Supplement 1: List of species and location of populations included in analyses

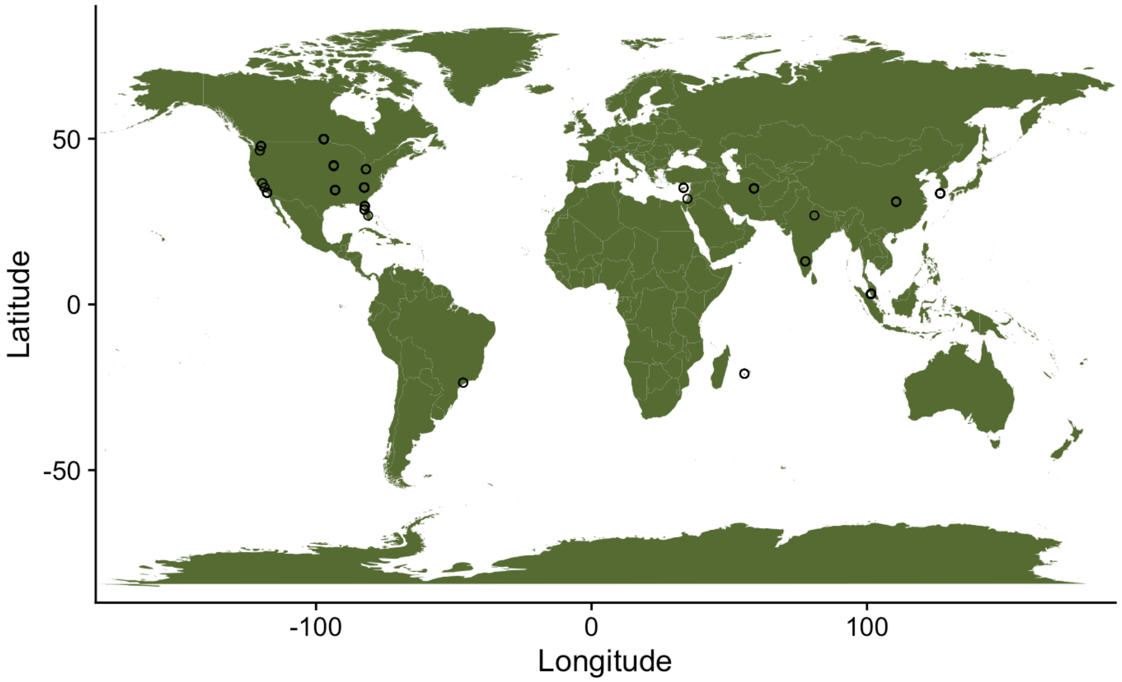


Figure S1. Location of study populations in the analytical data set. Figure generated using the R package "maps"[1].

Table S1. List of 26 species constituting the analytical data set.

Species	family
Herpetogramma phaeopteralis	Crambidae
Chilo sacchariphagus	Crambidae
Keiferia lycopersicella	Gelechiidae
Ascotis selenaria	Geometridae
Marmara gulosa	Gracillariidae
Spalgis epius	Lycaenidae
Mamestra configurata	Noctuidae
Peridroma saucia	Noctuidae
Chilo auricilius	Noctuidae
Lacanobia subjuncta	Noctuidae

Spodoptera exigua	Noctuidae
Cerconota anonella	Oecophoridae
Ectomyelois ceratoniae	Phycitidae
Ephestia figulilella	Phycitidae
Homadaula anisocentra	Plutellidae
Metisa plana	Psychidae
Pteroma pendula	Psychidae
Elasmopalpus lignosellus	Pyralidae
Ameyelois transitella	Pyralidae
Orthopygia glaucinalis	Pyralidae
Lista haraldusalis	Pyralidae
Rhyacionia frustrana	Tortricidae
Ancylis comptana	Tortricidae
Episimus utilis	Tortricidae
Argyrotaenia velutinana	Tortricidae
Cydia pomonella	Tortricidae

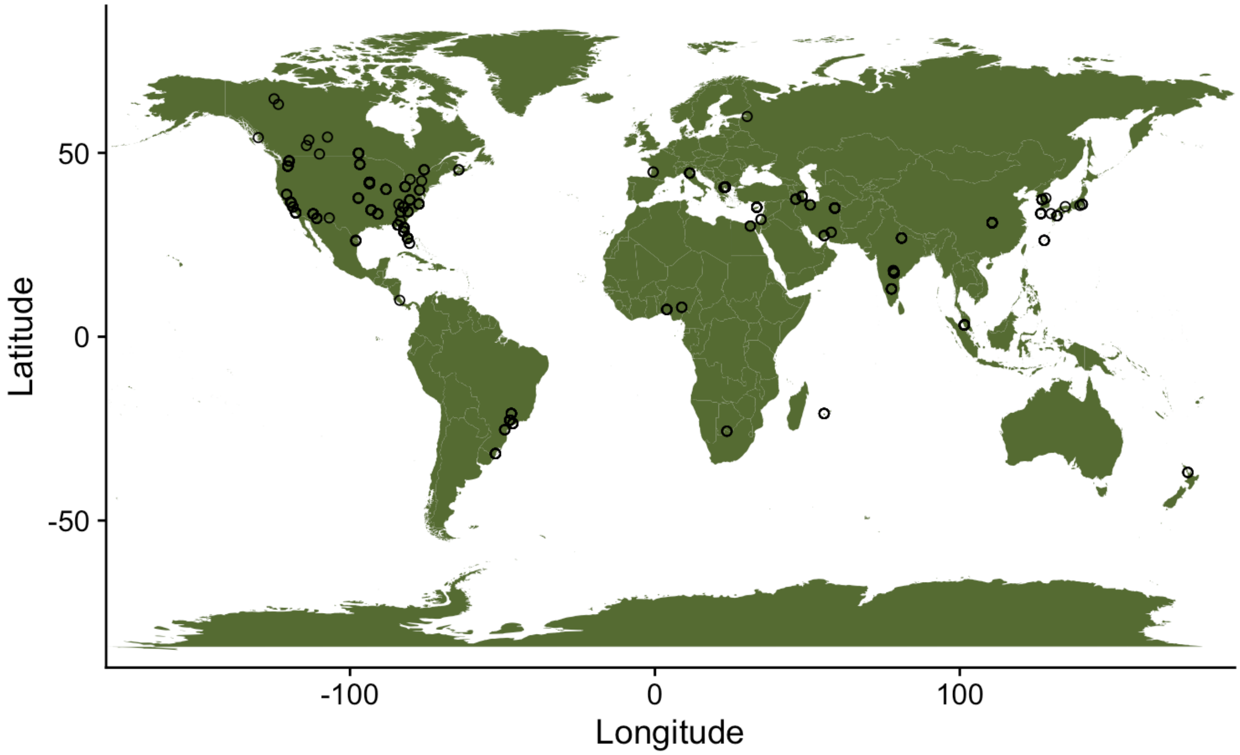


Figure S2. Location of study populations included in the full data set (analysis of this data set is reported in supplement 2). Figure generated using the R package “maps”[1].

Table S2. List of 89 species constituting the full data set.

Species	Family
Utethesia ornatrix	Arctiidae
Bedellia somnulentella	Bellelliidae
Carposina sasakii	Carposinidae
Cochylis hospes	Cochylidae
Herpetogramma phaeopteralis	Crambidae
Chilo sacchariphagus	Crambidae
Pediasia trisecta	Crambidae
Diaphania nitidalis	Crambidae

Diaphania indica	Crambidae
Ostrinia nubilalis	Crambidae
Diatraea grandiosella	Crambidae
Palpita nigropunctalis	Crambidae
Neoleucinodes elegantalis	Crambidae
Cnaphalocrocis medinalis	Crambidae
Stenoma catenifer	Elachistidae
Lymantria albescens	Erebidae
Lymantria xylina	Erebidae
Keiferia lycopersicella	Gelechiidae
Anarsia lineatella	Gelechiidae
Tuta absoluta	Gelechiidae
Pectinophora gossypiella	Gelechiidae
Aproaerema modicella	Gelechiidae
Phthorimaea operculella	Gelechiidae
Ascotis selenaria	Geometridae
Marmara gulosa	Gracillariidae
Phyllonorycter blancardella	Gracillariidae
Spalgis epius	Lycaenidae
Lycaeides argyrognomom	Lycaenidae
Mamestra configurata	Noctuidae
Peridroma saucia	Noctuidae
Argyrogramma albostriata	Noctuidae
Chilo auricilius	Noctuidae
Sesamia nonagrioides	Noctuidae
Spodoptera cosmioides	Noctuidae
Lacanobia subjuncta	Noctuidae
Spodoptera exigua	Noctuidae
Panolis flammea	Noctuidae
Heliothis subflexa	Noctuidae
Heliothis virescens	Noctuidae

Heliothis zea	Noctuidae
Hypantria cunea	Noctuidae
Leucania separata	Noctuidae
Pseudaletia unipuncta	Noctuidae
Simyra henrici	Noctuidae
Trichoplusia ni	Noctuidae
Egira curialis	Noctuidae
Spodoptera litura	Noctuidae
Naranga aenescens	Noctuidae
Sesamia cretica	Noctuidae
Anticarsia gemmatalis	Noctuidae
Inachis io	Nymphalidae
Danaus plexippus	Nymphalidae
Cerconota anonella	Oecophoridae
Atrophaneura alcinous	Papilionidae
Sericinus montela	Papilionidae
Ectomyelois ceratoniae	Phycitidae
Ephestia calidella	Phycitidae
Ephestia figulilella	Phycitidae
Homadaula anisocentra	Plutellidae
Plutella xylostella	Plutellidae
Metisa plana	Psychidae
Pteroma pendula	Psychidae
Diatraea saccharalis	Pyralidae
Dioryctria amatella	Pyralidae
Ameyelois transitella	Pyralidae
Cactoblastis cactorum	Pyralidae
Maruca vitrata	Pyralidae
Euzopherodes vapidella	Pyralidae
Elasmopalpus lignosellus	Pyralidae
Orthopygia glaucinalis	Pyralidae

Hypocosmia pyrochroma	Pyralidae
Lista haraldusalis	Pyralidae
Cadra cautella	Pyralidae
Corcyra cephalonica	Pyralidae
Plodia interpunctella	Pyralidae
Diatraea lineolata	Pyralidae
Hypsipyla grandella	Pyralidae
Attacus ricini	Saturnidae
Platynota idaeusalis	Tortricidae
Rhyacionia frustrana	Tortricidae
Ancylis comptana	Tortricidae
Cydia pomonella	Tortricidae
Episimus utilis	Tortricidae
Ctenopseustis obliquana	Tortricidae
Adoxophyes orana	Tortricidae
Choristoneura fumiferana	Tortricidae
Argyrotaenia velutinana	Tortricidae
Croesia curvalana	Tortricidae
Lobesia botrana	Tortricidae

References

1. Becker OScbRA, Minka ARWRvbRBEbTP, Deckmyn. A (2022). _maps: Draw Geographical Maps_. R package version 3.4.1, <https://CRAN.R-project.org/package=maps>.

Supplement 2: Model results from the “analytical” and “full” data sets

We performed the analyses described in the “analyses” section on two data sets the “Analytical data set”, which includes only sets from which all three performance curves could be estimated and the full data set, which also includes studies reporting at least one of them. The **“full dataset”** consisted of overlapping suites of sets reporting development time (n = 75 species, 173 sets, 24% inferred locations) and/or survival (n = 54 species, 117 sets, 31% inferred locations) data.

Table 1: Model results from the “analytical dataset”. Interactive or additive models were chosen by AIC. When the models did not differ significantly, the additive model was chosen. Significant terms are marked with asterisks (*: p < 0.05, **: p < 0.01, ***: p < 0.001)

A) D_h			
Fixed effects	**Estimate**	**SE**	**t-value**
absolute latitude	-0.06	0.04	-1.32
egg	36.20	1.39	26.09
larva	36.11	1.40	25.69
pupa	36.85	1.39	26.47
larva:absolute latitude	-0.01	0.03	-0.34
pupa:absolute latitude	-0.06	0.03	-2.12
Random effects	**SD**		
species	2.12		
residual	0.82		
N = 35 obs., 20 species			
B) D_l			
Fixed effects	**Estimate**	**SE**	**t-value**
absolute latitude	-0.15	0.04	-3.90**
egg	25.68	1.28	20.01
larva	25.37	1.32	19.20
pupa	26.45	1.33	19.88
Random effects	**SD**		
Species	1.91		
residual	1.28		
N = 37 obs., 21 species			
C) $D_{breadth}$			
Fixed effects	**Estimate**	**SE**	**t-value**
absolute latitude	0.07	0.02	2.89*
egg	11.16	0.86	12.97
larva	11.29	0.90	12.53
pupa	9.54	0.86	11.09**
Random effects	**SD**		

species	1.16		
residual	0.90		
N = 26 obs., 15 species			
D) S_h			
Fixed effects	**Estimate**	**SE**	**t-value**
absolute latitude	-0.05	0.05	-0.98
egg	35.32	1.68	21.02
larva	35.32	1.70	20.82
pupa	36.43	1.68	21.63
larva:absolute latitude	-0.05	0.03	-1.69
pupa:absolute latitude	-0.08	0.03	-2.92*
Random effects	**SD**		
species	2.64		
residual	0.85		
N = 35 obs., 20 species			
E) S_l			
Fixed effects	**Estimate**	**SE**	**t-value**
absolute latitude	-0.20	0.06	-3.46**
egg	22.29	1.90	11.70
larva	22.23	1.96	11.34
pupa	21.38	1.97	10.83
Random effects	**SD**		
species	2.83		
residual	1.91		
N = 37 obs., 21 species			
F) $S_{breadth}$			
Fixed effects	**Estimate**	**SE**	**t-value**
absolute latitude	0.20	0.08	2.67*
egg	11.70	2.43	4.82
larva	12.09	2.49	4.85
pupa	16.87	2.47	6.84**
larva:absolute latitude	-0.08	0.05	-1.60
pupa:absolute latitude	-0.17	0.05	-3.36**
Random effects	**SD**		
species	3.51		
residual	1.52		
N = 26 obs., 15 species			
G) P_h			
Fixed effects	**Estimate**	**SE**	**t-value**
absolute latitude	-0.06	0.04	-1.36
egg	35.91	1.48	24.33

larva	36.42	1.49	24.50
pupa	36.87	1.48	24.93
larva:absolute latitude	-0.05	0.02	-2.31*
pupa:absolute latitude	-0.08	0.02	-3.66**
Random effects	**SD**		
species	2.37		
residual	0.64		
N = 35 obs., 20 species			
H) P_l			
Fixed effects	**Estimate**	**SE**	**t-value**
absolute latitude	-0.14	0.04	-3.70**
egg	25.41	1.25	20.26
larva	24.99	1.32	18.97
pupa	26.28	1.33	19.74
Random effects	**SD**		
species	1.55		
residual	1.89		
N = 37 obs., 21 species			
I) $P_{breadth}$			
Fixed effects	**Estimate**	**SE**	**t-value**
absolute latitude	0.03	0.04	0.68
egg	11.58	1.33	8.70
larva	12.09	1.40	8.62
pupa	10.14	1.33	7.61
Random effects	**SD**		
species	1.73		
residual	1.54		
N = 26 obs., 15 species			

Table 2: Model results from the full datasets. Interactive or additive models were chosen by AIC. When the models did not differ significantly, the additive model was chosen.

A) D_h			
Fixed effects	**Estimate**	**SE**	**t-value**
absolute latitude	-0.05	0.03	-1.62
egg	35.32	1.02	34.56
larva	34.97	1.01	34.66
pupa	34.91	1.01	34.52
Random effects	**SD**		
species	2.60		
residual	1.07		
N = 84 obs., 41 species			
B) D_l			
Fixed effects	**Estimate**	**SE**	**t-value**
absolute latitude	-0.96	0.021	-4.64
egg	23.74	0.72	33.1
larva	23.45	0.73	32.22
pupa	24.17	0.73	33.27
Random effects	**SD**		
species	1.81		
residual	1.18		
N = 167 obs., 71 species			
C) $D_{breadth}$			
Fixed effects	**Estimate**	**SE**	**t-value**
absolute latitude	0.031	0.02	1.28
egg	12.47	0.86	14.51
larva	12.01	0.84	14.39
pupa	11.09	0.84	13.14
Random effects	**SD**		
species	3.06		
residual	1.50		
N = 82 obs., 39 species			
D) S_h			
Fixed effects	**Estimate**	**SE**	**t-value**
absolute latitude	-0.09	0.034	-2.50
egg	34.89	1.32	26.44
larva	34.68	1.36	25.45
pupa	34.64	1.34	25.79
Random effects	**SD**		
species	2.35		
residual	1.90		
N = 65obs., 36 species			
E) S_l			

Fixed effects	**Estimate**	**SE**	**t-value**
absolute latitude	-0.26	0.49	-5.37
egg	23.51	1.60	14.65
larva	20.89	1.49	13.99
pupa	19.28	1.81	10.66
absolute latitude: larva	0.12	0.05	2.68
absolute latitude: pupa	0.14	0.05	2.6
Random effects	**SD**		
species	2.80		
residual	1.75		
N = 61 obs., 34 species			
F) $S_{breadth}$			
Fixed effects	**Estimate**	**SE**	**t-value**
absolute latitude	0.11	0.05	2.30
egg	14.32	1.83	7.83
larva	11.36	1.88	6.05
pupa	13.83	1.91	7.24
Random effects	**SD**		
species	2.40		
residual	3.28		
N = 41 obs., 24 species			
G) P_h			
Fixed effects	**Estimate**	**SE**	**t-value**
absolute latitude	-0.07	0.04	-1.95
egg	35.00	1.25	28.01
larva	34.86	1.27	27.36
pupa	34.65	1.27	27.25
Random effects	**SD**		
species	2.32		
residual	1.08		
N = 62 obs., 36 species			
H) P_l			
Fixed effects	**Estimate**	**SE**	**t-value**
absolute latitude	-0.12	0.03	-4.31
egg	24.61	0.95	25.82
larva	24.69	1.00	24.80
pupa	25.11	0.97	25.80
Random effects	**SD**		
species	1.60		
residual	1.80		
N = 96 obs., 46 species			
I) $P_{breadth}$			

Fixed effects	**Estimate**	**SE**	**t-value**
absolute latitude	0.02	0.04	0.44
egg	11.18	1.26	8.86
larva	11.50	1.32	8.74
pupa	10.77	1.30	8.31
Random effects	**SD**		
species	2.095		
residual	1.59		
N = 60 obs., 34 species			

Supplement 3: Phylogenetic analyses

We searched for 11 full-length, commonly sequenced (Wahlberg and Wheat, 2008) genomic DNA markers (Table 1), across all 102 species using GeneDumper, a toolkit designed to search GenBank for certain loci given a taxonomy. The taxonomy used for input was generated from the NCBI taxonomy database in R v3.6.3 using the *tax_name* command from the package taxise. Sequences were validated and curated using a detailed pipeline available in the GeneDumper toolkit to remove paralogs, uninformative and mislabeled sequences. Five species were not available on Genbank, and in those cases, we opted to search for and utilize a congener as a surrogate (Table 2). Given that sampling covered a significant breadth of Lepidoptera, utilizing surrogates within the same genus will have a negligible effect on downsteam use of the tree in phylogenetic linear mixed modeling.

Sequences were aligned with mafft v7.294b (Katoh & Standley, 2014) employing the --adjustdirection and --localpair options. AliView v1.26 (Larsson, 2014) was used to view and edit the alignments by hand if needed. Nearly identical sequences (>95% identity and within 50 bp in length) with the same species label were randomly chosen. Sequences covering different areas of the same loci (<100 bp overlap) within the same species were merged together using a degenerate consensus technique employed in AliView. Locus alignments containing 10 or less species were removed, leaving a total of 8 usable loci. A supermatrix for the final dataset was generated using FasConCat-G v1.0 (Kück & Longo, 2014). The supermatrix contained 64% missing data, but all 102 species were represented by the common barcode *COI*, followed by a *Ef-1a* representation (50% coverage) and *Wgl* and *CAD* (each with 32% coverage).

An unpartitioned maximum likelihood tree was built using RAxML-NG v0.9.0 (Kozlov et al. 2019) under a GTR-G substitution model. The phylogeny was constrained by superfamily, due to the small number of species across a large order that diverged over 100 million years ago (Kawahara et al. 2019). We ran 60 analyses (30 starting from random trees and 30 starting from a maximum parsimony tree). The phylogeny with a log-likelihood closest to 0 was chosen as the final phylogeny (-119586.886). FigTree v2.0 (Rambaut, 2010) was used to visualize and root the tree to superfamily Tineoidea (Mitter et al. 2017, Kawahara et al. 2019, Kristensen et al. 2007). See Figure 1 for final phylogeny colored by superfamily.

All analyses were run using the high-performance cluster (HPC) at the University of Florida, HiperGator 2.0. Raw data and cleaned products (uncleaned FASTA files, final alignment and final tree file) are available (DOI: 10.5061/dryad.qjq2bvqk4).

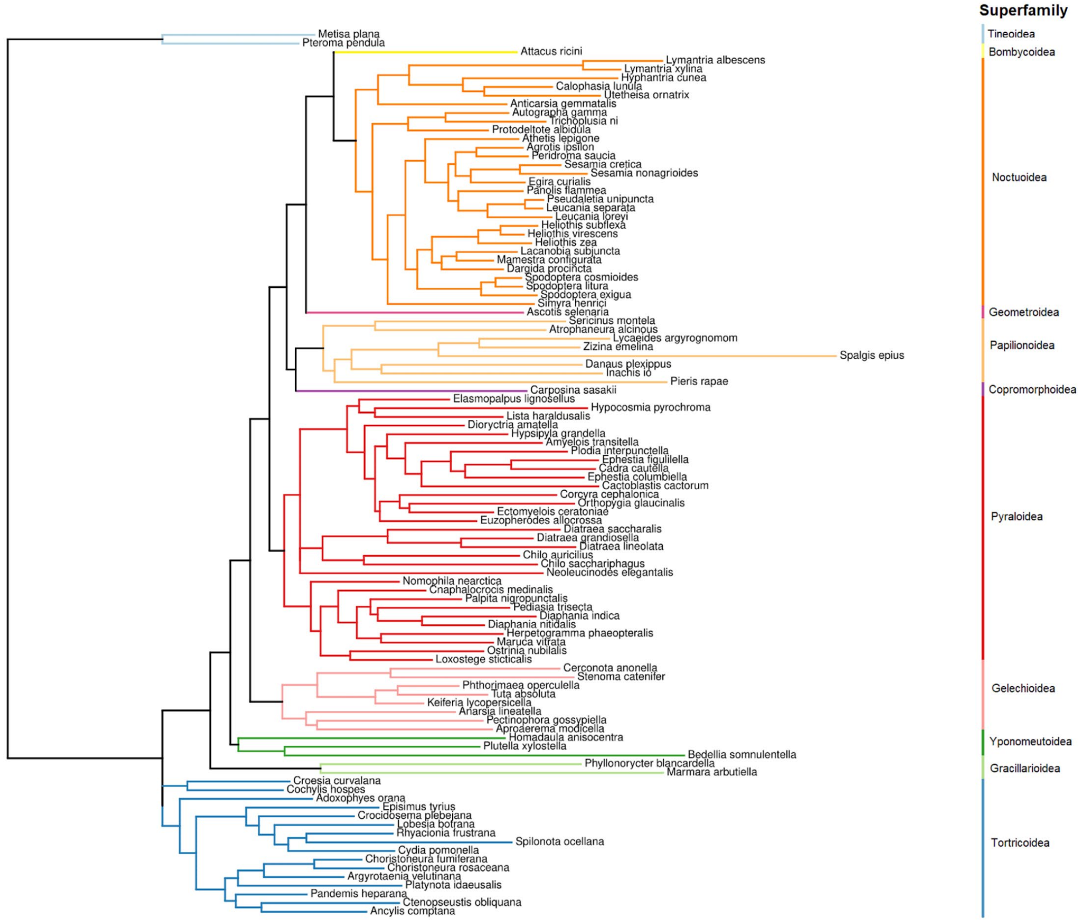
Table 1: The names and lengths of the 11 loci used as the starting sequence for input into GeneDumper.

Locus Name	Locus Length (bp)
ArgKin	596
CAD	2,211
COI_trnL_COII	2,271 (COI: 1,531; trnL: 67; COII: 673)
DDC	957
EF1a	1,240
GAPDH	609
IDH	709
MDH	733
RpS2	474
RpS5	614
Wgl	453

Table 2: Species substitutions made due to lack of DNA information.

Species	Replacement Species
Ephestia calidella	*Ephestia columbiella*
Episimus utilis	*Episimus tyrius*
Euzopherodes vapidella	*Euzopherodes allocrossa*
Marmara gulosa	*Marmara arbutiella*
Naranga aenescens	*Protodeltote albidula*

Figure 1: Final phylogram colored by superfamily, rooted to Tineoidea.



References

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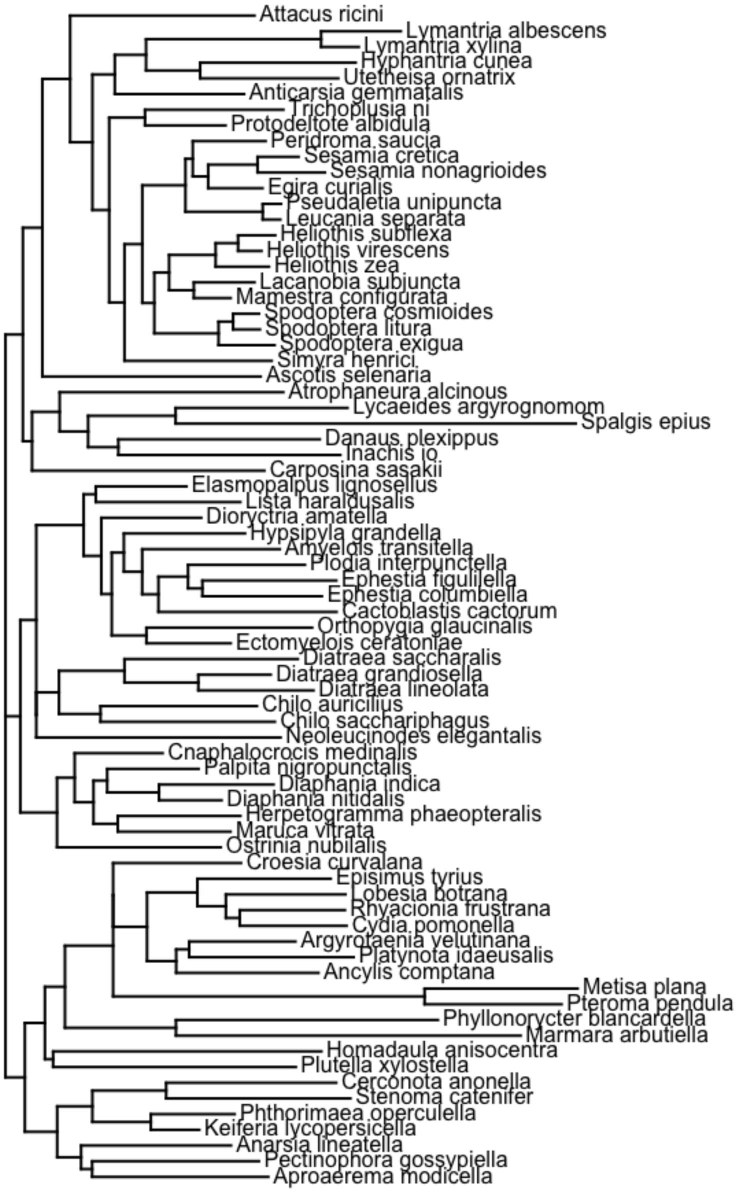
Supplement 4: Models with phylogenetic correction

1. Phylogenetic tree used in analysis of development variables



D_l

Fixed effects	**Estimate**	**SE**	**Z score**
absolute latitude	-0.087	0.0260	-4.05
egg	23.5	0.896	30.04
larva	23.22	0.911	29.27
pupa	23.94	0.910	30.25
Random effects	**SD**		
species	0.85		
residual	1.18		
N = 167 obs., 71 species			

R^2_{lik} (phylogenetic vs non-phylogenetic model): 0.0026

D_h

Fixed effects	**Estimate**	**SE**	**Z score**
absolute latitude	-0.048	0.029	-1.623
egg	35.32	1.022	34.548
larva	34.97	1.010	34.651
pupa	34.91	1.011	34.514
Random effects	**SD**		
species	0.004		
residual	1.066		
N = 84 obs., 41 species			

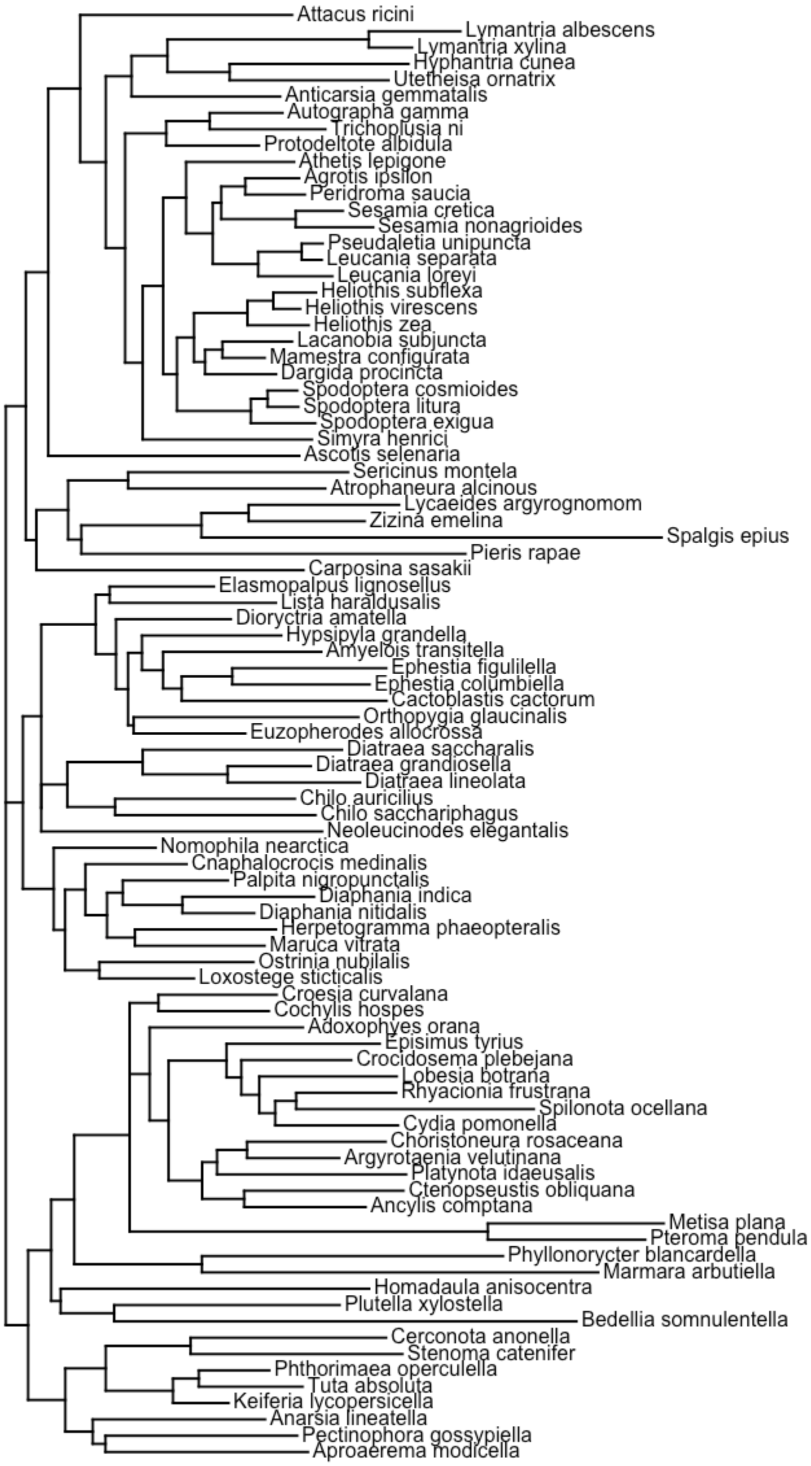
R^2_{lik} (phylogenetic vs non-phylogenetic model): < 0.0001

$D_{breadth}$

Fixed effects	**Estimate**	**SE**	**Z score**
absolute latitude	0.031	0.025	1.276
egg	12.471	0.859	14.513
larva	12.012	0.835	14.386
pupa	11.088	0.843	13.139
Random effects	**SD**		
species	0.001		
residual	1.226		
N = 82 obs., 39 species			

R^2_{lik} (phylogenetic vs non-phylogenetic model): < 0.0001

2. Phylogenetic tree used in T_0 analysis

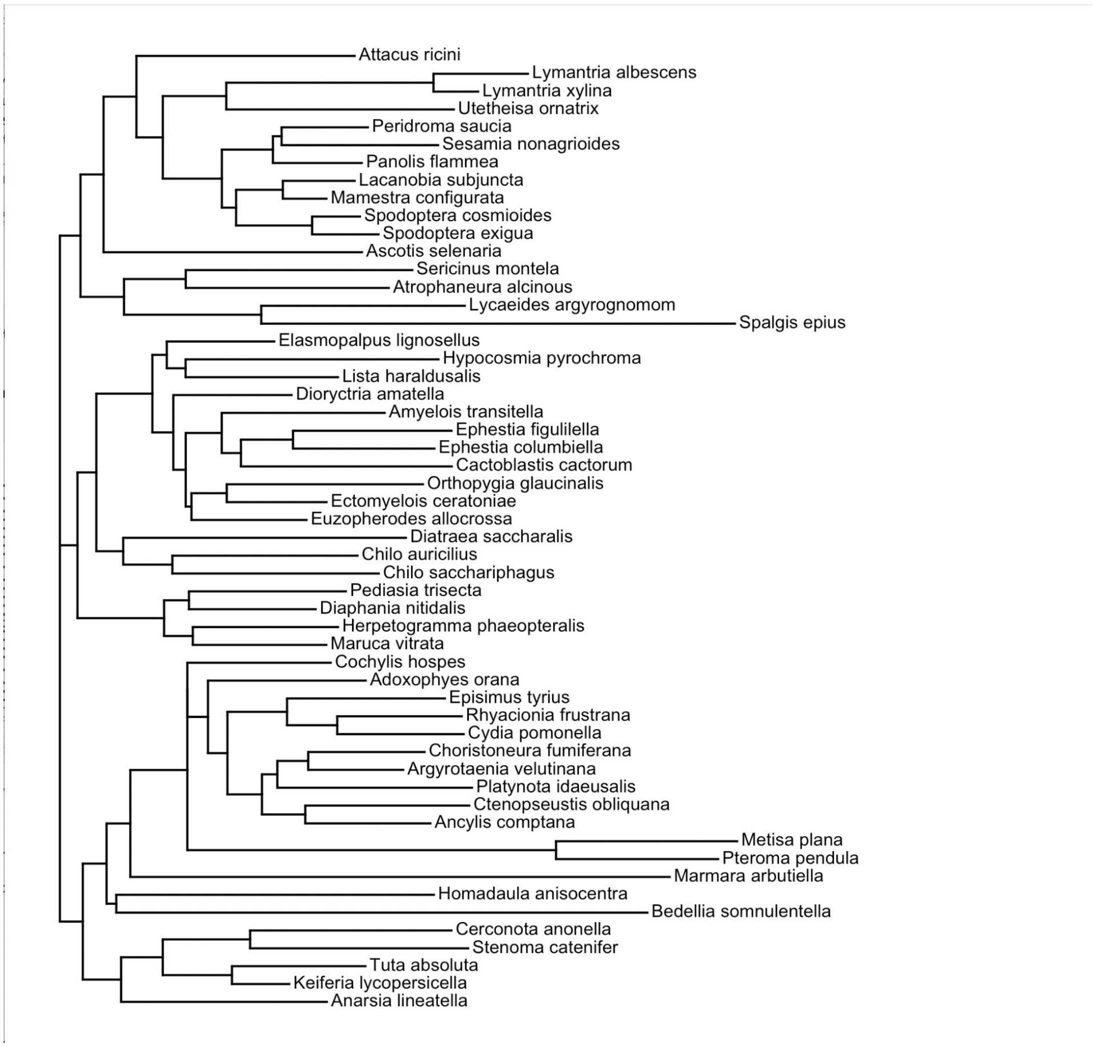


T_0

Fixed effects	**Estimate**	**SE**	**Z score**
absolute latitude	-0.0312	0.021	-1.509
egg	11.43	0.835	13.700
larva	10.72	0.844	12.700
pupa	11.63	0.830	14.011
Random effects	**SD**		
species	1.30		
residual	1.583		
N = 235 obs., 89 species			

R^2_{lik} (phylogenetic vs non-phylogenetic model): < 0.0001

3. Phylogenetic tree used in analysis of survival variables



S_l

Fixed effects	**Estimate**	**SE**	**Z score**
absolute latitude	-0.258	0.053	-4.837
egg	23.367	1.841	12.694
larva	20.569	1.692	12.161
pupa	19.108	2.044	9.346
Random effects	**SD**		
species	1.92		
residual	1.75		
N = 61 obs., 34 species			

R^2_{lik} (phylogenetic vs non-phylogenetic model): - 0.02

S_h

Fixed effects	**Estimate**	**SE**	**Z score**
absolute latitude	-0.051	0.044	-1.157
egg	33.710	1.603	21.026
larva	33.233	1.644	20.209
pupa	33.248	1.635	20.34
Random effects	**SD**		
species	1.76		
residual	1.75		
N = 65 obs., 36 species			

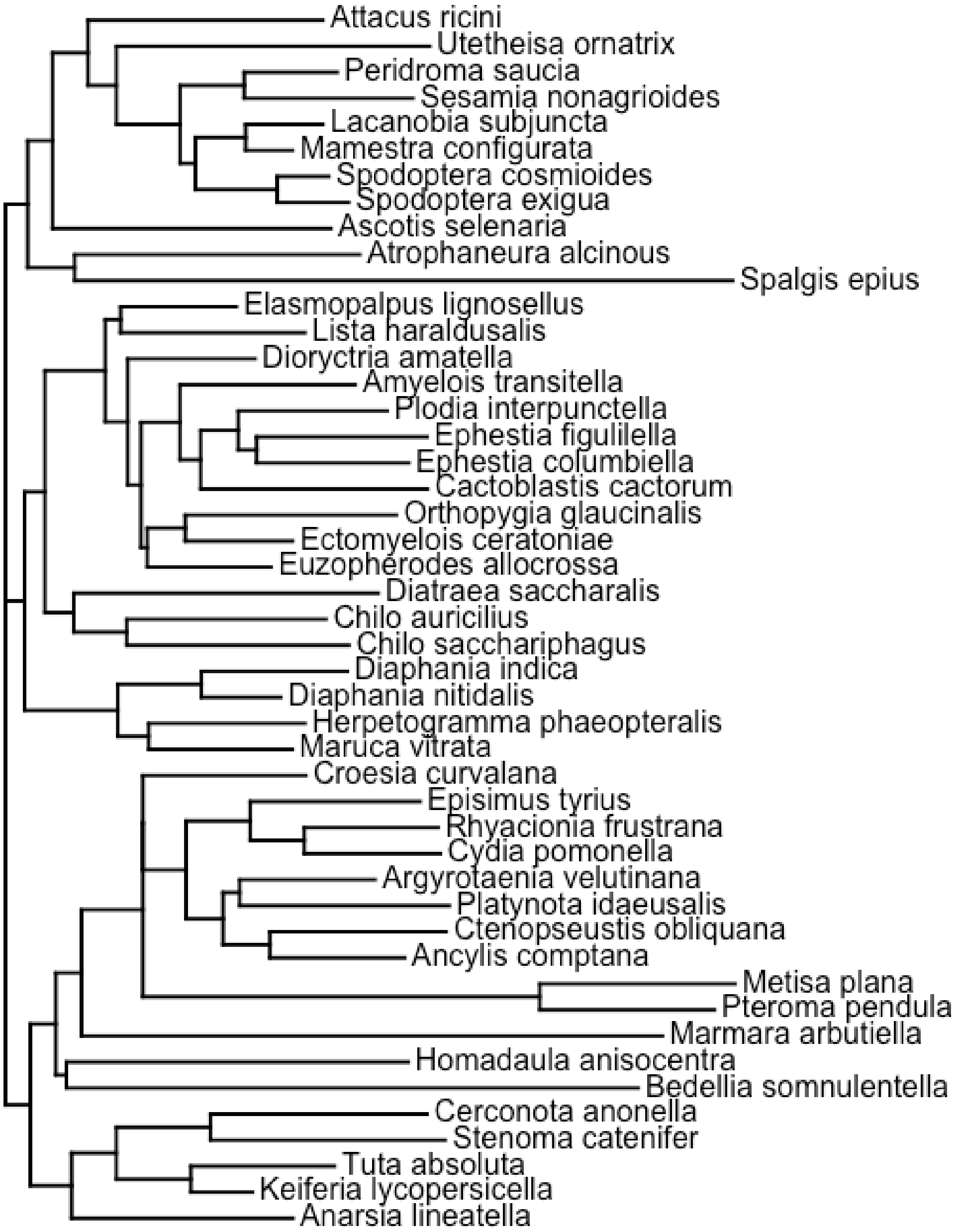
R^2_{lik} (phylogenetic vs non-phylogenetic model): 0.003

$S_{breadth}$

Fixed effects	**Estimate**	**SE**	**Z score**
absolute latitude	0.121	0.087	1.381
egg	13.333	3.199	4.167
larva	10.996	3.216	3.419
pupa	12.620	3.246	3.888
Random effects	**SD**		
species	3.462		
residual	2.415		
N = 41 obs., 24 species			

R^2_{lik} (phylogenetic vs non-phylogenetic model): -0.287

4. Phylogenetic tree used in analysis of performance variables



P_l

Fixed effects	**Estimate**	**SE**	**Z score**
absolute latitude	-0.109	0.036	-3.069
egg	24.366	1.252	19.466
larva	24.424	1.285	19.012
pupa	24.881	1.271	19.574
Random effects	**SD**		
species	1.355		
residual	1.646		
N = 96 obs., 46 species			

R^2_{lik} (phylogenetic vs non-phylogenetic model): -0.0263

P_h

Fixed effects	**Estimate**	**SE**	**Z score**
absolute latitude	-0.041	0.040	-1.021
egg	33.979	1.383	24.56
larva	33.772	1.415	23.86
pupa	33.593	1.414	23.764
Random effects	**SD**		
species	1.846		

residual	1.073		
N = 62 obs., 36 species			

R^2_{lik} (phylogenetic vs non-phylogenetic model): 0.023

$P_{breadth}$

Fixed effects	**Estimate**	**SE**	**Z score**
absolute latitude	0.016	0.037	0.442
egg	11.177	1.261	8.860
larva	11.498	1.314	8.746
pupa	10.769	1.296	8.309
Random effects	**SD**		
species	2.093		
residual	1.589		
N = 60 obs., 34 species			

R^2_{lik} (phylogenetic vs non-phylogenetic model): < 0.0001