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FUNCTIONAL DIVERSITY AND RESTORATION OF MEADOWS IN NORTHEAST OHIO

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ABSTRACT

Restoration outcomes can be variable and there is a need to understand the short- and long-term responses of the vegetation community. It is important to see if management goals are being met by evaluating restoration outcomes. Restoration goals often include establishing native species, increasing conservation value, and providing pollinator resources throughout the year. Assessing communities is commonly done though a taxonomic approach by using species presence and abundance. Another method of evaluation is through functional traits or species traits and their abundance. Both give different perspectives on how the community is achieving management goals. While taxonomic assessments can give insight into native species metrics, a functional trait approach can give insight into the processes influencing the assembly of species. This research evaluates restoration through a taxonomic and functional trait approach.

A seeding experiment at Observatory Park, Geauga County, was conducted to see if there are differences in functional diversity before and after a restoration as well as between methods of broadcast and drill seeding. I found that broadcast seeding from the seed mix had a greater richness and abundance of species and a higher mean coefficient of conservatism than in the drill seeded plot. However, the drill seeded plot had a greater diversity of native species. Functional composition analysis found individual traits differed between treatments. Multivariate functional trait analyses, which included the traits of leaf dry matter content, height, seed mass and reproductive phenology, did not identify differences between treatments. This survey characterized the plant community in the early stage of restoration.

To understand regional patterns of restoration and functional diversity, I surveyed 5 paired restored and unrestored sites in the Cleveland, Ohio Metropolitan Area. Restored plots had a significantly higher coefficient of conservatism than plots that were not restored. There was no difference in native richness or diversity between plots, but native abundance increased as a restoration progressed. Flowering phenology was most abundant in summer and tended to have lower abundance in spring and in fall. There was no difference in functional diversity between restored and unrestored plots. These insights into restoration can guide natural resource managers in planning restorations.

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CHAPTER I

INTRODUCTION TO FUNCTIONAL DIVERSITY AND RESTORATION

Prairies and meadows provide a suite of ecosystem services that are relevant to human health and well-being. These ecosystem services include water regulation, nutrient and soil retention, pollination, carbon sequestration and providing a refuge for biodiversity. Prairie ecosystems have an expansive range, the eastern edge of which ends in Ohio. Ohio may not have had a great expanse of prairie, but they are still an important part of its natural history. It has been estimated that historically Ohio had about 260,000 – 294,000 ha of prairie prior to European settlement (Klips 2004; Selbo & Snow 2005). Prairie remnants in Ohio now occupy about 1% of their former range (Selbo & Snow 2005). There is potential to restore prairie and meadow habitats, especially as agricultural fields are taken out of production.

Meadow restoration provides an opportunity to convert areas with low diversity or conservation value into areas with enhanced ecological value. Restoration projects have the common goal of establishing native vegetation and enhancing ecosystem services (Cadotte, Carscadden & Mirotchnick 2011; Bach, Baer & Six 2012; Petursdottir, Aradottir & Benediktsson 2013). Although restoration goals may be similar, project successes can vary, and there is a need to understand variability in outcomes. Taxonomic and functional diversity are two ways to assess a restoration and determine if project goals are met. Taxonomic diversity takes a species identity approach by using species richness and abundance. A functional diversity approach uses the characteristics, or traits, of a species. Each of these approaches can be used to evaluate different components of a community.

Often restoration outcomes are measured by comparing taxonomic richness and the abundance of target species. Taxonomic metrics can be useful to assess diversity and compare species composition across sites. This is especially true when a reference site is used to highlight differences in native plant richness in comparison to restored sites. Species diversity has also been related to ecosystem functions. For instance, high plant diversity has been associated with mitigating drought stress in a community (Klaus et al. 2016). However, functional diversity has been found to be a better predictor of ecosystem functions than species diversity alone (Zhang et al. 2015b).

Taxonomic diversity is important when managing species, but only using this index might omit important qualities structuring a community. A trait-based approach is a way to analyze how species are distributed and assembled within an ecosystem. Plant functional traits include morphological, physiological or life history features of a species (Cadotte et al. 2011). A plant's leaf area, nutrient composition and seed size are all examples of functional traits. These functional traits have a practical application to understanding ecosystems because they determine the processes underlying ecosystem functions and services. For example, traits of vegetative height and leaf dry matter content were the best predictors of ecosystem services of fodder production, biomass production and soil water retention (Lavorel et al. 2011). Using traits as a response to the environment, rather than species identity, allows for generalizations that can then be applied broadly and to other ecosystems (McGill et al. 2006; Laughlin 2014a).

A variety of plant traits can be chosen and used to evaluate a community or ecosystem. It is important to consider which traits to use in an analysis when taking a trait-based approach to evaluating a community. In a meta-analysis by Laughlin, traits that reflected the whole plant and specific organs best predicted community assembly (2014a). Using traits common to all plants also helps define which traits are best to include. Since all plants have to meet the challenges of growth, dispersal and persistence, traits that reflect these life history traits are good candidates for inclusion in analysis (Weiher et al. 2011). Such traits can include leaf, height and seed measurements, which are supported theoretically as a core list of traits (Westoby 1998). This core list of traits also aligns with research that suggested traits that represent the whole plant as well as individual plant organs (Westoby 1998; Weiher et al. 2011; Laughlin 2014a).

Plants have many more traits that can be measured and analyzed to describe a community. Common traits used to assess communities include specific leaf area (SLA), leaf dry matter content (LDMC), seed mass and height, but other traits such as stem density, flowering phenology, and root traits are also found in the literature (Lavorel et al. 2011; Weiher et al. 2011; Laughlin 2014a; Verheijen et al. 2016). Such traits identify trade-offs regarding life history strategies or function (Westoby 1998; Laughlin 2014a). Continuous trait measurements are often used since they can be any value within the range of a particular trait. These types of traits are preferred because it gives a greater dimensionality to characterize a community (Weiher et al. 2011; Laughlin 2014a).

Using more traits in analyses may at first seem beneficial, however only 4-8 traits are needed to describe a community (Laughlin 2014a; Lefcheck, Bastazini & Griffin 2015; Verheijen et al. 2016). Studies taking a functional trait approach have been done with more than 8 traits. For example, Valencia et al. used 10 traits related to plant architecture or leaf characteristics (2015) and Mokany et al. (2008) used 13 continuous traits and a few categorical traits. However, there is the possibility that choosing too many traits, or traits that distinctly discriminate species may negate a functional trait approach. This is because it will likely simulate traditional taxonomic diversity indices (Lefcheck et al. 2015). It has also been suggested traits should be analyzed individually and cumulatively to better understand the relationships and trends between traits (Lefcheck et al. 2015).

There are a variety of ways single or multiple functional traits can be analyzed. Functional trait analysis can describe the range in value, abundance and distribution of traits represented in an ecosystem (Díaz et al. 2007; Cadotte et al. 2011). Functional diversity collectively defines many different indices and dimensions and therefore cannot be distilled into one value. These indices of diversity can be used similarly to species diversity and composition metrics, where values are not absolute, but used as a tool for comparison between communities. Unlike taxonomic diversity indices though, functional diversity considers not just species and abundances, but also species trait values. This creates a trait space in which to describe a range of trait values (Schleuter et al. 2010). Both one dimensional and multidimensional indices are recommended, because of the dimensionality of traits and what they describe about a community or ecosystem (Butterfield & Suding 2013). Traits can then be analyzed individually or together. A one-dimensional trait evaluates only one trait and is often used for finding the mean or abundance of a trait. This would place trait values on the x-axis and their abundance on the y-axis. When multiple traits are used the space occupied by the traits becomes multidimensional (Villéger, Mason & Mouillot 2008). If this relationship is visualized in a plot, species would be points and each trait would be represented along an axis.

There are many different indices used to assess functional composition. Three indices frequently used to compare traits in a community are the community weighted mean (CWM), a central tendency metric of functional composition, as well as functional evenness and functional dispersion, which are two functional diversity indices.

CWM is used to evaluate single traits and weights the value of the trait by its abundance. Weighting the trait by its abundance relates to the idea that those species with the greatest abundance will have the most influence over the function of a community (Grime 1998; Laughlin 2014b). This has been termed the ‘mass ratio’ hypothesis and when used with soil, nutrient or other environmental data can be used to evaluate ecosystem function and processes. This theory has been empirically studied in a grassland system, and is shown to be a good predictor of ecosystem processes (Mokany et al. 2008). Additionally, CWM is more consistent at predicting restoration success than taxonomic metrics (Laughlin et al. 2017).

Functional evenness measures how traits are distributed within the environment. It considers how resources are used and if the traits are complementary or redundant (Schleuter et al. 2010; Butterfield & Suding 2013). Redundant traits can be important because they act to stabilize a community by buffering the effects of species loss and subsequent reduction of traits (Garcia et al. 2015). A removal experiment in a natural grassland community demonstrated that complete removal of a plant functional group negatively affected ecosystem functions (Pan et al. 2016). A diversity of traits, on the other hand, can complement each other and add variation (Engst et al. 2016). This variation can increase resource use efficiency, as an example.

Functional dispersion is another multidimensional way to analyze traits. This index of functional diversity calculates how species are placed in space based on their traits (Laliberte & Legendre 2010). It can be used in place of functional richness and divergence and uses abundance of species as a weighting factor. A high functional dispersion index could indicate that many functional traits are present and infers niche-complementarity (Zuo et al. 2016).

There is growing support for the use of functional diversity as a way to connect traits, ecosystem function and services (Funk et al. 2008; de Bello et al. 2010; Cadotte et al. 2011; Engst et al. 2016). Pollinators are an excellent example of this relationship between traits and ecosystem services. An ecosystem service often associated with meadows is pollination. Pollination is primarily animal mediated, and is essential for the majority of flowering plants in agriculture and native plant populations (Fontaine et al. 2006). Meadow habitats provide food resources to support pollinators through abundant floral resources and a wide diversity of floral traits. In turn, insect pollination of native plants can increase genetic diversity, seed set and seed recruitment. The diversity of plants and pollinators are both important to the stability and perpetuation of the plant community (Fontaine et al. 2006). Diversity in flowering phenology is a trait of particular importance to pollinators that need floral resources throughout the year. This plant and pollinator network is beneficial to both sides of the relationship and enhances the pollination services of the meadow habitat.

Assessing plant communities through functional diversity can give insight into how the community is organized (Engst et al. 2016). One way traits and their diversity help to explain how a community is organized is through community assembly. Understanding how species and their traits assemble can then be applied to restoration efforts (Zirbel et al. 2017). For example, selecting and seeding native plants with traits similar to invading non-natives can competitively exclude invading plants (Byun, de Blois & Brisson 2013). In a study by Zirbel et al. (2017) vegetative height, pollination mode, SLA and seed mass, were used to investigate the relationship between functional traits, environmental conditions and ecosystem function in a grassland restoration. These traits were selected because of their importance to dispersal, establishment and persistence of plant species in a community as well as to ecosystem functions (Zirbel et al. 2017). Restoration directly from tillage seemed to have a significant effect on seed mass, SLA and vegetative height. In addition, these traits influenced the ecosystem functions of pollination, decomposition rate and belowground biomass. This research applied functional traits in the context of restoration and demonstrated how traits can inform management decisions. It also has the potential to predict ecosystem function at restoration sites on a broader scale (Zirbel et al. 2017).

Plant traits have also been used to compare functional diversity indices in restored and reference fens (Hedberg et al. 2013). Restoration treatments were found to have higher canopy height and greater functional richness than the reference site. Further analysis revealed that restoration through tree cutting increased light abundance causing a shift in abundance of competitive plants. This indicates that to reach reference conditions, which are characterized by narrower functional richness, a strong environmental filter favoring traits specific to fen ecosystems may be needed.

Trait measurements can be collected in the field, literature or from open sources databases. Open source databases such as TRY Plant Trait Database, USDA Plants Database can contain plant trait records for hundreds of thousands species and traits (Kattge et al. 2011; USDA, NRCS. 2019). Many studies with a functional trait approach use these data sources because of the advantage of a reduction in time and labor associated with measuring all the traits for all species present at a study site. This trade-off was acknowledged by Hedberg et al. (2013) who also recognized intraspecific trait variation within species as a potential variable, particularly when using trait values from regions other than the one being studied. The authors argue that the potential drawbacks are overruled by the benefits of using traits databases. For some species, intraspecific variation is low and may be less of a concern for traits not collected in situ. LDMC is one trait that supports this argument since it has low intraspecific variation, and therefore is an appropriate trait to use from databases (Smart et al. 2017).

This project focuses on meadow restorations in Northeast Ohio with the overall question of how restoration changes taxonomic and functional diversity. Evaluating meadows using both taxonomic and functional diversity will enhance our understanding of how species traits influence the function of the community. There is a great need to understand these ecological connections so that best practices can be applied to the management of natural areas. Knowledge gained from this research has the potential to inform meadow restoration planning to enhance the provisioning of ecosystem services.

This research has two complementary studies. The first (Chapter 2) examines changes in vegetation before and after restoration. I explored how functional diversity changes after seeding as well as between seeding methods at Observatory Park. A second study (Chapter 3), is a regional survey of multiple restorations in Northeast Ohio, that compares seeded restored meadows to those that were not seeded. The overall research question investigates how restoration changes taxonomic and functional diversity in meadows. I predicted that areas where restoration methods used seeding will be more functionally diverse than areas that were not seeded. I also predicted seeded areas will have greater native species richness and abundance.

CHAPTER II

CHANGES IN VEGETATION BEFORE AND AFTER RESTORATION: OBSERVATORY PARK

Summary

Restoring areas that have a heavy legacy of disturbance can be challenging, as the native seedbank may be completely depleted. Therefore, seeding a mix of native species is a common method used to restore land and increase its conservation value. Changes in species composition due to restoration can be detected through taxonomic evaluations, but this does not consider how community traits might change over time. I focused on differences in functional diversity between two methods of restoration, broadcast and drill seeding. Functional traits of the community were compared for individual trait community weighted mean and through the use of multivariate functional diversity indices of evenness and dispersion. Broadcast seeding established more species and had greater abundance of species from the seed mix. Additionally, broadcast seeding had a higher coefficient of conservatism than drill seeding. In contrast to broadcast seeding, drill seeding had a higher diversity of native species. Single-trait indices were significantly different between broadcast and drill methods and over years. Multivariate functional diversity of evenness and dispersion indicate no significant differences in trait composition between methods or over years. This may indicate that differences arise

early in restoration in terms of individual traits but are not evident in multivariate analyses.

Introduction

Restoration is often used as a way to establish native species, decrease non-native and invasive species, provide wildlife habitat and increase biodiversity. Seeding to restore natural areas can help achieve many of these goals simultaneously, including increasing native diversity while also reducing non-natives (Eastburn et al. 2018). Applying a mix of target native species seed can be desirable because of the effect it has on species assembly and final composition of the restored community. Without seeding, spontaneous succession can be slow due to limited and fragmented source populations which create barriers for target species (Standish et al. 2007). Seeding, however, tends to establish target species sooner than spontaneous revegetation, particularly in disturbed sites (Baasch, Kirmer & Tischew 2012).

Additionally, seeding can mitigate the effects of colonizing non-native species, which can be problematic for land managers. For example, a study on resistance to invasion found that even when propagule pressure from the invasive *Phragmites australis* was high, a dense cover of already established species was capable of reducing invasion (Byun, de Blois & Brisson 2015). Another strategy is to establish target species early to exclude exotic species that may come later (Grman & Suding 2010; Martin & Wilsey 2012). Such priority effects can influence how the community is structured (Von Gillhaussen et al. 2014), pointing to seeding as a practical way to reach a desired plant community.

The seeding method can potentially impact the outcome of a restoration due to the way seeds are applied. For example, two commonly used seeding methods, broadcast and drill, differ in their application, affecting both seeding depth and distribution. Broadcast seeding can result in variable distances between seeds which are distributed on the soil surface, whereas drill seeding is more structured with equally spaced rows of seeds at similar distances from each other and planted at specified depths (Yurkonis et al. 2010a). These differences in spatial distribution can result in differences in community composition as well. C3 grasses were more abundant in drill seeded plots compared broadcast seeded in restored prairies in Iowa (Yurkonis et al. 2010a). Similarly, C4 grasses had higher germination rates in prairies in the arid Southwest (Bernstein et al. 2014). Drill seeding can also create larger patches of grasses compared to broadcast seeding (Yurkonis et al. 2010b).

Another consideration is how restoration may influence functional traits and their diversity. Functional traits describe morphology, physiology and phenology of a species (Cadotte et al. 2011). The collection of these traits, together with abundance, provides an index of diversity that can be used to compare communities. Functional diversity can be applied to answer questions on how traits effect ecological processes (effect traits) and they can be employed to identify shifts in plants traits due to changes in the environment (response traits) (Garnier & Lavorel 2002). Response traits can identify more than changes in the environment; they can also mediate species interactions and assembly (Laughlin 2014b).

Traits associated with persistence, dispersal and establishment are often used as guides to trait selection in functional diversity analyses because they are common challenges faced by the majority of plants (Weiher et al. 2011). Similarly, leaf morphology, maximum plant height and seed mass are cited as important to include in a functional trait analysis (Westoby 1998). Plant trait values are most informative when considered in the context of its life history strategy and its relationship to plant function. Leaf dry matter content (LDMC), for example, relates to the plants nutrient acquisition strategy and rate of biomass production (Garnier et al. 2001; Li et al. 2017).

It has been suggested that functional diversity assessments include indices that assess traits individually as well as together in a multidimensional trait space (Butterfield & Suding 2013). A trait index commonly used to assess individual trait values is the community weighted mean (CWM). For this index, the trait value of a plant is weighted by its abundance in the community. Restoration might impact the CWM of a trait depending on the ecosystem and goals of the project. In a study evaluating the restoration of a fen, height was considered in the analysis as fens typically have shorter canopies when compared to a forest, the ecosystem they were restoring from (Hedberg et al. 2013).

Multivariate analyses, in contrast, use multiple traits and can assess how the trait space of a community is being filled. Functional evenness as a multivariate analysis can determine how regularly the abundance of trait values are represented in an environment (Schleuter et al. 2010; Karadimou et al. 2016). It may be important for restoration to consider functional evenness, because an even abundance of traits has a potential link to invasion resistance (Funk et al. 2008). Functional dispersion, another multivariate index, calculates how similar traits are and if they are complementary or redundant (Laliberte & Legendre 2010; Karadimou et al. 2016; Zuo et al. 2016). This index of dispersion has important applications to restoration and has been linked to weed suppression (Suter, Hofer & Lüscher 2017).

Depending on the goals of the restoration, the mean value, abundance, or similarity of traits can all be of interest and describe different components of a community. Since traits and their valuation can be context dependent, it is important to note that diversity indices are not absolute values but are tools for comparisons between communities. The valuation of the index may also be dependent on the trait and the goals of restoration. For example, we may be interested the CWM of a leaf trait like LDMC, since it may tell us something about the competitiveness of the species in that community. In contrast to this, functional evenness may be more important for phenology and pollinator resources throughout the year, but we may be less concerned about this metric for leaf traits.

Assessing traits can give insight into the assembly of plant communities as well, which is often of interest to restoration ecology. Indeed, studies using metrics of functional diversity have indicated its usefulness for assessing restorations. For example, functional traits have been used to compare restoration efforts with reference communities, and to observe changes in traits in response to management (Hedberg et al. 2013). Studies have also highlighted the dynamic relationships between traits, species assembly and ecosystem functioning (Hedberg et al. 2013; Engst et al. 2016; Zirbel et al. 2017).

Since a functional trait approach has been used to assess restorations and functional traits often respond to environmental change, we were interested in the differences in trait distribution both before and after restoration treatments, and between broadcast and drill seeding methods. To address questions about differences in species and functional diversity as a function of seeding method (broadcast and drill seeding), the vegetation was monitored over 3 years, pre and post restoration, in a meadow restoration project. I predicted that there would be differences pre and post-restoration as well as between seeding treatments. Seed mix species were predicted to establish themselves in both treatments but with differences in richness and abundance between the two treatments. Functional diversity was predicted to increase after seeding, due to treatments and the addition of species to the community. Comparing the seeding methods, I predicted that drill seeding would lead to a more taxonomically and functional diverse plant community due to grasses establishing in greater abundance from this method.

Methods

Observatory Park, part of the Geauga Parks District in Northeastern Ohio, was chosen as a location for this study (Coordinates: 41.58722500 degrees N, -81.08277778 degrees W). Before the Park District acquired the land, it was previously used for agriculture. Once taken out of production, the field underwent succession without planting a cover crop. Restoration of native meadow habitat was proposed for 14 acres within this park.

Before the restoration began, I surveyed the plant community using the North Carolina Vegetation Survey protocol, involving collecting data on species presence and abundance as percent cover classes (Peet, Wentworth & White 1998). The protocol uses a 20 x 50 m plot with a multiscale, nested design. Within each plot there are 10 subplots, or modules, that are 10 x 10 m. Four of the subplots are nested and provide a systematic approach to identifying species. This method has numerous benefits, one of which is its compatibility with other survey designs, due to its modular shape and multiple scales. Another benefit of this design, is that it performs well in patchy environments (Goslee 2006). Two plots were permanently staked with metal nails, one plot for each seeding treatment. In June of 2016 each plot was surveyed to provide a baseline for analyzing changes in the community.

Site preparation prior to seeding included mowing and herbicide treatment to reduce standing vegetation. A native seed mix of 43 species from Ohio Prairie Nursery was applied in October of 2016 to allow for stratification of seeds over winter. The 14 acre area was divided to implement two seeded methods used in this experiment, drill and broadcast seeding. The western half of the site was drill seeded and the eastern half broadcast seeded. Plots were resurveyed after seeding in June 2017 and 2018 at the permanently staked plots.

Analyses focused on comparing the community before seeding and the final year of survey to understand the early changes in vegetation composition. Differences between seeding treatments of broadcast and drill were compared as well. Species composition was evaluated by comparing the abundance and richness of species that established from the seed mix and through overall taxonomic diversity. Taxonomic diversity was calculated using the Shannon index. The diversity for all the species identified and for only the natives was found.

Functional traits were selected and obtained from the TRY plant trait database, USDA plants, from the field and from literature (Kattge et al. 2011; USDA, NRCS. 2019; see Appendix for references of all trait data used). The TRY Plant Trait Database includes approximately 11.8 million trait records and 279,000 plant taxa (Kattge et al. 2011). One major advantage to using trait databases is the reduction in time and resources to measure all the species traits present at the site (Hedberg et al. 2013). I selected traits that were closely related to the functions all plants perform in order to disperse, establish and persist (Weiher et al. 2011). Within the potential traits available, I focused on representative traits that were the most complete set of traits for the species observed at the site: leaf dry matter content (LDMC; g/g), plant height at maturity (m), seed mass (mg) and flowering phenology. Root length (m) was analyzed separately due to missing values for many of the species, as too many missing values can potentially misrepresent the outcome of the functional diversity indices (Lefcheck et al. 2015).

In addition to the trait values from the TRY database, LDMC was collected for 4 species (*Cyperus esculentus, Ranunclus pennsylvania, Taraxacum officinale*, and *Agrostis scabra*) that were the most abundant but did not have the trait available in the TRY database. Data collection for LDMC followed protocols by Cornelissen et al. (2003). Seven to 10 individuals per species were collected and rehydrated overnight in the dark at four degrees Celsius before removing the leaves. At least two leaves, including petiole, per individual were removed from the stem and a water saturated mass was recorded. Leaves were then dried in an oven at 60 degrees Celsius for 72 hours and measured again to obtain a dry mass.

A coefficient of conservation (C of C) was assigned to each plant following the Vegetation of Index of Biotic Integrity (VIBI) for Ohio (Andreas, Mack & McCormac 2004). This metric ranks species based on their perceived value to the environment as well as ecological tolerances. Including the coefficient of conservation provides a way to compare the conservation value of sites which might not be captured by taxonomy alone.

Traits were analyzed by evaluating functional diversity indices for each trait separately and with a multivariate approach using multiple traits (leaf dry matter content (LDMC;

g/g), height (m), seed mass (mg) and flowering phenology) proposed by Lefcheck et al. (2015; but also see Hedberg et al. 2013). Plants that were only identified to genus were removed from the analyses since traits could not be evaluated at this level of identification.

For individual trait analysis, the community weighted mean (CWM) was determined. Trait values included coefficient of conservatism (C of C), leaf dry matter content (LDMC), height, seed mass, phenology and rooting depth. The CWM weights the mean trait values in a community by the species abundance. This measure of trait distribution identifies the most dominate trait values in the community (Valencia et al. 2015). Comparing the CWM may distinguish different communities in terms of structure, as in the CWM of height, or if they differ in overall competitiveness, as CWM of LDMC may indicate (Garnier et al. 2001). CWM of abundance for phenology by season was used to compare timing and abundance of flowering species for each treatment, and before and after restoration. The greater abundance of species flowering during a certain time, the more pollinator resources are available.

Functional evenness and dispersion indices included for 4 main traits, LDMC, height, seed mass and phenology. Each individual trait was analyzed separately and together using the multivariate index. Rooting depth was not included in the multivariate analysis but was calculated separately because there were many null values which can fail to truly represent the trait value in the community (Lefcheck et al. 2015).

Functional evenness describes how traits are distributed relative to one another within the available trait space. The index is constrained between 0 and 1 where values closer to 0 indicate traits are less evenly distributed and values closer to 1 indicate traits that are more evenly distributed (Schleuter et al. 2010). How traits are distributed can then be used to interpret how resources are being used. A value closer to 1 may indicate resources are being used efficiently or that there is competition (Mouchet et al. 2010; Schleuter et al. 2010).

Functional dispersion describes how species are placed in trait space by calculating the distance of each species from the centroid of all trait values and averaging them (Laliberte & Legendre 2010). This index evaluates how similar traits are relative to one another. A value of 0 would be expected in a monoculture, or communities with only one species present. However, unlike functional evenness, dispersion can be greater than 1. A low index value would indicate that the traits in the community are redundant (Karadimou et al. 2016) and a higher value would mean that many functional traits are present and different from each other (Zuo et al. 2016).

I also calculated the functional trait composition, including CWM, evenness, and dispersion for all the species and their relative abundances in the seed mix. This allows a comparison between the actual functional composition and what the potential functional composition could be if all the species established in the abundances they were seeded.

Statistical analysis. Functional trait analysis for CWM and functional diversity indices were calculated using the 'FD' package in R (R Core Team 2017; Laliberte & Legendre 2010; Laliberte, Legendre & Shipley 2014). Repeated measures ANOVA was used to determine differences between broadcast and drill seeded plots and between years for each index also using R (R Core Team 2017, packages 'nlme', Pinheiro, et al., 2018 and 'multcomp', Hothorn, Bretz and Westfall, 2008). Survey years 2016, prior to seeding, and 2018, after seeding, were used in the analysis to be able to make a comparison between the initial community and resulting community two years after seeding. Interactions that were not significant at alpha = 0.05 were removed from the model. Tukey's test was used for post hoc analysis on those models that indicated significant differences in the interaction between treatment and year. NMDS was used to see differences in community composition between broadcast and drill seeding. Distances in the ordination used Bray-Curtis dissimilarity index. A Mantel test was used to test the correlation between the distances in broadcast and drill seeded plots. A species indicator analysis was used to find the species driving community differences (R package ‘labdsv’, Roberts 2016).

Results

A species accumulation curve indicated that the vegetation survey had sufficient size to characterize the plant community (Figure 2-1). Species richness curves come to an asymptote where species are accumulating more slowly as the sampled area increases. The curves for the years of sampling also indicate that diversity was higher in both broadcast and drill seeded plots in 2017 than other years.

The pre-restoration survey identified 50 species. When considering both broadcast and drill plots together, four species comprised most of the cover (*Cyperus esculentus*, *Lepedium campestre*, *Poa palustris*, *Trifolium repens*) (Table 2-1). All but *Poa palustris* are non-native. Three non-native species (*Cyperus esculentus*, *Lepidium campestre*, *Trifolium repens*) accounted for approximately 80% of the total cover (60% of the relative abundance). Nineteen native species were identified and made up only about 24% of the total cover (18% of the relative abundance).

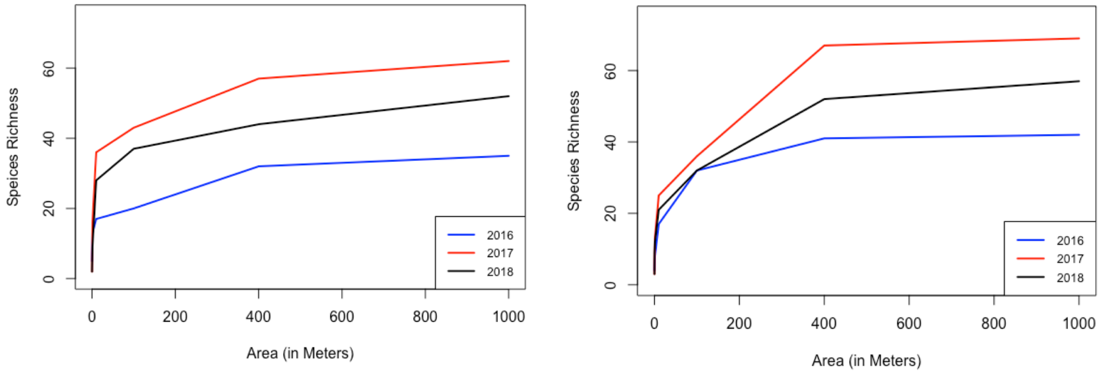

Figure 2-1. Species accumulation curves for broadcast plot (Left) and drill plot (Right). Species accumulation curves saturate in all cases, indicating that the plot size of the North Carolina Vegetation Survey was sufficient to capture the species at Observatory Park. The curves also indicate that there was greater species richness the first year after seeding in 2017 in both the broadcast and drill plots.

In the first summer after seeding (2017), an average of 4.8 species (eight seeded species for the whole plot, 18.6% of the species from the mix) were identified and made up about an average of 2.5% cover in the broadcast seeded plot (Figure 2-2). The drill seeded plot had an average of 2.6 for species richness (also eight species for the whole plot) established from the seed mix which made up about 1.4% of the cover. Each plot had similar species establish except for *Elymus canadensis* (Canada wild rye) which was only identified in the drill plot and *Symphytrichum novae-angliae* (New England aster) which was only identified in the broadcast plot. Low species richness and percent cover of species from the seed mix could be because the survey was conducted in June of 2017 which was less than a year after seeding (eight months).

Broadcast 2016	**Average Percent Cover**	**Drill 2016**	**Average Percent Cover**
Cyperus esculentus	60.0	*Lepedium campestre*	43.5
Trifolium repens	17.1	*Trifoilum repens*	16.9
Poa palustris	15.5	*Poa palustris*	13.5
Lepedium campestre	14.3	*Cyperus esculentus*	8.1
Barbarea vulgaris	10.7	*Anthoxanthum odoratum*	5.2
Total cover	117.6		87.2

Table 2-1. The five most abundant species in the plots before seeding.
Prior to seeding both plots had a high cover of non-native species. In both plots all species but *Poa palustris* are non-native.

In June 2018, the last year of the survey, target species richness increased in both broadcast and drill plots (Figure 2-2). An average of 6.5 species were identified (14 species total from the whole plot, about 32.6% of the seed mix) in the drill seeded plot and made up 8.3% of the cover for the plot. On average, 9.7 species (17 species from the whole plot or 39.5% of species from seed mix) were identified in the broadcast plot and comprised 10% of the cover. *Schizachyrium scoparium* (little blue stem) was found in the drill but not in the broadcast seeded plot. More graminoids were found in the drill seeded plot (3 species) and had a higher percent cover (2.1% cover) than in the broadcast seeded plot. In contrast to the graminoids, more forb species were found in the broadcast plot (15 species, 9.9% cover). *Lobelia siphilitica* (great blue lobelia), *Coreopsis lanceolata* (lance leaf coreopsis), *Helenium autumnale* (sneezeweed), and *Tradescantia ohiensis* (spiderwort) were found in the broadcast but not the drill seeded plot.

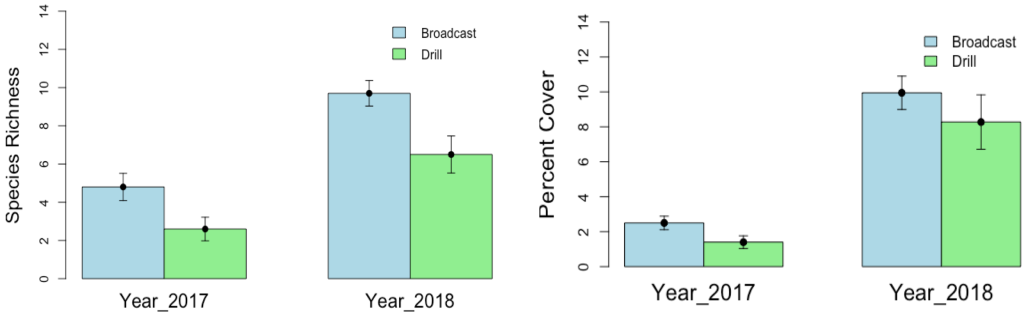

Figure 2-2. Richness and abundance from the seed mix.
The figure on the left is the average species richness identified from the seed mix in 2017, one year after seeding, and in 2018, two years after seeding. The figure on the right is the abundance (average abundance) of the species identified from the seed mix. These figures indicate that broadcast seeding may establish more species and have a higher abundance of those species. Error bars are one standard error of the mean.

Overall, 21 of the 43 species (48%) from the seed mix were found in 2017, 2018 or both years (Table 2-2). The top five species with the most cover from the broadcast and drill seeded plots in 2018 were mostly non-native species (Table 2-3). *Trifolium hybridum* and *Trifolium pratense* were common in both plots and are non-natives. *Erigeron annuus*, a native species, was also found in both plots but was only the 5th most abundant in the broadcast and 3rd in the drill seeded plots.

Species that established	Species from the mix not identified
Schizachyrium scoparium	*Aster umbellatus*
Asclepias incarnata	*Baptisia australis*
Asclepias syriaca	*Bouteloua curtipendula*
Carex lurida	*Carex comosa*
Carex vulpinoidea	*Carex crinita*
Chamaecrista fasciculata	*Carex stipata*
Coreopsis lanceolata	*Echinacea purpurea*
Elymus canadensis	*Eryngium yuccifolium*
Elymus virginicus	*Eupatorium maculatum*
Helenium autumnale	*Gaillardia pulchella*
Heliopsis helianthoides	*Lespedeza capitata*
Lobelia siphilitica	*Liatris spicata*
Monarda fistulosa	*Lobelia cardinalis*
Ratibida pinnata	*Monarda citriodora*
Rudbeckia hirta	*Penstemon digitalis*
Silphium integrifolium	*Ratibida pinnata*
Silphium perfoliatum	*Scirpus atrovirens*
Symphyotrichum novae-angliae	*Scirpus cyperinus*
Tradescantia ohiensis	*Scirpus validus*
Verbena hastata	*Solidago rigida*
Zizia aurea	*Solidago ulmifolia*
	Sporobolus heterolepis

Table 2-2. Species that established from the seed mix.
Species were identified in 2017 (1 year after seeding) and 2018 (2 years after seeding). About half the species were identified in the survey either in the first or second year or in both years after seeding.

Broadcast 2018	Average Percent Cover	Drill 2018	Average Percent Cover
Poa palustris	57.0	*Trifoilum hybridum*	61.5
Trifolium hybridum	64.3	*Trifolium pratense*	25.5
Trifolium pratense	12.9	*Erigeron annuus*	13.5
Phleum pretense	12.2	*Leucanthemum vulgare*	11.9
Erigeron annuus	8.0	*Phleum pratense*	7.0
Total cover	154.4		119.4

Table 2-3. The five most abundant species in each plot after seeding in 2018. Non-native species are still abundant after seeding. The most abundant species are different than those identified before seeding. Native species include *Erigeron annuus* and *Poa palustris*.

Shannon diversity. Diversity was calculated using the Shannon index of diversity for all species and also for native species only (Figure 2-3 and Figure 2-4, respectively). When considering all species, there was not a significant difference in diversity between years or between the two seeding methods (ANOVA, Treatment, p-value = 0.74, F-value = 0.11, df= (1,18); Year, p-value = 0.92, F-value = 0.01, df = (1,19); Figure 2-3). However, there is a difference in diversity when considering only native species present in the plots (Figure 2-4). In the second year after seeding, the broadcast plot seems to increase only slightly in native diversity while the drill seeded plot had a greater increase in native diversity. The drill seeded plot after seeding is statistically significantly different from all other treatments and prior years (ANOVA, Interaction, p-value = 0.02, F-value = 6.93, df= (1,18); Treatment, p-value < 0.01, F-value = 9.33, df = (1,18); Year, p-value < 0.001, F-value = 27.62, df= (1,18); Tukey's test, p-value < 0.001).

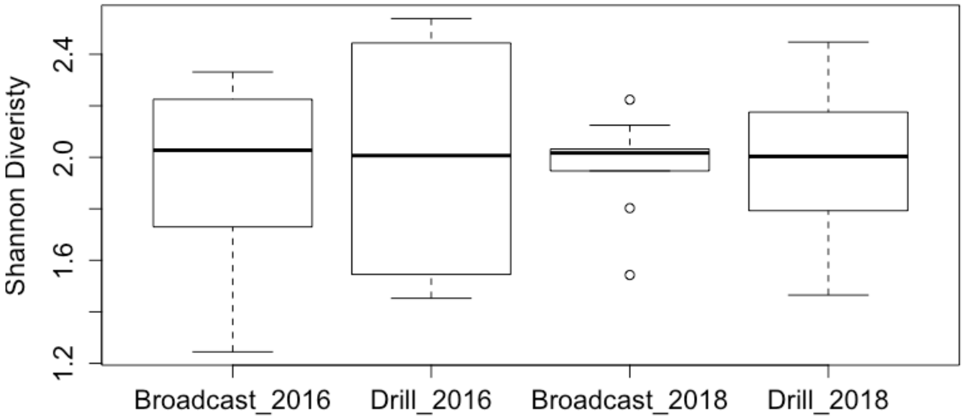

Figure 2-3. Shannon diversity for all species.
There was no difference in the Shannon index of diversity between 2016, before seeding, and 2018, after seeding (ANOVA, p-value > .05).

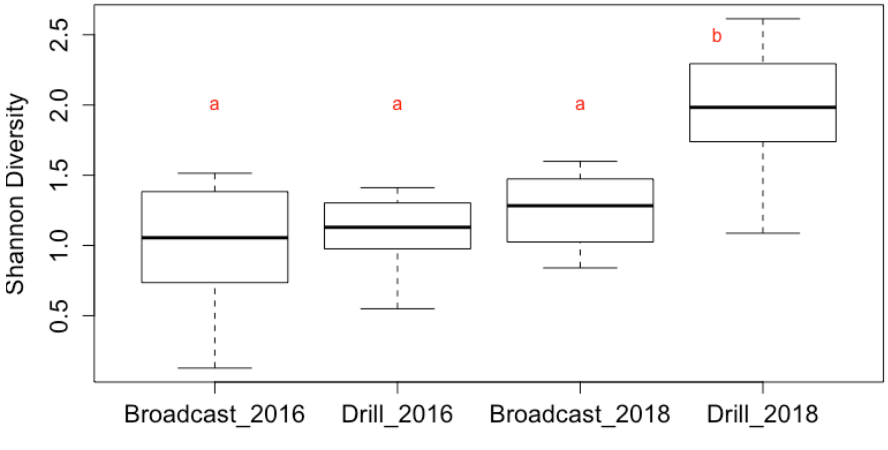

Figure 2-4. Shannon diversity for native species.
Native species diversity between broadcast and drill seeding shows that native diversity was greatest in the drill seeded plot in 2018 (mean =1.96). Overall, the mean native diversity broadcast changed from 0.99 to 1.28. In the drill seeded plot, the mean native diversity increased steadily from 1.1 to 1.96. Red lettering indicates significant differences.

Coefficient of conservatism. Since the Shannon diversity index considers all species, whether or not they are target or desired species, using the coefficient of conservatism (C of C) can give weight to the species restoration practitioners might be interested in. The community weighted mean of the C of C between plots was highest in the broadcast plot two years after seeding (Figure 2-5). A repeated measures ANOVA found a significant difference in the interaction between treatments and years (ANOVA, Treatment, $p < 0.001$, F-value = 21.08, df = (1,18); Year, p-value = 0.008, F-value = 9.08, df = (1,18)). The C of C in broadcast plots two years after seeding was greater than drill seeding, both before and after seeding (Tukey's test, $p < 0.001$). The drill seeded plot prior to seeding was also different compared to the drill seeded plot two years after seeding, and C of C decreased from 2016 to 2018 (Tukey's test, p-value = 0.05).

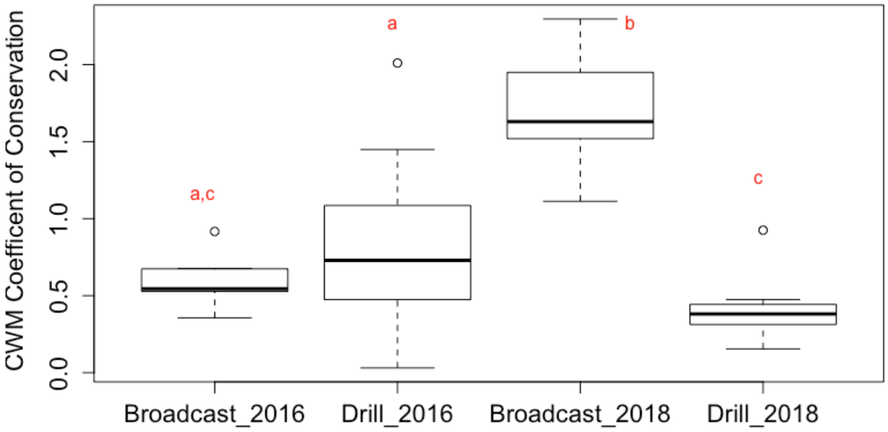

Figure 2-5. Community weighted mean of coefficient of conservation.
The community weighted mean (CWM) of coefficient of conservation was determined to see if there were differences in the conservation value of the plots. Broadcast seeding had the greatest average CWM of the coefficient of conservation (CWM C of C = 1.675) the second year after seeding. Red lettering indicates significant differences.

Phenology. The phenology of species was used to create a chart to understand the patterns of floral resources (Figure 2-6 and 2-7). Each species flowering period was determined and designated into the categories of early, mid, late, and spring, summer and fall. Species in the broadcast plot primarily bloom in late spring (Figure 2-6). Abundance of wind pollinated plants decreased after seeding but were still abundant. Similarly, in the drill seeded plot, late spring flowering plants were most abundant (Figure 2-7). There was also a greater abundance of summer flowering plants after seeding in the drill plot (21% relative abundance) compared to broadcast seeding (9% relative abundance).

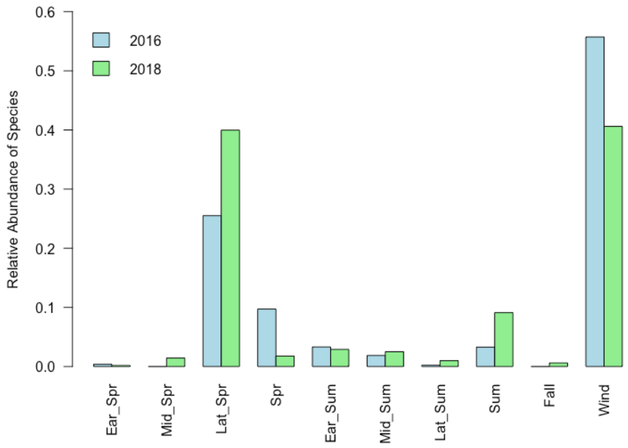

Figure 2-6. Broadcast plot phenology prior to and post seeding.
The bar graph shows the abundance of flowering plants and their phenology prior to seeding (2016) and post seeding (2018). The peak of flowering both prior to and after seeding are during late spring. Restoration seemed to increase the abundance of spring flowering plants, however, this abundance is likely due to the abundance of *Trifolium spp*. There is also an abundance of wind pollinated plants.

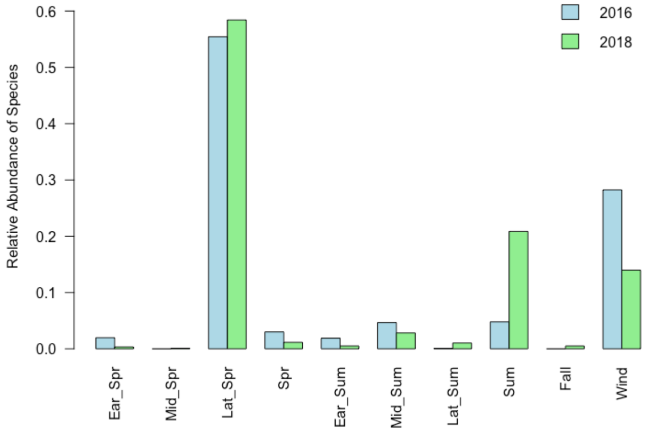

Figure 2-7. Drill plot phenology prior and post seeding.
The bar graph at left shows the abundance of flowering plants and their phenology prior to seeding (2016) and post seeding (2018). The peak of flowering both prior to and after seeding are during late spring. The abundance of summer flowering plants increased after seeding.

Other individual traits. Leaf dry matter content CWM was determined to be different between years, treatments, and there was an interaction (Figure 2-8; ANOVA, Interaction, p-value = 0.03, F-value = 5.35, df = (1,18); Treatment, p-value < 0.001, F-value = 36.91, df = (1,18); Years, p-value = 0.04, F-value = 5.05, df = (1,18)). Post hoc testing identified that the broadcast plot prior to seeding was different from all other years and treatments (Tukey's test, p-value< 0.01). Broadcast plot after seeding was also different from the drill plot before and after seeding (Tukey's test, p-value = 0.03, z-value = 2.74 and p-value = 0.04, z-value = -2.69 respectively). The ranges in LDMC seem to be wider in 2016 compared to 2018, which seemed to be narrower. Potential differences in the range of LDMC could be due to the abundance of *Cyperus esculentus* and *Lepidium campestre* in 2016 before restoration and their extreme LDMC values. *Cyperus esculentus* had one of the greatest abundances and has an LDMC value of 0.41 g/g which was also one of the highest LDMC values of all the species. *Lepidium campestre* was also abundant and had one of the lowest LDMC values (0.19 g/g). Since CWM is weighted by abundance of species, this could have resulted in a higher range for modules with higher abundances of *Cyperus esculentus* and in those modules with greater abundance of *Lepidium campestre*, which brought the CWM lower. Similarly, after seeding, *Trifolium spp*. (LDMC = 0.22-0.25*), Poa palustris* (LDMC = 0.32), and *Phleum pratense* (LDMC = 0.31) were abundant and have LDMC values that are relatively close to each other, narrowing the range of the CWM for this trait.

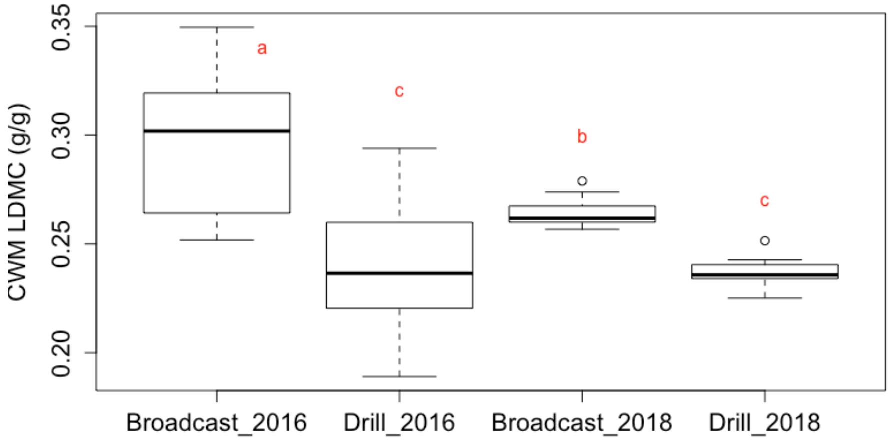

Figure 2-8. Community weighted mean of leaf dry matter content.
LDMC had a wider range in CWM prior to seeding. Broadcast had a greater mean CWM than drill seeding both prior to and after seeding. Red lettering indicates significant differences.

The CWM height of plants increased in the broadcast plot after seeding, while in the drill seeded plot there seems to be little change over years (Figure 2-9). An ANOVA found that treatment, year and the interaction of treatment and year all were significantly different (ANOVA, Interaction, p-value < 0.001, F-value = 22.77, df = (1,18); Treatment, p-value = 0.01, F-value = 9.86, df = (1,9); Year, p-value < 0.001, F-value = 67.33, df = (1,18)). Plant height in the broadcast seeded plot after seeding was different from the drill seeded plot both before and after seeding and the broadcast plot prior to seeding (Tukey's test, p-value < 0.001). There was also a different in means between the broadcast seeded plot prior to seeding and the drill seeded plot after seeding (Tukey's test, p-value = 0.002).

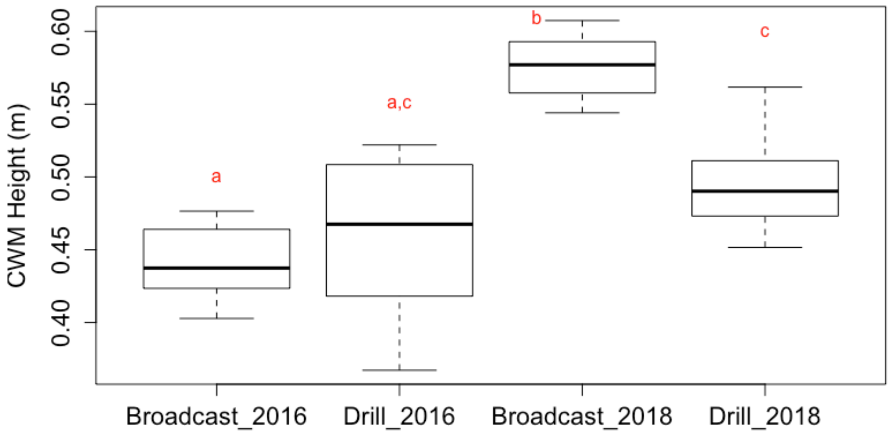

Figure 2-9. Community weighted mean of height.
Height of vegetation changed over time in the broadcast seeded plot. Little change was observed in the drill seeded plot after seeding. Red lettering indicates significant differences.

For the CWM seed mass of plants surveyed, there was little change before and after seeding (Figure 2-10). An effect of treatment was found (ANOVA, p-value = 0.01, F-value = 10.15, df = (1, 9)) and an interaction between year and treatment as well (ANOVA, p-value = 0.01, F-value = 8.21, df = (1,18)). The drill plot prior to seeding had a higher mean CWM seed mass than the broadcast plot before and after seeding (Tukey's test, broadcast 2016, p-value < 0.001; broadcast 2018, p-value = .004). Mean seed mass decreased after seeding in the drill seeded plot (Tukey's test, p-value = 0.01).

Rooting depth community weighted mean increased in both treatments, and rooting depth was greatest in the drill seeded plot after seeding (Figure 2-11). A main effect of treatment and of year was found (ANOVA, Treatment, p-value = 0.002, F-value = 18.56, df = (1,9); Year, p-value = < 0.0001, F-value = 182.43, df = (1,19)).

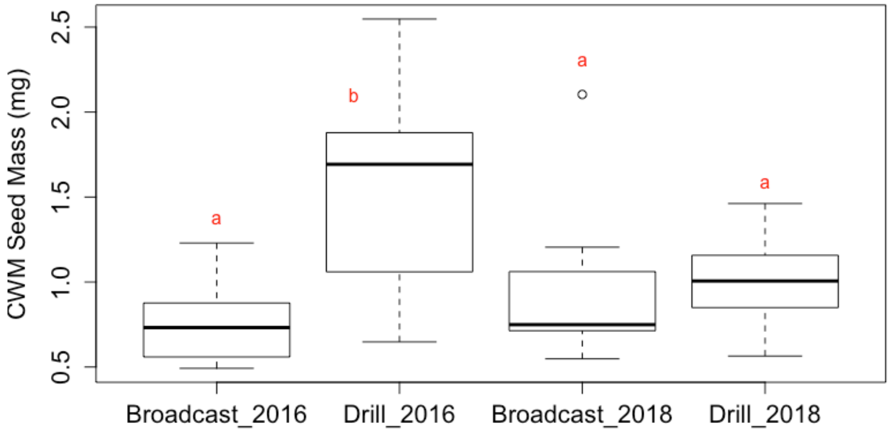

Figure 2-10. Community weighted mean of seed mass.
Seed mass of plants showed little change after seed. Post hoc testing found that the drill seeded plot in before seeding was different from all other years and treatments (Tukey's test, p-value < 0.01). Red letters indicate significant differences.

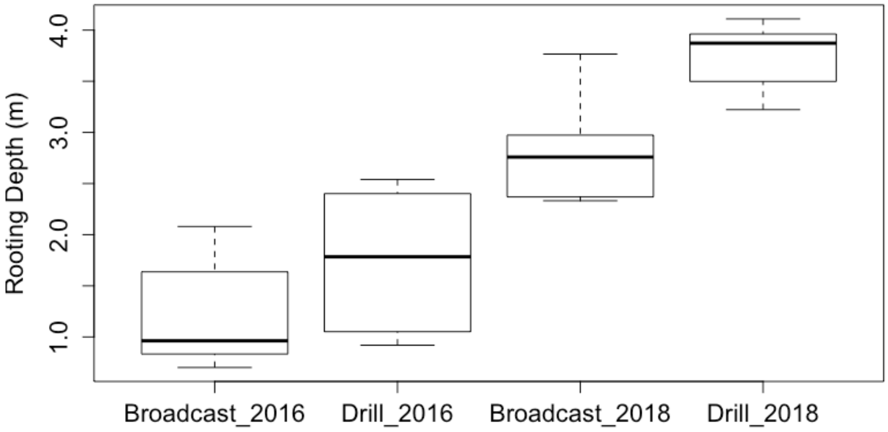

Figure 2-11. Community weighted mean rooting depth.
Root depth increase in both plots after seeding. The greatest mean CWM rooting depth was in the drill seeded plot in after seeding. An ANOVA found a main effect of year and a main effect of treatment.

Functional Evenness. Functional evenness was analyzed for each trait, LDMC, height, and seed mass, individually (Figure 2-12). Functional evenness is a measure of how equally distributed species, traits and their abundances are, relative to one another (Mouchet et al. 2010). In the model for LDMC there was a main effect of year (ANOVA, Treatment, p-value = 0.07, F-value = 3.61, df = (1,18); Year, p-value = 0.02, F-value = 6.08, df = (1,19)). Evenness of LDMC increased slightly after seeding in both broadcast and drill seeded plots. For height, there was only a main effect of year (ANOVA, Treatment, p-value = 0.09, F-value = 3.13, df = (1,18); Year, p-value < 0.001, F-value = 31.45, df = (1,19)). After seeding functional evenness of height decreased for both broadcast and drill seeded plots. For seed mass, there was no significant difference in functional evenness between broadcast and drill seeding or between years (ANOVA, Treatment, p-value = 0.12, F-value = 2.59, df = (1,18); Year, p-value = 0.07, F-value = 3.79, df = (1,19)). Roots were analyzed separately (Figure 2-13) and only a main effect of year was found (ANOVA, Treatment, p-value = 0.63, F-value = 0.24, df = (1,18); Year, p-value = 0.02, F-value = 6.46, df = (1,19)).

To better understand the distribution of LDMC, height and seed mass and phenology together, a multivariate functional evenness analysis was used. Functional evenness was calculated for all species and was also calculated for natives only (Figure 2-12). An analysis considering all species found no main effects of treatment of years (ANOVA, Treatment, p-value = 0.18, F-value 1.91, df = (1,18); Year, p-value = 0.055, F-value = 4.18, df = (1,19)). Similarly, for functional evenness of native species, no significant difference was found between treatments or years (Broadcast 2016 Module 9 was removed from analysis because there were more species than traits in this module and therefore functional diversity could not be calculated, ANOVA Treatment, p-value = 0.09, F-value = 0.02, df = (1,18); Year, p-value = 0.95, F-value = 0.004, df = (1,18)). When comparing all species and only natives, native species had a slightly higher index for functional evenness. This could be due to the abundance of non-natives and their influence to lower the functional evenness on this index.

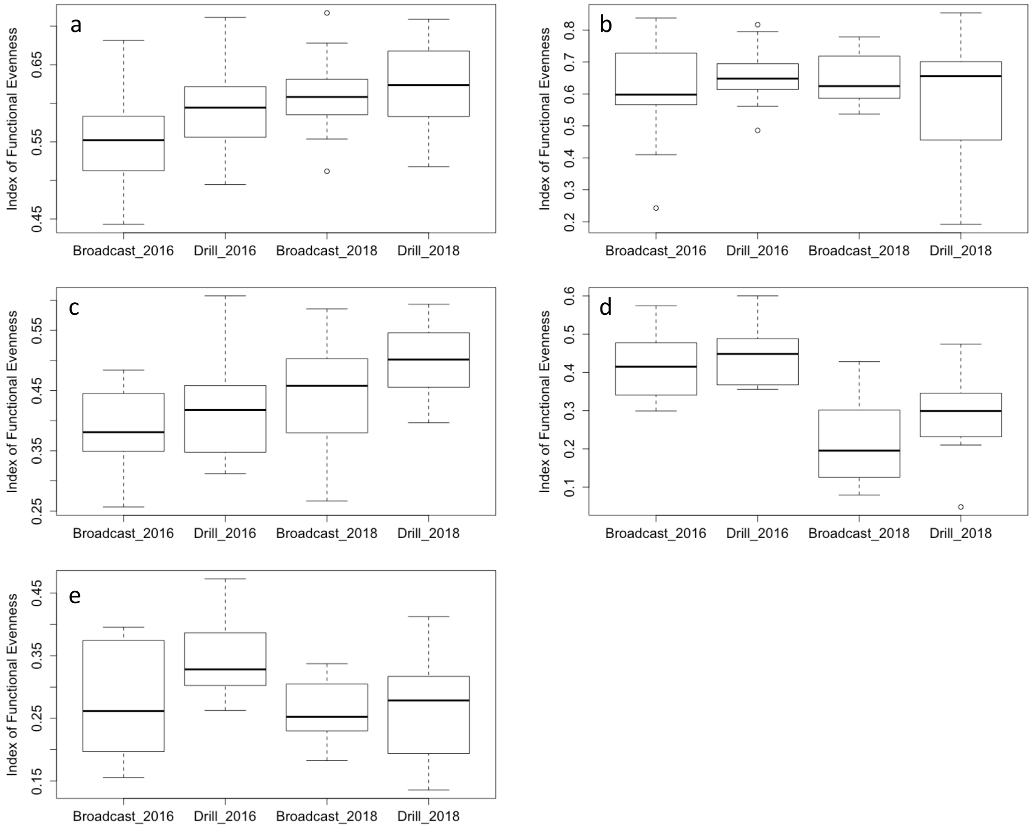

Figure 2-12. Functional evenness analyses.
Functional evenness analyses for all species (a) and for native species only (b). Traits were analyzed individually for functional evenness for the traits LDMC, height, and seed mass (c, d, and e, respectively). Functional evenness was similar between all species and when considering only natives. Individual traits were similar as well with LDMC and height having a main effect of year.

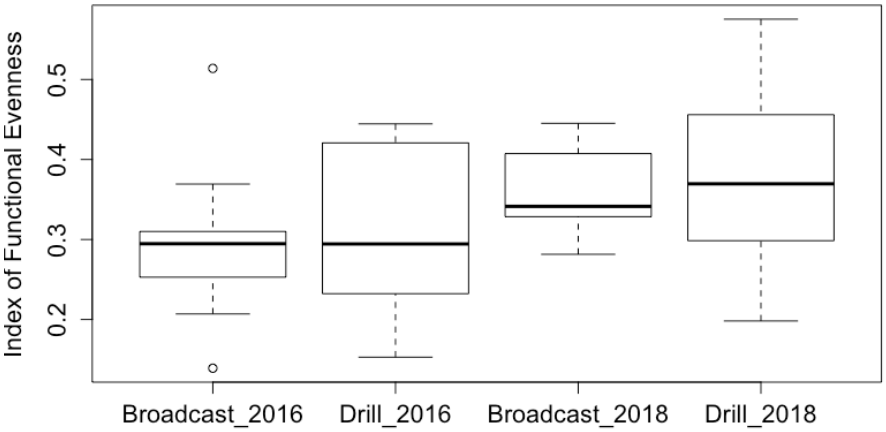

Figure 2-13. Functional evenness of rooting depth.
An ANOVA found a main effect of year (ANOVA, Year p-value = 0.02, F-value = 6.46, df = 19). Both plots increased in functional evenness of rooting depth after seeding.

Functional dispersion. Functional dispersion was analyzed to determine if traits are complementary in the community. Similar to the analysis of functional evenness, traits were assessed individually and together (Figure 2-14). For individual traits, LDMC functional dispersion results indicated only main effects of treatment and year (ANOVA, Treatment, p-value < 0.0001, F-value = 27.57, df = (1,18); Year, p-value < 0.0001, F-value = 48.48, df = (1,19)). For height, only the interaction was significant in the model (ANOVA, Interaction, p-value = 0.002, F-value = 13.32, df = (1,18); Treatment, p-value = 0.69, F-value = 0.16, df = (1,18); Year, p-value = 0.65, F-value = 0.22, df = (1,18)). Prior to seeding, the drill seeded plot had a higher mean functional dispersion of height than the broadcast plot before seeding and the drill plot after seeding (Tukey's test, broadcast plot 2016, p-value = 0.02; drill plot 2018, p-value = 0.02). Functional dispersion of seed mass found only the interaction to be significant (ANOVA, Interaction, p-value = 0.01, F-value = 8.03, df = (1,18); Treatment, p-value = .7, F-value

= 0.15, df = (1,18); Year, p-value = 0.06, F-value = 3.86, df = (1,18)). There was a significant difference between the drill seed plot prior to and after seeding (Tukey's test, p-value = 0.004). For roots (Figure 2-15), there was a main effect of year and the broadcast plot prior to seeding was different from the broadcast plot after seeding (ANOVA, Interaction, p-value = 0.004, F-value = 11.09, df = (1,18); Treatment, p-value = 0.99, f-value = 0, df = (1,18); Year, p-value = 0.003, F-value = 11.82, df = (1,18); Tukey's test, p-value < 0.001).

Assessing the traits of LDMC, height, seed mass and phenology together found only a main effect of treatment (ANOVA, Treatment, p-value = .01, F-value = 7.3, df = (1,18); Year, p-value = 0.07, F-value = 3.67, df = (1,19)). Functional dispersion decreased from after seeding and the drill seeded plot tended to have lower mean functional dispersion then the broadcast plot. When analyzing only the natives, there was a main effect of treatment and year (ANOVA, Treatment, p-value = 0.04, F-value = 5.05, df = (1,18); Year, p-value = 0.04, F-value = 4.82, df = (1,19)). The drill plot had a higher mean functional dispersion of native species after seeding.

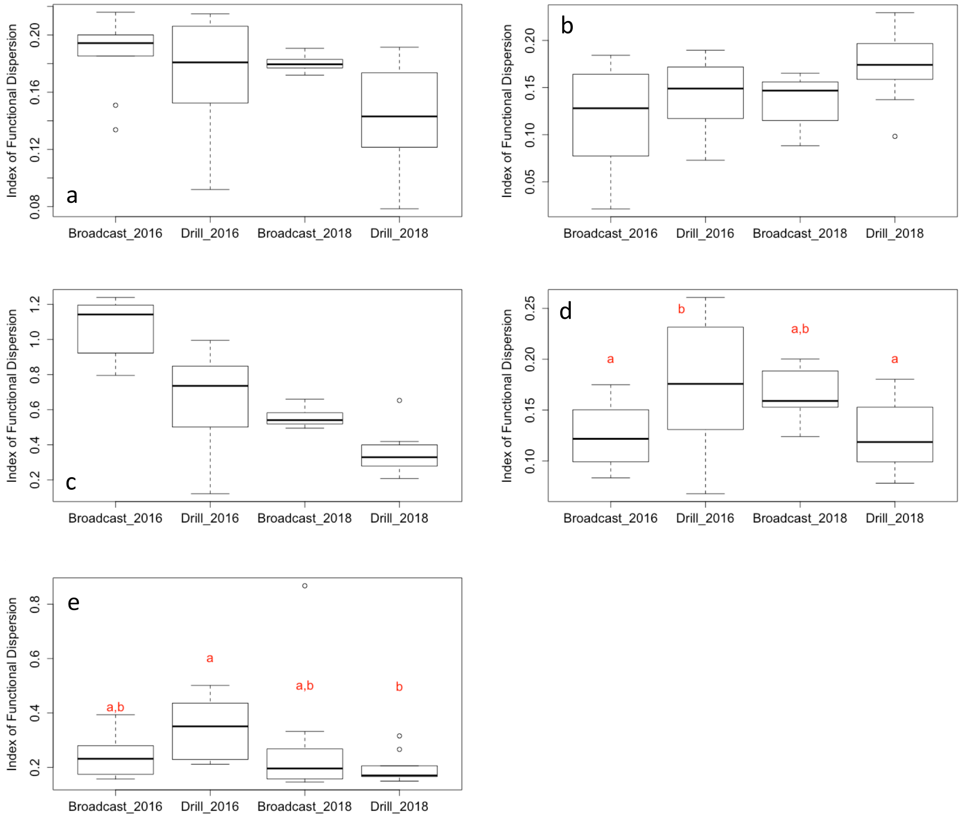

Figure 2-14. Functional dispersion analysis.
Functional dispersion analyses for all species (a) and for native species only (b). Traits were analyzed individually for functional evenness for the traits LDMC, height, and seed mass (c, d, and e, respectively). For all species, functional dispersion analysis found a main effect of treatment, while native species analysis found a main effect of year. Each of the individual trait analyses were different as well with LDMC having a both year and treatment effects, height found drill 2016 was different from drill 2018 and broadcast 2016, and seed mass only the drill plots were different. Red lettering indicates significant differences.

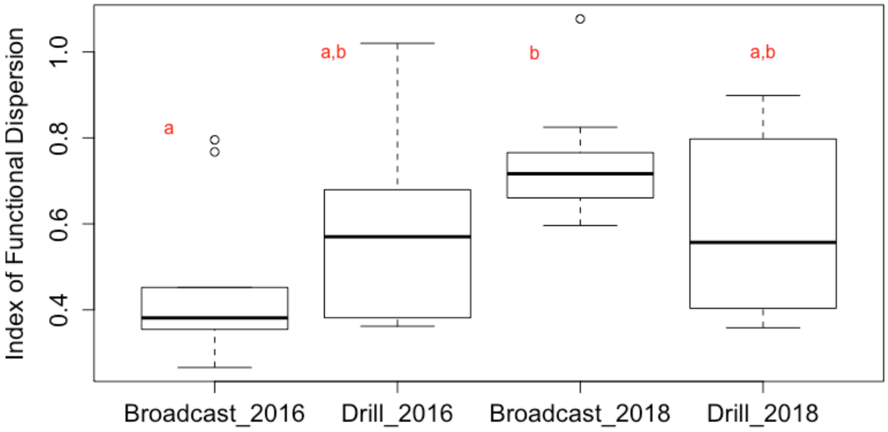

Figure 2-15. Functional dispersion of rooting depth.
The rooting depth of species in broadcast plot prior to seeding was different than the broadcast plot after seeding. There was also a main effect of year. Red letters indicate significant differences.

Functional diversity of the seed mix. Similarly to the analyses described above for actual plant communities, I also examined the functional diversity of the seed mix. This allows a comparison between the observed community and the seed mix, if every species established in the same abundance as in the seed mix. The CWM of the coefficient of conservation was 3.78, which was lower than expected considering all the species in the mix were native and desirable for restoration applications. Phenology of the seed mix includes species representing all seasons, however, wind pollinated species have the greatest abundance (Figure 2-16). CWM for the individual traits LDMC, height, seed mass and rooting depth were 0.32, 0.77, 2.75, and 0.55 respectively. Functional evenness was 0.62 and functional dispersion was 0.21.

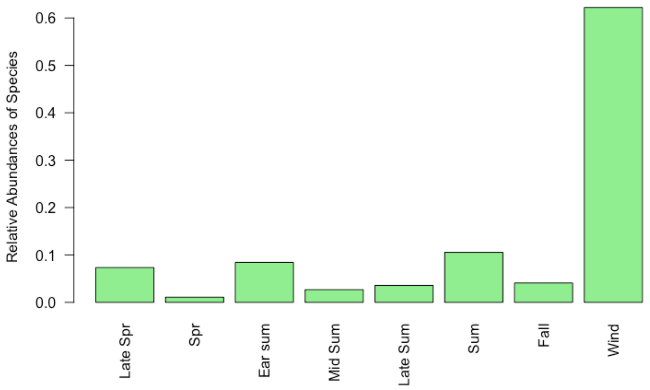

Figure 2-16. Phenology of seed mix of all species established.
There was a high abundance of wind pollinated plants in the seed mix. Flowering species that are important to insect pollinators are represented throughout the year.

Community Analysis. An NMDS ordination was used to visualize the differences in the communities before and after seeding as well as between the two treatments of broadcast and drill (Figure 2-17). The plant communities in both treatment plots before restoration grouped together, while the plots after restoration also seemed to group together. This may indicate a shift in the community after restoration for both broadcast and drill seeding treatments. The resulting community after two years after seeding was also analyzed in a separate ordination. An NMDS ordination of the plot two years after seeding grouped the broadcast and drill seeded plots separately (Figure 2-18). A Mantel test indicated the two treatments were different (p-value = 0.001, r = 0.49). A total of ten indicator species were identified, seven for the broadcast plot and three for the drill plot (Table 2-4.). Of the seven indicator species for the broadcast seeded plot, only one was a non-native and three were from the seed mix. In the drill seeded plot, all three indicator species were non-natives.

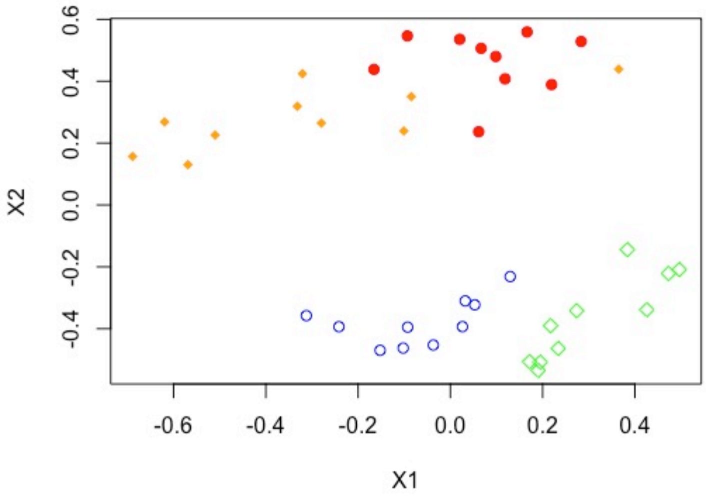

Figure 2-17. NMDS of Observatory Park before and after restoration.
NMDS ordination of broadcast and drill plots before and after restoration. The red filled circles are the broadcast modules before seeding, orange diamonds are the drill modules before seeding, blue open circles are the broadcast modules two years after seeding, and the open green diamonds are the drill modules two years after seeding. This figure visualizes the differences between the communities before and after seeding as well as between the two seeding treatments, broadcast and drill. In both the broadcast and drill plots the communities shifted in composition two years after seeding.

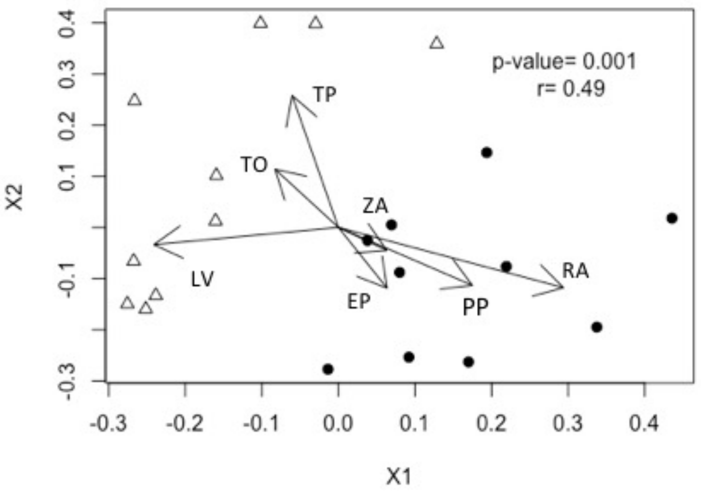

Figure 2-18. NMDS of Observatory Park modules two years after restoration. NMDS plots the modules at Observatory Park two years after restoration. Triangles are drill seeded modules and circles are broadcast modules. A mantel test found that the two groups are statistically different (p-value = 0.001, r = 0.49). Vectors are from the indicator species analysis (Table 4.). The indicator species for the drill seeded modules are all non-native species. In the broadcast plot *Ziza aurea* was the strongest indicator species from the seed mix. LV - *Leucanthemum vulgare*, TP - *Trifolium pretense*, TO - *Taraxacum officinale*, RA - *Ranunculus acris*, PP - *Poa palustris*, EP - *Erigeron philadelphicus*, ZA - *Zizia aurea*.

Species	Cluster	Indicator value	Probability
Ranunculus acris	1	0.9286	0.002
*Poa palustris**	1	0.9005	0.001
*Erigeron philadelphicus**	1	0.8	0.001
*Zizia aurea***	1	0.671	0.035
*Symphyotrichum novae-angliae***	1	0.6667	0.026
*Sisyrinchium angustifolium**	1	0.6545	0.022
*Lobelia siphilitica***	1	0.6	0.009
Leucanthemum vulgare	2	0.8322	0.002
Trifolium pretense	2	0.6641	0.039
Taraxacum officinale	2	0.6061	0.013

Table 2-4. Indicator species analysis for broadcast and drill seeded plot.
Seven species were indicators of the broadcast plot (cluster 1). The three species that had the greatest indicator values for the broadcast plot were *Ranunculus acris*, *Poa palustris*, *Erigeron philadelphicus*. Only the broadcast plot had indicator species that were from the seed mix. Three species, *Leucanthemum vulgare*, *Trifolium pratense*, and *Taraxacum officinale*, were indicators of the drill seeded plot (cluster 2). * Indicate native species, ** indicate species from the seed mix.

Discussion

A taxonomic comparison between seeding methods found differences in which species established successfully. In the last survey year (2018), the drill plot had a greater richness and abundance of seeded grasses than the broadcast plot. I expected to find more of the seeded grasses in the drill plot and this finding is also consistent with what has been reported in other research (Yurkonis et al. 2010b).

There was lower establishment of species richness and abundance of species from the seed mix in the drill than in the broadcast plot. In the drill seeded plot, 14 species accounted for an average of 8.3% of the total cover and in the broadcast plot, 17 species made up an average of 10% of the total cover. These results are similar to Kimball et al. (2014) who found higher establishment of seeded species in hand seeded plots than in drill seeded plots. For restoration practitioners, this may suggest the use of broadcast seeding as a better method for meeting the goal of establishing new species. This is evidenced by the establishment of a greater abundance of natives and more flowering forbs that provide pollinator resources that established in the broadcast plot. This study is focused on the early-stage of restoration, so there is potential for more species to establish or the composition to change. Many restoration studies mention the value of long term monitoring to see changes that occur over longer time scales (Barr, Jonas & Paschke 2017). Subsequent surveys will be needed to see if this trend continues since species composition will likely continue to shift over time.

Seeding did not seem to change the overall diversity of the meadow since there was no significant difference between seeding method or years. I predicted that drill seeding would increase diversity due to the establishment of seeded grasses, but the species that did establish did not change the diversity. A similar experiment testing the differences between drill and broadcast seeding methods also found no difference in diversity (Yurkonis et al. 2010b). In my study, however, a difference was found when comparing native species diversity. In this case, the drill seeded plot had a greater native species diversity than the broadcast seeded plot.

The coefficient of conservation was highest in the broadcast plot after seeding. Broadcast seeding should be a preferred method of restoration if species with high conservation value is a main goal. It is important to note, that even species with lower C of C can be effective and beneficial in restorations. For example, *Andropogon gerardii* (big blue stem), is a common grassland species used in restoration with a fairly wide range of environmental tolerances in prairie type habitats. Because it is common and has a wide distribution, it is in the middle of the range of C of C with a value of 5 (Andreas et al. 2004). These same qualities that assign *A. gerardii* a mid-value C of C are the same qualities that make it an ideal species to use in restoration seed mixes. Seeding rapidly growing, tolerant natives may be a preferred method of an early restoration success compared to seeding rare, habitat specific, high conservation value species. This could be particularly true in areas where the native soil seed bank is depleted. C of C provides insight on the conservation value of species in a community and is useful in combination with other diversity indices, but C of C should not be the only index used to assess whether restoration was successful.

Phenology was examined for patterns of timing of flowering and to determine if pollinator resources are being provided throughout the year. In both the broadcast and drill plots, spring flowering and wind pollinated species are abundant. The same was true for wind pollinated species abundance from the seed mix. Wind pollinated plants were typically grasses and, while important for diversity and structure of a habitat, provide few resources for insects relying on nectar and pollen as food. Pollinator resources were most abundant in spring, likely from the high cover of exotic clovers (*Trifolium sp.*) identified in the survey. The seed mix has spring flowering native species, but few became established and those that did had low abundances. *Ratibida pinnata* and *Zizia aurea* where the only spring flowering species that were established from the seed mix. Seeding did seem to increase the abundance of summer flowering species. The abundances of fall flowering species was low in both plots and it may be useful to add fall flowering species to insure continuous pollinator resource availability.

No significant differences were observed between the indices when comparing before and after seeding, indicating that neither seeding method significantly increased functional diversity more than the other. Some traits in the community did shift depending on treatment. Additionally, the CWM of LDMC decreased in the broadcast plot after restoration, while it remained unchanged in the drill plot. This may suggest that there are more species with lower LDMC in the broadcast plot, and the plants in the community tend to be represented by species with faster growth and biomass production (Garnier et al. 2001; Li et al. 2017). CWM of height also significantly increased in the broadcast plot compared to the drill plot. An increase in height suggests a greater abundance taller more competitive plants in the broadcast plot. Hedberg (2013) also found changes in canopy height in restored fen communities where restored communities had a greater canopy height than reference sites. The greatest seed mass was in the drill seeded plot before seeding the native mix. This suggests that there was an abundance of species with larger seeds prior to restoring. The results also showed that seed mass of broadcast and drill seeding in the final year of survey had similar weights. Seed weight is related to dispersal distance, stress tolerance and fecundity, so similar seed weight infers similar function in both plots (Muller-Landau 2010). Roots did show a trend of deeper rooting species establishing after seeding. This could be related to the species that established from the seed mix. The CWM of rooting depth for the seed mix was 0.55m which was greater than the CWM of both broadcast and drill plots before seeding. Deeper rooted species could potentially access to water and nutrients unavailable to shallow rooting species.

Contrary to what I predicted, functional evenness for all species and for native species only did not change with time or seeding method. A study on succession in grasslands found similar results with little change in evenness of traits over time (Kelemen et al. 2017). LDMC had minor increases in evenness but was not statistically different for all plots, while evenness in height decreased in both broadcast and drill seeded plots. Decreasing functional evenness over time may indicate that traits became less evenly distributed across the range of observed values after restoration (Schleuter et al. 2010).

Functional dispersion of LDMC decreased and may indicate redundancy for this trait. The drill seeded plot in 2018 had the lowest functional dispersion which may indicate the LDMC values for the species in this plot are similar to each other. Besides trait redundancy, low functional dispersion can be an indicator of environmental filtering (Hedberg et al. 2013). It could be that seed placement under the soil surface by drill seeding acted as an environmental filter and selected species that are able to germinate under these conditions. Since this study only investigated two years after seeding, it is also possible for functional dispersion to change over time. In a study of fen restoration, functional dispersion remained unchanged in the first three years after restoration and then increased between 3-8 years after restoration (Hedberg et al. 2013).

Overall, restoration did not change the functional evenness or dispersion of traits in the plot. There were, however, differences in some traits when analyzed individually. This trend is evident in the CWM of LDMC, height, seed mass and rooting depth. In these analyses the trait values changed after seeding.

Although there were no strong trends across functional indices for either broadcast or drill seeding, some of the indices of functional diversity did identify community shifts, particularly for CWM of traits. Thus, functional diversity indices can identify trait shifts within a community resulting from management activities. Additionally, by tracking changes in functional diversity managers can add species with traits that are needed to support manager goals.

In the community analysis, the species composition of the broadcast and drill plots were different two years after seeding. The broadcast seeded plot had more natives and more seed mix species that were significant indicators than the drill seeded plot. This finding further supports that the practice of broadcast seeding establishes seeded species early in restoration when compared to drill seeding.

Assessing restorations through functional diversity can give insight into the structure and function of a community but it is also meaningful for management. In this context, trait assessments could potentially be a guide when planning management activities. Managers can identify gaps in floral resources by determining the abundance of flowering phenology. In our analysis we were able to make recommendations on what phenology types might be beneficial. Plant traits and their diversity may not be top priority for all managers, but should still be considered as part of a comprehensive restoration plan because of the potential benefits. Increasing functional trait diversity in a community also has implications for controlling unwanted non-native species (Pokorny, Sheley & Engel 2005). Another added advantage of assessing functional trait information is planning for resiliency and stability in the community facing future climate change. Future planning should consider not only how complementary plant traits are but also how redundant they are so that ecosystems can continue to provide services important to management goals (Klaus et al. 2016; Kohler et al. 2017).

CHAPTER III

NORTHEAST OHIO REGIONAL MEADOW SURVEY

Summary

Understanding how restoration seeding practices can influence plant communities is important to future planning of natural areas. Restoration outcomes can be variable, and it is important to assess restoration success at many sites, as well as over longer time periods. One way to assess changes in plant communities in a restoration context is to examine the functional traits of the new plant communities. Five paired restored and unrestored areas across the Cleveland, Ohio Metropolitan Area were surveyed in 2017 and 2018. I used functional diversity indices to assess differences in plant communities between restored meadows that received a seeding treatment and unrestored adjacent areas. I found that native species richness and diversity were similar, but that native species abundance increased with time after restoration. From a functional diversity perspective, there was no difference between restored and unrestored meadows. However, I did find significant differences in the coefficient of conservatism, an indicator of conservation value, between restored and unrestored areas. Phenology patterns also revealed that seed mixes might benefit from additions of spring and fall flowering plants.

Introduction

Anthropogenic changes to the landscape have put increasing pressure on the delivery of ecosystem services (Arico et al. 2005; Kohler et al. 2017). Some of these anthropogenic disturbances include changing land use and land abandonment which have led to low diversity sites dominated by non-native and exotic species. These sites, however, can also be considered as opportunities to enhance biodiversity and ecosystem services through restoration (Fischer et al. 2013). Restoration through seeding a native species mix is a widely used method that can overcome the challenges associated with spontaneous succession. Some of these challenges include lack of or limited source populations for recruitment and high abundances of non-native species (Baasch et al. 2012; Prach, Jongepierová & Řehounková 2013; Hill & Fischer 2014). By seeding a mix of desired species, land managers can attain restoration goals by establishing native vegetation, increasing conservation value, and enhancing pollinator resources.

Monitoring vegetation over time helps determine how restoration is progressing and how the community is changing. Characterizing changes in an ecosystem is often done though taxonomic assessments. A taxonomic approach can be useful in assessing species composition and diversity, and it allows monitoring of the presence of native and non-native plant species. In contrast to a species identity approach, functional traits use a plant's morphology and physiology, as they often relate to how plants respond to, or affect their environments (de Bello et al. 2010). Functional traits can also help identify how plant traits and strategies might differ between ecosystems or how they are changing over time (D’Astous et al. 2013; Piqueray et al. 2015; Kelemen et al. 2017). For example, in a study of old field succession, leaf traits identified a shift in community composition over time resulting in plants with more conservative resource use strategies (Kelemen et al. 2017). Additional information about the patterns of vegetation changes in a community are revealed by including both species and traits in assessments. Zhang et al. (2015a) were able to conclude that the change in trajectory for species assembly was different from the direction of change in trait assembly by analyzing both species and functional traits of plants. By applying both species and functional trait analyses, a complete assessment and comparison of changes can be made.

Functional traits and their diversity can be useful since they are correlated to ecosystem services and processes (Mokany et al. 2008; de Bello et al. 2010; Kohler et al. 2017). It is important to understand the relationship between traits and ecosystem function for proper management and species selection in restoration. In a study by Rayome et al. (2018), species were categorized based on their strategy for carbon storage and were planted in different combinations. Having different categories of carbon storage helped identify that redundant carbon storage traits sequestered more carbon than complementary storage traits (Rayome et al. 2018).

Target trait values can be flexible and necessary depending on the ecosystem and the goals of restoration. In a study of fen restoration, functional diversity indices increased in response to restoration, but reference sites had lower functional diversity overall (Hedberg et al. 2013). Lower functional diversity may be appropriate in the context of fens and their specific environmental conditions, but perhaps less so if the goal, for example, is efficient resource use. In the latter case, a higher functional diversity and complementary traits would be the restoration goal (Zuo et al. 2016). It is important to note that such indices provide a comparison between communities or sites rather than an absolute value that must be met.

The objective of this large-scale regional survey is to understand patterns of restoration, establishment of native vegetation and functional diversity between restored areas and those that were not restored. To investigate this, I surveyed the plant community in 5 paired restored and unrestored areas, over two years. I expected that sites that were restored would be more taxonomically and functionally diverse. Functional evenness is predicted to be greater in restored areas, especially for flowering phenology since seed mixes often include forbs. I also expected that restored areas will have a greater abundance of native plants due to the addition of seed, than those that were not restored and that this abundance would increase with time after restoration.

Methods

Location. Five locations in Northeast Ohio were included in this study, each with a plot that was seeded as a method of restoration (restored) and a plot that was not seeded but with similar management (unrestored) within at least 3 miles of each other (Table 3-1 and Figure 3-1). All sites were 2 or more acres and were previously in agricultural production prior to becoming a park. All restored sites were restored using a native seed mix, typically after burning, mowing or using herbicide to remove weedy and invasive plants. Sites selected include Frohring Meadow in Geauga County, Skok Meadow in Lake County, Circle Emerald in Cuyahoga County, Tallmadge Meadows in Summit County, and Dix Park and Morgan Preserve in Portage County. An additional site surveyed was Springfield Bog in Summit County, which met the criteria for selection of a restored plot but did not have an analogous unrestored plot within the 3 miles. Sites are managed by local park districts who used controlled burning and mowing intermittently to reduce woody vegetation.

The seed mixes used varied in richness, from 12 to 37 species, and in diversity, with different species making up different percentages in the mixes. Sites were either drill or broadcast seeded. The year seeding took place also varied with the earliest seeding in 1999 and most recent in 2016.

Site	Restored - Method/ Unrestored	Park District	GPS Coordinates	Year Restored	Size of Meadow (appox. Acres)
Dix Park	Restored - Drill	Portage Park District	41.190380°, -81.245610°	2016	1.5
Morgan Preserve	Unrestored	Portage Park District	41.232180°, -81.227310°	NA	40.1
Frohring Meadows	Restored - Drill	Geauga Park District	41.408670°, -81.361930°	2012	3.3
Frohring Meadows	Unrestored	Geauga Park District	41.410230°, -81.362140°	NA	16.7
Tallmadge Meadows	Restored - Broadcast	Summit Metro Parks	41.129730°, -81.434300°	2010	3.8
Tallmadge Meadows	Unrestored	Summit Metro Parks	41.129160°, -81.435830°	NA	22.5
Skok Meadow - Skok	Restored – Broadcast/Drill	Lake Metroparks	41.657897°, -81.190619°	2010	19.5
Skok Meadow – Girdled Rd. Res.	Unrestored	Lake Metroparks	41.645280°, -81.174750°	NA	2.7
Springfield Bog	Restored - Drill	Summit Metro Parks	41.011040°, -81.396540°	2010	95.2
Circle Emerald	Restored - Drill	Cleveland Metroparks	41.383500°, -81.567380°	1999	4.8
Circle Emerald	Unrestored	Cleveland Metroparks	41.382880°, -81.563740°	NA	18.7

Table 3-1. Summary of Sites.
Study sites are listed with information on the park district they are in, GPS coordinates, the year they are restored and size of the park.

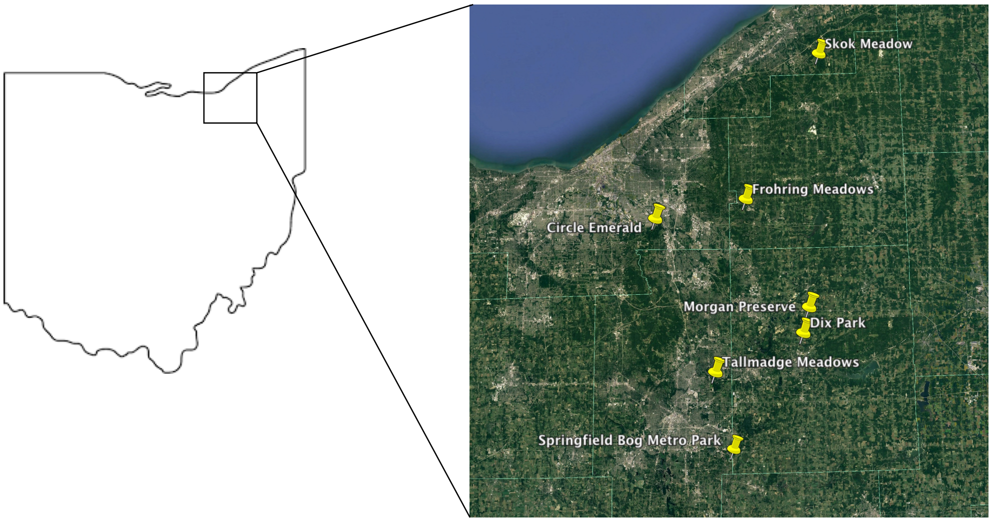

Figure 3-1. Map of site locations.
Map includes the 5 paired sites and Springfield bog, the unpaired restored site.

Vegetation Surveys. A pre-survey was done in 2016 and collected data at Frohring Meadows, Skok Meadow, and Circle Emerald. All parks were surveyed in 2017 and 2018 between June and August. I used the North Carolina Vegetation Survey protocol, which involves collecting data on species presence and abundance as percent cover classes (Peet et al. 1998). The protocol uses a 20 x 50 m plot with a multiscale, nested design. Within each plot there are 10 subplots, or modules, that are 10 x 10 m. Four of the subplots are nested and provide a systematic approach to identifying species. This method has numerous benefits, one of which is its compatibility with other survey designs due to its modular shape and multiple scales. Another benefit of this design is that it performs well in patchy environments (Goslee 2006). Plots were permanently marked at the corners with metal nails. The plot at Morgan Preserve did change position and had to be shifted 90 degrees in 2018 due to park improvements and trail maintenance.

Functional traits. Plants that were only identified to genus were removed from the analyses since traits could not be evaluated at this level of identification. Additionally, species that composed at least 1% cover were used for functional traits analysis. In total, 78 species were used and these species made up at least 90% of the total cover. This follows other functional diversity research that supports including species that make up the majority of cover (Mokany et al. 2008; Costa et al. 2017; Kohler et al. 2017). Functional traits used for analysis were leaf dry matter content (LDMC), plant height, seed mass, flowering phenology and rooting depth (Laughlin 2014a). Traits were chosen following the leaf, height, seed (LHS) approach proposed by Westoby (1998). Rooting depth was analyzed separately because there were many missing trait values (only 70% of traits were available for all the species used and only 66% of the native species),which can potentially skew the results of the functional diversity indices (Lefcheck et al. 2015). Traits were retrieved from TRY Plant Trait Database and the USDA Plants Database (Kattge et al. 2011; USDA, NRCS. 2019; see Appendix for references of all trait data used). The USDA Plants Database was also used to determine if species were native or non-native.

LDMC was collected for 18 species that did not have the traits available in the TRY database. Data collection for LDMC followed protocols by Cornelissen et al. (2003). Seven to 10 individuals per species were collected and rehydrated overnight in the dark at 4 degrees Celsius before removing the leaves (except for *Solidago rigida*, where 2 individuals were sampled as most leaves wilted after rehydrating in fridge). At least two leaves, including petiole, per individual were removed from the stem and a water saturated mass was recorded. Leaves were then dried in an oven at 60 degrees Celsius for 72 hours and measured again to obtain a dry mass.

Taxonomic diversity metrics were calculated to understand species composition. Additionally, the coefficient of conservatism (C of C) was assigned to each plant following the Vegetation of Index of Biotic Integrity (VIBI) for Ohio (Andreas et al. 2004). This metric ranks species based on expert knowledge and the species perceived value to the environment as well as ecological tolerances. The coefficient of conservatism provides a way to compare the conservation value of sites which might not be captured by taxonomy alone.

For individual trait analysis, the community weighted mean (CWM) was determined. The CWM weights the mean trait values in a community by the species abundance. This measure of trait distribution identifies the most dominate trait values in the community (Valencia et al. 2015). Comparing the CWM may distinguish different communities in terms of structure, as in the CWM of height, or if they differ in overall competitiveness, as the CWM of LDMC may indicate (Garnier et al. 2001). CWM of abundance for phenology by season was used to compare timing and abundance of flowering species. The greater the abundance of species flowering during a particular season, the more pollinator resources are available.

Trait diversity was analyzed by evaluating functional diversity indices for each trait separately, and with a multivariate approach using multiple traits (leaf dry matter content (LDMC; g/g), height (m), seed mass (mg) and flowering phenology) proposed by Lefcheck et al. (2015; but also see Hedberg et al. 2013).

Functional evenness and dispersion indices for all traits and for each individual trait were calculated to understand how traits within the community are assembled. Functional evenness describes how traits are distributed relative to one another within the available trait space. The index is constrained between 0 and 1 where values closer to 0 indicate traits are less evenly distributed and values closer to 1 indicate traits that are more evenly distributed (Schleuter et al. 2010). How traits are distributed can then be used to interpret how resources are being used. A value closer to 1 may indicate efficient resource use or that there is competition (Mouchet et al. 2010; Schleuter et al. 2010). Functional dispersion describes how species are placed in trait space by calculating the distance of each species from the centroid of all trait values and averaging them (Laliberte & Legendre 2010). This index evaluates how similar traits are relative to one another. A value of 0 would be expected in a monoculture, or communities with only one species present. However, unlike functional evenness, dispersion can be greater than 1. A low index value would indicate that traits in the community are redundant (Karadimou et al. 2016) and a higher value would mean that many functional traits are present and different from each other (Zuo et al. 2016).

Statistical analysis. All statistical analyses were calculated using R (R Core Team 2017). Because results were similar in both years, 2018 was used for the analyses presented. Functional trait analysis for CWM and functional diversity indices were calculated using the ‘FD’ package in R (Laliberte & Legendre 2010; Laliberte, Legendre & Shipley 2014). To determine if the means of the indices were different between restored and unrestored areas, a paired t-test was used. Springfield Bog was not used for these analyses because it did not have an analogous unrestored plot within the specified

3-mile radius. Linear regression was used use to determine if there was a relationship between time since restoration and percent change in abundance of natives. This regression analysis did not include Springfield Bog because there was no unrestored plot to calculate the difference in native species abundance. A regression of time since restoration and native diversity evaluated only restored plots and included Springfield Bog.

Results

The survey identified 201 species from all six sites. Species richness was not different between restored and unrestored plots (Figure 3-2; Paired T-test, t = 0.93, df = 4, p-value = 0.41). Native species richness was slightly higher in the restored plots, but this difference was only marginally significant (Figure 3-3; Paired T-test, t = 2.72, df = 4, p-value = 0.053).

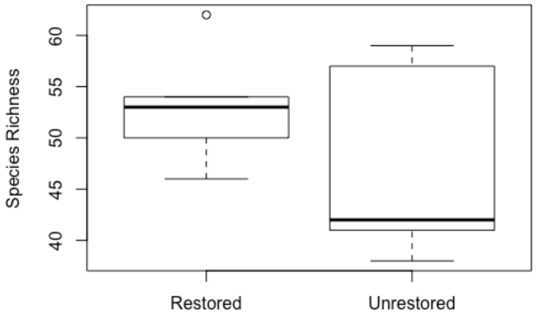

Figure 3-2. Species richness.
There was no difference between species richness in restored and unrestored plots (Paired T-test, t = 0.93, df = 4, p-value = 0.41).

Figure 3-3. Native species richness.
Native species richness was greater in restored plots, but this difference was not statistically significant (Paired T-test, t = 2.72, df = 4, p-value = 0.053).

The percent cover of native species was greater in the restored plots than unrestored plots, but this difference was not statistically significant (Figure 3-4; Paired T-test, t = 1.62, df = 4, p-value = 0.18). Native species were also assessed to compare differences in abundance of natives at each site (Figure 3-5). Three out of the five sites had more native abundance in restored plots than unrestored plots. Skok Meadow and Circle Emerald had the greatest differences between the restored plot and unrestored plot. Frohring Meadows also had more native abundance in the restored plot than the unrestored plot. Tallmadge Meadows had more native abundance in the plot that was unrestored, but this difference was smallest. Portage Parks was the most recently restored and had more native species in the plot that was unrestored.

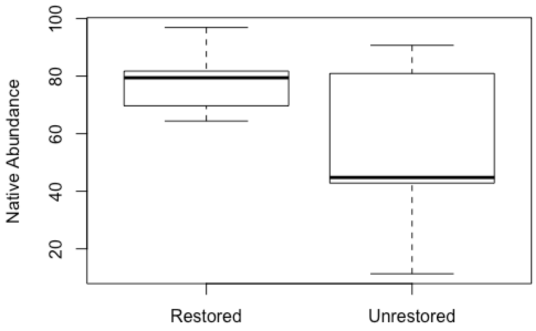

Figure 3-4. Percent native species abundance in restored and unrestored plots.
The figure to the left shows that the mean of abundance of native species is higher, however it is not statistically significant (Paired T-test, t = 1.62, df = 4, p-value = 0.18).

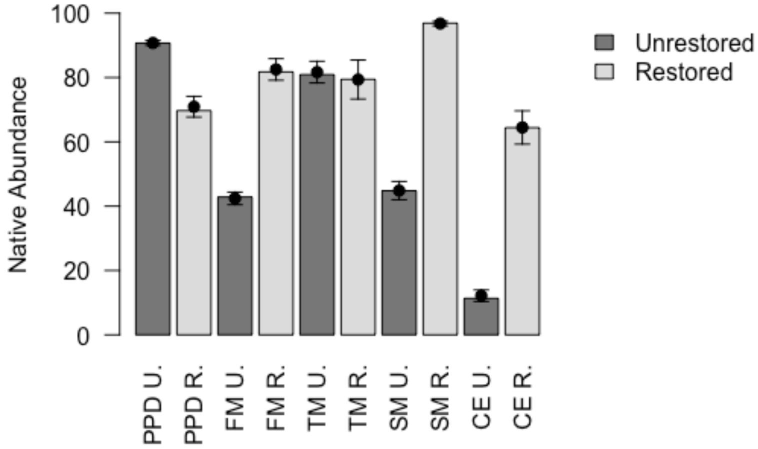

Figure 3-5. Abundance of native species in areas that restored and unrestored.
Sites are in order of time since restoration. Sites, PPD – Portage Parks District; FM – Frohring Meadows; TM – Tallmadge Meadows; SM – Skok Meadow; CE – Circle Emerald. Portage Parks and Tallmadge Meadows are the only two sites where the areas that were not seed have a greater abundance of native species.

There is a significant relationship between percent change in native abundance and time since restoration (Figure 3-6; Regression; p-value = 0.02, R^2 = .89). This may indicate that seeding as a method of restoration increases native abundance compared to those areas that were not restored. A similar pattern is seen when considering native diversity and time since restoration, but this relationship is not statistically significant (Figure 3-7; Regression, p-value = 0.54, $R^2 = 0.1$).

Figure 3-6. Percent change in native species abundance.
As time since restoration increases the percent change in abundance of native species between restored and unrestored plots also increases. This may indicate that as a restoration progresses native will increase in abundance (Regression; p-value = 0.02, $R^2 = 0.89$).

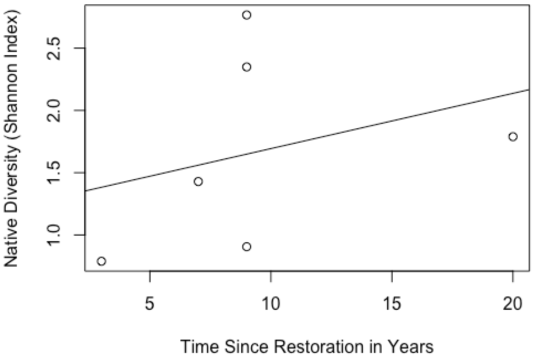

Figure 3-7. Native diversity and time since restoration.
A weak, non-significant relationship was found between time since restoration and diversity. (This analysis includes Springfield Bog; Regression analysis p-value = 0.54, $R^2 = 0.1$).

Species diversity of all species and only natives was not significantly different between restored and unrestored areas (Figures 3-8 and 3-9 respectively; All species diversity, Paired T-test, t = -0.7, df = 4, p-value = 0.522; Native diversity, Paired T-test, t = -0.94, df = 4, p-value = 0.4).

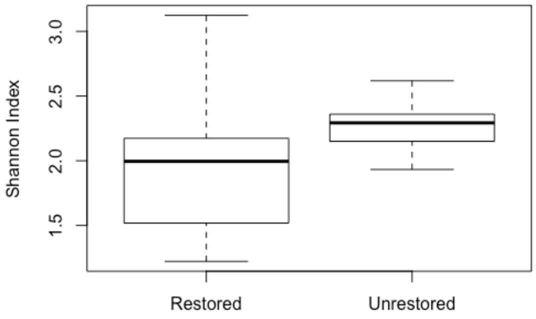

Figure 3-8. Species diversity in restored and unrestored plots.
There was no difference in species diversity between restored and unrestored meadows (Paired T-test, t = -0.7, df = 4, p-value = 0.522).

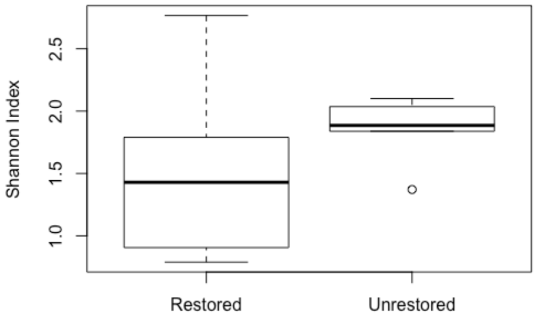

Figure 3-9. Native species diversity in restored and unrestored plots.
The mean of the Shannon Index of Diversity for the unrested plot was slightly higher than the mean of the restored plot. This difference was not significant though (Paired T-test, t = -0.94, df = 4, p-value = 0.4).

A significant difference was found between restored and unrestored plots in the coefficient of conservatism were a higher mean coefficient value was found for the restored plots (Figure 3-10; Paired T-test, t = 2.97, df = 4, p-value = 0.04).

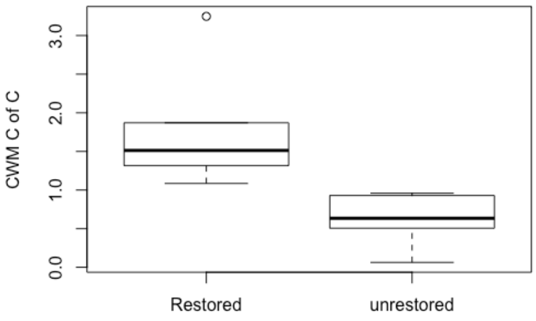

Figure 3-10. Community weighted mean of coefficient of conservatism.
The mean conservation value was higher in the restored plots than unrestored plots (T-test, t = 2.97, df = 4, p-value = 0.04). This indicates seeding to restore meadows can increase the conservation value.

Restoration does not appear to have shifted mean values of individual traits. Analysis of community weighted mean of individual traits found no difference between restored and unrestored plots (Figure 3-11; Paired T-test, LDMC, t = 0.88, df = 4, p-value = 0.43; height, t = -0.93, df = 4, p-value = 0.41; seed mass, t = -0.52, df = 4, p-value = 0.64; rooting depth, t = -1.04, df = 4, p-value = 0.36). Similarly, when considering only the native species, there was no difference between restored and unrestored plots (Figure 3-12; Paired T-test, LDMC, t = 1.24, df = 4, p-value = 0.28; height, t = -2.16, df = 4, p-value = 0.097; seed mass, t = -0.52, df = 4, p-value = 0.628; rooting depth, t = -0.63, df = 4, p-value = 0.56).

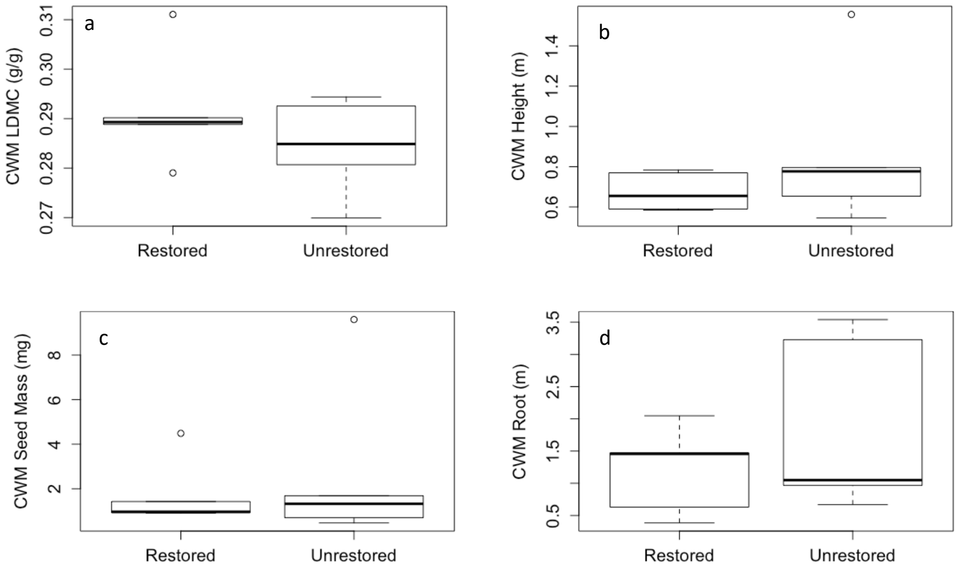

Figure 3-11. Community weighted mean of individual traits.
Individual traits showed no significant differences between restored and unrestored sites. Traits top left LDMC (a), top right height (b), bottom left seed mass (c) and bottom right rooting depth (d).

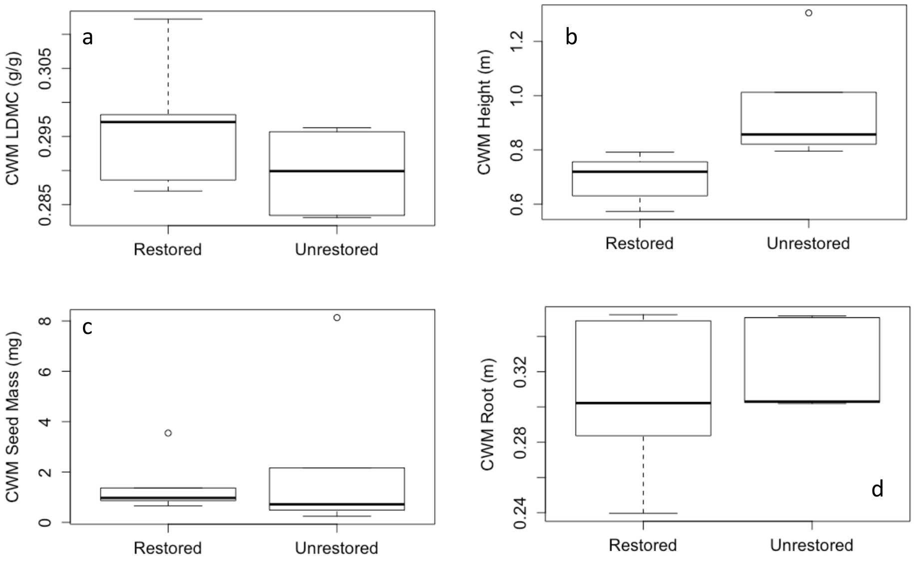

Figure 3-12. Native species community weighted mean of individual traits.
There was no difference between restored meadows and unrestored for CWM of individual traits. Top left LDMC (a), top right height (b), bottom left seed mass (c), bottom right rooting depth (d).

Flowering phenology varied from site to site and between restored and unrestored plots (Figures 3-13 – 3-18). Most sites had the greatest abundance of flowering species in summer. There were some spring flowering species, but these were not as abundant as the summer blooming species. Fall flowering species were the least abundant. Wind pollinated plants were also considered in this analysis but not shown in the graphs since the focus was on determining the evenness of abundance in timing of floral resources. Wind pollinated species ranged from 1.4% to 79% abundance in restored plots and 17% to 77% in plots that were unrestored. (see wind pollinated species abundances in respective graph captions).

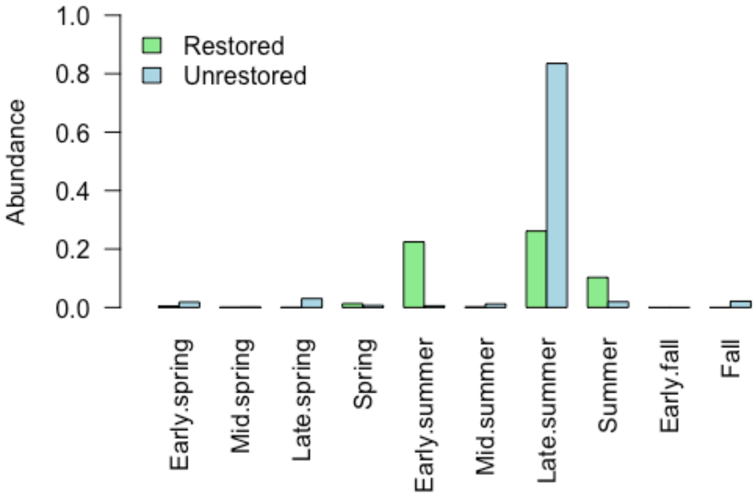

Figure 3-13. Portage Parks phenology of insect pollinated plants.
Wind pollinated species abundance was 39% in restored plots and 50% in unrestored plots.

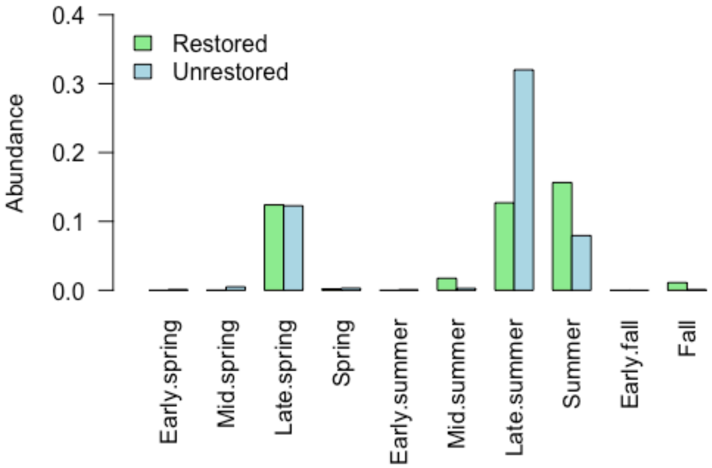

Figure 3-14. Frohring Meadows phenology of insect pollinated plants.
Peak flowering abundance was in summer for plots that were unrestored. Restored plots seem to be more even in the distribution of floral resources throughout the year with spring, summer and fall seasons represented. Wind pollinated plants accounted for 56% of the abundance in restored plots and 46% in unrestored plots.

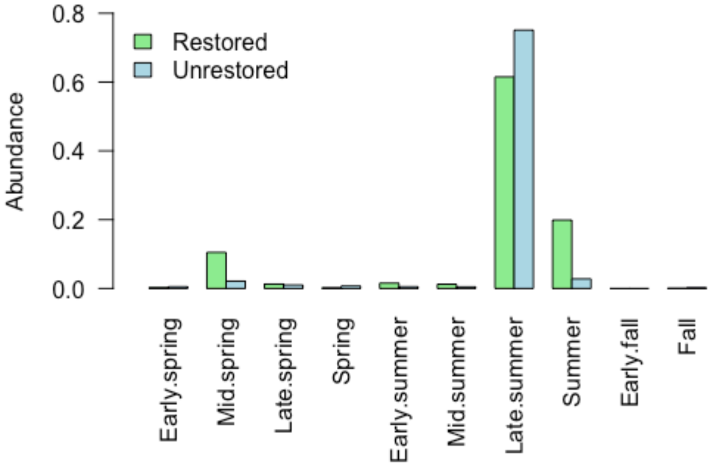

Figure 3-15. Tallmadge Meadows phenology of insect pollinated species.
Peak abundance of flowering was in summer for both restored and unrestored plots. Abundances of wind pollinated species was 3% in restored plots and 17% in unrestored plots.

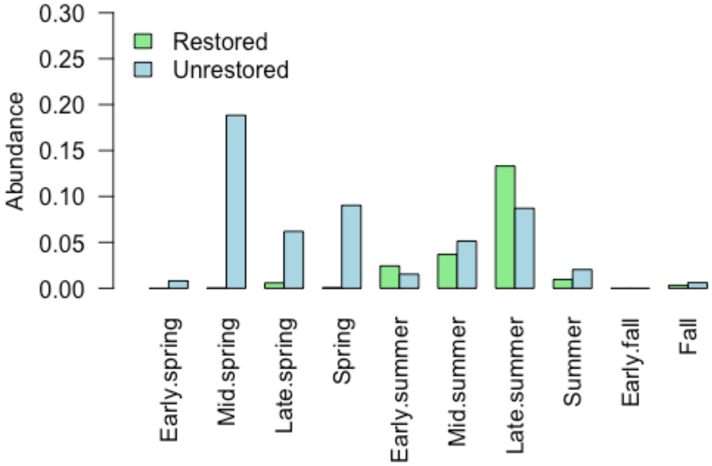

Figure 3-16. Skok Meadow phenology of insect pollinated plants.
The plot that was unrestored had a more even distribution of floral resources throughout the year than the restored plot. Peak flowering time for the plot that was unrestored is mid spring while the restored plot had a peak flowering abundance in late summer. Wind pollinated species abundances was 79% in restored plots and 47% in unrestored plots.

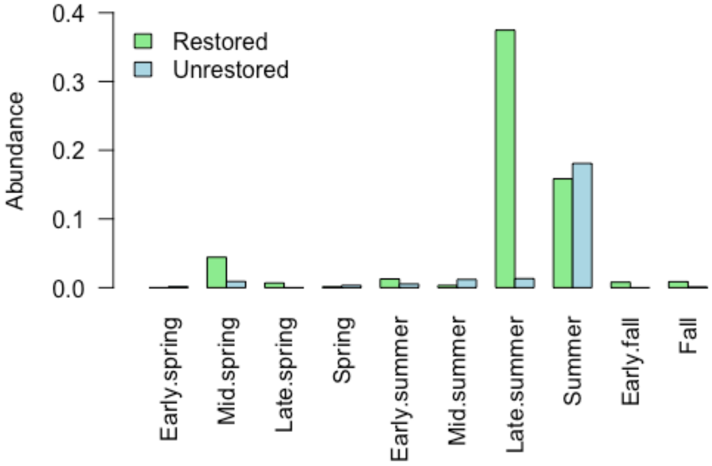

Figure 3-17. Circle Emerald phenology of insect pollinated plants.
Peak flowering time for both plots was in summer. The unrestored plot had more wind pollinated species abundance than insect pollinated species. Species with wind pollination made up 38% of the abundance of restored plots and 77% of unrestored plots.

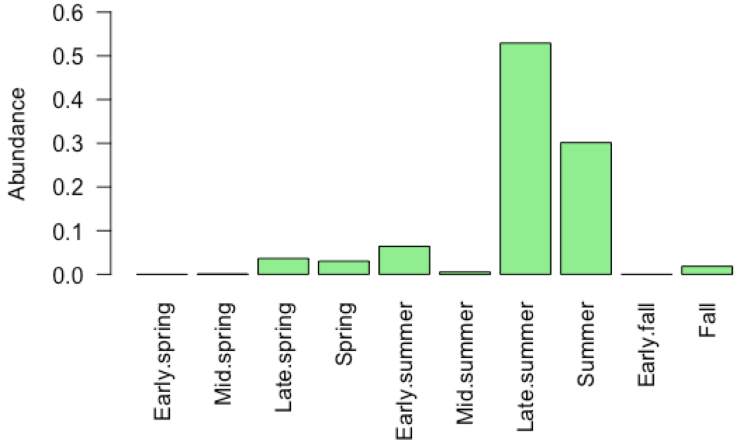

Figure 3-18. Springfield Bog phenology of insect pollinated species.
Peak floral abundance is in summer. Spring and fall abundances are low but still present. Abundances of wind pollinated species was 1.4%. Only the restored plot at Springfield Bog is shown. This site did not have analogous unrestored area to compare with the restored area of the park.

Functional trait values tended to be more even in plots that were unrestored, but there was no statistical difference between plots (Figure 3-19; Paired T-test results; all traits and species, t = -0.86, df = 4, p-value = 0.44; Native species, t = -0.79, df = 4, p-value = 0.48; LDMC, t = -0.84, df = 4, p-value = 0.45; height, t = -1.28, df = 4, p-value = 0.27; seed mass, t = -1.5, df = 4, p-value = 0.21). Rooting depth evenness also had a similar pattern where the plots that were unrestored had higher evenness, but it was not significant (Figure 3-20; Paired T-test, t = -2.51, df = 4, p-value - 0.07).

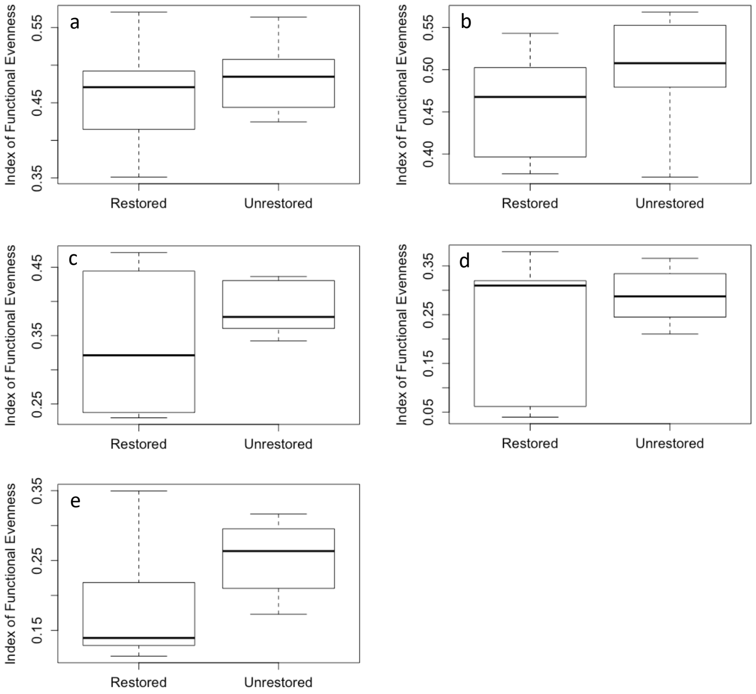

Figure 3-19. Functional evenness of regional survey.
Boxplots compare restored plots with unrestored plots. Functional evenness of all species (a), only natives (b), LDMC (c), height (d) and seed mass (e). Mean evenness tended to be greater in plots that were unrestored, but there was no statistical difference.

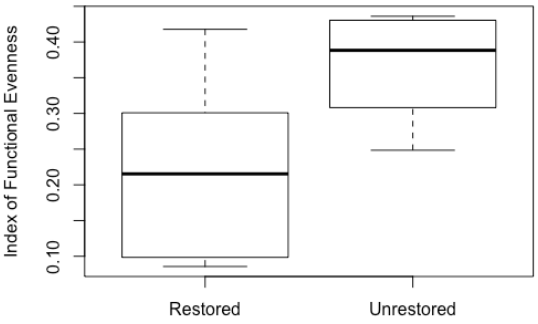

Figure 3-20. Functional evenness of root traits.
Rooting depth was more evenly distributed in plots that were unrestored than plots that were restored, but this difference was not significant (Paired T-test, t = -2.51, df = 4, p-value - 0.07).

Functional dispersion tended to be higher in the restored plots meaning that traits were less similar to each other, but again there was not a significant difference (Figure 3-21; Paired T-test, Functional dispersion for all traits, t = 0.21, df = 4, p-value = 0.85; Native species and all traits, t = 0.43, df = 4, p-value = 0.7; LDMC, t = 1, df = 4, p-value = 0.37; height, t = -0.96, df = 4, p-value = 0.39; seed mass, t = -0.6, df = 4, p-value = 0.59). The difference in dispersion of rooting depth was also not significant and dispersion values were similar in both restored and unrestored plots (Figure 3-22; Paired T-test, t = -0.46, df = 4, p-value = 0.67).

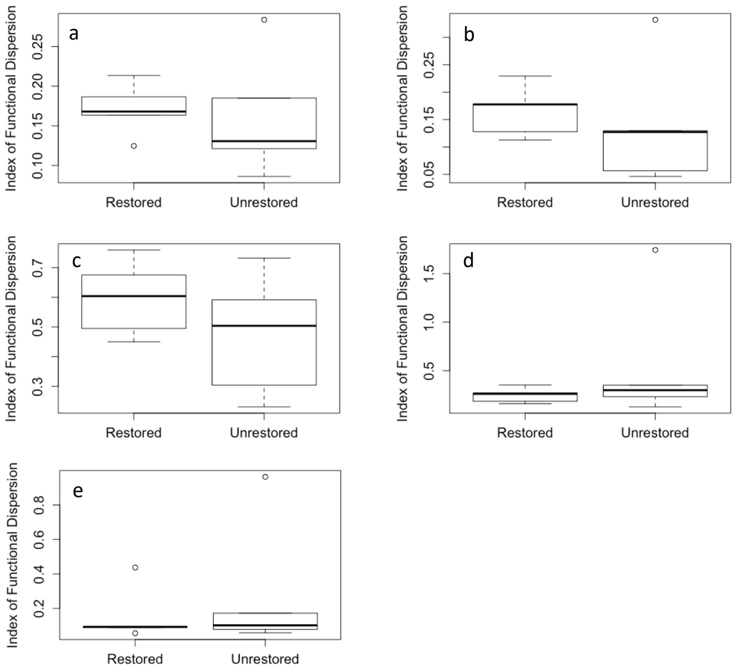

Figure 3-21. Functional dispersion of regional survey.
Boxplots compare seeded restored plots and not seeded, not restored plots. Functional dispersion of all species (a), only natives (b), LDMC (c), height (d) and seed mass (e). There was no difference in functional dispersion between restored plots and those that were not restored.

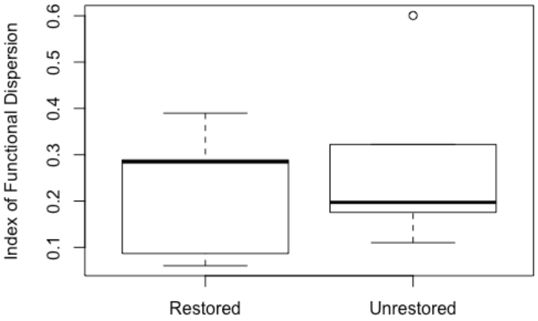

Figure 3-22. Functional dispersion of rooting depth.
There was no difference in dispersion of rooting depth between restored and unrestored plots (Paired T-test, t = -0.46, df = 4, p-value = 0.67).

Discussion

Diversity indices did not identify differences between restored plots and those that were unrestored. Native species abundance and richness generally had higher mean values, but these differences were not statistically significantly different between sites. Native diversity had an opposite pattern where there was higher diversity in plots that were not restored compared to the restored sites. This comparison however, did not consider time since restoration, which can be an important aspect of community assembly. Restorations can take many years to reach communities that are comparable to reference sites and some components might be more quickly reestablished then others (Engst et al. 2016). While species richness and diversity were not significantly different between restored and unrestored plots, the abundance of natives did increase over time. For percent change in native abundance over time, it is clear restoration can alter the community composition and place it on a path of increasing native species cover. This suggests that seeding can establish natives and meet restoration goals of increasing native abundance.

Another positive indication of the benefits of seeding was the increase in conservation value between restored and unrestored meadows. This is could be due to the presence and abundance of species from the seed mixes. Since the mixes contain native seeds, direct addition of these species influences both native species richness and abundances. Indeed, richness and abundance of native species was greater in restored areas, however, there was not a significant difference. Weighting the coefficient by the abundances of these species demonstrates that this metric has value in determining differences in the plant communities. Other restoration research using coefficient of conservatism have reported an increase in the mean of the coefficient of conservatism as a restoration ages, even while diversity metrics showed differing tends (Carter & Blair 2012). Additionally, a higher conservation value for restored areas confirms that seeding is meeting some management goals.

One of the most frequently mentioned management goals was increasing pollinator resources. Insect pollinated species were assessed for abundance and timing of flowering to visualize the evenness of resources throughout the year. This information is important for determining how sites might be providing floral resources for pollinators. A common factor among all the sites was that summer blooming species had the greatest abundance when compared to other seasons. Spring and fall were under-represented in the restored plots, except for Frohring Meadows where spring flowering species were abundant. Carter and Blair (2012) also found that species with spring phenologies had lower abundances than late phenology species. They also emphasized the implications this has for functional diversity and when formulating seed mixes for restoration. Increasing the diversity of the flower community is one way to ensure pollinator resources are available throughout the year (Dorado & Vázquez 2014). Wind pollinated species abundance was high in some restored plots (up to 79%). The addition of flowering forbs could shift the abundance so that insect pollinated species have a greater presence. Assessing restorations in this way can inform management decisions regarding what species and phenology would most benefit the site.

CWM functional evenness and functional dispersion showed no difference between restored and unrestored plots when analyzing trait composition. No difference in CWM of traits due to restoration has been reported (Laughlin et al. 2017), but other research has been able to detect differences in trait composition due to restoration (D'Astous et al. 2013; Hedberg et al. 2013). In one study, differences were found for individual traits as well as for functional dispersion between restoration and reference sites (Hedberg et al. 2013). Similarly, trait composition monitored over time also found variation between restoration stages (D'Astous et al. 2013). One reason for this result could be because of similar environmental factors and land use. This has been seen in other grassland studies where trait composition depended on the land-use history and whether or not a site was restored after tillage (Zirbel et al. 2017). All of the sites chosen for this research had similar management histories of agricultural production followed by a fallow period and management by mowing and periodic burning.

Trait assessments can also be valuable to understanding how plant communities assemble and to predict the outcome of a restoration (Engst, Baasch & Bruelheide 2017; Zirbel et al. 2017). Functional diversity concepts can also be applied to restoration management decisions. One practical application for future restoration plans is to consider planting species with high functional dispersion as a means to suppress unwanted, weedy non-natives (Suter et al. 2017). High functional dispersion as well as CWM of traits have been associated with resource use efficiency of nutrients such as nitrogen (Zuo et al. 2016). This is especially applicable to restorations where previous land use was agriculture. In such cases, land often has a legacy of high soil fertility, leading to competitive exclusion of some species (Prach et al. 2013). With the increasing anthropogenic pressure on natural areas it may be necessary to prioritize function diversity in restoration (Laughlin 2014b).

This research highlights that restoration outcomes depend on which metric is used to evaluate the plant community. Taxonomic assessments identifying the species present and their diversity can be used to see if restoration has met the goals of establishing and increasing native species. Functional diversity metrics of evenness and dispersion measure the regularity of trait values and how similar these traits are. These functional trait assessments evaluate what traits might be needed in the community to meet ecosystem service goals. Considering both metrics gives a comprehensive overview of the differences between communities and can better identify the potential needs of a restoration project.

CHAPTER IV

RESEARCH DISCUSSION AND MANAGEMENT RECOMMENDATIONS

Restoration is a dynamic process where outcomes can be context dependent and variable. It is important to understand the processes influencing restoration outcomes so that land managers can use their time and resources effectively. Restoration ecology is complex and there is an opportunity for functional diversity to help understand the biological and environmental interactions influencing a community. Functional diversity analyses have already been recognized as a useful tool and are currently being applied in this context. In fact, there has been in increase in publications over the last 20 years that combine restoration and functional traits (Wainwright et al. 2018). The research presented here adds valuable functional trait and plant community information that can aid management in decision making. This conclusion aims to summarize the findings from this research, suggest recommendations for future restoration planning and highlight import aspects of functional diversity.

Land managers often identify conservation value, pollinator habitat, and native species of high importance when restoring native habitat. The coefficient of conservatism can be a good indicator of how restoration is meeting its conservation goals. Seeding to restore a meadow, specifically by broadcasting seeding, increases the conservation value of the site. This may be important to managers that are interested in restoring certain plant species of high conservation value. Broadcast seeding can be recommended to meet the goal of increasing the conservation value of a meadow. Establishing rare species may not be a priority for all restorations, and even natives with low C of C values can still provide important components of a restoration. For example, big blue stem (*Andropogon gerardii*) is a common species in restoration seed mixes, but only has a C of C value of 5 (Andreas et al. 2004). One must also consider that species with higher C of C tend to have narrow habitat preferences and that such habitats might not be restored to reference condition because of previous land use legacies.

Providing pollinator resources throughout the year is a commonly mentioned priority for restoration. This study provided insight into the phenology of flowering species for species present in the survey and in the seed mix. By assessing the abundance of flowering plants, gaps in provisioning pollinator resources can be identified. Abundance of flowering plants varied before and after seeding, as well as between restored and unrestored sites. Flowering was most abundant during spring, whereas summer and fall flowering abundance was low. A different pattern was found between restored and unrestored sites. In this case, summer flowering plants were abundant in restored sites while spring and fall flowering plants were under-represented. The seed mix used at Observatory Park also had a high abundance of wind pollinated species. While grasses are important to meadow systems, there is an opportunity to increase forb species in mixes. Flowering species proportions should be assessed so that species with phenologies missing from the site can be added.

It is clear from the species composition in the seed mix that native species are a priority in restorations. This research indicated that drill seeding is recommended for those interested in increasing native diversity. In contrast, broadcast seeding establishes a higher richness and abundance of species from the seed mix. The results from the seeding experiment at Observatory Park reflect early-stage restoration. Richness and abundance of species from the seed mix could change over time. However, from the regional survey it seems that either broadcast or drill seeding will increase native species abundance over time. It is known that restorations can take many years to approach reference communities. Additionally, every restoration project can have a different trajectory, and monitoring over time can reveal these patterns (Bullock et al. 2011). Therefore, long term monitoring is recommended to detect changes that may occur over longer time spans.

Functional traits and their diversity may not be among the top priority of land managers when restoring meadows, but there are many benefits for including these in planning. One potential benefit is excluding non-native and invasive plants. This can either be achieved through developing high functional diversity (Pokorny et al. 2005), or by selecting native species with traits that can competitively exclude unwanted species (Funk et al. 2008). Another benefit is building resiliency to environmental change such as drought or climate change (Valencia et al. 2015). Considering plant traits in this way could have long term benefits and maintain stability of the restored community.

This research contributes to the growing number of studies that combine restoration and plant functional traits. This area of research has implications for both the planning stages of restoration as well as long term management of natural areas. As with all restorations, monitoring the progression of the plant community as well as the functional trait composition will be needed.

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APPENDIX

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