

1 **Supplementary materials**

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3 **Supplementary methods**

4 **(a) Phylogenetic tree construction**

5 We constructed a phylogenetic tree for the 30 species in our experiment using Bayesian
6 methods on ITS1/5.8S/ITS2 and rbcL nucleotide sequence regions. These regions were chosen
7 because they are relatively fast and slow evolving, respectively, and are thus good complements
8 for estimating divergence times at different depths in the phylogenetic tree. Separately for each
9 region, sequences were retrieved from GenBank, aligned using the MUSCLE algorithm in
10 MEGA (version 4.0), and combined into a single sequence matrix for analysis. We then loaded
11 the aligned sequence data from both sequence regions into BEAST (version 2.3.1) and generated
12 a Bayesian tree using a GTR substitution model selected by ModelTest (version 3.7) and an
13 uncorrelated lognormal relaxed molecular clock for branch length estimation; the site and clock
14 models of the two sequence regions were unlinked. We set lognormal priors on four internal
15 nodes (Poales = 1.8 [mean], 0.5 [standard deviation], 68.1 [minimum age in millions of years];
16 Fabales = 1.5, 0.5, 59.9; Caryophyllales = 1.5, 0.5, 83.5; Lamiales = 1.5, 0.5, 44.3) based on
17 published node calibrations for these groups, to calibrate the tree to real-time (in millions of
18 years) with the minimum age constraints based on the fossil record [47]. We constrained the tree
19 topology at nodes above the family-level based on well-resolved relationships in the angiosperms
20 [48,49], and thus did not require an outgroup to root the tree because BEAST automatically
21 performs molecular clock rooting above the constrained nodes. We ran the MCMC chain for
22 100,000,000 generations, with a 10,000,000 burn-in and data logging every 9,000 generations.
23 This analysis generated 10,000 posterior trees, which were summarized into a single ultrametric

24 maximum clade credibility tree with median node heights. The resulting tree (figure S1) is fully
25 resolved and consistent with Angiosperm Phylogeny Group III classifications and estimated
26 divergence times of major groups [49]. We used the ‘cophenetic.phylo’ function in the R
27 package ‘ape’ to calculate all pairwise phylogenetic distances based on the branch length
28 information of the 30 study species.

29 **(b) Details of lambda estimation**

30 As described in the *Materials and methods*, we grew plants at low densities with seven
31 replicate pots per species \times soil moisture environment. These replicates were used to calculate
32 the distribution of log-transformed finite rates of increase (λ) for each combination of species \times
33 soil moisture environment by fitting separate linear models. The linear models tested the effects
34 of the number of individuals in each low density pot on finite rate of increase, to identify species
35 for which competition might affect our estimates of λ . These linear models were possible
36 because, although we thinned pots to eight individuals, low germination rates or post-thinning
37 germination/mortality caused some variation among pots in the numbers of individuals that were
38 present (mean = 6.3, sd = 2.2 individuals). For species with a significant to marginally-
39 significant slope ($P < 0.1$), we confirmed that significance was not driven by outlying
40 observations, and then used the intercept (\pm standard deviation [sd]) of the population growth
41 rate as λ . For species with a non-significant slope, we used the mean (\pm sd) population growth
42 rate across all replicates as λ . In both cases, these estimates were used as informative priors in the
43 Bayesian analysis described in the *Materials and methods*. For those species that have been
44 studied elsewhere, our estimated λ values were, on average, within one standard deviation (mean
45 = 0.56 standard deviations, $n = 3$) of existing estimates in the literature [28].

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47 **Supplementary equations**

48 Equations for stabilizing differences (Eq. **S1**) and fitness differences (Eq. **S2, S3**) as described in

49 *Materials and methods*:

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$$1 - \rho = 1 - \sqrt{\frac{\alpha_{ij}}{\alpha_{jj}} \cdot \frac{\alpha_{ji}}{\alpha_{ii}}} \quad (\text{S1})$$

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$$\kappa_j / \kappa_i = \frac{\lambda_j - 1}{\lambda_i - 1} \cdot \sqrt{\frac{\alpha_{ij}}{\alpha_{jj}} \cdot \frac{\alpha_{ii}}{\alpha_{ji}}} \quad (\text{S2})$$

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$$K = \max(\kappa_j / \kappa_i, \kappa_i / \kappa_j) \quad (\text{S3})$$

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66 **Table S1**

67 **Taxonomic and sequence accession (ITS1/5.8S/ITS2 and rbcL regions) information for the 30 study species, organized to show**
 68 **each focal species and its sympatric and allopatric competitor**

Species names	Order	Family	Origin	ITS1/5.8S/ITS2	rbcL
<i>Lasthenia glabrata</i>	Asterales	Asteraceae	California	AF391593.1	AIW51855.1*
<i>Lasthenia californica</i>	Asterales	Asteraceae	California	AF467195.1	NA
<i>Centaurea melitensis</i> ¹	Asterales	Asteraceae	Spain	HQ540425.1	EU384954.1
<i>Uropappus lindleyi</i>	Asterales	Asteraceae	California	AF386495.1	NA
<i>Madia elegans</i>	Asterales	Asteraceae	California	AF413612.1	AY215141.1*
<i>Crepis capillaris</i> ¹	Asterales	Asteraceae	Spain	AJ633353	KM360738.1
<i>Phacelia campanularia</i>	Boraginales	Boraginaceae	California	AF091188.1	KF158107.1
<i>Nemophila menziesii</i>	Boraginales	Boraginaceae	California	AF091183.1	KF158108.1
<i>Myosotis arvensis</i>	Boraginales	Boraginaceae	Spain	AY092908.1	HM850186.1
<i>Chenopodium berlandieri</i>	Caryophyllales	Amaranthaceae	California	HE577429.1	JF941268.1*
<i>Claytonia perfoliata</i> ²	Caryophyllales	Montiaceae	California	AY764040.1	AF132093.1
<i>Portulaca oleracea</i>	Caryophyllales	Portulacaceae	Spain	JF508578.1	HQ621340.1
<i>Monolepis nuttalliana</i>	Caryophyllales	Amaranthaceae	California	HE577375.1	AY270108.1
<i>Atriplex patula</i> ²	Caryophyllales	Amaranthaceae	California	DQ499332.1	HM849801.1
<i>Silene gallica</i>	Caryophyllales	Caryophyllaceae	Spain	U30959/U30985	HM850354.1
<i>Lupinus bicolor</i>	Fabales	Fabaceae	California	DQ524209.1	Z70056.1*
<i>Lotus purshianus</i>	Fabales	Fabaceae	California	AF467067.1	HM850139.1*
<i>Trifolium incarnatum</i>	Fabales	Fabaceae	Spain	AF053160.1	HM850415.1
<i>Salvia columbariae</i>	Lamiales	Lamiaceae	California	DQ667219.1*	AY570408.1
<i>Collinsia heterophylla</i>	Lamiales	Lamiaceae	California	AF385337.1	AF026825.1*

<i>Salvia viridis</i>	Lamiales	Lamiaceae	Spain	DQ667222.1*	AY570450.1
<i>Bromus carinatus</i>	Poales	Poaceae	California	AY367948.1	KM360707.1
<i>Hordeum depressum</i>	Poales	Poaceae	California	AJ607894.1	NA
<i>Hordeum vulgare</i>	Poales	Poaceae	Spain	FJ593180.1	AY137456.1
<i>Vulpia microstachys</i>	Poales	Poaceae	California	EF584981.1	NA
<i>Vulpia octoflora</i>	Poales	Poaceae	California	EF584982.1	KJ773986
<i>Vulpia myuros</i>	Poales	Poaceae	Spain	AY118092.1	KF713076.1
<i>Eschscholzia caespitosa</i>	Ranunculales	Papaveraceae	California	JF892592.1	NA
<i>Eschscholzia californica</i>	Ranunculales	Papaveraceae	California	DQ912884.1	HM849984.1
<i>Papaver dubium</i>	Ranunculales	Papaveraceae	Spain	DQ250322.1	HM850229.1

69 Notes: Species contrasts are delineated by row shading, with the focal species in bold type. Superscripts represent contrasts with
70 partial branch length overlap, one of which (*M. nuttalliana*/*A. patula*²) was excluded from analysis because the latter species failed to
71 flower. *Sequences were unavailable, and were replaced with those of known sister species (*S. columbariae* = *S. clevelandii*, *S. viridis*
72 = *S. sclarea* [46]) or congeners as appropriate. ‘NA’ means that sequences were unavailable for that specific region and species.

73 **Table S2**74 **Comparing fits of alternative annual plant models**

Model	AICc scores
1 $N_{i\ t+1} = N_{i\ t} \cdot \frac{\lambda_i}{1 + \alpha_{ii}N_{i\ t} + \alpha_{ij}N_{j\ t}}$	2236
2 $N_{i\ t+1} = N_{i\ t} \cdot \lambda_i e^{-\alpha_{ii}N_{i\ t} - \alpha_{ij}N_{j\ t}}$	2468
3 $N_{i\ t+1} = N_{i\ t} \cdot \frac{\lambda_i}{1 + N_{i\ t}^{\alpha_{ii}} + N_{j\ t}^{\alpha_{ij}}}$	2556
4 $N_{i\ t+1} = N_{i\ t} \cdot \frac{\lambda_i}{1 + (\alpha_{ii}N_{i\ t} + \alpha_{ij}N_{j\ t})^{b_i}}$	2625
5 $N_{i\ t+1} = N_{i\ t} \cdot \lambda_i e^{-\alpha_{ii}\ln(N_{i\ t+1}) - \alpha_{ij}\ln(N_{j\ t+1})}$	2748
6 $N_{i\ t+1} = N_{i\ t} \cdot \frac{\lambda_i}{(1 + \alpha_{ii}N_{i\ t} + \alpha_{ij}N_{j\ t})^{b_i}}$	2892

75 Notes: All models were simultaneously fit to each focal species i vs. sympatric species j and
76 allopatric species k . The AICc scores were summed across each three-species contrast \times soil
77 moisture environment for model comparison. The parameters are described in the *Materials and*
78 *methods*, except for b_i which allows individuals to vary in competitive impacts as their density
79 increases. Model formulations are taken from Levine and HilleRisLambers [28].

80 **Table S3**81 **Parameter estimates used to calculate stabilizing and fitness differences (Eqs. S1 and S2)**

Species				Parameter estimates									
<i>i</i>	<i>j</i>	<i>k</i>	Soil env	λ_i	λ_j	λ_k	α_{ii}	α_{jj}	α_{kk}	α_{ij}	α_{ji}	α_{ik}	α_{ki}
<i>B. carinatus</i>	<i>H. depressum</i>	<i>H. vulgare</i>	wet	79.0	155.1	22.8	0.175	0.138	0.227	0.001	0.795	0.623	0.006
<i>C. berlandieri</i>	<i>C. perfoliata</i>	<i>P. oleracea</i>	wet	69.4	8.6	509.2	0.223	0.007	279.72	<0.001	0.065	<0.001	219.90
<i>E. caespitosa</i>	<i>E. californica</i>	<i>P. dubium</i>	wet	67.0	53.7	947.4	0.004	0.012	0.705	3.573	2.388	15.10	0.008
<i>L. bicolor</i>	<i>L. purshianus</i>	<i>T. incarnatum</i>	wet	4.3	58.4	1136.3	0.563	12.01	20.18	0.796	0.096	7.845	0.945
<i>L. glabrata</i>	<i>L. californica</i>	<i>C. melitensis</i>	wet	389.8	839.0	1.8	0.054	0.098	0.180	0.003	0.219	0.001	0.728
<i>M. nuttalliana</i>	<i>A. patula</i>	<i>S. gallica</i>	wet	587.5	0.1	989.4	0.263	0.001	0.119	0.003	<0.001	8.227	<0.001
<i>P. campanularia</i>	<i>N. menziesii</i>	<i>M. arvensis</i>	wet	63.6	9.6	352.4	0.142	0.140	0.107	0.006	0.004	0.004	<0.001
<i>S. columbariae</i>	<i>C. heterophylla</i>	<i>S. viridis</i>	wet	318.9	727.9	75.6	0.231	2.358	0.126	0.403	0.001	0.128	0.070
<i>U. lindleyi</i>	<i>M. elegans</i>	<i>C. capillaris</i>	wet	35.9	75.5	323.6	0.384	1.271	1.342	0.069	0.001	0.003	0.002
<i>V. microstachys</i>	<i>V. octoflora</i>	<i>V. myuros</i>	wet	235.8	923.8	314.8	0.099	0.456	0.200	0.083	0.302	0.227	0.002
<i>B. carinatus</i>	<i>H. depressum</i>	<i>H. vulgare</i>	dry	563.3	138.0	15.7	2.176	0.036	0.266	0.001	1.291	2.85	0.005
<i>C. berlandieri</i>	<i>C. perfoliata</i>	<i>P. oleracea</i>	dry	44.1	14.5	331.1	0.267	0.022	0.017	0.001	0.072	0.001	221.85
<i>E. caespitosa</i>	<i>E. californica</i>	<i>P. dubium</i>	dry	100.9	52.2	617.4	0.010	3.091	0.829	9.309	0.002	56.02	0.004
<i>L. bicolor</i>	<i>L. purshianus</i>	<i>T. incarnatum</i>	dry	7.1	13.1	392.8	3.983	3.551	13.42	2.158	0.003	8.221	0.009
<i>L. glabrata</i>	<i>L. californica</i>	<i>C. melitensis</i>	dry	468.7	666.3	1.6	0.157	0.214	0.438	0.042	0.105	0.066	0.689
<i>M. nuttalliana</i>	<i>A. patula</i>	<i>S. gallica</i>	dry	1148.4	0.1	923.8	0.045	0.001	0.153	0.611	<0.001	8.303	<0.001
<i>P. campanularia</i>	<i>N. menziesii</i>	<i>M. arvensis</i>	dry	103.9	3.8	303.2	0.361	0.009	0.136	0.006	0.026	0.002	<0.001
<i>S. columbariae</i>	<i>C. heterophylla</i>	<i>S. viridis</i>	dry	305.3	124.3	69.8	0.130	0.518	0.177	0.847	<0.001	0.444	0.038
<i>U. lindleyi</i>	<i>M. elegans</i>	<i>C. capillaris</i>	dry	38.3	120.3	166.9	0.505	3.608	0.855	0.001	0.005	0.001	0.002
<i>V. microstachys</i>	<i>V. octoflora</i>	<i>V. myuros</i>	dry	152.9	1126.9	677.3	0.082	0.515	0.248	0.002	0.574	0.097	0.022

82 Notes: See table S1 and figure S1 for full species names and taxonomic information. Focal species *i* (bold) were competed against83 both species *j* (sympatric) and *k* (allopatric).

84 **Table S4**

85 **Germination (g) and species-specific seed bank viability (s) rates used for alternative seed**
 86 **bank viability scenarios**

i	Species		Germination			Seed bank viability		
	j	k	g_i	g_j	g_k	s_i	s_j	s_k
<i>B. carinatus</i>	<i>H. depressum</i>	<i>H. vulgare</i>	0.39	0.24	0.49	0.17	0.17	0.00
<i>C. berlandieri</i>	<i>C. perfoliata</i>	<i>P. oleracea</i>	0.62	0.25	0.35	0.00	0.35	0.11
<i>E. caespitosa</i>	<i>E. californica</i>	<i>P. dubium</i>	0.17	0.08	0.28	0.18	0.59	0.28
<i>L. bicolor</i>	<i>L. purshianus</i>	<i>T. incarnatum</i>	0.14	0.17	0.22	0.01	0.08	0.07
<i>L. glabrata</i>	<i>L. californica</i>	<i>C. melitensis</i>	0.58	0.46	0.48	0.13	0.23	0.00
<i>M. nuttalliana</i>	<i>A. patula</i>	<i>S. gallica</i>	0.36	0.24	0.80	0.59	NA	0.00
<i>P. campanularia</i>	<i>N. menziesii</i>	<i>M. arvensis</i>	0.54	0.28	0.61	0.47	0.64	0.23
<i>S. columbariae</i>	<i>C. heterophylla</i>	<i>S. viridis</i>	0.55	0.40	0.66	0.29	0.56	0.00
<i>U. lindleyi</i>	<i>M. elegans</i>	<i>C. capillaris</i>	0.32	0.07	0.09	0.61	0.03	0.23
<i>V. microstachys</i>	<i>V. octoflora</i>	<i>V. myuros</i>	0.54	0.51	0.63	0.88	0.71	0.58

87 Notes: See table S1 and figure S1 for full species names and taxonomic information. Focal

88 species i (bold) were competed against both species j (sympatric) and k (allopatric). Rates g and s

89 were calculated separately, from the germination of seeds in the low-density λ pots (for g) and

90 through a germination trial comparing germination rates before and after gibberellic acid

91 application (for s); the 0% and 100% seed bank viability scenarios were $s = 0$ and $s = 1$ for all

92 species, respectively (figure 2*b,e*). The same values of g and s were used in wet and dry

93 environments, because the watering treatments were imposed post-germination.

94 **Table S5**

95 **Effects of phylogenetic distance (PD), biogeographic history (BH), soil moisture (SM), and their interactions on stabilizing**
 96 **differences, fitness differences, and coexistence**

	logit(stabilizing differences)		log(fitness differences)		log(coexistence metric)	
	χ^2	<i>P</i> -value	χ^2	<i>P</i> -value	χ^2	<i>P</i> -value
PD	0.02	0.900	17.72	<0.001	2.08	0.149
BH	0.70	0.403	5.82	0.016	1.92	0.166
SM	0.01	0.922	0.26	0.613	1.94	0.164
PD × BH	8.75	0.003	2.60	0.107	3.89	0.049
PD × SM	1.15	0.283	1.21	0.271	2.07	0.151
BH × SM	1.12	0.290	0.38	0.537	0.18	0.675
PD × BH × SM	0.08	0.775	<0.01	0.960	<0.01	0.979
Variance weights	none		varIdent(form=~PD BH)		varPower(form=~PD)	

97 Notes: All *P*-values based on a χ^2 tests of maximum likelihood ratios with 1 degree of freedom, summarized using the ‘Anova’
 98 function in ‘car’ R package; significant *P*-values are in bold type.

99

100 **Table S6**

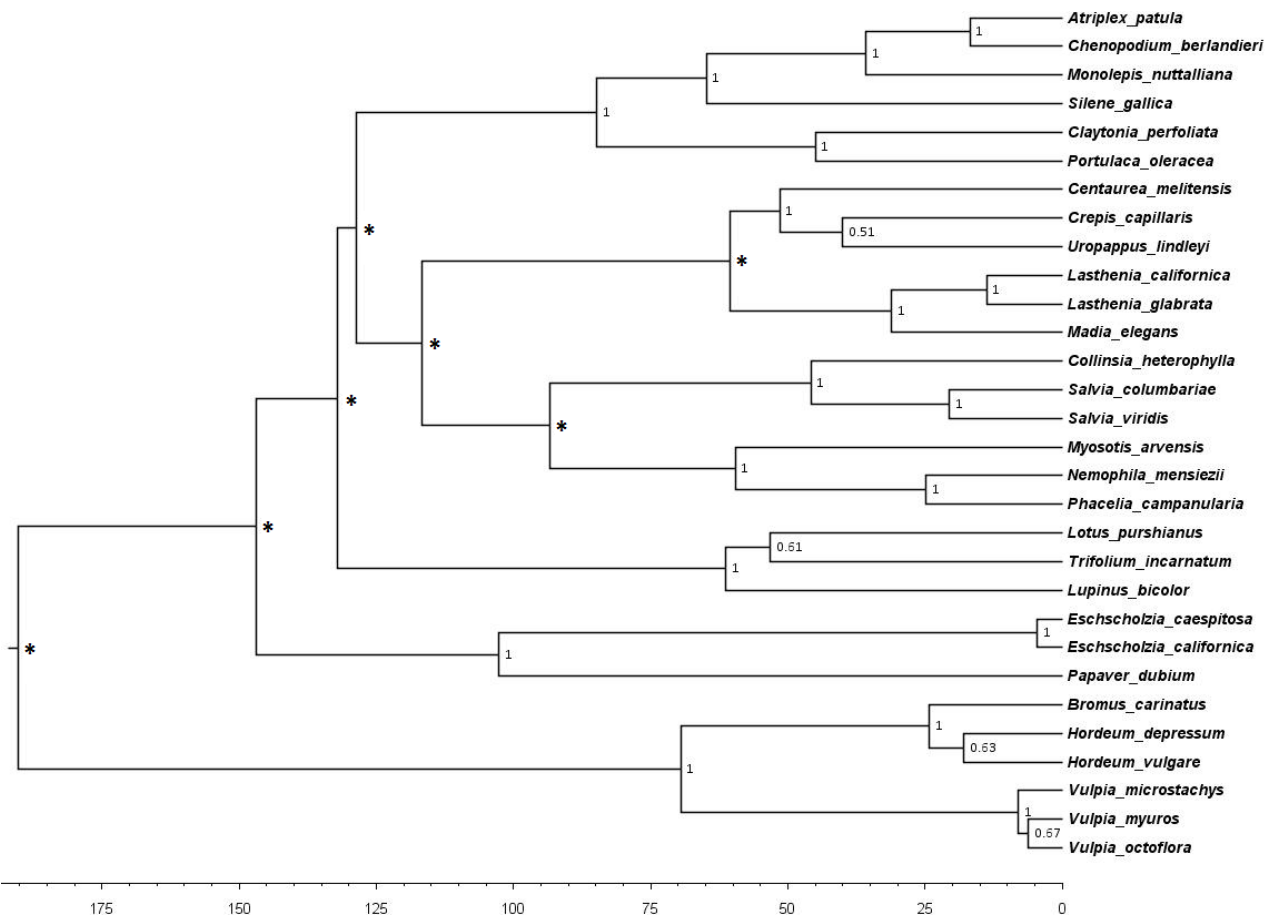
101 **Effects of phylogenetic distance (PD) on the fitness components of sympatric and allopatric species pairs**

	Sympatric		Allopatric	
	χ^2	<i>P</i> -value	χ^2	<i>P</i> -value
Demographic component	5.91	0.015	0.70	0.402
Competitive component	0.02	0.881	6.67	0.010
Fitness difference	11.39	<0.001	7.35	0.007

102 Notes: All *P*-values based on a χ^2 tests of maximum likelihood ratios with 1 degree of freedom, summarized using the ‘Anova’

103 function in ‘car’ R package; significant *P*-values are in bold type. Variance weights are varIdent(~PD) for allopatric pairs; no weights

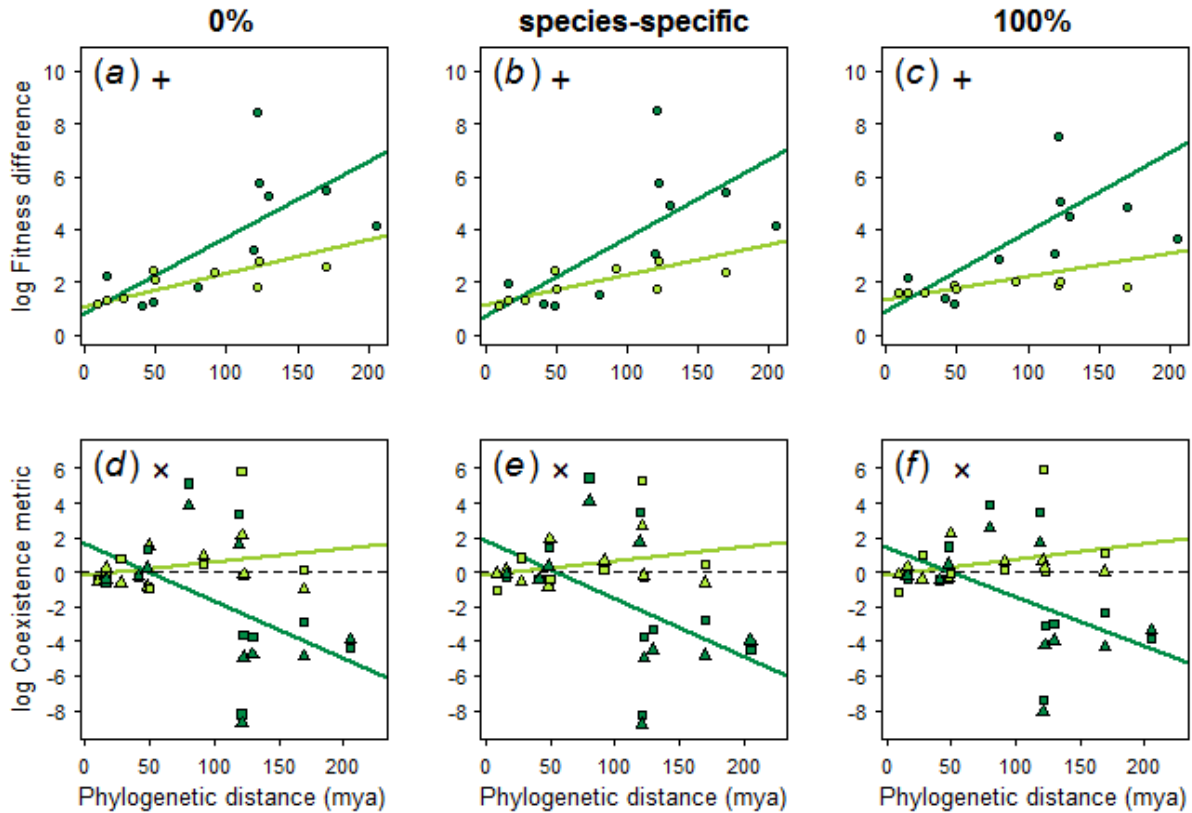
104 were necessary for sympatric pairs.



105

106 **Figure S1.**

107 Maximum clade credibility tree of the 30 annual plant species with median node heights. The
 108 tree was generated in BEAST using ITS1/5.8S/ITS2 and rbcL sequence data, and calibrated to
 109 real-time based on fossil records. The scale bar is in millions of years ago, and nodal support
 110 values are the posterior probabilities; * indicates nodes that were fixed based on *a priori*
 111 information. See table S1 for species information.



112

113 **Figure S2.**

114 Comparison of fitness differences and coexistence under three seed bank viability scenarios (0%,
 115 species-specific (table S4), and 100%); the 0% scenario is presented in the main text. We took
 116 the approach of Godoy & Levine [23] for incorporating germination rates, in which non-zero
 117 seed bank viability modifies our calculations of fitness differences and coexistence, but not
 118 stabilizing differences; as such, the latter is not shown. Data points represent sympatric (light
 119 green) and allopatric (dark green) species pairs, either averaged across soil environments
 120 (circles; *a-c*) or in wet (squares) and dry (triangles) soil moisture conditions (*d-f*); soil moisture
 121 was included in each analysis. + and × indicate significant main effects or a significant
 122 interaction, respectively, of phylogenetic distance and biogeographic history.