Supporting Information

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Table S1. Parameter estimates for calculating the magnitude of the storage effect

Parameter	Value
Species x time variance component for germination	1.46
Species x time variance component for per germinant fecundity	1.27
Species x time covariance component for germination and fecundity	0.49
Average survival of ungerminated seeds, $\bar{s}$	0.41
Average germination fraction	0.45
Average rate of loss from the seed bank, $\bar{\beta}$	0.77
Number of species	10

These are the parameters for Eqs. **30**, **32**, and **34** (*SI Appendix*) and are calculated from demographic data on winter annual plants at the University of Arizona Desert Laboratory (see *Materials and Methods*).

Table S2. Partitioning of the low-density log growth rate from the storage effect

Mechanism	Boost to $\bar{r}/\beta$	Boost to $\bar{r}$
Germination Variation	0.067	0.052
Reproduction Variation	0.032	0.025
Covariation of Germination and Reproduction	0.035	0.027
Total	0.133	0.103

Storage effect is partitioned into parts due to germination variation, reproductive variation, and the covariation of germination and reproduction calculated with Eqs. **30**, **32**, and **34** in *SI Appendix*.

Table S3. Demographic difference matrices

	ERCI	*ERLA*	*ERTE*	*EVMU*	*PERE*	*PLIN*	*PLPA*	*SCBA*	*STMI*
ERCI		1.57	0.86	2.47	1.02	1.02	1.39	1.11	1.04
ERLA	0.52		2.51	2.91	2.62	1.29	1.20	1.67	1.38
ERTE	0.05	0.89		3.90	1.96	0.85	1.54	2.17	2.72
EVMU	0.29	0.03	0.59		4.72	2.50	1.76	2.29	1.39
PERE	0.09	1.02	0.00	0.69		2.64	2.18	3.07	2.39
PLIN	0.03	0.77	0.00	0.49	0.02		1.12	1.46	1.48
PLPA	0.01	0.63	0.02	0.38	0.05	0.01		1.85	1.56
SCBA	0.32	0.02	0.63	0.00	0.74	0.53	0.41		1.23
STMI	0.19	0.08	0.45	0.01	0.54	0.36	0.26	0.02	

Species-by-year squared difference matrix given in upper diagonal. Species-by-precipitation squared difference matrix given in lower diagonal. Species abbreviations are the first two letters of the genus and specific epithet given in *Materials and Methods*.

Table S4. Functional trait difference matrices

	ERCI	*ERLA*	*ERTE*	*EVMU*	*PERE*	*PLIN*	*PLPA*	*SCBA*	*STMI*
ERCI		3.95	0.21	9.60	0.30	2.57	0.68	7.30	12.55
ERLA	4.12		5.99	1.23	2.08	0.15	1.35	0.51	2.42
ERTE	0.10	5.53		12.66	1.01	4.25	1.65	10.00	16.02
EVMU	16.51	4.14	19.24		6.51	2.24	5.17	0.16	0.20
PERE	1.90	11.61	1.11	29.61		1.12	0.08	4.65	8.98
PLIN	0.00	4.12	0.10	16.51	1.90		0.61	1.21	3.76
PLPA	0.11	2.90	0.42	13.96	2.91	0.11		3.53	7.39
SCBA	2.58	0.18	3.71	6.05	8.90	2.57	1.63		0.71
STMI	4.29	0.00	5.73	3.97	11.90	4.29	3.04	0.22	

Squared differences in principal component I score for analysis of variation in RGR and Δ are given in upper diagonal. Squared differences in principal component I score for analysis of variation in 5 key traits (Nleaf, LMR, Jmax:VCmax, SLA and RGR plasticity) are given in lower diagonal. Species abbreviations are the first two letters of the genus and specific epithet given in *Materials and Methods*.

Table S5. Comparison of results with and without phylogenetic distance correction

Functional trait difference matrix	Demographic difference matrix	Mantel *P* value	Partial Mantel *P* value
5 key traits	Species × year interaction	0.0003	<0.001
RGR-Δ	Species × year interaction	0.0410	0.048
5 key traits	Species × precip interaction	0.0068	0.009
RGR-Δ	Species × precip interaction	0.0453	0.042

Results are shown for partial Mantel tests calculated in the R package vegan with a phylogenetic distance matrix based on equal branch lengths. Results using a phylogenetic distance matrix based on pseudo branch length differences were qualitatively identical.

Other Supporting Information Files

SI Appendix