The Effect of Plant Distribution on Diversity and Exotic Species Invasion in Prairie Restoration

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Introduction

The most abundant plants in restored prairies are often distributed in large, single-species stands despite our efforts to establish high diversity plantings. This likely occurs as weaker species are excluded by stronger competitors during the first few years of establishment. The resulting distribution of plants into large patches in space may promote establishment of non-planted species in restored prairies, further compromising restoration success.

With this study we tested the effect that plant distribution has on species diversity and invasion within a simplified prairie restoration. We tested the hypothesis that 1) native species diversity will decline over time in plots with randomly distributed plants, and 2) invader abundance will be highest in plots with large single-species patches.

Materials and Methods

In May 2006 we planted 24, 4 m^2 plots with transplants of four prairie species to test the effects of plant distribution on diversity and invasion. Transplants (256 plants m^{-1}) were planted in one of three spatial arrays (random, low aggregation, and high aggregation) as simulated in program QRULE (Figure 1). Two C_4 grasses (Big bluestem, *Andropogon gerardii*; Little bluestem, *Schizachyrium scoparium*) and two forbs (Yellow coneflower, *Ratibida pinnata*; Wild bergamont, *Monarda fistulosa*) were planted at approximately equal densities (64 plants $plot^{-1}$). The species selected were abundant in biomass and frequency across local remnant prairies and our planting density was based on realistic plant density in a prairie remnant.

During the summer of 2006 all plots were weeded to allow transplant establishment and ensure homogeneity in the propagule pool across treatments. Subsequent volunteers were allowed to persist. Species abundance was measured through point intercept sampling in August 2007 and 2008 within each plot by recording the identity of every leaf and stem touched by each of 160 pins dropped uniformly across each plot. These data were used to determine native planted Simpson's diversity ($1/D$), where $D = \sum p_i^2$ and p_i = total touches for species i/total touches in the plot, evenness ($[1/D]/S$) and invader relative abundance at the plot scale.

We used repeated measures analysis of variance to test for differences in species diversity and invasion among the spatial arrays. Invader abundance was arcsine square root transformed to meet normality assumptions.

Results and Discussion

Two years after establishment, native-planted species diversity and species invasion were similar among plots planted in different spatial arrays (Table 1; Figure 2). Native species diversity and invasion were greater in 2008, likely due to the cool, wet spring facilitating establishment by weed species from the local propagule pool. Our results suggest that diversity and invasion are not affected by species distribution patterns in prairie restoration.

Future analyses will determine to what extent the initial plant distributions were maintained through time. Preliminary results suggest that the highly clonal *M. fistulosa* spread extensively through randomly planted plots during the first growing season. This change in the distribution of a single species may have resulted in loss of spatial pattern among treatments early in our experiment.

Our findings do not support the hypothesis that large single-species patches facilitate invasion and suggest that plant distributions are more important for controlling dynamics among established species. We need to further investigate if planting prairie restorations with large patches of conspecific individuals may promote species co-existence and increase restoration success.

Acknowledgements

Many thanks to the Horticulture Station staff who helped to prepare the site. Adam Asche, Andrea Blong, Ashley Conner, Tim Dickson, Tom Moeller, Joe Reynolds, Jenny Richter, Chris Swenson, Kim Wahl, and Susan Yurkonis assisted in planting and sampling the plots. This project was partially funded by the Iowa Department of Transportation Living Roadway Trust Fund and Prairie Biotic, Inc.

Table 1. F-values from RMANOVA of plot-scale native planted species diversity and invasion metrics for 2007 and 2008.

Source	df	Simpson's diversity	Evenness	Invader relative abundance
Spatial array (S)	2	0.50	0.77	0.90
Time (T)	1	7.88*	9.52**	179.71***
S x T	2	1.19	0.71	1.17
Error (time)	21			

*P < 0.05; ** P < 0.01; *** P < 0.001

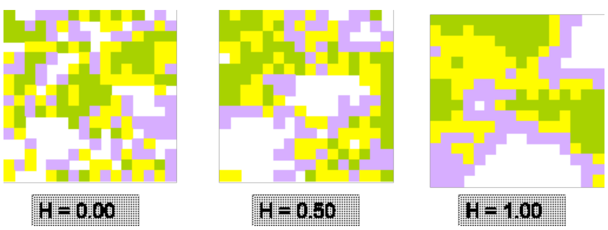

Figure 1. Representative maps of random (H = 0.00), low aggregation (H = 0.50), and high aggregation (H = 1.00) plots.

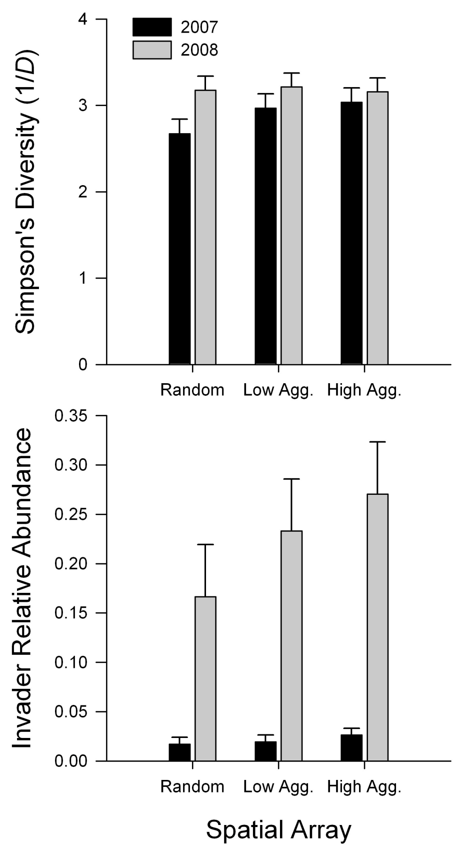

Figure 2. Diversity and invasion (untransformed data presented) were similar across spatial arrays.