Soil Feedback Mechanisms in Prairie Ecosystems

Christopher Bing[1], Dave Sollenberger[2], Louise Egerton-Warburton[2,3]

[1]University of California, Santa Barbara, [2]Chicago Botanic Garden, [3]Northwestern University

Abstract

In any community, feedback systems often define the abundance and composition of its inhabitants; positive feedbacks lead to increased abundance while negative feedbacks limit abundance. Our study investigates the feedback mechanisms occurring between arbuscular mycorrhizal (AM) fungi, soil fungal pathogens and *Andropogon gerardii* (Big Bluestem). Greenhouse experiments confirmed varying degrees of interaction between AM fungi, pathogenic fungi and target plants leading to differing feedback mechanisms. However, the nature of these mechanisms depends heavily on specific biotic and abiotic conditions present in the habitat. These factors include soil nutrient conditions and the presence or absence of both AM fungi and soil pathogens. Identifying the causes and effects of feedback mechanisms in prairie communities may lead to more effective management and restoration strategies in the future.

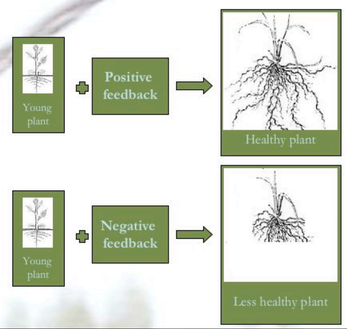

Figure 1: Illustration of positive and negative feedback systems between soil biota and plants.

Introduction

Feedback systems influence community structure often by increasing or decreasing the growth and abundance of a given individual or species. Our project focuses on the feedback mechanisms operating on *Andropogon gerardii,* a keystone prairie species, in relation to the soil biota. The soil biota may be either helpful or harmful to a plant depending on the type of feedback mechanism interacting with the plant. A positive feedback system may lead to enhanced plant growth and abundance while a negative feedback system may cause the individual to suffer and the population to decline (Figure 1). The nature of the feedback mechanism depends on the type of interactions occurring between involved species.

For the purposes of this experiment, we divided fungi into two categories, arbuscular mycorrhizal (AM) and non-mycorrhizal (pathogenic). *A. gerardii* shows varying degrees of dependency on AM fungi, ranging from relative independence to obligate mycotrophism (Anderson *et al.* 1994). The presence of AM fungi in the rhizosphere aids the uptake of available resources in the soil and the defense against certain pathogens (Newsham *et al.* 1994, Newsham *et al.* 1995). The nutritional benefits of AM fungi are greatest when the soil contains low levels of nutrients and resources such as P, N and water because AM fungi increase the overall surface area across which nutrients are absorbed. In addition, AM fungi deter root pathogens through both preemption of root space and the production antibiotic compounds.

In this study we first evaluated the abundance and composition of both mycorrhizal and pathogenic fungi in four prairie restoration settings. The abundance of *A. gerardii* found on these sites ranges from high in near pristine habitat (Schulenberg, Shaw Prairies) to a population in obvious decline (Dixon Prairie). The second part of the study is a greenhouse experiment in which we measured the net feedback effect of both the AM and pathogenic fungi found on *A. gerardii* roots at each restoration site by infecting *Zea mays* and recording the variation in growth and health. We used the results from these two studies to test our hypothesis that higher levels of AM fungi create a positive feedback mechanism in *A. gerardii* leading to increased growth and greater abundance. Similarly, we can hypothesize that higher levels of pathogenic fungi will create negative feedbacks that impede growth, resulting in lower abundance of *A. gerardii*.

Methods

Part 1: Observational Study

Soil cores were collected from beneath *A. gerardii* in four different prairie sites across Northern Illinois (Table 1). Each soil sample was analyzed for available P (Bray-1) and K-Cl extractable NH_4^+ and NO_3^{2-}. Root fragments were cultured on agar plates to determine the bacterial and fungal soil biota present under *A. gerardii.* Root fragments were also stained using Trypan blue (Koske and Gemma 1999) and percent root colonization quantified using the line intersect method (McGonigle *et al.* 1990). In addition, AM and pathogenic fungal hyphae were extracted from soil samples using the method of Jakobson *et al.* (1992) and quantified by microscopy.

Part 2: Greenhouse Experiment

Differential wet sieving was used to separate AM and pathogen components in soil from each of the four sites. *Zea mays* seedlings were planted into pots containing either AM only, pathogen only, combined or sterile inoculum (control) and maintained under greenhouse conditions (Temp °C max 27, min 20; 14:10 day:night). During that time, each seedling was analyzed for its physiological status using a TPS-1 Photosynthesis System. Seedlings were then destructively harvested and the shoots weighed and used as an indicator of different inoculum treatments.

Plate 1: Measuring *A. gerardii* transpiration using the TPS-1 Photosynthesis System.

Results

Part 1: Observational Study

We found four major differences in soil and fungal characteristics among the sites as follows (Table 1).

1. Soil P was high in Dixon Prairie soils relative to other sites indicating that the soil N:P ratio is therefore low.
2. The percentage of root length colonized by AM coils, i.e., the fungus-plant exchange interface, was lowest in Dixon Prairie soils.
3. Soil AM hyphal abundance, i.e., the exploration for nutrients and water by AM fungi, was lowest in Dixon Prairie soils.
4. The bacterial:fungal ratio was highest at Dixon Prairie indicating that less carbon was exuded into the rhizosphere.

Additionally, we found in the root fragment cultures of Dixon Prairie (Figure 2):

1. Low levels of Ascomycetes, a group of fungi with benign to protective effects on plants.
2. High relative levels of Mastigomycota and Zygomycota, two groups of fungi with effects on plants that are particularly detrimental (e.g., *Pythium* belongs to the Mastigomycota).

All other remaining soil and fungal factors did not differ significantly among the sites.

Part 2: Greenhouse Experiment

We found that both biomass and transpiration varied among sites and treatments (Figures 3-4).

1. Schulenberg Prairie treatments showed little difference between AM and control treatments while Almond Marsh and Dixon Prairies exhibited a clear reduction in biomass in AM treatments. By contrast, Shaw Prairie showed the presence of mycorrhizae that appeared to aid plant growth.
2. While transpiration patterns appear to be similar at each site, Schulenberg Prairie, showed the lowest transpiration rates while Dixon Prairie had the highest rates. Shaw and Almond Marsh Prairies exhibited intermediate transpiration rates.

Calculated values for AM fungi responsiveness proved negative for all sites except Shaw Prairie (Schulenberg -25%, Shaw +11%, Almond Marsh -73% Dixon -68%). The AM feedback responses in Dixon Prairie were negative compared to both Schulenberg and Shaw Prairies but positive compared to Almond Marsh.

Table 1: Observational Study Data

Site	Nutrient Concentration (ppm)					% Root Colonization		Soil Hyphal Abundance (m/g soil)		Bacterial Fungal
	P	NH4	NO3	Total N	N:P	Total	By Coils	AM	Pathogen	Ratio
Schulenberg	6.5	4.27	2.89	7.16	1.21	77.7	16.1	70.64	22.29	1.11
Shaw	5	6.36	0.88	7.24	1.55	79.8	4.4	60.83	23.69	1.54
Almond Marsh	10.1	4.79	1.35	6.14	0.66	77.4	8.5	25.15	17.34	1.06
Dixon	19.6	3.88	1.15	5.03	0.29	85.9	3.6	15.54	24.53	3.03
Statistical Signifigance (X^2)	*	ns	*	ns	*	ns	*	*	ns	*

* = p<0.05

NS = not significant

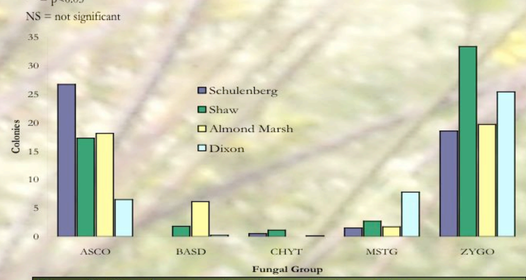

Figure 2: Fungal groups found at each site. Deuteromycota (not shown) ranged from 60-70% in each community and was therefore removed to reduce skew. ASCO, Ascomycota; BASD, Basidiomycota; CHYT, Chytridiomycota; MSTG, Mastigomycota; ZYGO, Zygomycota.

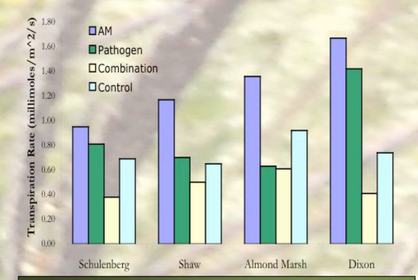

Figure 3: Measured transpiration rates of each treatment by site for *Zea mays*.

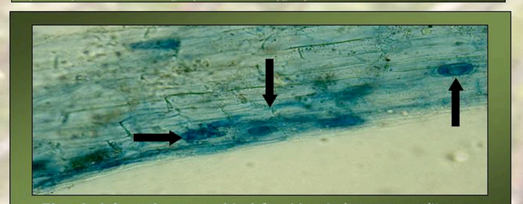

Plate 2: Arbuscular mycorrhizal fungi in *Andropogon gerardii* root. Arrows denote mycorrhizal structures (vesicles and hyphae).

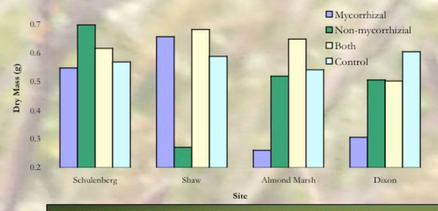

Figure 4: Mean dry biomass for AM, pathogenic, combination and control treatments by site in *Z. mays*..

Discussion

In the greenhouse experiment, AM fungi did not necessarily lead to greater plant growth. Instead, there was a gradient response with some mycorrhizae being mutualistic and others being saprophytic (Figures 4 and 5). Both Schulenberg and Shaw Prairies contained AM fungi that lead to increased seedling growth and decreased water usage whereas Dixon contained AM fungi that acted more as pathogens. Schulenberg and Shaw Prairies therefore support a positive feedback system whereas Dixon Prairie supports a negative feedback system.

The rest of our experiment illustrates how greater levels of AM colonization may deter pathogen infection. One can see this idea in effect based on the colonization and infection rates of different sites (Figure 3). Schulenberg, Shaw and Almond Marsh Prairies all show elevated levels of AM fungi and decreased levels of pathogens. Dixon Prairie shows just the opposite, with fewer AM fungi and increased levels of pathogens, particularly *Pythium*, a root disease.

Why are there so few mycorrhizae in Dixon Prairie? We believe this answer lies in the soil nutrient data (Table 1). In the other sites, soil nutrients are relatively low, thus one would expect mutualistic benefits from AM fungi. In Dixon Prairie, however, the soil contains abundant nutrients, especially P. Mycorrhizae in Dixon Prairie therefore are largely unnecessary from a resource-gathering standpoint and their relationship with plants approaches parasitic, e.g., in plant growth (low biomass) and functioning (high transpiration).

All these feedback mechanisms are reflected in the quality of the restoration sites. Schulenberg and Shaw Prairies represent healthy restoration sites where *A. gerardii* appears to flourish in the presence of positive feedbacks. Almond Marsh is of intermediate quality with some positive feedbacks. Dixon Prairie represents a struggling restoration site due to its numerous negative feedbacks.

Based on these results, we can accept our hypothesis that soil conditions create positive and negative feedback mechanisms for plants leading to increased or decreased growth influencing the progress of restoration efforts.

References

Anderson, R., Hetrick, B., Wilson, G. Mycorrhizal Dependence of *Andropogon gerardii* and *Schizachyrium scoparium* in Two Prairie Soils. American Midland Naturalist 132:366-376.

Jakobson, I., Abbot, L., Robson, A. 1992. External hyphae of vesicular-arbuscular mycorrhizal fungi associated with *Trifolium subrerraneum* L. 2. Hyphal transport of ^{32}P over defined distances. New Phytologist 120:509-516.

Koske, R. and Gemma. 1989. A modified procedure for staining roots to detect mycorrhizas. Mycological Research 92:486-488.

McGonigle, T., Miller, H., Evans, D., Fairchild, G. 1990. A new method which gives an objective measure of colonization of roots by vesicular-arbuscular mycorrhizal fungi. New Phytologist 115:495-501.

Newsham, K., Fitter, A., Watkinson, A. 1994. Root pathogenic and arbuscular mycorrhizal fungi determine fecundity of asymptomatic plants in the field. Journal of Ecology 82:805-814

Newsham, K., Fitter, A., Watkinson, A. 1995. Arbuscular mycorrhiza protect an annual grass from root pathogenic fungi in the field. Journal of Ecology 83: 991-1000.

Acknowledgments: We would like to thank E. Garl Smith, S. Dehn, M. Ingalls, S Finkelman, B. Clark, K. Dreisilker, K. Klick and the Administration of the Skokie River Nature Preserve. This research was supported by a National Science Foundation Research Experience for Undergraduates (REU) site grant and by the USDA Forest Services (NUCFAC; 03-DG-11244225-124).