

Supporting Information for: Ecological drivers of flower-leaf  
sequences: aridity and pollination success select for flowering-first in  
The American Plums

**Tables**

	species	n.FLS	n.petal	n.pdsi
1	alleghaniensis	17	39	114
2	americana	95	271	200
3	angustifolia	77	238	200
4	gracilis	85	289	200
5	hortulana	106	254	200
6	maritima	75	255	200
7	mexicana	64	284	200
8	munsoniana	117	279	200
9	nigra	118	230	200
10	rivularis	111	225	200
11	subcordata	46	71	30
12	texana	19	38	39
13	umbellata	70	284	200

Table S1: Sample sizes of each for each species used in this study

	species	index	index.nodoy
1	mexicana	0.85	0.90
2	umbellata	0.82	0.83
3	angustifolia	0.76	0.77
4	maritima	0.68	0.76
5	gracilis	0.64	0.68
6	americana	0.62	0.55
7	munsoniana	0.60	0.67
8	alleghaniensis	0.59	0.65
9	nigra	0.55	0.62
10	hortulana	0.51	0.52
11	texana	0.51	0.54
12	rivularis	0.44	0.53
13	subcordata	0.16	0.18

	Estimate	Est.Error	Q5.5	Q25	Q75	Q94.5
Intercept	0.34	0.23	-0.02	0.20	0.48	0.70
phi_Intercept	1.92	0.42	1.22	1.65	2.21	2.55
pdsi.z	-0.47	0.30	-0.96	-0.66	-0.28	0.01
petal.z	-0.14	0.24	-0.54	-0.29	0.01	0.23
pdsi.z:petal.z	-0.14	0.49	-0.91	-0.46	0.16	0.65

	Estimate	Est.Error	Q5.5	Q25	Q75	Q94.5
Intercept	0.49	0.25	0.09	0.33	0.65	0.88
phi_Intercept	1.77	0.41	1.09	1.50	2.06	2.39
pdsi.z	-0.43	0.32	-0.92	-0.63	-0.22	0.07
petal.z	-0.14	0.27	-0.56	-0.30	0.03	0.27
pdsi.z:petal.z	-0.16	0.54	-1.01	-0.50	0.17	0.69

## Figures

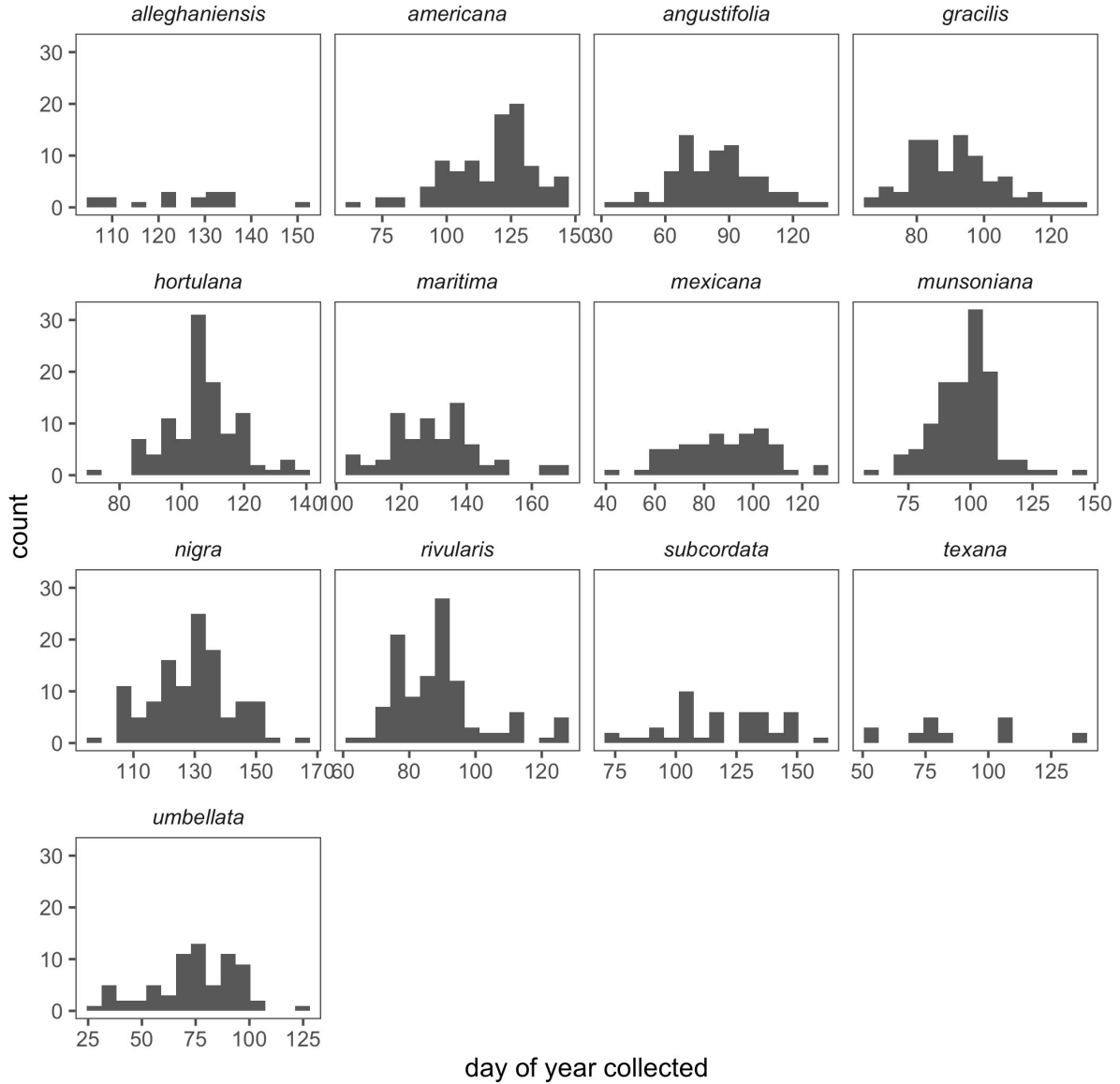


Figure S1: Sampling is uneven

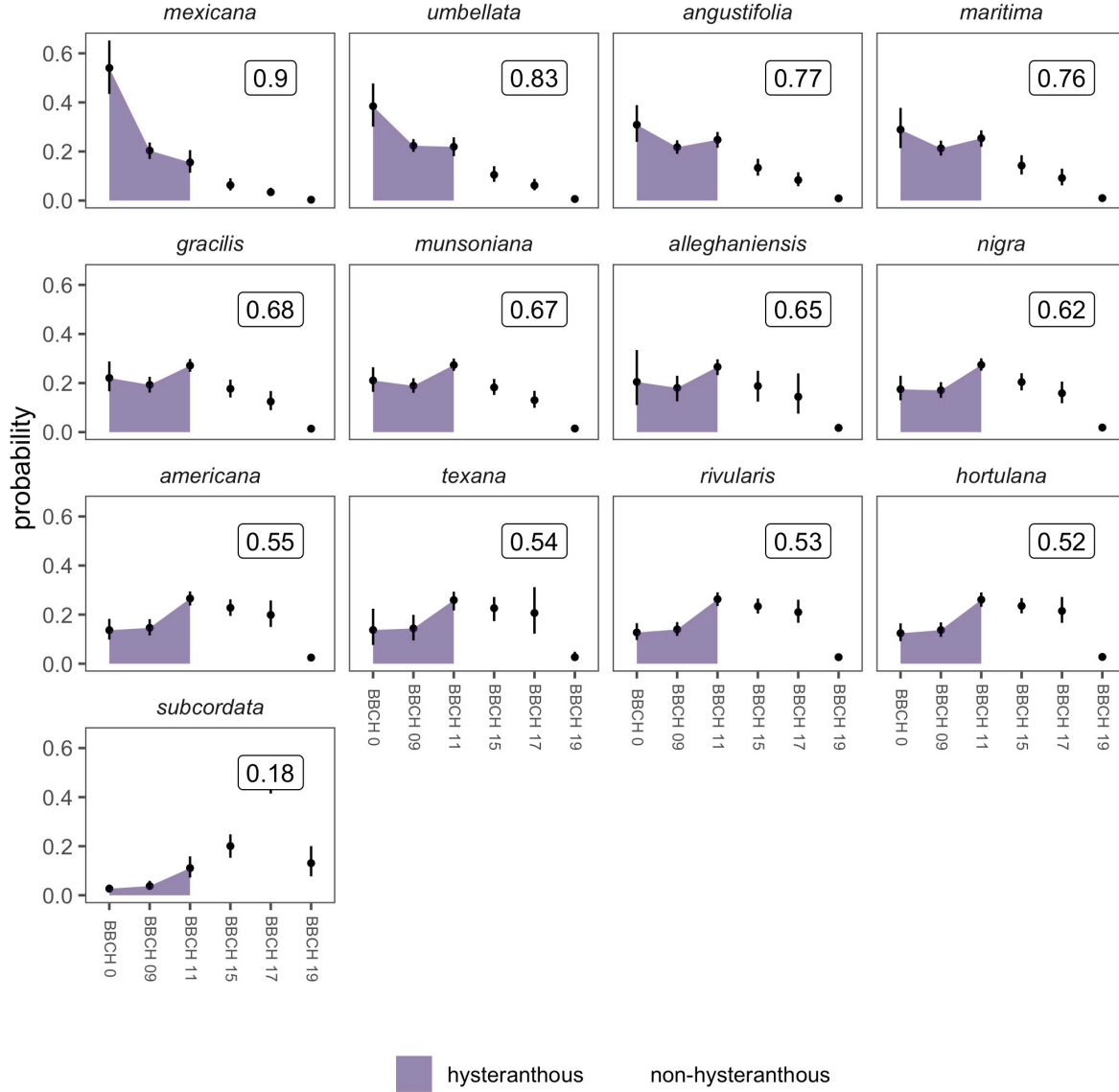


Figure S2: This the model predictions without doy

## Extended Methods:

Because single-predictor regressions can be formulated with either variable as the dependent one (say better and cite), this allowed us to both account for variation in within species PDSI and petal lengths and account for the phylogenetic structure of these variables as well. (Should everything below go to the supplement?)

In these models, we modeled species and phylogeny as above.

The model structure is:

$$y_{trait} = \alpha + \alpha_{sp} + \alpha_{phylo} + \beta_{hyst.index} * X_{hyst.index} + \epsilon$$

$$\epsilon \sim N(0, \sigma_y^2)$$

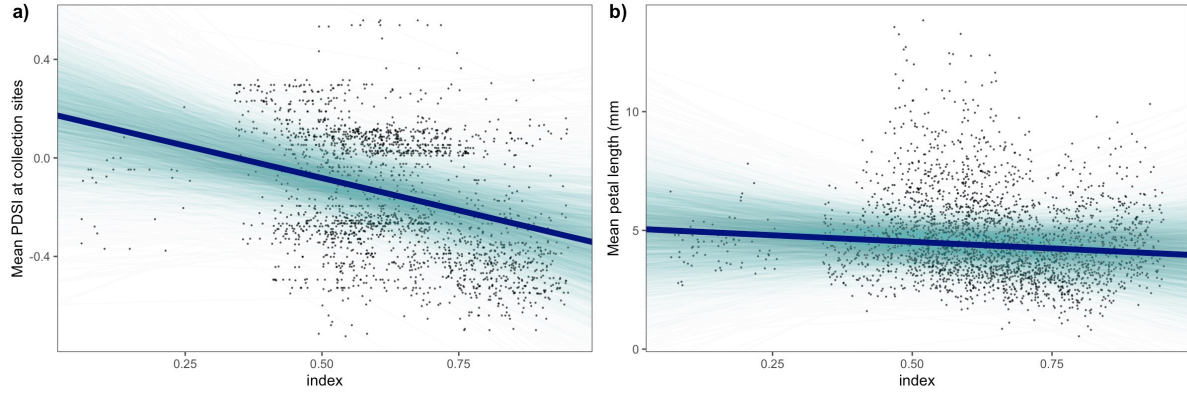


Figure S3: This is the separate model

where  $y_{trait}$  is observed trait values (PDSI or petal length), and the slope  $\beta_{hyst.index}$  describes the relationship between extended hysternathy (higher hysternathy index value) and the trait of interest.  $\alpha$  describes a grand intercept, and  $\alpha_{sp}$  and  $\alpha_{phylo}$  describe the species and phylogenetic effects respectively.