Biomass detection model

We assume that species are present in all plots in which they were planted, even when no biomass was observed, and that zero observations of biomass arise from lack of detection (as clipstrips only cover 3.75% area in the plot) rather than extinction. This is a reasonable assumption, because only three of the species were entirely absent, as biomass, percent cover or inflorescences, in any plots (and then, in only 3% of those plots). Plots in which no biomass is detected (i.e. zero biomass) presumably arise when biomass production in that plot is very low. We allow observations of zero biomass to contribute to the estimation of the latent variable biomass ($\hat{b}_{ijkl}$) by modeling biomass detection (o_{bijkl}, a vector of ones and zeros describing whether or not biomass was detected, i.e. greater than zero, in clipstrips) as a Bernoulli sample from the unobserved probability of biomass detection in that plot ($\hat{o}_{bijk}$) :

$$o_{bijkl} \sim \text{Bern}(\hat{o}_{bijkl}) \quad \text{(A1)}$$

We assume that biomass detection is linked to biomass production ($\hat{b}_{ijkl}$) through two parameters (f_{bi}, g_{bi}):

$$\text{logit}(\hat{o}_{bijkl}) = f_{bi} + g_{bi} \log(\hat{b}_{ijkl} - \overline{b_i}) \quad \text{(A2)}$$

We subtracted the average biomass observed for each species ($\overline{b_i}$) from the plot, ring and sample specific estimate of biomass production to reduce the natural tendency for slope and intercept parameters to be correlated; this technique is called covariate centering.

Percent cover detection model

As with biomass, we assumed that zero observations of percent cover arise from a lack of detection. Thus, percent cover detection (o_{pijkl}, a vector of ones and zeros describing whether or not percent cover was detected, i.e. greater than zero, in quadrats) is a Bernoulli sample from a plot-specific probability of observing percent cover values greater than zero ($\hat{o}_{pijkl}$) :

$$o_{pijkl} \sim \text{Bern}(\hat{o}_{pijkl}) \quad \text{(B1)}$$

Our percent cover detection process model links the probability of sampling percent cover that is greater than zero ($\hat{o}_{pijkl}$) to the expected (unobserved) percent cover in that plot and two parameters (f_{pi} , g_{pi}):

$$\text{logit}(\hat{o}_{pijkl}) = f_{pi} + g_{pi} \log(\hat{p}_{ijkl} - \overline{p}_i) \quad \text{(B2)}$$

In other words, the probability of observing a particular species is greater when there is more percent cover in the plot. We subtracted the average percent cover observed for each species ($\overline{p_i}$) from the plot, ring and sample specific estimate of biomass production to reduce the natural tendency for slope and intercept parameters to be correlated; this technique is called covariate centering.

Bayesian model fitting

Our Bayesian statistical models are characterized by hierarchical levels of variability (Fig A1, Fig A2), consisting of (1) data models (describing sampling distributions of biomass, percent cover, inflorescences, and seed weight), (2) process models (describing how global change affects biomass, inflorescence production and seed number; and how percent cover and biomass are related) and (3) parameter models (describing parameter and prior distributions). In the text, we describe data models (equations 1, 8 and 12).and process models (equations 2, 7, 9 and 13).

We briefly describe our 'parameter' models; that is, the priors. We used diffuse priors for all parameters in both models. Specifically, coefficients describing average global change effects over all species ($A_b, A_f, X_b, N_b, N_f, \Delta_{b9}, \Delta_{f9}, \Delta_{b4}, \Delta_{f4}, \Delta_{b1}, \Delta_{f1}, A_w, X_w, N_w, \Delta_{9w}, \Delta_{4w}, \Delta_{1w}$) were given diffuse normal priors – (mean 0, standard deviation 9). Parameters describing average intercept and slope parameters for all species in biomass detection (appendix A), percent cover detection (appendix B), and the relationship between biomass and percent cover relationship (equation 7) were also given diffuse normal priors with mean 0 and standard deviation 9. Parameters describing between-species variability in global change effects, variability in intercept and slope parameters for biomass detection, percent cover detection and biomass to percent cover translation were given diffuse inverse gamma priors (shape 0.1, scale 0.1). Parameter describing ring to ring variability in inflorescence production and inflorescence weight (eqns 3, 4 14, 15 - σ_{bri}, σ_{fri}, σ_{wri}) were also given diffuse inverse gamma priors (shape 0.1, scale 0.1), and not modeled hierarchically.

Because parameters for both biomass and inflorescence production are estimated on a log-scale, a normal distribution with mean 0 and standard deviation 9 represents an extremely wide range of possible parameter values. Priors are not as diffuse as those sometimes used in hierachical Bayesian statistics, but they generously encompass the largest possible range of values for these parameters (roughly based on extreme data values). We assured (with additional model fitting) that they were diffuse enough to have no effect on the means and credible intervals of the posterior densities of interest. Extremely diffuse priors run the risk of generating improper posteriors, which we wished to avoid.

Figure C1. Bayesian Hierarchical model structure for analyses determining effects of elevated CO_2, nitrogen deposition and declining diversity on biomass production and allocation to inflorescence production. Grey boxes indicate different hierarchical levels of the model, white squares indicate observed data, and white circles bordered with dashed lines indicate model elements estimated by Gibbs sampling. Oval white boxes represent the process models we specify in our model. Arrows indicate how parameters, process and data are related.

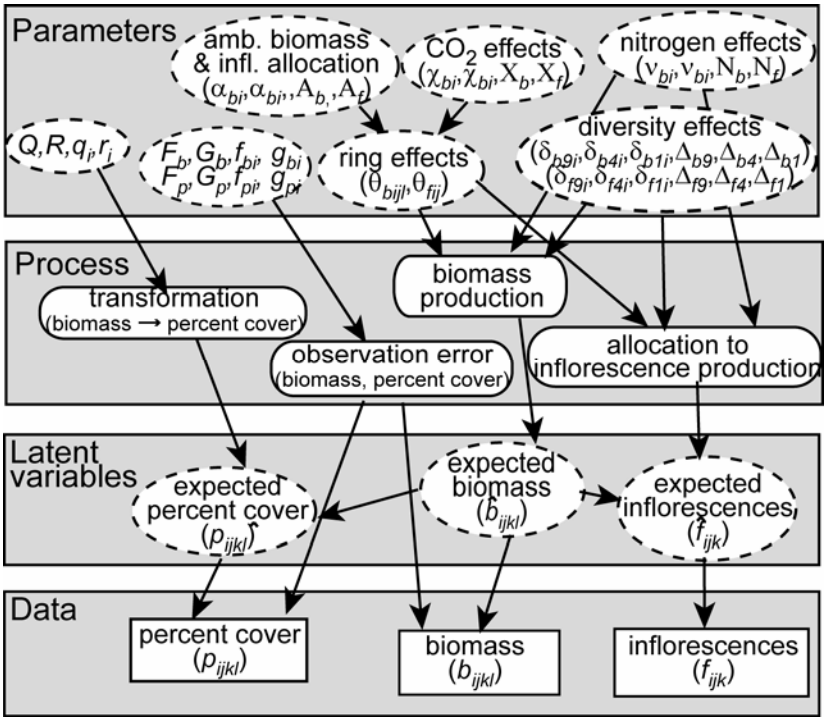
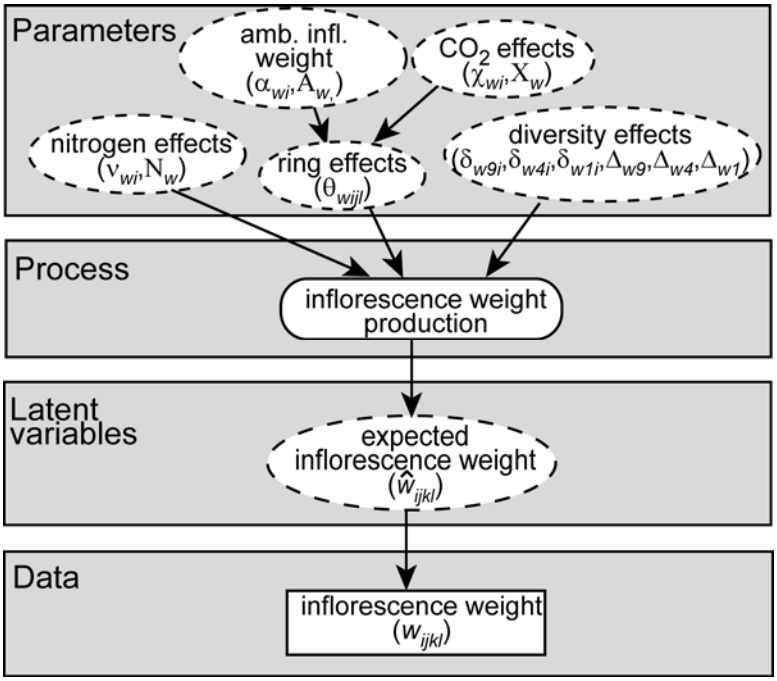


Figure C2. Bayesian Hierarchical model structure for analysis determining effects of elevated CO_2, nitrogen deposition and declining diversity on inflorescence weight. Grey boxes indicate different hierarchical levels of the model, white squares indicate observed data, and white circles bordered with dashed lines indicate model elements estimated by Gibbs sampling. Oval white boxes represent the process models we specify in our model. Arrows indicate how parameters, process and data are related.



Model fit

Our statistical model structure and parameter estimates (Table D1-D4) did a good job describing the observed data for most species and response variables (Figure D1-D4). The r^2 between predicted and observed response variables ranged from 0.10 to 0.55 for biomass data, from 0.47 to 0.72 for percent cover data, from 0.31 to 0.94 for inflorescence counts, and from 0.06 to 0.30 for inflorescence weights. Slope parameters describing the relationship between biomass and biomass detection, and percent cover and percent cover detection were always significantly positive, as expected (Table D2). The slope parameters describing the (inverse) relationship between biomass and percent cover were always negative (indicating a positive relationship between biomass and percent cover). Some parameter correlations existed, especially between slope (g_{bi}, g_{pi}, r_i) and intercept parameters (f_{bi}, f_{pi}, q_i). As we do not independently interpret the values of these parameters, these parameter correlations do not affect our conclusions about global change coefficients.

Table D1. Posterior means of parameters related to the biomass process model

Species	α_{bil}	χ_{bi}	δ_{b1i}	δ_{b4i}	δ_{b9i}	v_{bi}	ϕ_i	f_{bi}	g_{bi}	σ_{bi}
Agropyron repens	0.807	-0.044	1.181	0.188	0.741	0.958	-0.15	1.353	1.14	9.827
Andropogon gerardii	2.424	0.121	-0.335	0.014	0.127	0.062	0.897	0.828	0.9	12.81
Bouteloua gracilis	0.188	-0.318	2.251	1.844	0.804	-0.405	0.301	0.786	0.844	12.83
Bromus inermis	2.361	-0.047	-0.762	-0.382	-0.261	0.908	0.29	1.562	1.194	12.86
Koeleria cristata	0.97	0.143	1.066	0.493	0.542	0.592	0.321	2.093	0.895	21.73
Lespedeza capitata	3.232	0.297	-0.35	-0.198	0.182	-1.24	0.802	-0.279	0.761	9.681
Lupinus perennis	5.189	-0.027	-1.792	-1.134	-0.384	-0.219	-0.963	0.164	0.927	24.87
Poa pratensis	2.701	0.073	-1.551	-1.4	-0.693	0.941	0.785	1.464	1.104	22.59
Schizachyrium scoparium	0.85	0.103	1.158	0.3	0.257	-0.595	0.85	-0.886	0.944	15.05
Solidago rigida	0.933	0.336	1.63	1.842	1.007	0.048	0.163	-2.281	0.904	13.83
Sorghastum nutans	1.029	0.138	0.996	0.792	0.177	-0.587	0.909	-0.79	1.152	7.639
Means over all species	1.974	0.067	0.179	0.142	0.186	0.057	NA	0.484	0.995	NA
Between-species variances	1.879	0.062	1.025	1.025	1.025	0.44	NA	1.759	0.061	NA

Table D2. Posterior means of parameters related to the inflorescence allocation process model

Species	α_{fi}	χ_{fi}	δ_{f1i}	δ_{f4i}	δ_{f9i}	v_{fi}	σ_{fi}
Agropyron repens	-1.973	-0.3405	0.24	0.6823	0.277	-0.6423	10.24
Andropogon gerardii	-2.251	-0.3661	-0.4749	-0.0464	-0.1172	0.988	4.539
Bouteloua gracilis	-1.092	-0.379	0.776	1.558	0.3479	1.271	2.264
Bromus inermis	-1.588	-0.503	-0.5316	0.3122	0.1325	-0.4881	8.392
Koeleria cristata	-1.472	-0.3324	1.271	0.6015	-0.171	-0.518	18.15
Lespedeza capitata	-1.844	-0.3341	-1.06	-0.0178	-0.0522	0.536	15.64
Lupinus perennis	-0.8018	-0.227	-0.3037	0.0533	-0.0033	-0.0619	21.4
Poa pratensis	-2.049	-0.4574	1.705	0.6159	1.089	-0.7451	5.302
Schizachyrium scoparium	-0.1799	-0.2225	-0.3883	0.4049	-0.2257	0.6863	16.29
Solidago rigida	-2.274	-0.3437	0.2177	0.4099	0.5704	0.8524	12.71
Sorghastrum nutans	-1.257	-0.4046	-0.1753	-0.1568	-0.1741	0.7847	9.496
Means over all species	-1.585	-0.3588	0.1503	0.4184	0.1679	0.1893	NA
Between-species variances	0.438	0.0443	0.3708	0.3708	0.3708	0.4885	NA

Table D3. Posterior means of parameters related to the percent cover process model

Species	f_{pi}	g_{pi}	q_i	r_i	σ_{pi}
Agropyron repens	7.822	2.959	-3.78	-0.2505	2.155
Bromus inermis	7.392	3.396	-3.269	-0.2331	4.928
Koeleria cristata	6.809	3.663	-3.066	-0.2426	2.029
Poa pratensis	8.134	2.277	-3.62	-0.2371	4.471
Andropogon gerardii	7.561	3.086	-3.685	-0.2491	2.403
Bouteloua gracilis	7.04	3.448	-3.211	-0.2177	4.527
Schizachyrium scoparium	7.41	2.699	-4.663	-0.2963	4.805
Sorghastrum nutans	7.931	2.352	-3.7	-0.2605	3.929
Lespedeza capitata	7.044	4.198	-3.167	-0.2281	3.593
Lupinus perennis	6.721	4.12	-3.086	-0.2082	3.904
Solidago rigida	7.332	3.575	-3.367	-0.2365	2.739
Means over all species	7.359	3.206	-3.534	-0.2455	NA
Between-species variances	0.1438	0.2743	0.1952	0.0161	NA

Table D4. Posterior means of parameters related to the inflorescence weight process model.

Species	α_{wi}	χ_{wi}	δ_{w1i}	δ_{w4i}	δ_{w9i}	v_{wi}	σ_{wi}
Agropyron repens	-2.737	0.0847	0.059	-0.0971	-0.0218	0.0716	3.417
Bromus inermis	-2.157	-0.0699	-0.0575	-0.0248	-0.0209	0.1089	6.958
Koeleria cristata	-3.847	-0.1332	0.3614	0.2944	-0.0336	0.000818	8.057
Poa pratensis	-2.042	-0.1306	-0.1179	-0.1837	-0.0253	0.09598	1.635
Andropogon gerardii	-2.823	0.0864	0.135	-0.1288	-0.0096	0.09551	6.308
Bouteloua gracilis	-1.823	0.0319	0.3255	-0.0361	-0.1505	0.04792	0.6371
Schizachyrium scoparium	-0.8597	0.1344	-0.0687	0.1477	0.047	-0.03725	2.1
Sorghastrum nutans	-3.065	0.0969	-0.106	0.0434	-0.0228	0.08152	5.877
Lespedeza capitata	-2.645	-0.136	-0.1142	-0.0676	-0.1545	0.1286	2.441
Lupinus perennis	0.5105	-0.0268	-0.3236	-0.27	-0.017	0.1188	2.479
Solidago rigida	-1.354	0.0298	0.153	0.1471	0.1605	-0.05007	2.822
Across-species means	-2.04	-0.0031	0.0203	-0.0168	-0.0214	0.05965	NA
Across-species variances		0.0456	0.0447	0.0447	0.0447	0.025994	NA

Figure D1. The relationship between predicted biomass vs. observations of aboveground biomass for the eleven species. Predictions are based on the mean of 1000 MCMC samples of the model after convergence was achieved and chains were thinned to remove autocorrelation. Scatterplots are on a log scale, with the 1:1 line drawn and the r^2 of the predicted vs. observed indicated on graph.

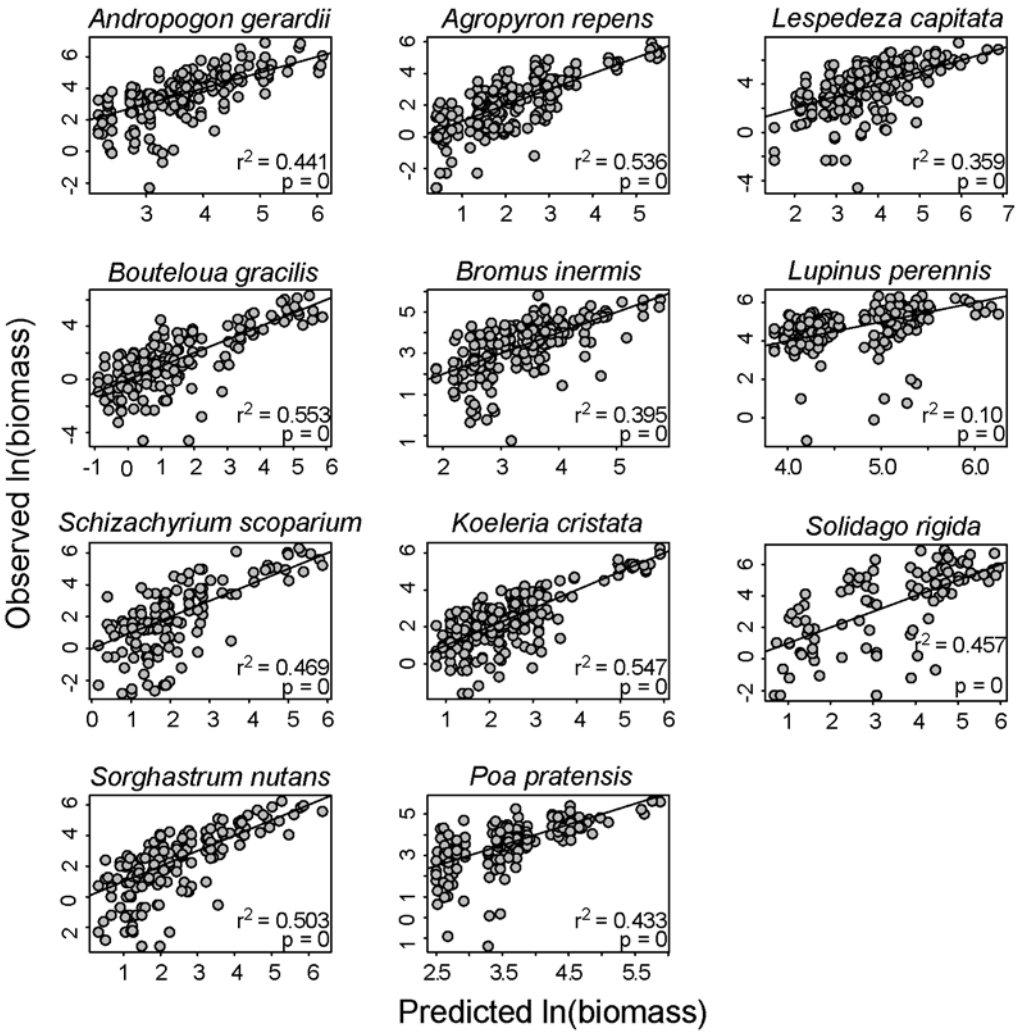


Figure D2. The relationship between predicted precent cover vs. observations of percent cover for the eleven species. Predictions are based on the mean of 1000 MCMC samples of the model after convergence was achieved and chains were thinned to remove autocorrelation. Scatterplots are on a log scale, with the 1:1 line drawn and the r^2 of the predicted vs. observed indicated on graph.

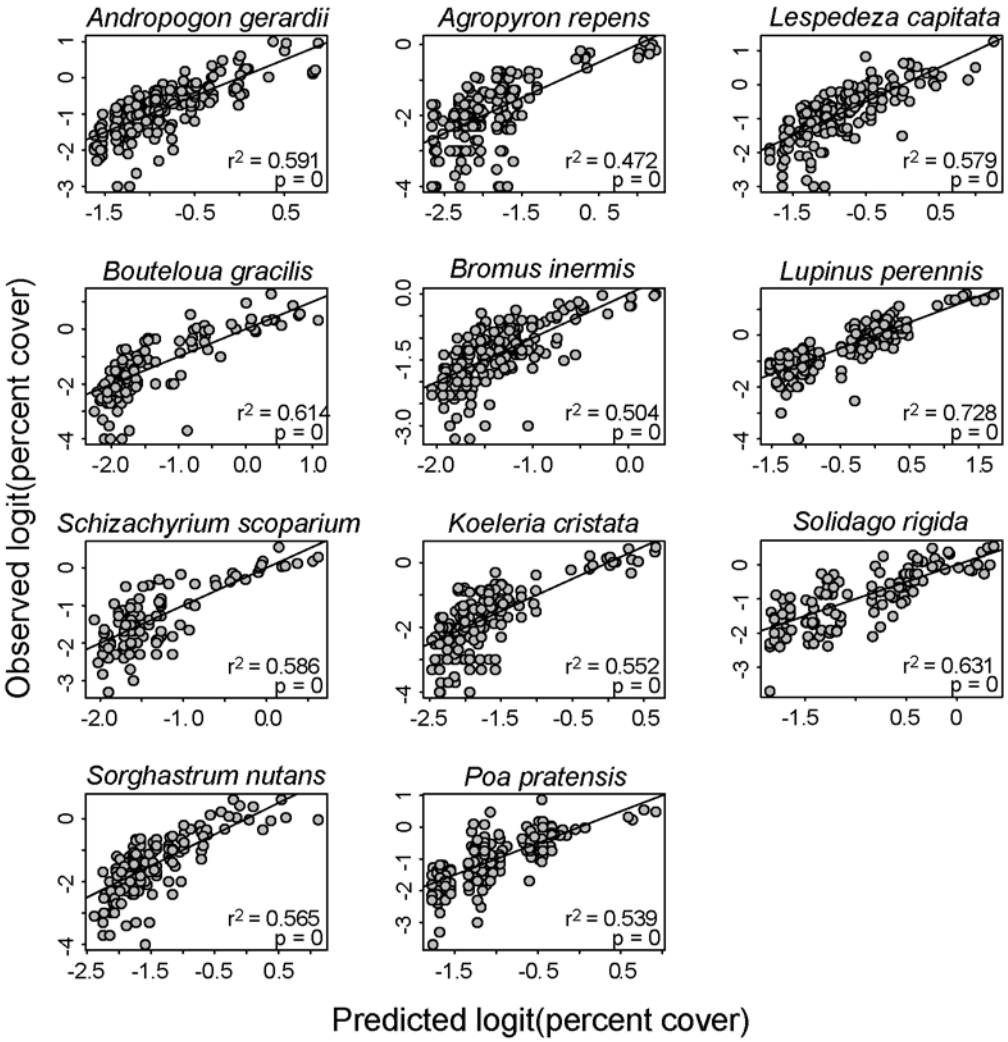


Figure D3. The relationship between predicted number of inflorescences per m^2 vs. observations observations of number of inflorescences for each of eleven species. Predictions are based on the mean of 1000 MCMC samples of the model after convergence was achieved and chains were thinned to remove autocorrelation. The 1:1 line and the r^2 of the relationship between predicted and observed are both indicated on graph.

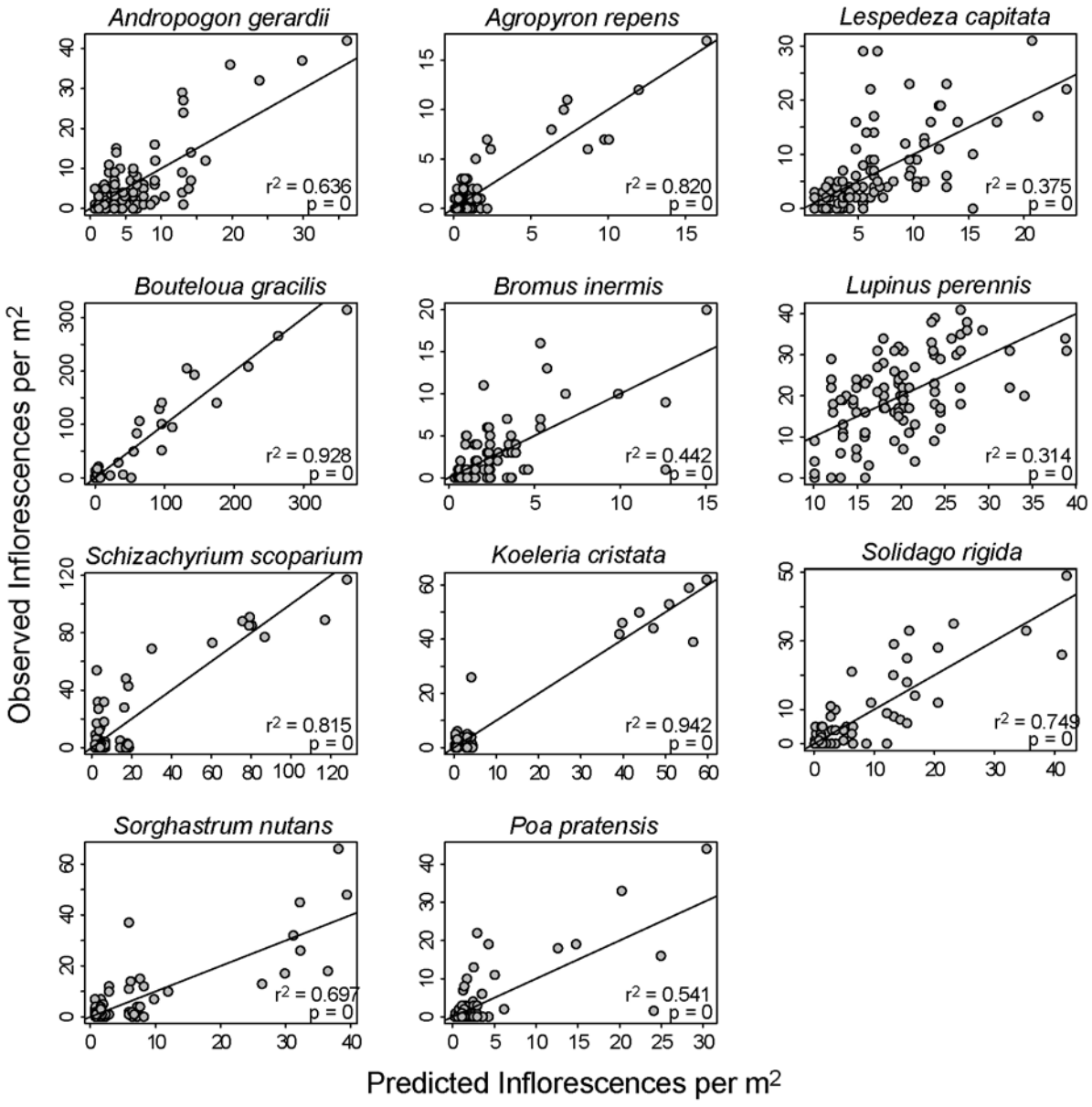


Figure D4. The relationship between predictions and observations of inflorescence weight for each of eleven species. Predictions are based on the mean of 1000 MCMC samples of the model after convergence was achieved and chains were thinned to remove autocorrelation. Scatterplots are on a log scale, with the 1:1 line drawn and the r^2 of the predicted vs. observed indicated on graph.