

Supplementary material for:
Quantitative assessment of observed and predicted responses to selection

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Supplement S1: Descriptive statistics for the selection experiment in Tovar

Means (μ), variances (σ^2) and covariance (σ_{zy}) for gland area (z) and upper bract area (y) estimated before selection at each generation for the up-selected, down-selected and control lines in Tovar (small gland species). S = selection differential and $\Delta\sigma^2_x$ is the change in the phenotypic variance due to selection. N = number of individuals; Traits in $\log(\text{mm}^2)$.

line	Gen.	μ_z	σ^2_z	S	$\Delta\sigma^2_z$	μ_y	σ^2_y	σ^2_{zy}	N	SE _z	SE _y
Up	1	2.925	0.018	0.191	-0.013	5.901	0.023	0.010	95	0.014	0.015
Up	2	2.958	0.017	0.142	-0.015	6.044	0.024	0.009	62	0.016	0.020
Up	3	3.022	0.020	0.148	-0.018	6.065	0.016	0.011	53	0.019	0.017
Up	4	3.048	0.013	0.144	-0.010	6.225	0.023	0.007	64	0.014	0.019
Up	5	3.017	0.020	NA	NA	6.103	0.015	0.009	83	0.016	0.013
Down	1	2.925	0.018	-0.206	-0.010	5.901	0.023	0.010	95	0.014	0.015
Down	2	2.759	0.013	-0.145	-0.009	5.910	0.024	0.008	63	0.014	0.019
Down	3	2.710	0.016	-0.153	-0.014	5.888	0.024	0.010	63	0.016	0.020
Down	4	2.675	0.025	-0.192	-0.016	5.988	0.030	0.009	59	0.020	0.023
Down	5	2.543	0.024	NA	NA	5.806	0.038	0.014	79	0.017	0.022
Control	1	2.925	0.018	NA	NA	5.901	0.023	0.010	95	0.014	0.015
Control	2	2.829	0.028	NA	NA	5.975	0.027	0.016	128	0.015	0.014
Control	3	2.854	0.019	NA	NA	5.979	0.021	0.007	90	0.014	0.015
Control	4	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
Control	5	2.837	0.026	NA	NA	5.966	0.022	0.014	91	0.017	0.016

Supplement S2: Descriptive statistics for the selection experiment in Tulum

Means (μ), variances (σ^2) and covariance (σ^2_{xy}) for gland area (x) and upper bract area (y) estimated before selection at each generation for the up-selected, down-selected and control lines in Tulum (large gland species). S = selection differential and $\Delta \sigma^2_x$ is the change in the phenotypic variance due to selection. S = selection differential. Traits in $\log(mm^2)$.

Line	Gen.	μ_x	σ^2_x	S	$\Delta \sigma^2_x$	μ_y	σ^2_y	σ^2_{xy}	N	SE _x	SE _y
Up	1	3.344	0.022	0.207	-0.014	6.112	0.028	0.014	100	0.015	0.017
Up	2	3.374	0.018	0.159	-0.016	6.191	0.017	0.008	68	0.016	0.016
Up	3	3.339	0.020	0.160	-0.013	6.178	0.033	0.011	58	0.018	0.024
Up	4	3.256	0.016	0.140	-0.014	6.101	0.023	0.009	65	0.015	0.019
Up	5	3.332	0.025	NA	NA	6.200	0.017	0.007	80	0.018	0.015
Down	1	3.344	0.022	-0.189	-0.017	6.112	0.028	0.014	100	0.015	0.017
Down	2	3.234	0.017	-0.172	-0.012	6.121	0.018	0.009	68	0.016	0.016
Down	3	3.111	0.025	-0.205	-0.017	6.090	0.019	0.006	55	0.021	0.019
Down	4	2.925	0.028	-0.189	-0.015	6.018	0.024	0.007	62	0.021	0.020
Down	5	2.935	0.039	NA	NA	6.096	0.013	0.009	76	0.023	0.013
Control	1	3.344	0.022	NA	NA	6.112	0.028	0.014	100	0.015	0.017
Control	2	3.293	0.016	NA	NA	6.097	0.021	0.010	142	0.011	0.012
Control	3	3.304	0.022	NA	NA	6.159	0.012	0.006	51	0.021	0.015
Control	4	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
Control	5	3.187	0.023	NA	NA	6.117	0.011	0.007	43	0.023	0.016

Supplement S3

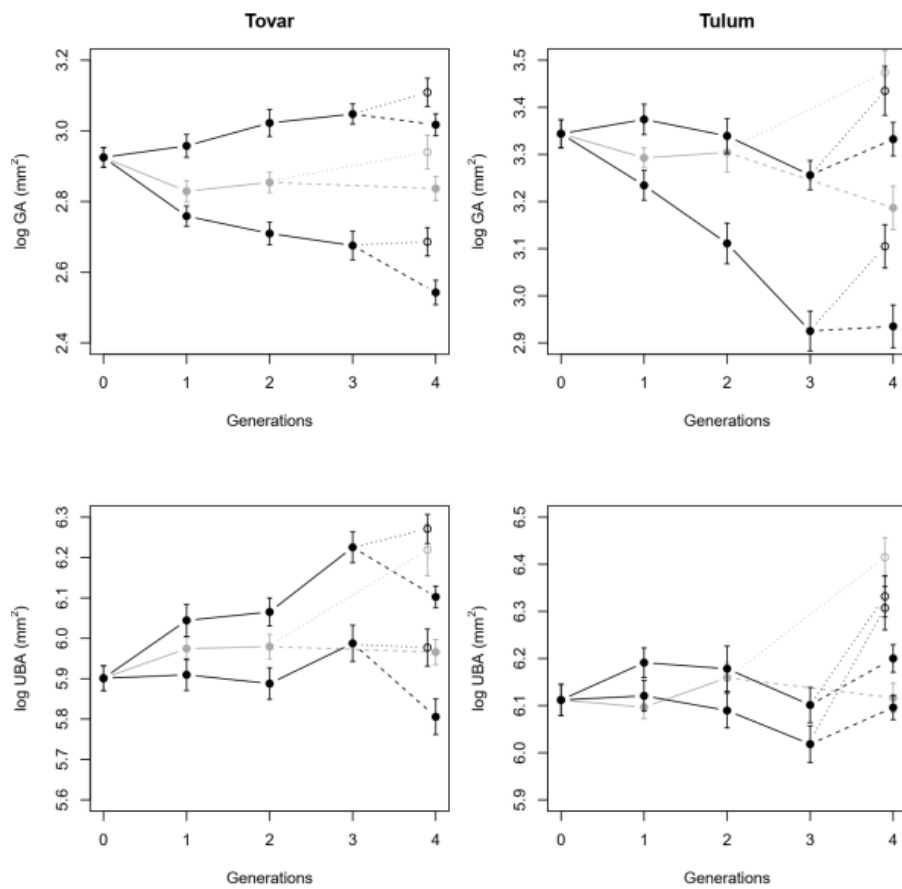


Figure S3. Observed response to selection of gland area (GA), and correlated response of upper bract area (UBA), in two species of *D. scandens*. The data presented here are the raw data and include the first series of measurements of generation 4 (open symbols and dotted lines between generation). Observed responses are represented by the trait means (± 2 SE). Control lines are reported in grey.

Supplement S4

Table S4. Genetic (**G**), environmental (**E**), and phenotypic (**P**) variance matrices for the Tovar (small-glanded species) and Tulum (large-glanded species) populations of *Dalechampia scandens* estimated from the diallel experiments when selfed individuals (diagonal from the diallel) are excluded from the analysis. Variances are reported on the diagonal, covariances above and correlations below the diagonal along with their standard error and credible intervals (genetic; calculated with HPDinterval.mcmc with default probability = 0.95) or confidence intervals (phenotypic) between parentheses. Means and SDs are in mm^2 . Variances are in $\log(mm^2) \times 100$. The number of observations is 616 for Tovar and 822 for Tulum.

			Gland area (GA)	Upper bract area (UBA)
Tovar	mean	(SD)	17.69 (3.30) mm^2	384.4 (72.4) mm^2
	G	GA	1.07 ±0.27 (0.52; 1.57)	0.54 ±0.22 (0.07; 0.94)
		UBA	0.44 ±0.12 (0.23; 0.67)	1.31 ±0.26 (0.80; 1.82)
	E	GA	2.26 ±0.22 (1.88; 2.72)	1.29 ±0.16 (0.99; 1.60)
		UBA	0.62 ±0.04 (0.54; 0.70)	1.87 ±0.18 (1.55; 2.22)
	P	GA	3.33 ±0.25 (2.87; 3.82)	1.83 ±0.21 (1.41; 2.23)
		UBA	0.56 ±0.04 (0.49; 0.64)	3.19 ±0.25 (2.71; 3.64)
Tulum	mean	(SD)	20.14 (5.23) mm^2	406.1 (80.4) mm^2
	G	GA	0.45 ±0.24 (0.00; 0.88)	0.36 ±0.17 (0.04; 0.72)
		UBA	0.60 ±0.18 (0.23; 0.91)	0.82 ±0.17 (0.53; 1.18)
	E	GA	5.98 ±0.37 (5.28; 6.67)	1.81 ±0.19 (1.48; 2.19)
		UBA	0.48 ±0.03 (0.42; 0.55)	2.34 ±0.16 (2.08; 2.66)
	P	GA	6.43 ±0.34 (5.77; 7.08)	2.17 ±0.19 (1.82; 2.54)
		UBA	0.48 ±0.03 (0.43; 0.54)	3.17 ±0.18 (2.80; 3.51)

Supplement S5

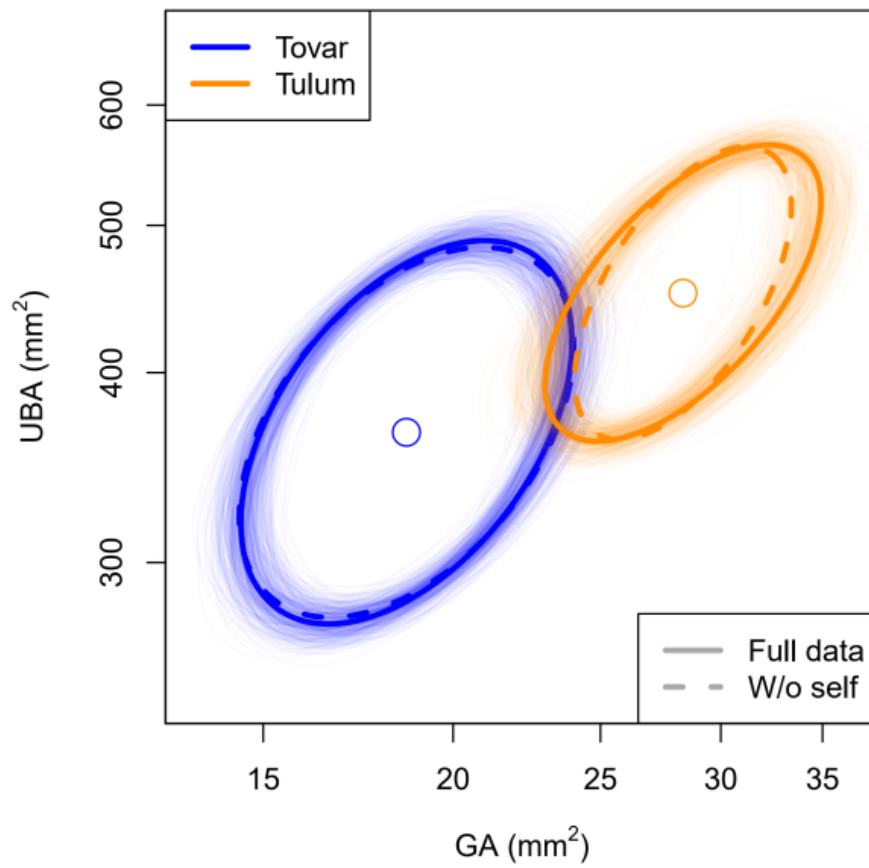


Figure S5: Visual representation of the changes \mathbf{G} when selfed individuals (diagonal of the diallel) are included (solid line) or not (dashed line) in the two species. The thin lines represent the stored iterations of the MCMCglmm model.

Supplement S6

Setting of the SRA model for two traits

The full dataset needed to fit the time-series model includes the sample size, the phenotypic means for both traits before and after selection, and their associated phenotypic variances for each generation (see Table S1 and S2). For the bivariate model, we also implemented the phenotypic covariance between the two traits.

Setting

Data set

Mean phenotype for trait A for T generations: $Y_A = \{y_{A1}, y_{A2}, \dots, y_{AT}\}$,

Mean phenotype for trait B for T generations: $Y_B = \{y_{B1}, y_{B2}, \dots, y_{BT}\}$,

Mean phenotype of breeders for trait A for T generations: $s_A^* = \{y_{A1}^*, y_{A2}^*, \dots, y_{AT}^*\}$,

Phenotypic variance for trait A for T generations: $s_A^2 = \{s_{A1}^2, s_{A2}^2, \dots, s_{AT}^2\}$,

Phenotypic variance for trait B for T generations: $s_B^2 = \{s_{B1}^2, s_{B2}^2, \dots, s_{BT}^2\}$

Phenotypic covariance between traits A and B for T generations: $s_{AB} = \{s_{AB1}, s_{AB2}, \dots, s_{ABT}\}$

Phenotypic variance among breeders for trait A for T generations: $s_A^{2*} = \{s_{A1}^{2*}, s_{A2}^{2*}, \dots, s_{AT}^{2*}\}$

Population size for the T generations: $N = \{N_1, N_2, \dots, N_T\}$

Inferred data

Selection gradient on trait A for T generations: $\beta_A = \{\beta_{A1}, \beta_{A2}, \dots, \beta_{AT}\}$, calculated as $\beta_{AT} = (y_{At}^* - y_{At}) / s_{At}^2$

where y_{At}^* is the average phenotype for trait A of the breeders chosen at generation t,

Selection differential on the variance of trait A for T generations: $\delta_A = \{\delta_{A1}, \delta_{A2}, \dots, \delta_{AT}\}$, calculated as $\delta_{At} = s_{At}^{2*} - s_{At}^2$,

It was assumed that there was no selection on trait B, i.e. $\beta_B = 0$ and $\delta_B = 0$.

Model

Model parameters

Initial phenotypic mean for trait A: μ_{A0} ,

Initial phenotypic mean for trait B: μ_{B0} ,

Initial additive genetic variance for trait A: G_{A0} ,

Initial additive genetic covariance between traits A and B: G_{AB0} ,

Environmental variance for trait A: E_A ,

Environmental variance for trait B: E_B ,

Effective population size N_e .

Model assumptions

No linkage disequilibrium before selection: $d_{A0} = d_{B0} = 0$,

The covariance G_{AB} is constant through time,

No selection gradient on trait B,

No non-additive genetic variances, so that phenotypic variances V_A and V_B can be obtained by adding additive and environmental components: $V_A = G_A + E_A$, $V_B = G_B + E_B$.

No environmental covariance: $V_{AB} = G_{AB}$,

The initial value of the additive genetic variance for trait B can be deduced from the observed regression slope, such that

$G_{B0} = G_{AB0} s_{B0}^2 / s_{AB0}$. In practice, the slope was calculated from the average over the whole time series.

Predicted response to selection

$$\begin{cases} \mu_{At+1} = \mu_{At} + G_{At} \beta_{At} \\ \mu_{Bt+1} = \mu_{Bt} + G_{ABt} \beta_{At} \end{cases}$$

$$\begin{cases} d_{At+1} = \frac{1}{2} \left(1 - \frac{1}{N_e}\right) \left(d_{At} + \frac{\delta_{At} G_{A1}^2}{G_{At} + E_A} \right) \\ d_{Bt+1} = \frac{1}{2} \left(1 - \frac{1}{N_e}\right) \left(d_{Bt} + \frac{\delta_{Bt} G_{B1}^2}{G_{Bt} + E_B} \right) \end{cases}$$

$$\begin{cases} G_{At+1} = G_{At} \left(1 - \frac{1}{2N_e}\right) + d_{At+1} \\ G_{Bt+1} = G_{Bt} \left(1 - \frac{1}{2N_e}\right) + d_{Bt+1} \end{cases}$$

$$\begin{cases} V_{At+1} = G_{At+1} + E_{At+1} \\ V_{Bt+1} = G_{Bt+1} + E_{Bt+1} \\ V_{ABt+1} = G_{AA} \end{cases}$$

Likelihood equation

Single generation

	Model prediction	Observed values
Mean trait A	$\bar{\mathbb{I}}_A$	y_A
Mean trait B	$\bar{\mathbb{I}}_B$	y_B
Var trait A	V_A	s_A^2
Var trait B	V_B	s_B^2
Cov A B	V_{AB}	s_{AB}
Number of observations		N

$$\rho = \frac{V_{AB}}{\sqrt{V_A V_B}}$$

$$\begin{aligned} \log(L) = & -N \log(2\pi \sqrt{V_A V_B (1 - \rho^2)}) - \frac{N}{2(1 - \rho^2)} \\ & \times \left(\frac{S_A^2 + (y_A - \mu_A)^2}{V_A} + \frac{S_B^2 + (y_B - \mu_B)^2}{V_B} - 2\rho \frac{s_{AB} + y_A y_B - \mu_A y_B - y_A \mu_B + \mu_A \mu_B}{\sqrt{V_A V_B}} \right) \end{aligned}$$

Time series generations are assumed to be independent, and the total likelihood is $\log(L) = \sum_t \log(L_t)$.

Supplement S7: Relative error in evolvability estimates

We compiled the relative error of evolvability estimates from 40 published studies. Using the data base from Hansen et al. 2011 as well as an unpublished data base on evolvability, we searched studies that reported trait mean, additive genetic variance as well as the standard error of the additive genetic variance to compute the relative error in evolvability. Evolvabilities, I_A , and standard errors in evolvability were estimated as the additive genetic variance or the standard error in genetic variance divided by the trait mean squared. We then calculated the relative error in evolvability as $100 \times$ the standard error in evolvability divided by the evolvability. Only traits expressed on a ratio scale were included and negative variance estimates were excluded.

Supplement S8: Experimental design of artificial-selection experiments in plants in evolutionary biology.

We conducted a search in ISI web of science core collection with the key words: “*artificial selection*” and “*plants*” within the categories “*Genetics Heredity*”, “*Ecology*” and “*Evolutionary Biology*”. This search on the 10/05/2020 returned 230 publications that were further considered. We also performed a systematic search of artificial selection experiments published in the journals *Evolution* and *Journal of Evolutionary Biology*. We took care of including only once selection experiments that were used in several publications. In one study, the details reported in the method section did not allow us to extract the necessary information about number of selected individuals and population size. Overall, we were able to extract the necessary information from 41 artificial selection experiment (including the present study). The information reported in the table is: Type of selection: individual or family selection; Number of families or individuals selected at each generation; Total population size; Number of replicates; Uni- or bidirectional selection; Presence of a control line; Number of episodes of selection.