

Supplementary Material

Supplementary Material S1: Analyses based on binary interactions

In the main text, we discussed a set of interaction-informed models whose optimal trait values were calculated as the weighted effective interaction trait (EIT) of hawkmoths in each selective regime, with weights given by the frequency of visits each hawkmoth made to each plant species. Here, we present simpler analyses of uEIT—the unweighted effective interaction trait—and hence optima are the arithmetic mean of plant corolla lengths where interaction frequency is not taken into account. The primary effect of this difference is that these additional models assume that interaction strength is not important in describing a hawkmoth’s interaction patterns and assumes that interaction presence/absence is the primary driving force of interaction-based selection.

When using uEIT, we see a similar phylogenetic signal and relationship to observed traits to that we observe with the version of EIT from the main text (Fig. S1). Regardless of whether or not EIT takes interaction frequency into account, the observed phylogenetic signal is less than would be expected under Brownian motion and not significant when EIT is not weighted by interaction frequency (weighted EIT: $K = 0.412$, $p = 0.008$, $n = 10000$; unweighted EIT: $K = 0.363$, $p = 0.086$, $n = 10000$). Likewise, a phylogenetic least-squares regression of observed hawkmoth proboscis length and EIT shows a significant trend regardless of weighting (uEIT: $\beta = 0.411$, $R^2 = 0.100$, $t = 2.851$, $p = 0.006$, and EIT: $\beta = 0.501$, $R^2 = 0.136$, $t = 3.386$, $p = 0.001$).

The role of including interaction frequency is not particularly clear to see (Table S1). In the case of species-, genus-, and global-scale models, the model fit improves when EIT is weighted by interaction frequency. However, for the modelling scenarios where we examine the interactions of functionally-similar hawkmoths the opposite is true. In all cases, the difference between models is not dramatic. This result suggests that the occurrence of an interaction regardless of the intensity appears to be enough for pollination interactions to capture pollinator traits. However, the degree of matching between proboscis and interactions in our interaction-informed models (as represented by the mean-squared error; MSE) does improve when EIT is weighted by interaction frequency. This second result suggests that while presence of an interaction may provide enough information to assess proboscis length, matching between the two improves when plant traits are weighted by interaction frequency.

Finally, we compared the best-supported of our hypothesis-based models (the six-functional-group model) to the most-likely model from SURFACE analysis (Fig. S2). Similar to the results for EIT weighted by interaction frequency, there is a significant, positive relationship between optimal proboscis length (as determined by SURFACE) and hawkmoth uEIT ($\beta = 1.991$, $t = 3.861$, $p < 0.001$, $R^2 = 0.169$). In addition, this relationship in our interaction-informed model had a larger slope than the SURFACE model.

TABLE S 1: Summary of model fit for each scenario for hawkmoth proboscis evolution.

Model	Type	α	σ	θ_N	nSR	$\ln L$	n	AICc	MSE
BM	—	—	25.240	40.604	—	-306.515	2	617.196	—
OU1	Global	0.410	27.143	31.672 [†]	1	-307.679	2	621.695	752.494
OU1 _w	Global	0.468	27.391	43.245 [†]	1	-307.591	2	621.520	590.562
OU2	Tax.	0.017	25.217	44.862	25	-308.722	3	623.783	662.603
OU2 _w	Tax.	0.030	24.770	43.329	25	-306.935	3	620.208	349.916
OU3	Tax.	0.025	23.583	22.347	75	-303.415	3	613.168	509.473
OU3 _w	Tax.	0.025	23.367	28.410	75	-302.702	3	611.742	404.395
OU4	Func.	0.017	25.203	19.710	2	-308.676	3	623.689	513.603
OU4 _w	Func.	0.012	25.177	17.840	2	-308.856	3	624.050	477.653
OU5	Func.	0.035	22.945	27.355	6	-301.037	3	608.412	452.476
OU5 _w	Func.	0.026	23.427	28.993	6	-302.855	3	612.048	395.813
SF	—	0.069	2.856	27.599*	7	-253.744	9	528.258	119.258

Notes: α : strength of attraction; σ : magnitude of variation; θ_N : intrinsic optimum; nSR: number of selective regimes in model (in interaction-informed models this is also the number of θ_g values fixed); $\ln L$: log-likelihood; n: number of free parameters; AICc: small-sample-size-corrected Akaike Information Criterion; MSE: mean-squared error between θ_g values and observed traits; BM: Brownian motion; OU1: global optimum; OU2: genus-specific optima; OU3: species-specific optima; OU4: two-functional-group-based optima; OU5: six-functional-group-based optima; SF: SURFACE implementation. “Tax.” refers to taxonomic groupings of species, “Func.” refers to groupings based on similarity of interactions, “Global” refers to no groupings. A “w” next to the model name indicates those models where optima were weighted by interaction frequency, a “—” indicates that the value is not applicable to the model, a “†” indicates that θ_N was equal to the fitted optima, and the “*” after the θ_N value for the SURFACE model refers to the estimated θ value at the root.

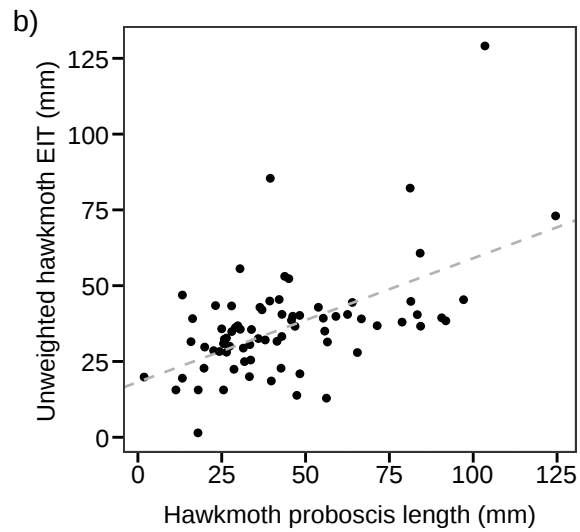
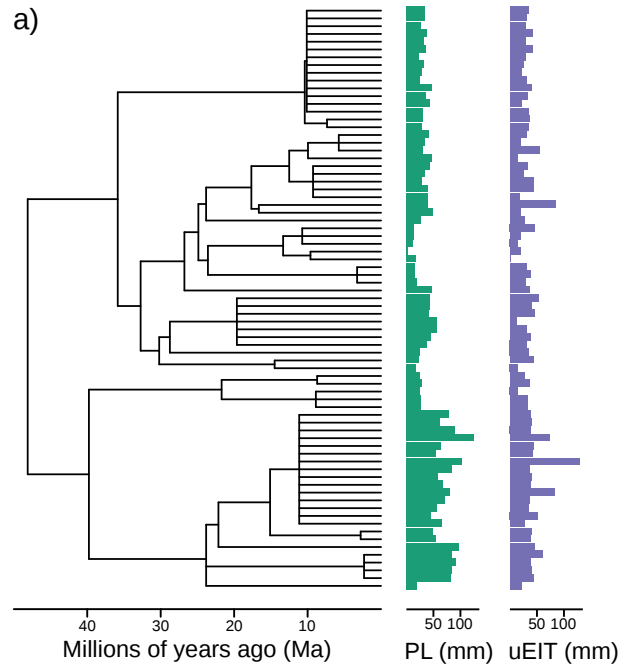


Figure S1: Relationship between hawkmoth phylogeny, proboscis length (PL; mm), and unweighted effective interaction trait (uEIT; mm). a) There is distinct phylogenetic signal of proboscis length compared to uEIT ($K = 1.169$, $p < 0.001$, $n = 10000$ and $K = 0.363$, $p = 0.086$, $n = 10000$, respectively; where $K > 1$ indicates greater phylogenetic clustering than expected under Brownian motion). b) There is a significant, positive relationship between proboscis length and uEIT, even when accounting for phylogenetic relatedness ($\beta = 0.411$, $t = 2.851$, $p = 0.006$, $R^2 = 0.100$).

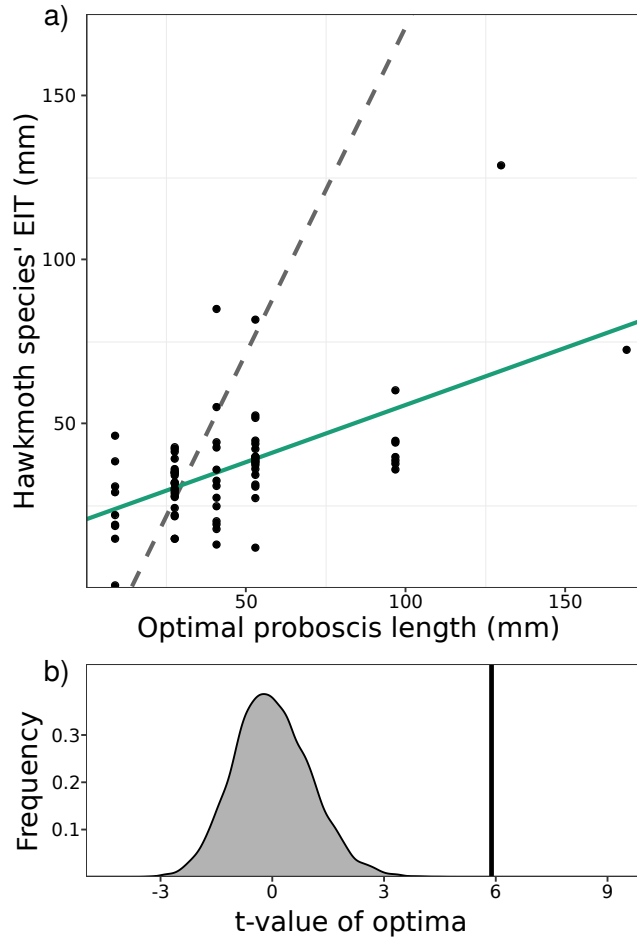


Figure S2: The relationship between a hawkmoth species' optimal proboscis length and its observed unweighted effective interaction trait (EIT). a) There is a significant, positive correlation between a species' EIT and its optimal proboscis length as determined by SURFACE. The solid green line shows the slope from a linear regression of the values while, for comparative purposes, the dashed grey line shows the same for our best-fitting interaction-informed model for comparative purposes. The observed slope between EIT and SURFACE optima is smaller ($\beta = 0.35$) than that from EIT and the optima of the interaction-informed model, where optima are based on EIT values ($\beta = 1.99$; dashed line). b) We show the degree to which the observed relationship between EIT and SURFACE optima is stronger than expected by chance. The vertical line indicates the observed t-value and the distribution represents 9,999 null models in which hawkmoth EIT is randomised.

Supplementary Material S2: Description of SURFACE best-fit model and results

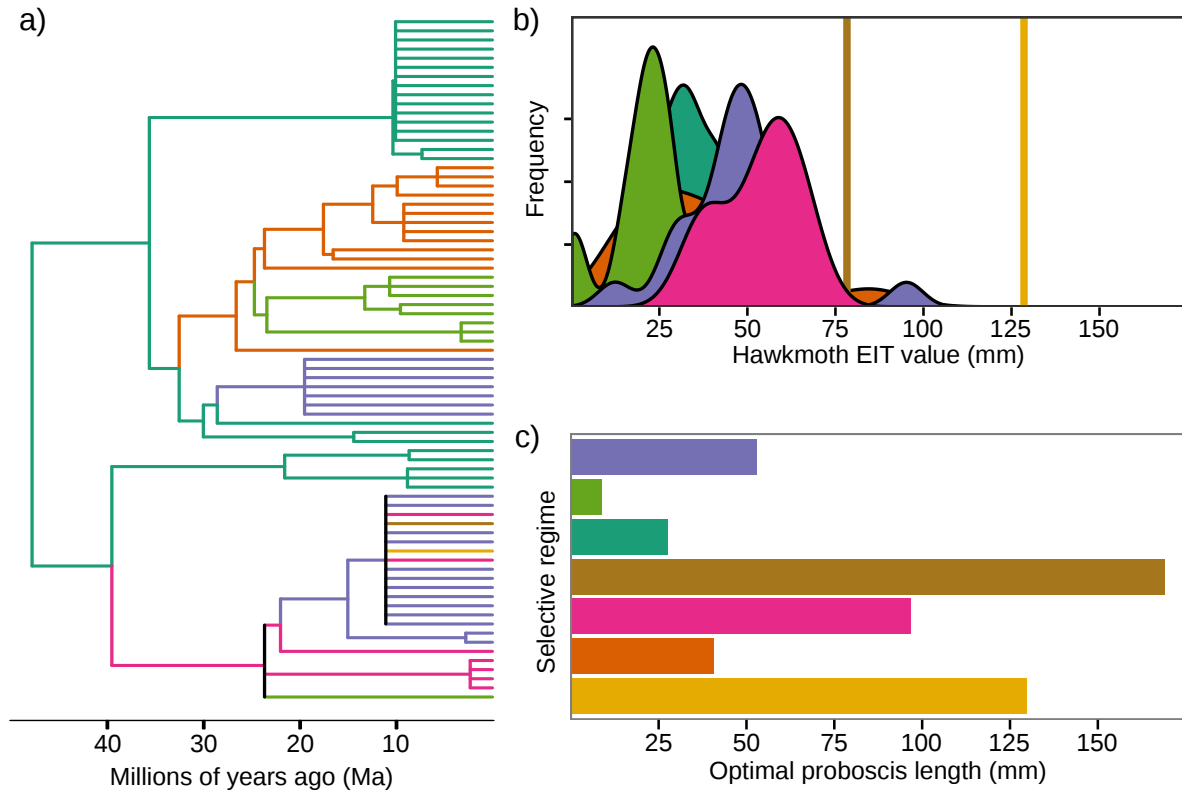


Figure S3: Summary of the best-fit Ornstein-Uhlenbeck model found by the SURFACE algorithm. SURFACE converges on a model that does a better job explaining the evolution of hawkmoth proboscis length than Brownian motion and all of our interaction-informed models ($\ln L = -253.744$, $\alpha = 0.069$, $\sigma = 2.856$, $AICc = 528.258$, $\#\theta = 7$). a) The phylogeny of hawkmoths in our dataset where different colours represent distinct selective regimes as estimated by SURFACE (black lines represent divergence from a polytomy with more than two optima). b) The hawkmoth trait space encompassed by each selective regime of SURFACE. Each distribution is made up of the EIT values of hawkmoths in that selective regime. The yellow and brown regimes are represented by vertical lines because only one hawkmoth species is found to be under those selective regimes. c) The optimal hawkmoth proboscis length for each selective regime estimated by SURFACE.

Supplementary Material S3: Comparisons to SLOUCH model

Finally, we compared the approach that we have introduced in this study to another recently-developed approach. The SLOUCH method was developed by Ref. [5] as a way to model the evolution of a trait based on a predictor variable. Other studies have expanded on this method [2] and implemented it to test Bergmann's rule [4], to show a relationship between haemoglobin genes in fish and ocean depth [1], and to investigate the diversification of bark beetles [3]. We wanted to examine how SLOUCH might compare to our approach as a way of asking how contemporary species interactions

can explain trait evolution. To do so, we modelled the evolution of hawkmoth proboscis length with SLOUCH while including EIT (to represent the pollination interactions) as a co-varying trait. First, we ran the simple case of no selective regimes (i.e. just proboscis length and species-level EIT as a covariate). Next, we implemented versions of the selective regimes used in our three best-fitting models (the two functional-group scenarios and the species-specific scenario) and the regime-level EIT values that were used as optima in our model.

TABLE S2: Summary of model fit between interaction-informed models and SLOUCH models with EIT.

Model	Type	α	σ	θ_N	$\ln L$	n	AICc
OU3	Tax.	0.025	23.367	28.410	-302.702	3	611.742
OU4	Func.	0.012	25.177	17.840	-308.856	3	624.050
OU5	Func.	0.026	23.427	28.993	-302.855	3	612.048
SL-OU3	Tax.	0.006	0.165	—	-80.755	76	<i>Inf</i>
SL-OU4	Func.	0.002	3.675	—	-305.802	6	624.839
SL-OU5	Func.	< 0.001	3.165	—	-296.043	10	615.524
SL-NR	—	0.004	3.507	—	-300.996	4	610.564

Notes: α : strength of attraction; σ : magnitude of variation; θ_N : intrinsic optimum; $\ln L$: log-likelihood; n: number of free parameters; AICc: small-sample-size-corrected Akaike Information Criterion; OU3: species-specific optima; OU4: two-functional-group-based optima; OU5: six-functional-group-based optima; SL-OU3: SLOUCH implementation of species-specific model; SL-OU4: SLOUCH implementation of two-functional-group model; SL-OU5: SLOUCH implementation of six-functional-group model; SL-NR: SLOUCH model with EIT and no selective regimes. “Tax.” refers to taxonomic groupings of species, “Func.” refers to groupings based on similarity of interactions, “Global” refers to no groupings. A “—” indicates that the value is not applicable to the model.

There are several points of interest when fitting these SLOUCH models compared to our own approach. First, the SLOUCH models do not tend to fit better than our approach with all models performing worse than or equivalent to our models (Table S2). Moreover, the species-specific model cannot be fit in SLOUCH as there are more parameters than data (indicated by the *Inf* for AICc in Table S2). The SLOUCH model with EIT and without selective regimes has a relatively good fit (Table S2). The SLOUCH models differ most to our implementation with respect to parameter estimates, with both α and σ values substantially lower in the SLOUCH versions.

References

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