Supporting Online Material

Estimating Measurement Error

Using the 305 specimens that were measured twice, repeatability of each trait was estimated using within-individual and among-individual variance components (which represent error and biological variation respectively) (1). The results indicated that every trait exhibited highly significant among-individual variation (all p < 0.001), and thus all traits were retained for further analysis. Repeatability was high in most instances (r > 0.75 for 8 of 11 traits) and we stress that even traits exhibiting moderate repeatability exhibited much greater among-individual versus within-individual variation such that their retention for further analysis is warranted (STable 1).

Correlation between divergent selection and trait divergence

Our central analysis tests for a correlation between the direction and magnitude of divergent selection and the direction and magnitude of trait divergence. The correlation reported in body of the paper stems from a parametric correlation analysis of the relationship between the difference in selection differentials on different hosts (i.e. divergent selection estimated using linear regression) and divergence in raw trait values between ecotypes. This correlation is sufficient and appropriate for evaluating the association between selection and trait divergence (2-4). However, to evaluate the robustness of this association, we also report this association using both raw and size-corrected trait values, selection estimates from both linear and logistic regression, and using parametric and non-parametric rank correlation of trait values against divergent selection. The results of these analyses are listed in Table 1 of the main text (mean raw and mean size-corrected standardized trait values for individuals from each host species are presented in Table S2 and directional selection differentials for each treatment estimated using linear (lin) and logistic (logit) regression are presented in Table S3).

In the presence of predation, the association between trait divergence and divergent selection was significant for 6 of 8 statistical approaches and marginally insignificant for the other two cases (p = 0.056). In contrast, the association did not approach significance in any cases when predation was absent (all p > 0.10). Thus the pattern of a positive association between trait divergence and divergent selection only in the presence of predation is relatively robust to different analytical techniques (note also that inter-trait correlations were generally modest such that different traits are relatively independent, particularly for size-corrected traits, Stable 4).

We conducted an explicit test for statistical differences between predation scenarios in the association between divergent selection and trait divergence by analyzing the interaction between predation scenario (present versus absent) and trait divergence. The analysis used repeated measures ANOVA because selection was estimated on the same sets of traits in the presence versus absence of predation such that a paired design is most appropriate (5). Divergent selection is the within-subject factor, with predation present versus absent as factor levels. Trait divergence is included as a continuous covariate. The interaction between divergent selection and trait divergence was highly significant in all cases (all p < 0.001; raw trait values, selection differentials estimated using linear regression - $F_{1,24} = 35.51$; size-corrected trait values, selection differentials estimated using linear regression - $F_{1,24} = 32.98$; raw trait values, selection differentials estimated using logistic regression - $F_{1,24} = 63.31$; size-corrected trait values, selection differentials estimated using logistic regression - $F_{1,24} = 62.11$). The results confirm statistical differences between predation scenarios in the association between selection and trait divergence.

Effect of host of origin and replicate number on selection estimates

We tested whether our selection estimates were independent from which host species the individuals used in the experiment originated from (i.e. ecotype), and independent from which replicate was considered within each treatment. This was accomplished by adding two interaction terms to the selection analyses described in the main text. Specifically, we examined the trait value by host of origin interaction and the trait value by replicate interaction in ANCOVA analyses within each treatment (the model included the two interaction terms and trait value as a covariate). These interaction terms analyze whether selection on a trait is dependent on host of origin or on replicate respectively. This procedure yielded a total of 88 interactions for analysis (2 interactions for each of 11 traits for each of 4 treatments). As reported in the main text, these analyses revealed that our estimates of selection on the 11 traits were generally independent from which host the individuals used in the experiment originated from (i.e. ecotype) and unaffected by variation among replicates within treatments. Thus only 5 of 88 interactions were significant at $p < 0.05$, and no interactions retain significance following correction for multiple comparisons (i.e. 11 traits). The full results are shown in Stable 5.

Analyses on uncorrelated Principal Components Analyses

Inter-trait correlations among the eleven traits examined were relatively low, but the traits are not completely independent. We thus also estimated the relationship between selection and trait divergence using principal components (PC) axes, which are completely uncorrelated. The analyses supported the analysis using individual trait values, thereby confirming a strong association between selection and trait divergence but only in the presence of predation. These analyses use the procedures described above, but applied them to PC axes calculated using standardized trait values, rather than the individual trait values themselves (the PC axes themselves were also standardized). The PC axes were extracted using correlation matrices. PC analyses using raw and size-corrected individual trait values yielded four and five PC axes respectively (see Stable 6 for trait loadings). Four and five PC axes were used for raw versus size-corrected traits respectively because they were the number of axes required to explain over 75% of the variation. In the presence of predation the correlation between divergent selection on PC axes and divergence between ecotypes in PC axes was strong and positive in all cases (all r $>=$ 0.80; Table 1 in the main text), with highly significant associations for PC axes generated using size-corrected trait values (note that significance was detected despite a loss of power given these analyses are on five PC axes rather than on eleven individual traits). Conversely, in the absence of predation the correlation between selection and divergence was much weaker, negative in some instances, and never approached statistical significance. These results using PC axes confirm that the results presented in the main text are not driven solely by inter-trait correlations.

References
1. Lessells, C.M. & Boag, P.T. (1987) *Auk* **104**, 116-121.
2. Janzen, F. J. & Stern, H.S. (1998) *Evolution* **52**, 1564-1571.
3. Lande, R. (1979) *Evolution* **33**, 402-416.
4. Lande, R. & Arnold, S.J. (1983) *Evolution* **37**, 1210-1226.
5. Sokal, R.R. & Rohlf, F.J. (1995) *Biometry* (W.H. Freeman and Company, San Francisco).

SFigure 1. Schematic of the experimental set-up. 24 insects were released onto each bush.
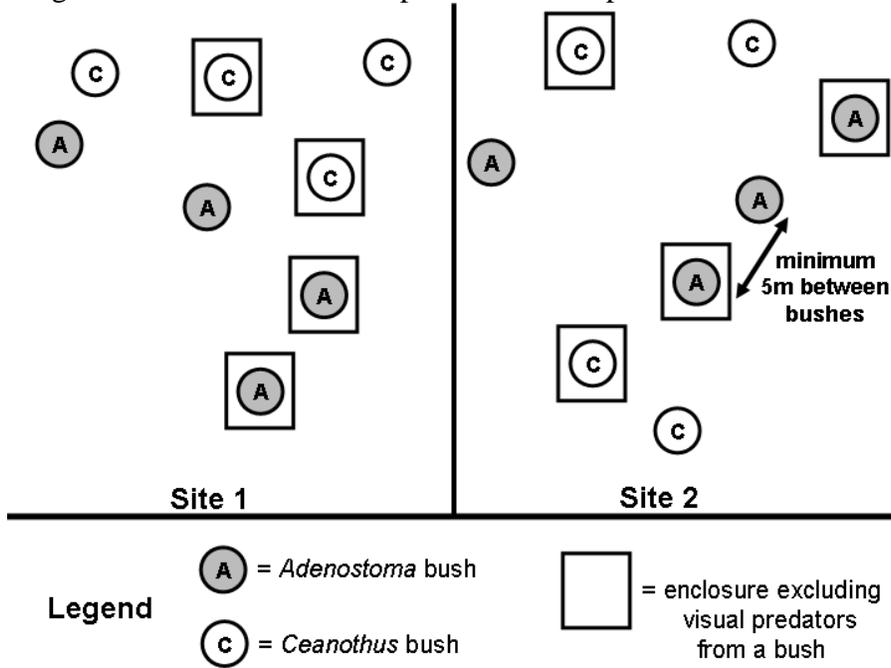
STable 1. Repeatabilities for the 11 morphological traits examined (n = 305 individuals). One-way ANOVA examined within-individual versus among-individual variance components (p-values refer to the statistical significance of the latter, estimated from F-ratios). See text for details.

trait	F-ratio	p	repeatability
Body hue	6.76	<0.001	0.74
Body saturation	42.58	<0.001	0.95
Body brightness	13.29	<0.001	0.86
Stripe hue	36.73	<0.001	0.95
Stripe saturation	27.00	<0.001	0.93
Stripe brightness	10.93	<0.001	0.83
Stripe area	10.01	<0.001	0.79
Head width	2.28	<0.001	0.40
Thorax width	13.47	<0.001	0.86
Femur length	4.89	<0.001	0.66
Body length	10.07	<0.001	0.82

STable 2. Mean raw and mean size-corrected standardized trait values for individuals from each host species.

Trait	*Ceanothus* raw mean	*Adenostoma* raw mean	*Ceanothus* size-corrected mean	*Adenostoma* size-corrected mean
Body hue	-0.099	0.088	-0.155	0.136
Body saturation	0.189	-0.167	0.094	-0.083
Body brightness	0.337	-0.297	0.271	-0.239
Stripe hue	0.014	-0.012	-0.044	0.039
Stripe saturation	0.368	-0.324	0.281	-0.248
Stripe brightness	-0.208	0.183	-0.189	0.166
Stripe area	-0.250	0.221	-0.202	0.178
Head width	0.157	-0.139	-0.085	0.075
Thorax width	0.233	-0.205	-0.012	0.011
Femur length	0.276	-0.243	0.131	-0.115
Body length	0.201	-0.178	-0.052	0.046

STable 3. Directional selection differentials for each treatment estimated using linear (lin) and logistic (logit) regression.

	C: predation		A: predation		C: no predation		A: no predation	
	lin	logit	lin	logit	lin	logit	lin	logit
Body hue	-0.094	-0.467	-0.012	-0.062	-0.012	-0.051	0.007	0.031
Body saturation	0.012	0.052	0.005	0.024	-0.001	-0.002	-0.038	-0.176
Body brightness	0.119	0.541	-0.024	-0.123	-0.085	-0.368	0.038	0.176
Stripe hue	0.017	0.075	-0.015	-0.080	0.015	0.064	0.036	0.165
Stripe saturation	0.001	0.006	-0.085	-0.446	-0.016	-0.670	0.017	0.077
Stripe brightness	-0.014	-0.059	0.135	0.744	-0.087	-0.378	0.013	0.059
Stripe area	-0.060	-0.256	0.057	0.306	-0.001	-0.004	-0.005	-0.023
Head width	0.021	0.091	-0.104	-0.596	0.022	0.094	0.014	0.063
Thorax width	0.013	0.057	-0.057	-0.308	0.008	0.033	0.000	-0.002
Femur length	0.060	0.259	-0.009	-0.046	-0.026	-0.112	-0.013	-0.059
Body length	0.051	0.218	-0.037	-0.198	0.030	0.128	0.053	0.241

STable 4. Inter-trait correlations (r-values from bivariate correlations) were generally weak such that different traits are relatively independent, particularly upon size-correction. Upper-diagonal shows correlations for raw traits and lower diagonal shows correlations for size-corrected traits (codes: body hue – 1; body saturation – 2; body brightness – 3; stripe hue – 4; stripe saturation – 5; stripe brightness – 6; stripe area – 7; headwid – 8; thorax width – 9; femur length – 10; body length – 11).

	1	2	3	4	5	6	7	8	9	10	11
1	X	0.30	0.19	0.86	0.11	-0.09	-0.37	0.06	0.29	0.13	0.21
2	0.24	X	0.15	0.21	0.79	0.08	-0.15	0.22	0.47	0.43	0.27
3	0.13	0.03	X	0.26	0.27	0.21	-0.38	0.24	0.32	0.26	0.25
4	0.86	0.14	0.21	X	0.03	-0.15	-0.47	0.09	0.28	0.15	0.23
5	0.02	0.74	0.14	-0.10	X	-0.18	-0.15	0.27	0.55	0.48	0.36
6	-0.07	0.12	0.25	0.13	-0.17	X	0.32	-0.02	-0.08	-0.05	-0.11
7	-0.34	-0.07	-0.34	-0.44	-0.06	0.31	X	-0.17	-0.22	-0.13	-0.19
8	-0.18	-0.22	-0.03	-0.16	-0.25	0.08	-0.01	X	0.68	0.47	0.63
9	0.27	0.29	0.08	0.19	0.30	-0.03	-0.06	-0.42	X	0.63	0.85
10	-0.04	0.21	0.04	-0.03	0.19	0.01	0.05	-0.37	-0.33	X	0.51
11	0.05	-0.23	-0.07	0.07	-0.18	-0.09	-0.01	-0.37	0.10	-0.53	X

Stable 5. The interaction between trait value and host of origin (ecotype) or the interaction between trait value and replicate number was significant for only 5 of 88 cases. No interactions retain significance following correction for multiple comparisons (i.e. 11 traits). Degrees of freedom are $F_{1,96}$ for the host of origin interactions and $F_{3,96}$ for the replicate interactions.

trait	interaction with	C: predation		A: predation		C: no predation		A: no predation	
		F	p	F	p	F	p	F	p
Body hue x	host	2.90	0.09	0.05	0.83	0.76	0.38	1.17	0.28
Body hue x	replicate	0.99	0.40	3.22	0.03	0.66	0.58	0.79	0.51
Body saturation x	host	0.66	0.42	0.20	0.66	0.56	0.46	0.27	0.61
Body saturation x	replicate	0.66	0.58	1.62	0.19	1.06	0.37	2.12	0.10
Body brightness x	host	0.56	0.46	2.38	0.13	1.62	0.21	0.52	0.47
Body brightness x	replicate	0.41	0.75	0.13	0.94	0.46	0.71	2.36	0.08
Stripe hue x	host	3.45	0.07	1.46	0.23	1.25	0.27	1.29	0.26
Stripe hue x	replicate	0.36	0.78	3.18	0.03	0.40	0.76	1.46	0.23
Stripe saturation x	host	0.10	0.75	0.13	0.72	0.33	0.57	1.50	0.22
Stripe saturation x	replicate	0.93	0.43	0.30	0.82	0.70	0.55	0.57	0.64
Stripe brightness x	host	0.10	0.75	2.87	0.09	0.03	0.86	0.04	0.84
Stripe brightness x	replicate	1.79	0.16	2.24	0.09	0.41	0.75	0.33	0.81
Stripe area x	host	5.33	0.02	2.50	0.12	1.08	0.30	0.06	0.81
Stripe area x	replicate	2.29	0.08	1.52	0.22	0.43	0.73	0.08	0.97
Head width x	host	0.01	0.91	0.04	0.85	0.00	0.96	0.81	0.37
Head width x	replicate	3.49	0.02	0.29	0.84	1.05	0.37	0.81	0.49
Thorax width x	host	1.29	0.26	0.84	0.36	0.09	0.76	1.59	0.21
Thorax width x	replicate	3.04	0.03	0.11	0.95	0.46	0.71	0.97	0.41
Femur length x	host	1.18	0.28	0.97	0.33	1.65	0.20	1.80	0.18
Femur length x	replicate	1.51	0.22	0.59	0.63	0.30	0.82	1.11	0.35
Body length x	host	0.39	0.54	1.31	0.26	0.10	0.75	0.81	0.37
Body length x	replicate	2.70	0.05	0.21	0.89	1.52	0.22	0.31	0.82

Stable 6. Trait loadings for principal components (PC) axes from PC analyses using raw and size-corrected trait values (which yielded four and five PC axes respectively). Shown in brackets is the percent of variance explained by that axis.

	PC on raw trait values				PC on size-corrected trait values				
	1 (37)	2 (18)	3 (11)	4 (11)	1 (24)	2 (19)	3 (14)	4 (12)	5 (10)
Body hue	0.49	-0.73	0.15	0.09	0.77	-0.34	-0.22	0.02	0.16
Body saturation	0.64	0.14	0.68	-0.11	0.57	0.63	0.10	0.14	-0.19
Body brightness	0.47	-0.13	0.03	0.56	0.32	-0.02	-0.35	0.54	0.04
Stripe hue	0.49	-0.79	0.01	0.10	0.73	-0.44	-0.32	-0.04	0.17
Stripe saturation	0.67	0.30	0.51	-0.30	0.47	0.68	0.23	-0.03	-0.37
Stripe brightness	-0.14	0.24	0.28	0.87	-0.18	0.17	-0.07	0.82	0.38
Stripe area	-0.45	0.55	0.14	0.12	-0.52	0.30	0.40	0.16	0.31
Head width	0.65	0.32	-0.45	0.11	-0.49	-0.17	-0.50	0.22	-0.60
Thorax width	0.89	0.23	-0.19	0.02	0.55	-0.01	0.55	0.26	-0.15
Femur length	0.71	0.30	0.00	-0.02	0.07	0.64	-0.40	-0.36	0.53
Body length	0.77	0.22	-0.40	0.02	0.04	-0.58	0.63	-0.02	0.17