Supplementary materials

Supplementary methods

(a) Phylogenetic tree construction

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

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

(b) Details of lambda estimation

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

Supplementary equations

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

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

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

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

Table S1

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

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

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

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

Table S2

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

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

Table S3

Parameter estimates used to calculate stabilizing and fitness differences (Eqs. S1 and S2)

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

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

Table S4

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

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

Notes: See table S1 and figure S1 for full species names and taxonomic information. Focal species *i* (bold) were competed against both species *j* (sympatric) and *k* (allopatric). Rates *g* and *s* were calculated separately, from the germination of seeds in the low-density λ pots (for *g*) and through a germination trial comparing germination rates before and after gibberellic acid application (for *s*); the 0% and 100% seed bank viability scenarios were $s = 0$ and $s = 1$ for all species, respectively (figure 2*b*,*e*). The same values of *g* and *s* were used in wet and dry environments, because the watering treatments were imposed post-germination.

Table S5

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

	logit(stabilizing differences)		**log(fitness differences)**		**log(coexistence metric)**	
	χ^2	*P*-value	χ^2	*P*-value	χ^2	*P*-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)	

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

Table S6

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

	Sympatric		**Allopatric**	
	χ^2	*P*-value	χ^2	*P*-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**

Notes: All *P*-values based on a χ^2 tests of maximum likelihood ratios with 1 degree of freedom, summarized using the 'Anova' function in 'car' R package; significant *P*-values are in bold type. Variance weights are varIdent(~PD) for allopatric pairs; no weights were necessary for sympatric pairs.

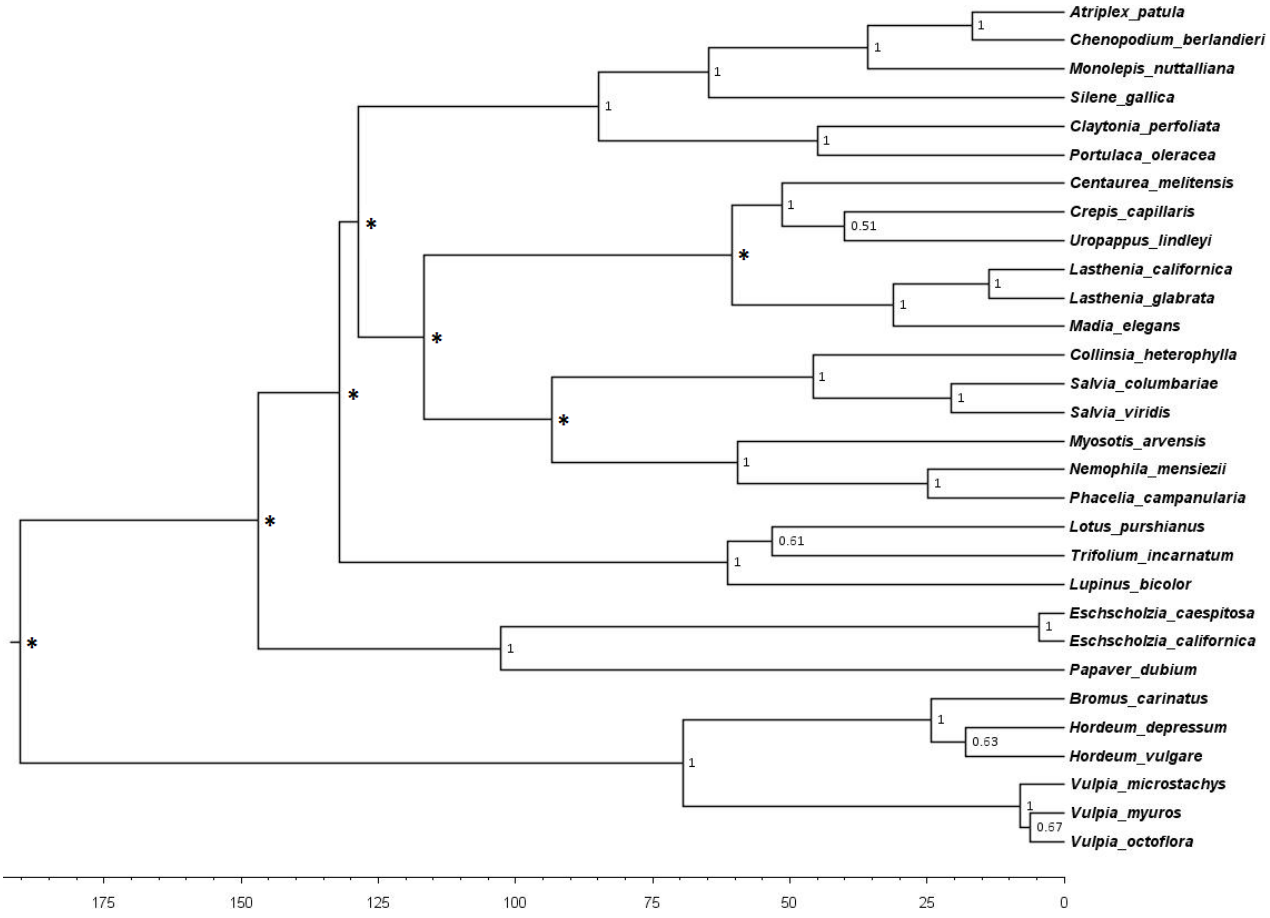

Figure S1.

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

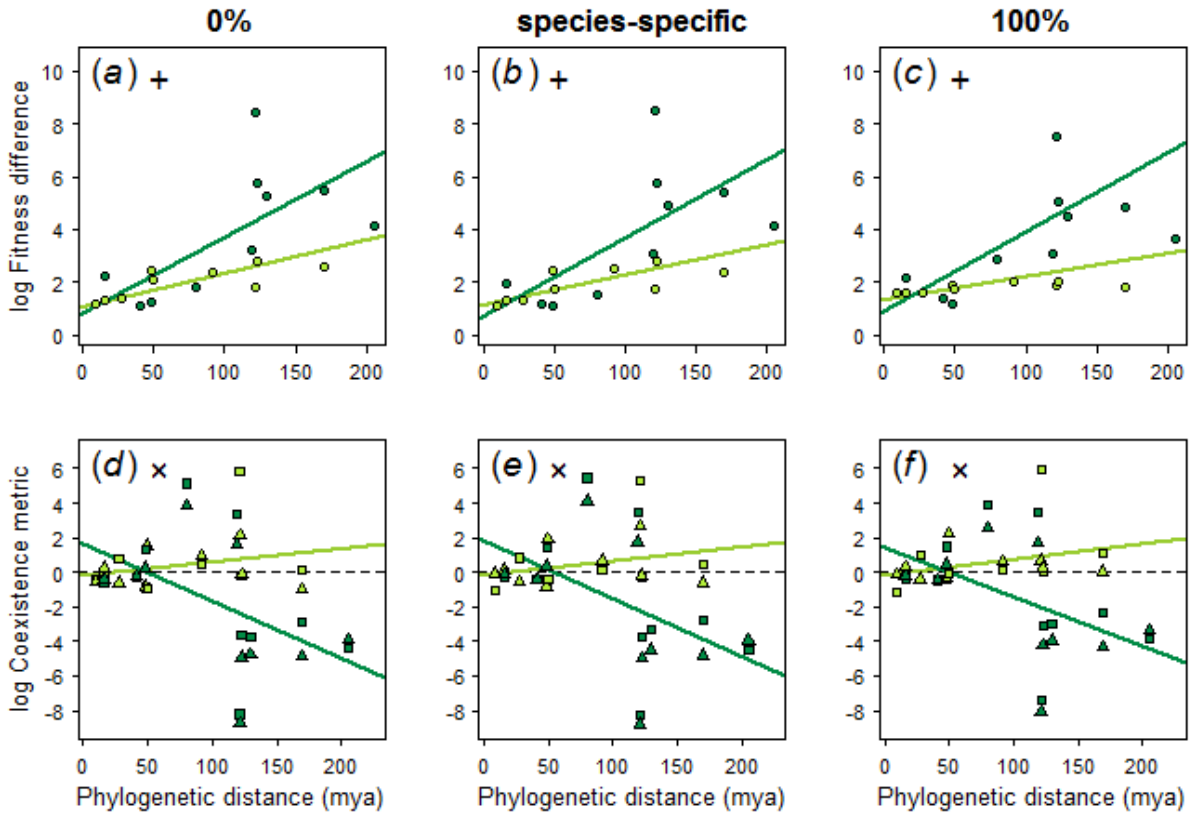

Figure S2.

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