^2 is the determination coefficient. The intercept (α) and slope (β) of the allometric curve $Y = \alpha X^{\beta}$, and their respective confidence intervals (CI) are shown for SMA regressions. P (H0: β=1) is the probability associated to the isometric hypothesis ($\beta = 1$). N = 307 species.

Component	R^2	α	$CI_{0.05}$	$CI_{0.55}$	β	$CI_{0.05}$	$CI_{0.55}$	$P_{(H0: \beta=1)}$
SMA								
Male	0.84	0.23	0.176	0.305	1.10	1.056	1.156	0.000019
Female	0.83	0.19	0.144	0.245	1.03	0.986	1.082	0.165551
Petals	0.90	0.64	0.517	0.802	1.10	1.063	1.143	0.000000
Sepals	0.85	0.25	0.194	0.318	1.03	0.986	1.076	0.182967
phySMA								
Male	0.83	0.29	-	-	1.12	-	-	0.000001
Female	0.83	0.15	-	-	1.00	-	-	0.836555
Petals	0.85	1.11	-	-	1.23	-	-	0.000000
Sepals	0.75	0.17	-	-	0.97	-	-	0.302173

Table S4. Sensitivity analyses for the influence of the top five species-rich angiosperm families. Estimated slopes from standardized major axis (SMA) regressions for the male and female organs, petals, and sepals against flower biomass, after removing species belonging to the five most species rich families. Slope (β) of the allometric curve $Y = \alpha X^{\beta}$, and their respective confidence intervals (CI) are shown. $P_{(H0:\ \beta=1)}$ is the probability associated to the isometric hypothesis ($\beta = 1$).

Flower organ	Removed family	N	(β)	CI$_{0.05}$	CI$_{0.95}$	$P_{(H0:\ \beta\ =\ 1)}$
Male	Fabaceae	281	1.110	1.057	1.165	0.00004
	Lamiaceae	285	1.103	1.051	1.157	0.00007
	Ericaceae	294	1.106	1.056	1.158	0.00002
	Brassicaceae	296	1.130	1.080	1.183	< 0.00001
	Malvaceae	296	1.109	1.058	1.163	0.00002
Female	Fabaceae	281	1.036	0.986	1.088	0.15634
	Lamiaceae	285	1.034	0.985	1.086	0.18122
	Ericaceae	294	1.034	0.986	1.084	0.16396
	Brassicaceae	296	1.042	0.993	1.094	0.09204
	Malvaceae	296	1.052	1.003	1.104	0.03718
Petals	Fabaceae	281	1.107	1.065	1.151	< 0.00001
	Lamiaceae	285	1.107	1.066	1.150	< 0.00001
	Ericaceae	294	1.101	1.061	1.142	< 0.00001
	Brassicaceae	296	1.098	1.057	1.140	< 0.00001
	Malvaceae	296	1.105	1.064	1.147	< 0.00001
Sepals	Fabaceae	281	1.029	0.982	1.079	0.23477
	Lamiaceae	285	1.037	0.991	1.085	0.11505
	Ericaceae	294	1.030	0.987	1.076	0.17736
	Brassicaceae	296	1.029	0.983	1.078	0.21541
	Malvaceae	296	1.018	0.973	1.065	0.44725

Table S5. Sensitivity analyses for the top five species-rich angiosperm orders. Estimated slopes from standardized major axis (SMA) regressions for the male and female organs, petals, and sepals against flower biomass, after removing species belonging to the five most species rich families. Slope (β) of the allometric curve $Y = \alpha X^{\beta}$, and their respective confidence intervals (CI) are shown. $P_{(H0:\ \beta=1)}$ is the probability associated to the isometric hypothesis ($\beta = 1$).

Flower organ	Removed order	N	(β)	$CI_{0.05}$	$CI_{0.95}$	$P_{(H0:\ \beta = 1)}$
Male	Lamiales	243	1.081	1.028	1.137	0.00239
	Fabales	278	1.102	1.049	1.157	0.00012
	Myrtales	282	1.093	1.043	1.145	0.00022
	Ericales	283	1.102	1.051	1.155	0.00006
	Malpighiales	291	1.100	1.050	1.152	0.00008
Female	Lamiales	243	1.026	0.970	1.085	0.37136
	Fabales	278	1.036	0.986	1.089	0.16446
	Myrtales	282	1.006	0.962	1.053	0.78935
	Ericales	283	1.036	0.987	1.087	0.15365
	Malpighiales	291	1.036	0.988	1.085	0.14598
Petals	Lamiales	243	1.101	1.055	1.149	0.00001
	Fabales	278	1.107	1.065	1.151	< 0.00001
	Myrtales	282	1.101	1.070	1.133	< 0.00001
	Ericales	283	1.102	1.062	1.145	< 0.00001
	Malpighiales	291	1.094	1.054	1.136	< 0.00001
Sepals	Lamiales	243	1.062	1.012	1.115	0.01538
	Fabales	278	1.035	0.987	1.085	0.15564
	Myrtales	282	1.023	0.978	1.070	0.32469
	Ericales	283	1.031	0.986	1.077	0.17814
	Malpighiales	291	1.032	0.988	1.079	0.15888

Table S6. Sensitivity analysis for showiness strategy. Estimated slopes from standardized major axis (SMA) regressions for the male and female organs, petals, and sepals against flower biomass, after removing species from different flower showiness strategies. The showiness categories were (A) inflorescence - species with flowers particularly clustered together in the branch, (B) showy sepals - species with flowers containing particularly colorful or enlarged sepals, (C) showy stamens - species with flowers containing particularly colorful or enlarged stamens, and (D) tepals - species with flowers containing relatively undifferentiated petals and sepals. Slope (β) of the allometric curve $Y = \alpha X^{\beta}$, and their respective confidence intervals (CI) are shown. $P_{(H0: \beta=1)}$ is the probability associated to the isometric hypothesis ($\beta = 1$).

Flower organ	Removed species	N	(β)	$CI_{0.05}$	$CI_{0.95}$	$P_{(H0: \beta = 1)}$
Male	showy stamens	239	1.108	1.051	1.168	0.00015
	showy sepals	271	1.085	1.034	1.138	0.00090
	tepals	289	1.098	1.049	1.150	0.00008
	inflorescence	270	1.129	1.079	1.182	< 0.00001
Female	showy stamens	239	1.042	0.986	1.100	0.14513
	showy sepals	271	1.030	0.981	1.081	0.23511
	tepals	289	1.029	0.980	1.080	0.25113
	inflorescence	270	1.027	0.977	1.080	0.28991
Petals	showy stamens	239	1.104	1.064	1.145	< 0.00001
	showy sepals	271	1.114	1.072	1.157	< 0.00001
	tepals	289	1.111	1.071	1.154	< 0.00001
	inflorescence	270	1.101	1.059	1.146	< 0.00001
Sepals	showy stamens	239	1.022	0.968	1.078	0.43113
	showy sepals	271	1.024	0.977	1.072	0.32222
	tepals	289	1.025	0.979	1.073	0.29796
	inflorescence	270	1.019	0.973	1.067	0.42246

Table S7. Ordinary least square (OLS) and phylogenetic generalized least square (PGLS) allometric regressions of the four flower components in relation to flower biomass. R^2 is the determination coefficient. The intercept (α) and slope (β) of the allometric curve $Y = \alpha X^\beta$, and their respective confidence intervals (CI) are shown for SMA regressions. P (H0: β=1) is the probability associated to the isometric hypothesis ($\beta = 1$). N = 307 species.

Component	R^2	α	$CI_{0.05}$	$CI_{0.95}$	β	$CI_{0.05}$	$CI_{0.95}$	$P_{(H0:\ \beta=1)}$
OLS								
Male	0.838	-0.85	-0.971	-0.732	1.01	0.961	1.062	0.650156
Female	0.831	-0.94	-1.052	-0.823	0.94	0.894	0.990	0.017303
Petals	0.897	-0.33	-0.421	-0.231	1.04	1.004	1.084	0.031828
Sepals	0.851	-0.79	-0.897	-0.682	0.95	0.905	0.995	0.028994
PGLS								
Male	0.882	-0.75	-1.137	-0.349	1.02	0.973	1.075	0.361434
Female	0.846	-1.00	-1.346	-0.649	0.90	0.862	0.949	0.000075
Petals	0.916	-0.15	-0.549	0.260	1.13	1.083	1.186	0.000001
Sepals	0.837	-1.03	-1.456	-0.602	0.84	0.789	0.894	< 0.000001

Dataset S1. (separate file). Species list and taxonomic classification for 307 angiosperm species used in this study. Taxonomic names were standardized following The Plant List database v1.1 (http://www.theplantlist.org).

SI References

1. G. B. Paterno, C. Penone, G. D. A. Werner, sensiPhy: An R-package for sensitivity analysis in phylogenetic comparative methods. *Methods Ecol. Evol.* **9**, 1461–1467 (2018).

2. D. I. Warton, I. J. Wright, D. S. Falster, M. Westoby, Bivariate line-fitting methods for allometry. *Biol. Rev.* **81**, 259 (2006).

3. S. A. Smith, J. W. Brown, Constructing a broadly inclusive seed plant phylogeny. *Am. J. Bot.* **105**, 302–314 (2018).