Supporting Information

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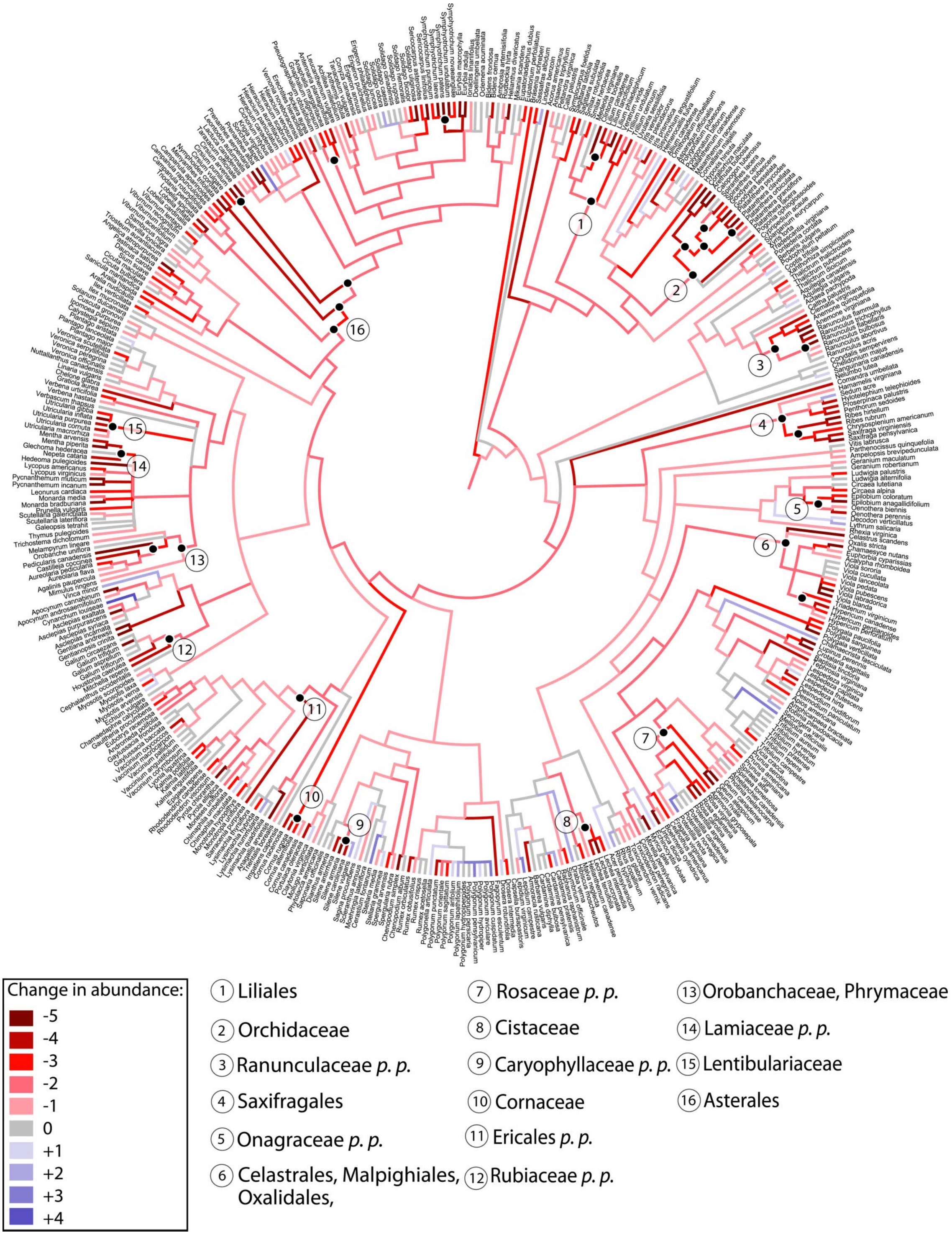

Fig. S1. Composite phylogeny of 429 flowering plant species from the Concord (Massachusetts) flora depicting changes in abundance from 1900 to 2007. Branch color illustrates parsimony character state reconstruction of change in abundance as summarized in Fig. 1. For character state scoring see color legend. Lineages that exhibited an average decline in abundance of 50% or greater are indicated by a black dot.

Table S1. Statistical tests of phylogenetic conservatism and trait correlations with change in abundance and with branch lengths on composite phylogeny set to 1

	Trait correlation								
	Model 1			Model 2			Model 3		
Trait	*n*	Estimate		*n*	Estimate		*n*	Estimate	
Flowering-time tracking of seasonal temperature	175	−0.92	***	166	−1.00	***	140	−1.33	***
Shift in flowering-time 1850–1900	319	−0.01	*	311	−0.01	*	140	0.01	—
Shift in flowering time 1900–2006	303	0.04	***	296	0.02	***	140	0.03	***
Shift in flowering time 1850–2006	271	0.03	***	253	0.02	***	140	—	—
Mean latitudinal range	414	−0.05	**	362	−0.05	***	140	−0.09	**
Change in abundance 1900–2006	—	—	—	—	—	—	—	—	—

The significance of phylogenetic conservatism was tested by comparing the rank of the observed standard deviation (SD) of descendent trait means with a null model based on 9,999 random iterations of trait distributions across the composite phylogeny. The observed rank is compared with a 2-tail test of significance, i.e., an observed (obs.) rank of 250 equals a P value of 0.05. Trait correlations were tested by using a general estimator equation (GEE). Estimates describe the direction and magnitude of the correlation (e.g., a negative estimate [−0.1] of mean latitude with change in abundance suggests that species from more southerly latitudes are increasing in abundance). Model 1 (univariate model), correlation of change in abundance with each trait; Model 2 (multivariate model), correlation of change in abundance with each trait and habitat, abundance (*ca*. 1900), flowering season, and native/introduced status as covariates; Model 3 (multivariate model), correlation of change in abundance with all traits and habitat, abundance (*ca*. 1900), flowering season, and native/introduced status as covariates (shift in flowering-time response 1850–2006 was excluded due to its high correlation with the other flowering-time shift traits). †, $P = 0.1$; *, $P = 0.05$; **, $P = 0.01$; ***, $P = 0.001$; n = sample size.

Table S2. Sensitivity analyses of phylogenetic uncertainty

	Trait correlation								
	Model 1			Model 2			Model 3		
Trait	*n*	Estimate		*n*	Estimate		*n*	Estimate	
Flowering-time tracking of seasonal temperature	175	−0.03	—	166	−1.24	***	137	−1.58	***
Shift in flowering time 1850–1900	319	0.02	***	311	0.01	*	137	0.01	—
Shift in flowering time 1900–2006	303	0.03	***	296	0.01	***	137	0.01	***
Shift in flowering time 1850–2006	271	0.03	***	253	0.01	***	137	—	—
Mean latitudinal range	414	−0.01	*	362	−0.03	*	137	−0.03	—
Change in abundance 1900–2006	—	—	—	—	—	—	—	—	—

Phylogenetic conservatism and trait correlations tested over 50 trees with randomly resolved polytomies. Median statistic of these analyses are reported in the table. The significance of phylogenetic conservatism was tested by comparing the rank of the observed SD of descendent trait means with a null model based on 9,999 random iterations of trait distributions across the composite phylogeny. The observed rank is compared with a 2-tail test of significance, i.e., an observed rank of 250 equals a *P* value of 0.05. Trait correlations were tested by using a GEE. Estimates describe the direction and magnitude of the correlation (e.g., a negative estimate [−0.1] of mean latitude with change in abundance suggests that species from more southerly latitudes are increasing in abundance). Model 1 (univariate model), correlation of change in abundance with each trait; Model 2 (multivariate model), correlation of change in abundance with each trait and habitat, abundance (*ca*. 1900), flowering season, and native/introduced status as covariates; Model 3 (multivariate model), correlation of change in abundance with all traits and habitat, abundance (*ca*. 1900), flowering season, and native/introduced status as covariates (shift in flowering-time response 1850–2006 was excluded due to its high correlation with the other flowering-time shift traits). †, $P = 0.1$; *, $P = 0.05$; **, $P = 0.01$; ***, $P = 0.001$; n = sample size.