

Figure S1. Histograms of species richness, species cover, size of glades in which study plots were located, and landscape glade cover in 1km surrounding study plots. Richness was calculated as the total number of herbaceous plants that occur within the each 1000 m<sup>2</sup> study plot. Plant cover was calculated as the average herbaceous plant cover in 20 - 0.25 m<sup>2</sup> quadrats within each study plot.

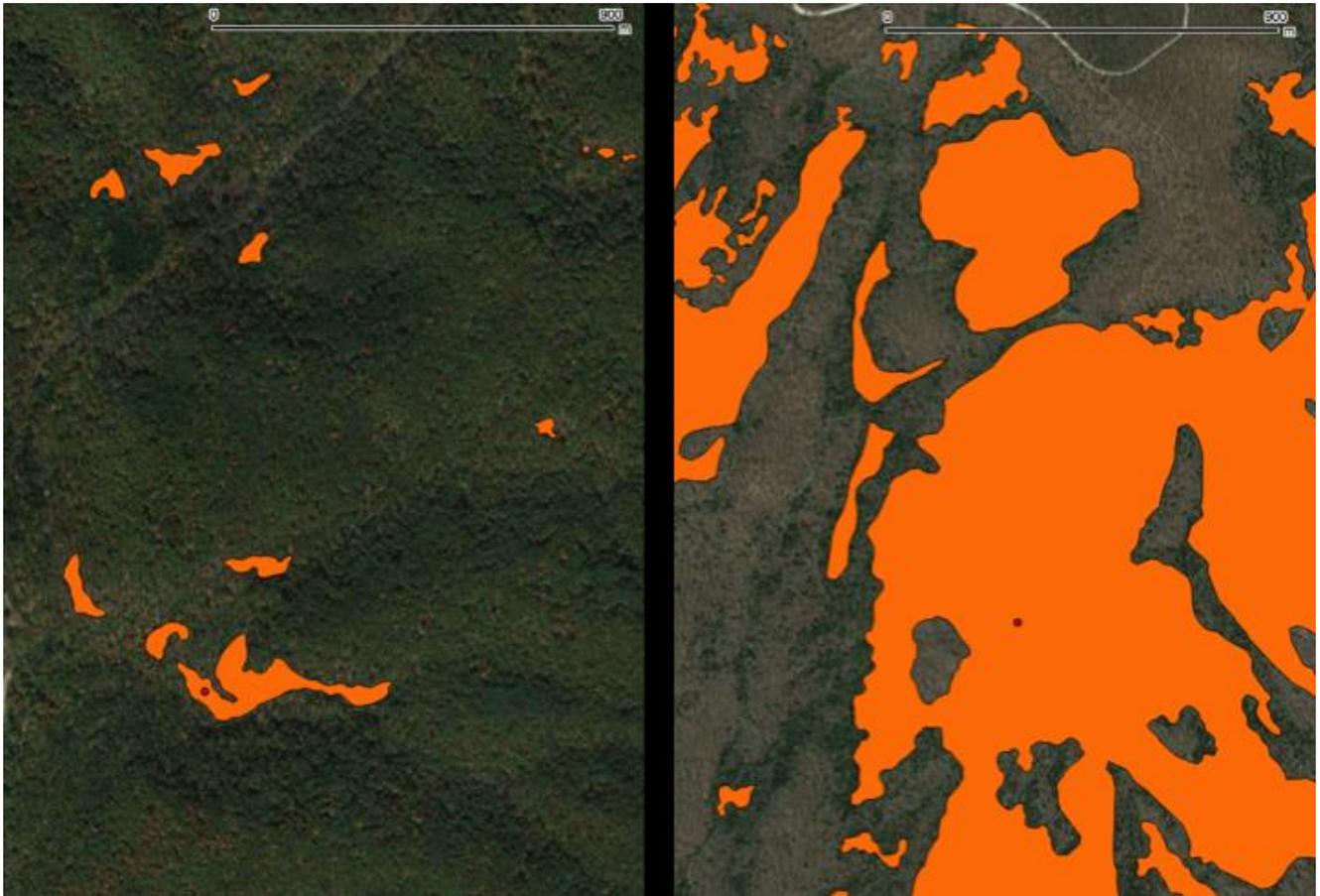


Figure S2. Aerial glade size comparison: small, isolated glades in St. Francois State Park (left), and a large, relatively well connected glade complex in Mark Twain National Forest (right). Glades are shown as orange polygons. The matrix surrounding glades is composed primarily of oak woodland, but is lighter in the right photo because it was taken in the winter. Red dots are locations of study plots.

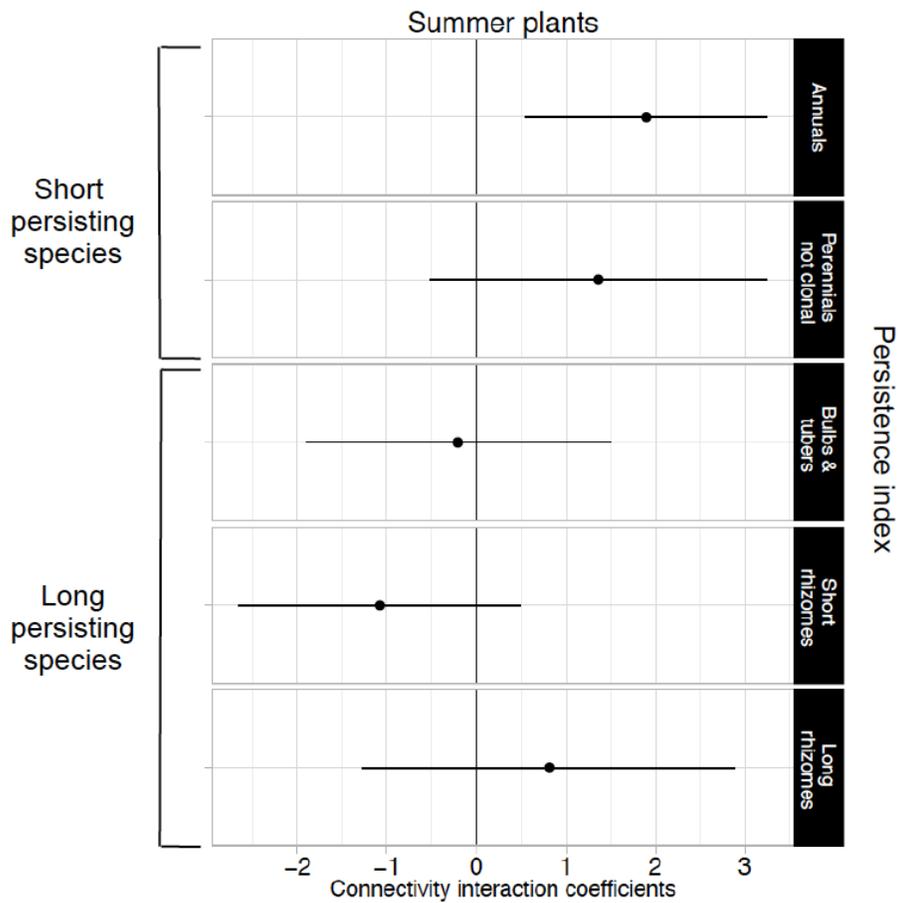


Fig. S3. Coefficients for interactions between landscape connectivity and the five-level persistence index. In the binary persistence index used in the full model (Fig. 5 and Fig. 6), species in the upper two categories (annuals and non-clonal perennials) are considered short persisting species, while the bottom three categories (bulbs & tubers, short rhizomes, and long rhizomes) are considered long persisting species. Bars give the standard errors of the coefficients. Note that the text reports the statistical differences between interaction coefficients for annual plants versus other groups, while the standard errors here are computed for each of the five groups separately.

Table S1. Correlation matrix showing Spearman rank correlation coefficients (lower left) and p-values (upper right) for functional traits. Significant ( $P < 0.05$ ) correlation coefficients are indicated with an asterisk (\*). Wind dispersal mode is represented as a binary variable.

	Flowering start	SLA	Seed mass	Persistence	Height	Wind dispersal mode
Flowering start	-	0.000	0.681	0.626	0.000	0.017
SLA	-0.446 *	-	0.930	0.005	0.000	0.201
Seed mass	-0.039	-0.008	-	0.897	0.493	0.000
Persistence	0.046	-0.262 *	-0.012	-	0.086	0.506
Height	0.596 *	-0.451 *	0.065	0.162	-	0.200
Wind dispersal mode	0.223 *	-0.121	-0.467 *	0.063	0.121	-

Table S2. Generalized linear mixed model (Eq. 1) for spring-blooming plant species.  $\alpha$  represents the mean intercept among species, and  $\sigma_a^2$  represents the variance among species in intercepts.  $\beta_{\text{Soil}}$  and  $\beta_{\text{Connectivity}}$  represent average species responses to soil resource availability and habitat spatial heterogeneity, and  $\sigma_{\text{Soil}}^2$  and  $\sigma_{\text{Connectivity}}^2$  represent the corresponding variances of species responses.  $\sigma_{\text{Site}}^2$  gives the site-to-site variance in presence/absence of species that is not explained by environmental variables. A total of 42 plant species distributed among 51 sites was analyzed. The model was fit using the function `glmer` (Bates et al. 2015) in the R computing language (R Core Team 2014).

Variable	Estimate	Standard Error	P-value
SLA	0.09	0.52	0.867
Persistence	-0.04	0.51	0.930
Seed mass	-0.49	0.46	0.292
Height	-1.07	0.61	0.079
Soil : SLA	0.27	0.35	0.441
Soil : persistence	0.33	0.34	0.339
Soil : Seed mass	0.62	0.31	0.045
Soil : Height	0.66	0.43	0.125
Connectivity : SLA	-0.04	0.37	0.925
Connectivity : persistence	-0.39	0.36	0.283
Connectivity : Seed mass	-0.10	0.33	0.753
Connectivity : Height	-0.50	0.45	0.265

$\alpha$	-1.60	0.44	<0.001
$\sigma^2_a$	3.46		
$\beta_{\text{Soil}}$	0.82	0.31	0.008
$\sigma^2_{\text{Soil}}$	0.90		
$\beta_{\text{Connectivity}}$	0.44	0.33	0.172
$\sigma^2_{\text{Connectivity}}$	1.02		
$\sigma^2_{\text{Site}}$	0.07		

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Table S3. Generalized linear mixed model (Eq. 1) for summer-blooming plant species.  $\alpha$  represents the mean intercept among species, and  $\sigma^2_a$  represents the variance among species in intercepts.  $\beta_{\text{Soil}}$  and  $\beta_{\text{Connectivity}}$  represent average species responses to soil resource availability and spatial heterogeneity, and  $\sigma^2_{\text{Soil}}$  and  $\sigma^2_{\text{Connectivity}}$  represent the corresponding variances of species responses.  $\sigma^2_{\text{Site}}$  gives the site-to-site variance in presence/absence of species that is not explained by environmental variables. A total of 71 plant species distributed among 51 sites was analyzed. The model was fit using the function `glmer` (Bates et al. 2015) in the R computing language (R Core Team 2014).

Variable	Estimate	Standard Error	P-value
SLA	-0.23	0.75	0.755
Persistence	0.40	0.72	0.581
Seed mass	-0.21	0.65	0.742
Height	-0.90	0.70	0.203
Soil : SLA	1.27	0.40	0.002
Soil : persistence	0.53	0.39	0.181
Soil : Seed mass	0.55	0.34	0.109
Soil : Height	1.14	0.40	0.005
Connectivity : SLA	-0.31	0.71	0.661
Connectivity : persistence	-2.25	0.68	0.001
Connectivity : Seed mass	1.25	0.62	0.044
Connectivity : Height	-0.13	0.68	0.846
$\alpha$	-1.32	0.57	0.021

$\sigma^2_a$	3.37		
$\beta_{\text{Soil}}$	0.77	0.35	0.029
$\sigma^2_{\text{Soil}}$	0.34		
$\beta_{\text{Connectivity}}$	1.79	0.57	0.002
$\sigma^2_{\text{Connectivity}}$	2.39		
$\sigma^2_{\text{Site}}$	0.29		

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Table S4. Table B3. Phylogenetic generalized linear mixed model (Eq. 1 and 2) for spring-blooming plant species.  $\alpha$  represents the mean intercept among species, and  $\sigma^2_a$  and  $\sigma^2_{a.phy}$  represents the non-phylogenetic and phylogenetic components of the variance among species in intercepts.  $\beta_{Soil}$  represents average species responses to soil resource availability, and  $\sigma^2_{Soil}$  and  $\sigma^2_{Soil.phy}$  represent the corresponding non-phylogenetic and phylogenetic variances of species responses;  $\beta_{Connectivity}$ ,  $\sigma^2_{Connectivity}$ , and  $\sigma^2_{Connectivity.phy}$  are defined similarly.  $\sigma^2_{Site}$  gives the site-to-site variance in presence/absence of species that is not explained by environmental variables. A total of 41 plant species distributed among 51 sites was analyzed. The model was fit using the function communityPGLMM (Pearse et al. 2015) in the R computing language (R Core Team 2014).

Variable	Estimate	Standard Error	P-value
SLA	0.08	0.44	0.858
Persistence	0.12	0.44	0.782
Seed mass	-0.31	0.40	0.437
Height	-0.88	0.53	0.094
Soil : SLA	0.22	0.33	0.508
Soil : persistence	0.22	0.33	0.508
Soil : Seed mass	0.58	0.30	0.055
Soil : Height	0.48	0.41	0.244
Connectivity : SLA	-0.03	0.35	0.933
Connectivity : persistence	-0.33	0.35	0.343
Connectivity : Seed mass	-0.16	0.31	0.621
Connectivity : Height	-0.31	0.43	0.464

$\alpha$	-1.88	0.58	0.001
$\sigma^2_a$	1.12		
$\sigma^2_{a,phy}$	0.25		
$\beta_{Soil}$	0.92	0.44	0.036
$\sigma^2_{Soil}$	0.14		
$\sigma^2_{Soil,phy}$	0.03		
$\beta_{Connectivity}$	0.08	0.44	0.858
$\sigma^2_{Connectivity}$	0.21		
$\sigma^2_{Connectivity,phy}$	0.01		
$\sigma^2_{Site}$	0.07		

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Table S5. Phylogenetic generalized linear mixed model (Eq. 1 and 2) for summer-blooming plant species.  $\alpha$  represents the mean intercept among species, and  $\sigma^2_a$  and  $\sigma^2_{a,phy}$  represents the non-phylogenetic and phylogenetic components of the variance among species in intercepts.  $\beta_{Soil}$  represents average species responses to soil resource availability, and  $\sigma^2_{Soil}$  and  $\sigma^2_{Soil,phy}$  represent the corresponding non-phylogenetic and phylogenetic variances of species responses;  $\beta_{Connectivity}$ ,  $\sigma^2_{Connectivity}$ , and  $\sigma^2_{Connectivity,phy}$  are defined similarly.  $\sigma^2_{Site}$  gives the site-to-site variance in presence/absence of species that is not explained by environmental variables. A total of 70 plant species distributed among 51 sites was analyzed. The model was fit using the function communityPGLMM (Pearse et al. 2015) in the R computing language (R Core Team 2014).

Variable	Estimate	Standard Error	P-value
SLA	0.41	0.77	0.591
Persistence	0.49	0.67	0.466
Seed mass	-0.36	0.61	0.552
Height	-1.06	0.68	0.120
Soil : SLA	0.79	0.45	0.077
Soil : Persistence	0.53	0.39	0.174
Soil : Seed mass	0.54	0.36	0.136
Soil : Height	1.25	0.42	0.003
Connectivity : SLA	-0.27	0.71	0.702
Connectivity : Persistence	-2.04	0.67	0.003
Connectivity : Seed mass	1.14	0.62	0.064
Connectivity : Height	-0.05	0.67	0.935

$\alpha$	-1.30	0.83	0.117
$\sigma^2_a$	2.43		
$\sigma^2_{a,phy}$	0.20		
$\beta_{Soil}$	0.62	0.67	0.349
$\sigma^2_{Soil}$	0		
$\sigma^2_{Soil,phy}$	0.04		
$\beta_{Connectivity}$	1.68	0.56	0.003
$\sigma^2_{Connectivity}$	0.57		
$\sigma^2_{Connectivity,phy}$	0		
$\sigma^2_{Site}$	0.26		

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Table S6. Generalized linear mixed model for summer plant species with persistence as a 5-level factor. Persistence.1 represents annual and biennial species, Persistence.2 represents perennial species without rhizomes or storage structures (e.g., tubers and corms), Persistence.3 represents species with short rhizomes, Persistence.4 represents species with long rhizomes, and Persistence.4 represents species with long rhizomes. Persistence categorizations are based on Yatskievych (1999, 2006, 2013).  $\alpha$  represents the mean intercept among species, and  $\sigma^2_a$  represents the variance among species in intercepts.  $\beta_{\text{Soil}}$  and  $\beta_{\text{Connectivity}}$  represent average species responses to soil resource availability and spatial heterogeneity, and  $\sigma^2_{\text{Soil}}$  and  $\sigma^2_{\text{Connectivity}}$  represent the corresponding variances of species responses.  $\sigma^2_{\text{Site}}$  gives the site-to-site variance in presence/absence of species that is not explained by environmental variables. The model was fit using the function glmer (Bates et al. 2015) in the R computing language (R Core Team 2014).

Variable	Estimat	Standard Error	P-value
SLA	0.264	0.793	0.740
Persistence.2	-0.942	1.288	0.465
Persistence.3	0.012	1.203	0.992
Persistence.4	-0.174	1.191	0.884
Persistence.5	0.075	1.423	0.958
Seed mass	-0.689	0.775	0.374
Height	-0.129	0.797	0.872
Soil : SLA	1.086	0.412	0.008
Soil : Persistence.2	-0.128	0.708	0.856
Soil : Persistence.3	0.435	0.636	0.495

Soil : Persistence.4	0.501	0.632	0.428
Soil : Persistence.5	0.351	0.762	0.646
Soil:Seed mass	0.616	0.406	0.130
Soil:Height	1.058	0.441	0.016
Connectivity:SLA	-0.307	0.640	0.632
Connectivity : Persistence.2	-0.393	1.087	0.718
Connectivity : Persistence.3	-2.445	0.988	0.013
Connectivity : Persistence.4	-2.749	0.992	0.006
Connectivity : Persistence.5	-1.025	1.170	0.381
Connectivity : Seed mass	0.848	0.635	0.182
Connectivity : Height	0.108	0.663	0.871
$\alpha_{\text{intercept}}$	-0.802	0.860	0.351
$\sigma^2_{\text{intercept}}$	3.75		
$\beta_{\text{Soil}}$	0.772	0.455	0.090
$\sigma^2_{\text{Soil}}$	0.37		
$\beta_{\text{Connectivity}}$	2.102	0.717	0.003
$\sigma^2_{\text{Connectivity}}$	1.78		

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Table S7. Generalized linear mixed model for summer-blooming species for which terminal velocity was measured.  $\alpha$  represents the mean intercept among species, and  $\sigma^2_a$  represents the variance among species in intercepts.  $\beta_{\text{Soil}}$  and  $\beta_{\text{Connectivity}}$  represent average species responses to soil resource availability and spatial heterogeneity, and  $\sigma^2_{\text{Soil}}$  and  $\sigma^2_{\text{Connectivity}}$  represent the corresponding variances of species responses.  $\sigma^2_{\text{Site}}$  gives the site-to-site variance in presence/absence of species that is not explained by environmental variables. The model was fit using the function `glmer` (Bates et al. 2015) in the R computing language (R Core Team 2014).

Variable	Estimate	Standard Error	P-value
TV	-1.464	0.709	0.039
Soil : TV	0.541	0.396	0.172
Connectivity : TV	-2.122	0.575	< 0.001
$\alpha$	-0.766	0.354	0.031
$\sigma^2_{\text{intercept}}$	3.660		< 0.001
$\beta_{\text{Soil}}$	1.041	0.194	< 0.001
$\sigma^2_{\text{Soil}}$	0.453		0.057
$\beta_{\text{Connectivity}}$	0.274	0.280	0.327
$\sigma^2_{\text{Connectivity}}$	1.578		< 0.001

## Appendix S1. Phylogenetic models

Phylogenetic non-independence among species in either overall mean presence/absence ( $a_{\text{spp}[i]}$ ) or slope in response to the environmental variable ( $c_{\text{spp}[i]}$ ) can lead to type I errors (false positives; Li and Ives in press, Revell 2010). Therefore, we performed a parallel analysis incorporating phylogenetic information into the covariance matrices

$$\begin{aligned} a &\sim \text{Gaussian}(\mathbf{0}, \sigma_a^2 \mathbf{I}_n + \sigma_{a,\text{phy}}^2 \mathbf{C}_n) \\ c &\sim \text{Gaussian}(\mathbf{0}, \sigma_c^2 \mathbf{I}_n + \sigma_{c,\text{phy}}^2 \mathbf{C}_n) \end{aligned} \quad (2)$$

Here,  $\mathbf{C}_n$  is the phylogenetic covariance matrix generated under the assumption of Brownian motion evolution (Martins & Hansen 1997; Ives & Helmus 2011). Thus,  $\sigma_a^2$  and  $\sigma_{a,\text{phy}}^2$  represent the non-phylogenetic and phylogenetic components of the variance in the mean abundances of species among sites. We obtained the phylogeny for species from Phylomatic (Webb & Donoghue 2005; Smith *et al.* 2011). We fit the phylogenetic models using the R code communityPGLMM in the pez library (Li & Ives, in review; Pearse *et al.* 2015).

### Literature cited

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