

Project Title: **Plants and Pollinators of the Borders: Native wildflower field margin plantings and bee communities**

Final Report to Pheasants Forever (2014-2016, 2017 NCE)

Claudio Gratton and Kiley Friedrich, University of Wisconsin – Madison

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Executive Summary:

Biomass-based agricultural is expected to increase as policies promote more carbon-neutral forms of energy production in the US. Perennial grasslands offer promise for biomass production since they can be grown on marginal lands with minimal inputs. In addition, because of their unique configurations, there is the opportunity for innovative approaches to improving wildlife conservation. This project examined whether planting pollinator-friendly mixtures of forbs in the 10 m borders areas around biomass production fields is a way to increase the number of both flowering plant and bees.

In 2014 at 4 different sites south-central Virginia, this project established 94 acres of high (49 species) and low (9 species) diversity border plantings adjacent to biomass production fields that were primarily using switchgrass as the primary perennial biomass plant. In 2015 (in the second summer after the initial establishment), we sampled plant and bee communities within replicated the border areas (n=39) in different planting treatments.

We found that plant communities in high diversity, low diversity, and control border treatments had about the same number of flower species. However, plant communities in the flower plantings had slightly shifted to be more represented by plants in the seeding mixtures. Yet, there were few differences between the High and Low diversity treatments. The lack of large differences may be expected as this was only the second summer after initial establishment. Little within-season management had been practiced in the border areas and plant communities were characterized by common agricultural weeds (nightshade, wild carrot, ragweed, maretail, smartweed), though in the pollinator borders, early-successional plants were becoming evident (coreopsis, mistflower, New England aster, yarrow).

Bee communities similarly shifted in the border plantings likely reflecting differences in the plant communities. There were significant differences in communities between the control borders, and the flower plantings, but again, only small differences between the high and low diversity plants. Over 75 species of native bees were found in the field edges, with small solitary bees in the genera *Lasioglossum*, *Agopostemon*, *Halictus* and *Augochlora* most common.

Due to the short duration of the study, it is too early to tell if the extra expense to plant the high diversity borders was worth the effort. Additional management efforts will likely be required to increase diversity in the border plantings and suppress agricultural weeds. The bee community responses are promising, but additional work is need to examine whether changes in community composition merely reflect behavioral differences among bees, or whether overall population-level effects are occurring and truly improving bee populations. This study was not designed to examine long-term population level responses of bees.

Introduction

Bioenergy crops have been promoted as beneficial for reducing greenhouse gas emissions through essentially a carbon-neutral production system. However, whether they also provide additional ecosystem services remains to be examined in detail (Sims et al. 2006). Most evidence to date suggests that corn-based systems - so-called first-generation biofuel crops - although they are highly productive, are energy-neutral, and provide few, if any, benefits for wildlife. In contrast, perennial-based bioenergy cropping systems (second-generation bioenergy crops), such as those based on native grasses, have a more favorable energy balance, and accrue additional benefits such as greater carbon sequestration below ground, and enhanced wildlife habitat (Werling et al. 2014). Moreover, native grasses are adapted to growing on marginal soils, with low fertility and low moisture retention capacity (Sanderson & Adler, 2008). This makes second-generation bioenergy crops ideal for perennial bioenergy cropping systems.

How to best manage grassland-based bioenergy crops for wildlife benefits is not well established since currently, perennial, native grasslands are not in widespread use as energy-production systems (Landis et al, 2017). After stand establishment, bioenergy production involves at the very least annual harvesting of the biomass. Current work suggests that changes in stand composition due to repeated harvesting, and exposing of bare ground favors some species of ground-nesting bees over stem-nesting bees (Spiesman et al. in review).

Bioenergy grasslands also offer unique opportunities for creative field designs. In particular, the grasslands in the eastern US often occur as small parcels within matrices of forests. Yet, areas immediately adjacent to forest edges are undesirable due to the risks to farm equipment from fallen tree limbs, debris, or rocks. These field edges go unharvested and offer opportunities for establishing undisturbed wildlife set-asides as part of the energy production system (Vaughn et al, 2015). The ability to incorporate field-level conservation measures makes grass-based bioenergy production systems particularly amenable to designs that not only produce energy crops, but can be engineered to support wildlife as well (Scherper et al, 2013).

In collaboration with Pheasants Forever and FDC Enterprises, this USDA-CIG funded project examined the effects of creating field-edge set-asides for bee conservation as part of bioenergy production systems.

Objective

The principal objective of this project was to work on production-scale bioenergy production systems based on switchgrass (*Panicum virgatum*) in west-central Virginia and to examine whether sowing of pollinator-friendly forb and grass mixtures in field edges benefitted native bee communities in these areas. We specifically focused on native bees because of the potential opportunity for enhancing bee populations through planting of forb rich habitats.

The **specific hypothesis** that was examined was whether bee-friendly plantings adjacent to bioenergy production fields (hereafter “pollinator borders”) had a greater abundance and richness of native bee species than fields that were left as grass or bare. Moreover, we examined whether planting of high diversity border areas (49 flowering plants) resulted in a greater abundance and richness of bees compared to more typically used low diversity plantings (9 species).

Experimental Design and Methods

The general approach in this study was to establish replicated fields with borders in either high diversity flowering-plant mixtures, low diversity mix, or control areas where switchgrass fields went to the edges of the field. Establishment of planting treatments occurred in May-June 2014, and sampling of plant communities and native bees occurred in June-August 2015.

With our FDC partners and in cooperation with private landowners, 4 general locations or “sites”, were selected for this study in 3 counties in southcentral Virginia (**Appendix 1**). The site locations included two small cooperators at Elzay and Inge-Mann and a larger site at Falcons in the eastern part of the study region. A large site in the western part of the region at Sweet Briar College was also established. These sites were chosen based on their relative proximity to the final destination of the bioenergy crop – a bioenergy burner at a geriatric hospital in the area.

At each site, we identified switchgrass production fields that would be amenable for establishment of field-edge border plantings. Site maps were created using a GIS (ArcGIS™ 9.3 ESRI) and Google Earth Images. Sampling fields were chosen based on field characteristics, distribution across our study areas, and field vicinity to one another. In addition, fields needed to be larger than 2 acres and sampling transects needed to be located at least 200 meters apart, ideally with a windbreak or similarly wooded barrier between them with similar distances from bodies of water and roads.

At each site, the core field in production for biomass had previously (before 2013) been planted with mixes of Switchgrass (*Panicum virgatum*), Little Bluestem (*Schizachyrium scoparium*), Big Bluestem (*Andropogon gerardii*), Splitbeard Bluestem (*Andropogon ternarius*). Field sizes ranged from 0.77 acres to 68.12 total acres. A 10 m border around each field was assigned to the three different wildflower conservation plantings (**Appendix 2A**).

PF and FDC worked with local seed distributors and ecologists to create a variety of seed mix diversities appropriate for the area. Plants were chosen based on their native ranges, perennial nature, and overlapping bloom periods. By increasing the number of plant species in the High diversity mix by an order of magnitude greater than the Low diversity mix, we could examine whether a commensurate effect on bees observed.

We assigned fields to be in one of the 3 border planting categories: High, Low or Control. “High Diversity” borders included up to 49 different wildflower species, the

“Low Diversity” borders include up to 9 different wildflower species and were typical of standard NRCS mixtures similar to CRP mixes, and the “Control” sites were planted without a pollinator border (**Appendix 3**). At the larger sites (Falcons and Sweet Briar) we were able to have all three treatments represented at the sites. At the smaller sites (Inge-Mann and Elzay) we were not able to establish control sites due to lack of sufficient number of fields and space. High diversity planting treatments were placed as far as possible from Control areas to minimize the potential effects of these plantings on the control treatments (presumably areas of low plant diversity) (**Appendix 4**).

At the 4 selected sites, 57 individual fields were planted by PF and FDC with bioenergy grasses for a total of 995.57 field acres. Wildflower borders contributed 93.49 acres of the total acreage, of which 67.92 acres were planted with High diversity seed mix and 27.14 acres planted with the Low diversity mix.

In the second summer (June-August 2015) year after field border establishment, the plant and bee communities were sampled. Sampling was performed at 39 of the 57 planted fields.

Plant Community Sampling

The plant community was assessed through a vegetation survey to determine the plant species abundance, diversity, and richness in the pollinator borders. Plant communities were examined twice during the growing season. The first plant sampling session was conducted from June 28 to July 10, 2016. The second plant sampling session was conducted from August 8 to August 20, 2016.

At each of the 39 study sites, two 50 m sampling transects were identified. Within each field, sampling occurred at two locations – the field “Edge” (within the pollinator border) and the field “Core” (within the bioenergy crop) (**Appendix 2B**). Each location included a 50 m transect. Each transect included 6 stations, 10 m apart (**Appendix 2C**). Bee and plant data was collected at each station.

One transect was placed in the central corridor of the pollinator border. This was referred to as the “Edge” measurement. The second transect was placed perpendicular to the “Edge” transect, approximately 10-25 m from the nearest edge of the pollinator border into the planting of bioenergy grass crop. This transect offered a measurement referred to as the “Core.”

At each sampling station along a transect, a 2x2 m quadrat was used to identify and quantify the vegetation inside the quadrat. To estimate percent cover of the vegetation, we used a calibrated ocular estimation technique to ensure standardized measurements across all quadrats. The vegetation was categorized by type and assigned a percent cover of the entire quadrat. These categories were “% Grasses” (all graminoids - rushes, sedges, warm and cool season grasses), “% Bare Ground” (exposed soil or other substrate), “% Litter” (dead organic plant material accumulated in the quadrat) and “% Forbs” (herbaceous and flowering plants). If vegetation was in bloom, the plant was

identified to species and recorded as present in the quadrat. Each flowering species was identified using field guides and local species lists.

Bee Community

The bee community composition was assessed through specimen collection using pan trap arrays, also known as “bee bowls.” Unbaited passive pan trap arrays were distributed at stations along the same border transect used for the plant community assessment. Each set of traps contained three 16 oz cups in alternating white, fluorescent blue, and fluorescent yellow, (Solo® Cup Company, Highland Park, IL) filled with 250 ml of a 1 % non-fragranced, phosphate-free dish soap (Seventh Generation™ Natural Dish Liquid) solution to ensure retention of a wide range of bee specimens. Bee bowls were distributed evenly along the center of pollinator border at each station in full sun for a portion of the day. These traps were deployed for one 48-hour period in each of the three trapping sessions in June, July and August. Trap catch was collected on June 24-27, July 22-23, and August 6-7 and August 10 of 2015. Specimens were collected from the field, preserved in 70 % ethanol and taken back to the lab for processing and identification.

Species-level identification was done using published keys and revisions, the online key to bees of the eastern U.S. available at www.discoverlife.org, comparison with the reference collections held at the University of Wisconsin, and the professional taxonomic assistance of Dr. Jason Gibbs, Michigan State University.

Data Analysis

The influence of the pollinator border field margins was evaluated both in terms of the plant communities and native bee communities in the second summer (2015) after initial establishment. Species richness, abundance, and diversity of plants and bees were evaluated using univariate statistical methods (ANOVA). Plant data was analyzed as early and late season measures, and as a season-long composite value for each field. Bee data was aggregated from all three sampling session (June, July, August 2015) for season-long data set.

We examined how communities as a whole (relative abundance and composition of species assemblage) varied across treatments using multivariate analyses (PERMANOVA and ANOSIM) and ordination visualization techniques (PCO and NMDS).

The primary factors that were included in the analyses were the planting treatments (High diversity, Low diversity, and Controls). Because of the differences in management, age of bioenergy grass plantings, and wide geographic separation among sites, we also included site locations (geographic groupings of fields: Sweet Briar College, Inge-Mann, Elzay, Falcons) to account for this additional set of factors influencing plant communities and bees. For plant communities, we separated analyses

for measurements taken in the pollinator plantings (“Edge”) and in the biomass production areas (“Core”), and separated samples from early and late season as well.

Results

Plant community data

Plant species richness data are segregated by sampling session (“Early” – June 2015, “Late” – July/August 2015) and field location (“Core” and “Edge”). The Core transects, toward the middle of the fields, averaged between 2.2 and 3.6 species present across the treatments in both Early and Late sampling sessions (**Figure 1**). The most common plant species in the Core areas were grasses. The few flowering plant species that did occupy the biomass production areas included nightshade (*Solanum spp.*), pennsylvania smartweed (*Polygonum pensylvanicum*), marestalk (*Erigeron canadensis*), and velvetleaf (*Abutilon theophrasti*).

In the pollinator borders, plant species richness varied depending on the planting treatment imposed. Control borders, where no seeding occurred, had on average 4 species in Early and Late sampling sessions (**Figure 2A, B**). The most common plant species present in the Control borders were wild carrot (*Daucus carota*), pennsylvania smartweed (*Polygonum pensylvanicum*), slender lespedeza (*Lespedeza virginica*), nightshade (*Solanum spp.*), showy partridgepea (*Chamaecrista fasciculata*), and pokeweed (*Phytolacca americana*) (**Table 1**). In contrast, pollinator borders that were seeded with either the Low or High treatments had about twice the number of species Early and Late sampling session compared to Controls (Session 1- “Early”: $F_{2,36} = 16.39$, $P < 0.001$; Session 2- “Late”: $F_{2,36} = 13.98$, $P < 0.001$) (**Figure 2A, B**). However, there was no statistical difference in species richness between Low and High diversity seeding treatments ($P = 0.344$). Interestingly, when combining species richness estimates over the entire season, there were no differences among any of the three treatments ($F_{2,36} = 0.41$, $P = 0.67$, **Figure 2C**) suggesting a wide range of variability in plant species richness among sites not related to planting treatments. For example, some Control pollinator borders had as many as 18 plant species, similar to that observed in some High diversity borders; conversely some High diversity borders had only 3 flowering plant species observed, comparable to some Control pollinator borders (**Figure 3**).

Plant community composition across the different pollinator borders (i.e., Edge transects) varied both as a function of site (i.e. geographic location) as well as planting treatment (High, Low, or Control). NMDS ordinations using Bray-Curtis dissimilarities from season-long averaged frequency data show clear differences between fields at Sweet Briar in the western region the study and Falcons in an eastern county (**Figure 4**). The smaller sites (those with fewer fields and treatments) of Elzay and Inge-Mann fell between Sweet Briar and Falcons in the ordination. Within each of the larger sites, the planting treatments formed separate groupings with plant species composition in Low and High diversity plantings occupying different parts of the ordination space compared to Control fields. Treatment fields at Inge-Mann and Elzay, which did not

include Controls, were in ordination space near other Low and High treatments fields at Sweet Briar and Falcons (**Figure 4**). Statistical analyses further support these graphical patterns (ANOSIM overall $R = 0.58$, $P < 0.001$; Control vs. Low, $P < 0.001$; Control vs. High, $P < 0.001$, High vs. Low, $P < 0.02$).

These patterns suggest that in addition to site-level effects on plant species composition, that High and Low pollinator borders had a different species composition than fields with unplanted Control borders. The differences between the Control and Low and High treatments are the result of different species being relatively more or less common across sites and treatments. When no prescribed seed mix was planted (Control), the background existing seed bank resulting in species such as Echinops spp. (*Echinops spp.*), Alsike Clover (*Trifolium hybridum*), Fleabane (*Erigeron spp.*), Ragweed (*Ambrosia spp.*), Pennsylvania Smartweed (*Polygonum pennsylvanicum*), Wild Carrot (*Daucus carota*), and Nightshade (*Solanum spp.*) (**Table 1**). Most of these are considered common agricultural weeds. Interestingly, Gray Goldenrod (*Solidago nemoralis*), was relatively common at all sites including the Control borders, despite not being intentionally planted at the Control sites.

The plant species most associated with the Low and High pollinator borders at both Falcons and Sweet Briar include Mistflower (*Eupatorium coelestinum*), Common Yarrow (*Achillea millefolium*), Blackeyed Susan (*Rudbeckia hirta*), and Gray Goldenrod (*Solidago nemoralis*) – all species intentionally planted in the mixes (**Table 1**). Other “unintended” plant species (e.g., nightshade) overlapped those observed in the Control areas likely due to the existing seed bank.

Plant – summary. One year after establishment, pollinator borders had a plant composition that was significantly different than both the biomass production areas (Core) and the field margins (Edge) where no plantings were made (Control treatments) (**Figure 5**). The differences were in large part due to flowering plants that were part of the High and Low seeding mixes. There were small, but significant, differences in plant community composition between High and Low diversity planting treatments. These differences had more to do with the relative abundance of flowers present, rather than differences in species richness *per se*. Nevertheless, even Control areas that were not intentionally planted with flowers had as high species richness as some of the High diversity plantings. This indicates that the existing seed bank (of mostly common agricultural weeds) provided a diverse and abundant flower supply in addition to anything that was intentionally sown. Given that on average, only 10-12 flowering species occurred in the pollinator borders (max of 18 species), and that these numbers were no different among treatments, we can conclude at least in the year immediately following the plant establishment, there were no large differences in species richness among the treatments. Rather, any differences among treatments had more to do with the relative abundance of a few intentionally planted species such as Mistflower (*Eupatorium coelestinum*), New England Aster (*Aster novae-angliae*), Common Yarrow (*Achillea millefolium*) and Plains Coreopsis (*Coreopsis tinctoria*).

It is too soon to tell if future years after the establishment would further alter the trajectories of the plant communities, as has been often observed in many restoration projects with the appropriate management. However, the significant effort and investment placed in the High diversity treatments were not evident in the year after establishment when compared to Low diversity treatments. This may, in part, reflect that common, easy-to-establish plants, are often the first to become established in a restoration, with rarer species taking longer to establish and emerge as part of the community in later years.

Bee community data

A total of 5,623 bees were collected using pan traps across the three sampling period in the summer of 2015. Approximately 9 % of the specimens (528) were excluded from the final dataset since they were not identified to species, representing a subset of genera – *Augochlora* spp. (n = 199), *Augochlorella* spp. (n = 78), *Bombus* spp. (n = 11), *Halictus* spp. (n = 35), *Megachile* spp. (n = 18), *Melissodes* spp. (n=73), and *Svastra* spp. (n = 12). In total, 5095 bees were identified to species, representing 76 different species. (**Appendix 5**). Overall, the most abundant species collected were *Lasioglossum imitatum* (n = 1701), *Lasioglossum pilosum* (n = 394), *Halictus poeyi/ligatus* (n = 382), *Agapostemon virescens* (n = 382), and *Lasioglossum hitchensi* (n=297). These 5 species represented 60% of all individuals collected of the course of the summer (**Figure 6**).

Bee species richness was similar across all pollinator border treatments ($F_{2,36} = 0.466$, $P=0.63$, **Figure 7**). However, bee abundance varied greatly across the planting treatments ($F_{2, 36} = 5.6132$, $P= 0.0037$, **Figure 8**) with abundance slightly higher in the Low diversity treatments than in the Control and High diversity planting treatments. Overall, the most abundant bee species in the Low diversity areas, *Lasioglossum imitatum*, was more than three times as abundant than all other bee species in the Low treatment pollinator borders (**Table 2**). In addition, *L. imitatum* abundance was nearly twice as high in borders of Low and High treatment borders than in the Control treatment pollinator borders.

Bee community composition across all treatments and sites varied as a function of site and treatment. NMDS ordinations using Bray-Curtis dissimilarities from abundance data show clear differences between sites, especially between the larger sites - Sweet Briar and Falcons (**Figure 9**) a pattern that was statistically significant (ANOSIM, $R = 0.429$, $P<0.001$).

More directly relevant to the central hypothesis posed for this study, bee communities were significantly different among planting treatments even when accounting for variation among sites. Using a 2-way ANOSIM there was a significant planting treatment effect ($R=0.56$, $P<0.001$), with Low diversity treatments different than Controls ($P<0.001$) and High Treatments different from controls ($R = 0.065$, $P<0.001$), but only weak differences between Low and High planting treatments ($R=0.251$, $P=0.024$). Using a perMANOVA for the two larger sites only, there was again a significant

difference in bee communities across sites (Site effect, pseudo-F = 10.9, $P=0.001$) and a significant difference across treatments (pseudo-F=3.2, $P=0.001$). [The species most associated with the High and Low diversity treatments were: *Bombus impatiens*, *Lasioglossum zephyrum*, and *Apis mellifera*. In contrast, species more typical of control border areas were *Lasioglossum versatum*, *Lasioglossum callidum*, and *Melissodes bimaculatus*. Common species at all three treatments included *Lasioglossum imitatum*, *Lasioglossum bruneri*, *Lasioglossum pilosum*, *Agapostemon virescens*, and *Halictus poeyi/ligatus*. (**Table 2**)

There was no relationship between total plant species richness in a field border and neither bee abundance ($r = 0.11$, $P=0.49$) nor bee species richness ($r=0.26$, $P=0.10$).

Discussion

Plant communities

When wildflower seed mixes are applied to field borders, plant community composition shifted compared to unplanted Control areas, irrespective of the site at which this occurred. As may be expected at this early stage of establishment - in the second growing season after initial planting – only a 42 % ($n=21$) of plants included in seed mixes became established across all planting treatments. Yet, differences in species richness between treatments were not evident – all sites had on average 11 plant species present during sampling irrespective of treatment.

However, there were significant differences in species *composition* among treatments. There were large differences in plant communities between pollinator borders and unplanted controls, but the differences between Low and High planting treatments were small. The differences among treatments were evident even when plant species composition is examined in terms of presence/absence rather than frequency (as a measure of relative abundance). This suggests that these differences are not just due to the relative abundance of species contributing to differences among sites, but also to which species are present.

One of the most obvious and consistent differences seen in this study was the contrast in plant communities between the eastern sites at Falcons and the western sites at Sweet Briar. Examining only the Control borders, as an example of what would have come up without any experimental intervention of seeding, it is clear that these locations are different. There are likely many reasons for this, not the least of which is the length of time these sites have been under management for biomass crops. Most fields at Falcons had been under grass production for at least 5 years. Border areas prior to the establishment of pollinator borders were in Switchgrass from fencerow to fencerow. In contrast, Sweet Briar sites had just been converted to biomass plantings in 2014. These fields were previously used for agricultural production of feed hay and cool-season grasses. Other differences among sites in land use history, soils, or geographic location would likely create additional differences in initial plant community composition, as well as different conditions for establishment of pollinator

plantings. Falcons has been established as a persistent Switchgrass production site with far less turnover in each field and its use, contrary to the Sweet Briar fields which have been in this system a much shorter time and had regular turnover throughout the college's history of haying for the equestrian program, recreation, and agricultural uses over the years.

Differences in management of the pollinator borders could also contribute to differences among sites. Some Controls were mowed and others remained bare and untouched while others still were planted with the same bioenergy crops used in the core areas. This inherently provides different substrates and seed banks to apply the different plantings. Implementing a wildflower diversity planting over these different border management practices may further enhance differences among sites.

Bee communities

We hypothesized that an increase in the abundance, richness, and diversity of the plant community would increase the abundance, richness, and diversity of the native and wild bee community (Ahern et al. 1992, Albrecht et al. 2007, Blaauw et al. 2014, Haaland et al. 2011). Simple metrics of bee responses to treatments, such as abundance or species richness, did not show any differences among planting treatments.

However, bee community composition was significantly different between sites (seen most clearly at the Sweet Briar and Falcons sites) as well as among the pollinator planting treatments. This effect was mostly driven by differences in the relative abundance of different bee species since an analysis using presence/absence failed to show any strong differences among treatments (although there was a differences among sites even with presence/absence data).

The degree of community differences in bee composition was strikingly similar to the patterns observed in the plant communities. Sites with significantly different bee communities were also sites that differed the most in species community composition in the field borders. The natural history of these bee species suggests that there exist a set of resource and nesting requirements for the variety of wild bees (Adamson 2011, Ascher & Pickering 2016, Carvell 2002, Michener 2007). By providing a variety of plants, and therefore a variety of resource niches, we are more likely to positively impact a wide range of bees according to their different environmental requirements or innate preferences. The higher the quantity or diversity of resources available to these species, the more likely it is that the plant community will have a beneficial impact on an equally diverse or abundant bee community (Potts et al. 2003, Tscharntke & Brandl 2004).

It is important to remember that this study focused on the second summer after initial establishment. It is well-known that these forb-rich plant communities require multiple growing seasons to come into their fullest performance and require intensive management in the first few years (e.g., by mowing or burning) to control unwanted weedy and invasive species.

Conclusions and Future directions

In the summer immediately following establishment of border areas adjacent to bioenergy crops, there was shift in the community of plant species towards more relative cover of flowering species that were part of the seeding mixtures. This was the hoped-for and expected pattern. Species richness was generally low, relative to desired outcomes, and communities were dominated by early establishing species from the sown mixtures as well as common agricultural weeds. Given the short time after establishment (2nd summer) and the large differences in land-use history and prior management between the sites, this should be viewed as a promising start towards shifting the plant communities toward more desirable flowering species. One important finding of this study is that after the second summer, there were only small differences in both plant and bee communities between the low and high diversity border planting treatments. Given the short duration of this study it is too soon to tell if the significantly greater level of effort required to establish the 49-specied high diversity planting was worth the effort.

This shift in plant communities was paralleled by a shift in bee communities as well. In addition to shifts in the relative abundance of species in the border plantings, additional species that are typically not part of unplanted controls also started appearing. These findings are consistent with other studies that show a generally positive association between plant diversity and bee diversity (Williams et al. 2015). This suggests that putting an emphasis on altering plant community composition through grassland restoration efforts is way to influence bee communities.

What remains to be tested in studies such as this one, is whether an increase in observed bee abundance and a change in community composition is related to actual increases in the populations of specific bees. The response observed may be merely a spatial aggregation of bees to newly available resources (i.e., flowers), at the expense of other areas in the landscape. While more food in theory should result in greater survival, reproduction and population growth, this was not tested in this study. Follow up studies that focus on actual population-level responses (rather than shifts in community patterns) would be a natural next step.

In addition, how both the plant and bee community change over time would be important to examine. It is not clear if continued management of the border areas will be done (e.g., periodic mowing to keep annual weeds down in favor of perennial flowering plants). This will have a large effect on the trajectory of the plant community, and with it, the bee community. Longer terms studies that explore these trajectories, as well as more direct measures of bee population growth would enhance our understanding of whether these conservation approaches are in fact achieving the desired goals of improving pollinator populations. This project helped establish the baseline data upon which future studies can build.

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Table 1. Most abundant plant species (>90% total plant abundance) recorded by treatment type (top 10 average abundances highlighted). Plant species **bolded** were part of the planting seed mixes for the Low and High diversity treatments.

Species Common Name	Control (n = 12)	Low (n = 13)	High (n = 14)
Echinops spp.	0.9	0.3	
Alsike Clover	0.8		
Fleabane	0.7	0.39	0.27
Unidentified Fabaceae Family	0.7	0.13	0.2
Gray Goldenrod	0.6	0.4	0.6
Oxalidaceae Family 1	0.5		0.8
Ragweed	0.5		
Lobelia	0.4	0.12	0.13
Pennsylvania Smartweed	0.4	0.11	0.11
Wild Carrot	0.39	0.36	0.23
Nightshade	0.31	0.21	0.15
Plantain	0.2	0.5	0.6
Pokeweed	0.2	0.2	0.1
Curly Dock	0.2	0.15	0.9
Slender Lespedeza	0.2	0.12	0.3
Marestail	0.18	0.45	0.38
Oxalidaceae Family 2	0.18	0.2	0.7
Showy Partridgepea	0.17	0.3	0.2
Common Yellow Woodsorrel	0.13	0.8	0.15
White Clover	0.12	0.38	0.37
Sweet Everlasting		0.8	
Mistflower		0.76	0.41
New England Aster		0.7	
Common Yarrow		0.53	0.35
Plains Coreopsis		0.48	0.19
Common Mullein		0.4	0.8
Blackeyed Susan		0.37	0.53
Blanketflower		0.3	0.13
Deptford Pink		0.2	0.9
Purple Coneflower		0.2	0.19
Wild Bergamot		0.2	0.15
Dotted Bee Balm		0.2	0.13
Panicked Tick-trefoil		0.2	0.11
Butterfly Milkweed		0.13	
Purple Prairieclover			0.9
Lemon Bee Balm			0.25
Lanceleaf Coreopsis			0.24

Birdsfoot Trefoil			0.13
Average Within Group Similarity	48.14	63.76	38.14
Average Between Group Dissimilarity	75.67		
		59.14	
	79.30 between Control & High		
Based on Bray Curtis Index			

Table 2: Average bee species (>90% total bee abundance) by treatment (top 10 average abundances per treatment highlighted in light blue).

Species	Control (n = 12)	Low (n = 13)	High (n = 14)
Lasioglossum imitatum	3.74	7.54	5.62
Lasioglossum bruneri	2.64	1.58	2.12
Lasioglossum pilosum	2.34	2.45	1.92
Agapostemon virescens	2.16	2.47	2.12
Lasioglossum versatum	2.07	1.01	0.76
Halictus poeyi/ligatus	2.06	3.94	2.62
Lasioglossum callidum	1.91	1.15	1.16
Lasioglossum hitchensi	1.77	2.69	2.6
Augochlora pura	1.69	1.75	1.79
Melissodes bimaculatus	1.57	0.99	0.69
Hylaeus affinis	1.17	1.14	0.97
Bombus impatiens	1.16	1.52	1.74
Lasioglossum gotham	1.1	1.35	0.86
Lasioglossum zephyrum	1.09	2.18	1.68
Ceratina calcarata	1.01	1.26	1.38
Lasioglossum weemsi	0.87	0.53	0.83
Apis mellifera	0.87	0.53	1.53
Lasioglossum tegulare	0.72	0.69	0.21
Hylaeus modestus	0.67	1.03	0.58
Ceratina dupla	0.64	0.37	0.53
Bombus griseocollis	0.57	0.87	0.91
Lasioglossum trigeminum	0.57	0.45	0.63
Melitoma taurea	0.57	0.42	0.49
Lasioglossum weemsi/hitchensi	0.45	0.23	0.45
Bombus vagans	0.42	0.47	0.52
Lasioglossum cressonii	0.42	0.43	0.51
Dieunomia heteropoda	0.4	0.34	0.24
Lasioglossum pectorale	0.39	0.71	0.66
Xylocopa virginica	0.39	0.34	0.46
Hylaeus mesillae	0.39	0.32	0.29
Lasioglossum coreopsis	0.35		0.63
Bombus bimaculatus	0.33	0.08	0.53
Melissodes comptoides	0.33		
Lasioglossum coeruleum	0.32	0.48	0.17
Lasioglossum illinoense	0.31	0.23	0.27
Lasioglossum quebecense	0.28		0.39
Lasioglossum oblongum	0.24	0.31	0.17
Agapostemon sericeus	0.2	0.75	0.29
Bombus citrinus/variabilis	0.17	0.37	0.21

Svastra obliqua	0.08	0.49	0.14
Lasioglossum paradmirandum	0.08	0.34	0.86
Average Within Group Similarity	48.36	52.75	54.99
Average Between Group Dissimilarity	52.29		
		47.67	
	50.39 between Control & High		
Based on Bray Curtis Index			

Figure 1: Average plant species richness in biomass crop. i.e., “Core” areas of fields.

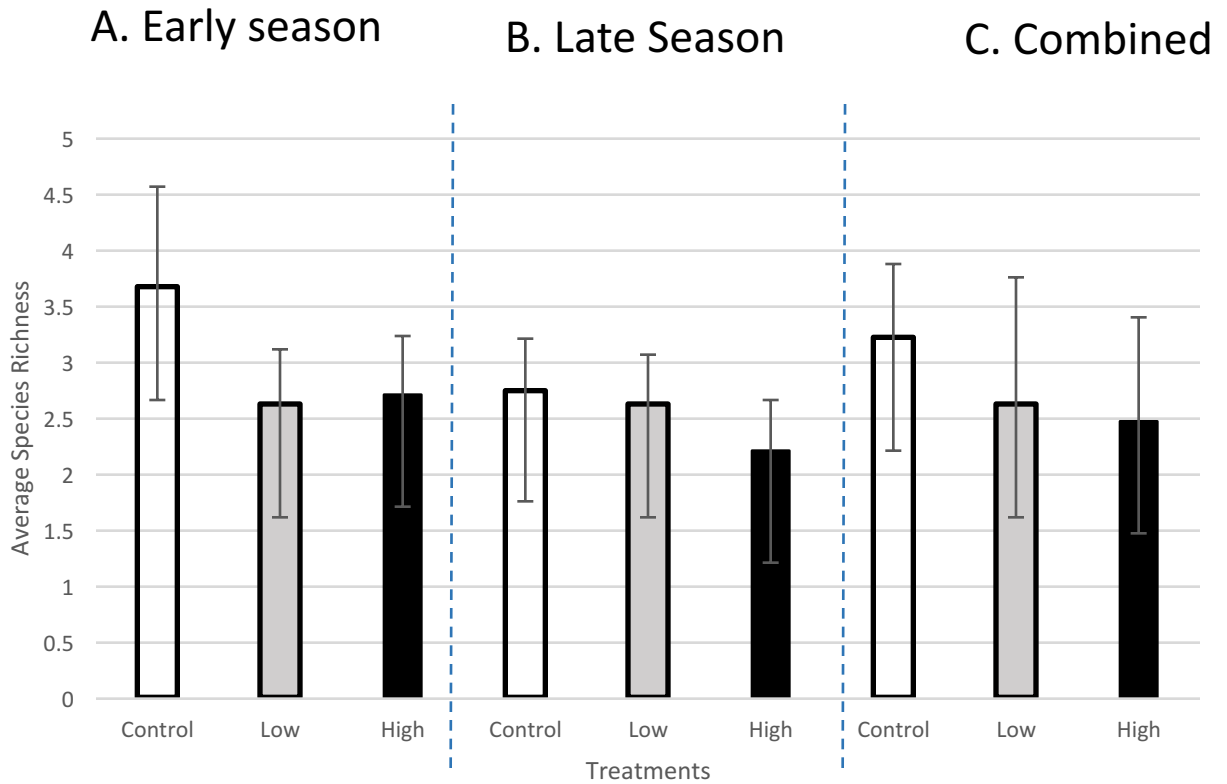


Figure 2: Average plant species richness in pollinator borders, i.e., "Edge" area of fields.

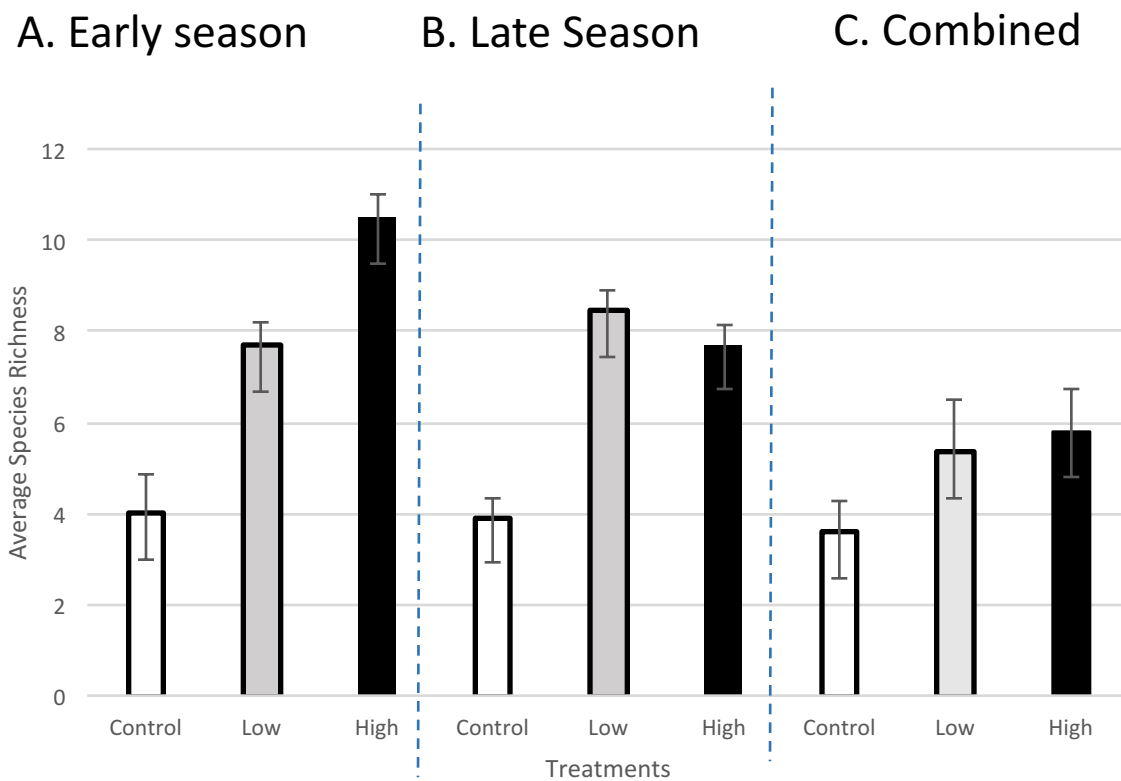


Figure 3: Season-long plant species richness tends to fall along a gradient, rather than the discrete categorical divisions of the treatments.

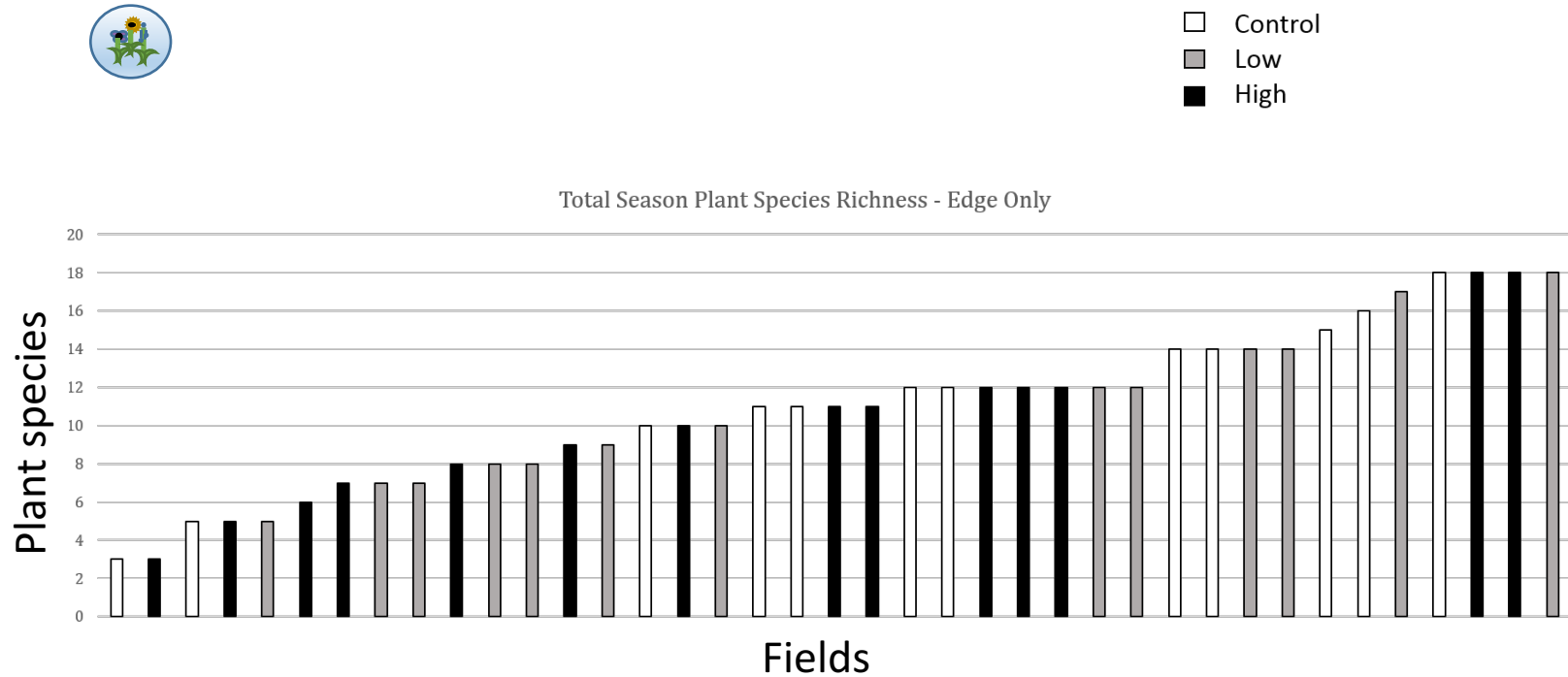
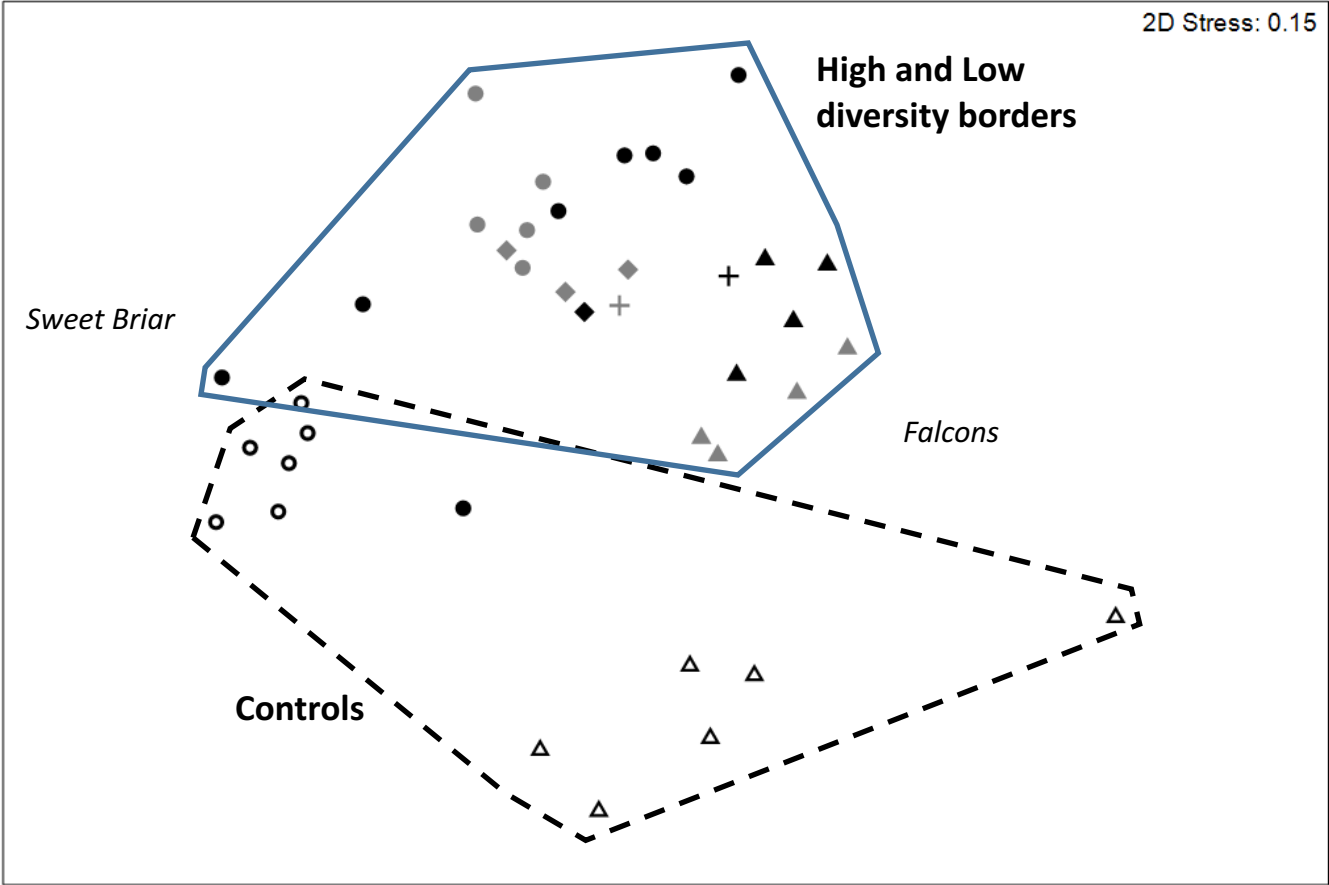


Figure 4: NMDS ordinations of all fields based on averaged plant species frequency over the course of the 2015 season (Square Root transformed, Bray-Curtis dissimilarity). The significant effect of border treatments on plant community composition is evident as the Control fields (dashed polygon) fall in a distinctly separate region of the ordination, away from the Low and High sites (solid polygon). In addition, the site effect can also be seen as Sweet Briar fields (circles) are on the left, while fields from Falcons are on the right (triangles).



	SB	FAL	INGE	ELZAY
CONTROL	○	△	NA	NA
LOW	●	▲	+	◆
HIGH	●	▲	+	◆

Figure 5. Examples of two 10 m wide control borders (A and B) at Sweet Briar College site, and High diversity borders (C, Falcons) and (D, Sweet Briar) intended to serve as pollinator enhancements adjacent to biomass production fields.



Figure 6. Examples of most four numerous bee genera collected within pollinator borders - (A and B) *Lasioglossum* spp. (C) *Halictus* spp. (D) *Agapostemon* spp. Photos by Heather Holm.



Figure 7: Bee species richness across the pollinator border planting treatments (Control, Low and High diversity).

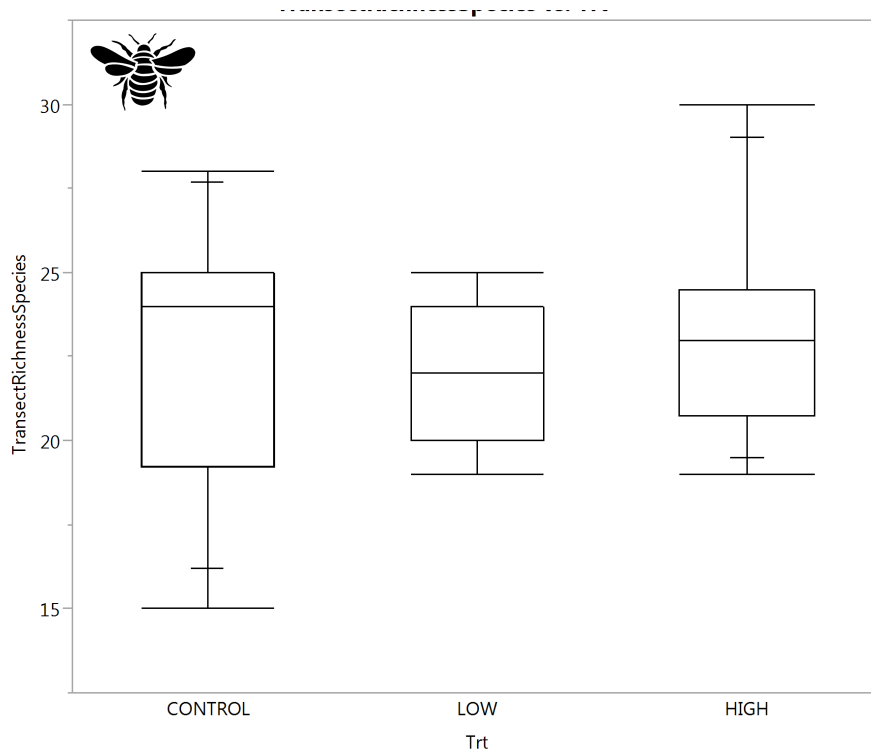


Figure 8: Bee species abundance across the pollinator border planting treatments (Control, Low and High diversity).

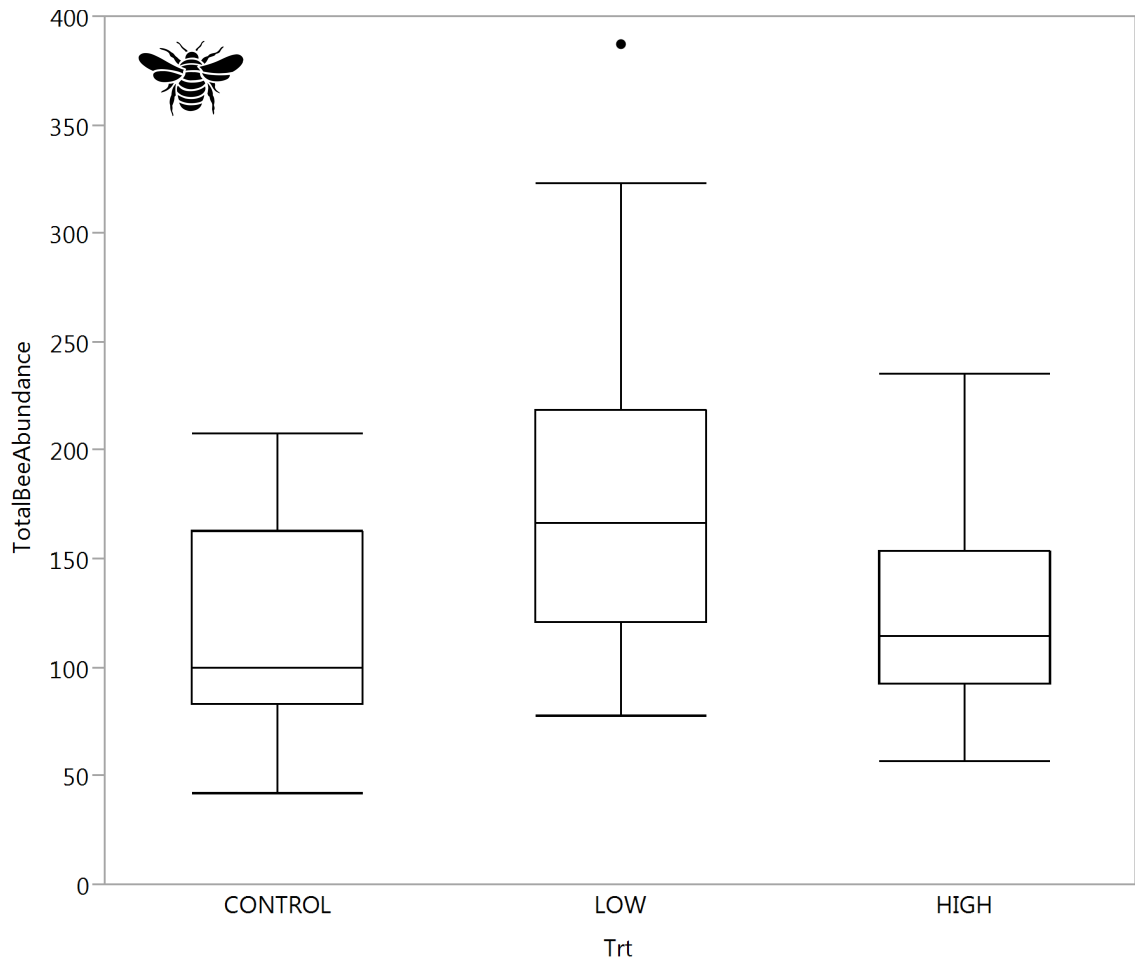
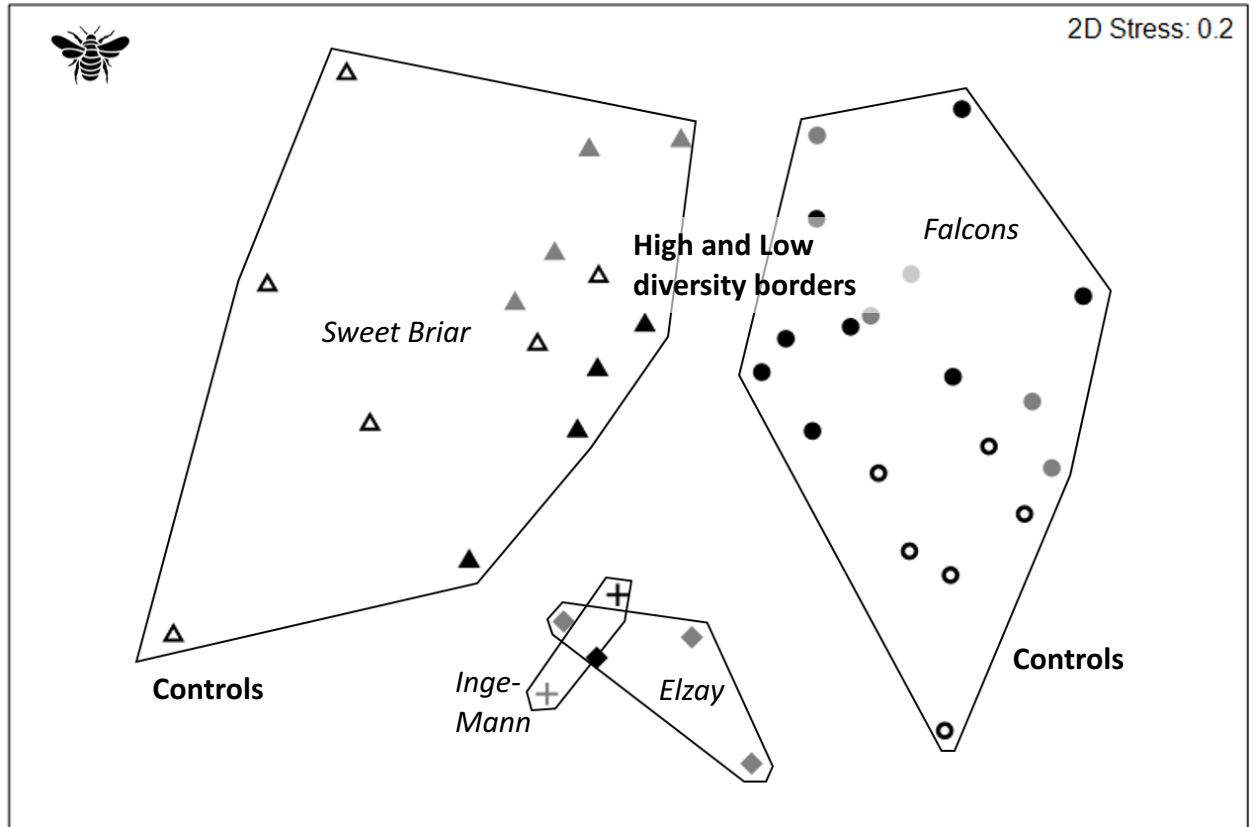
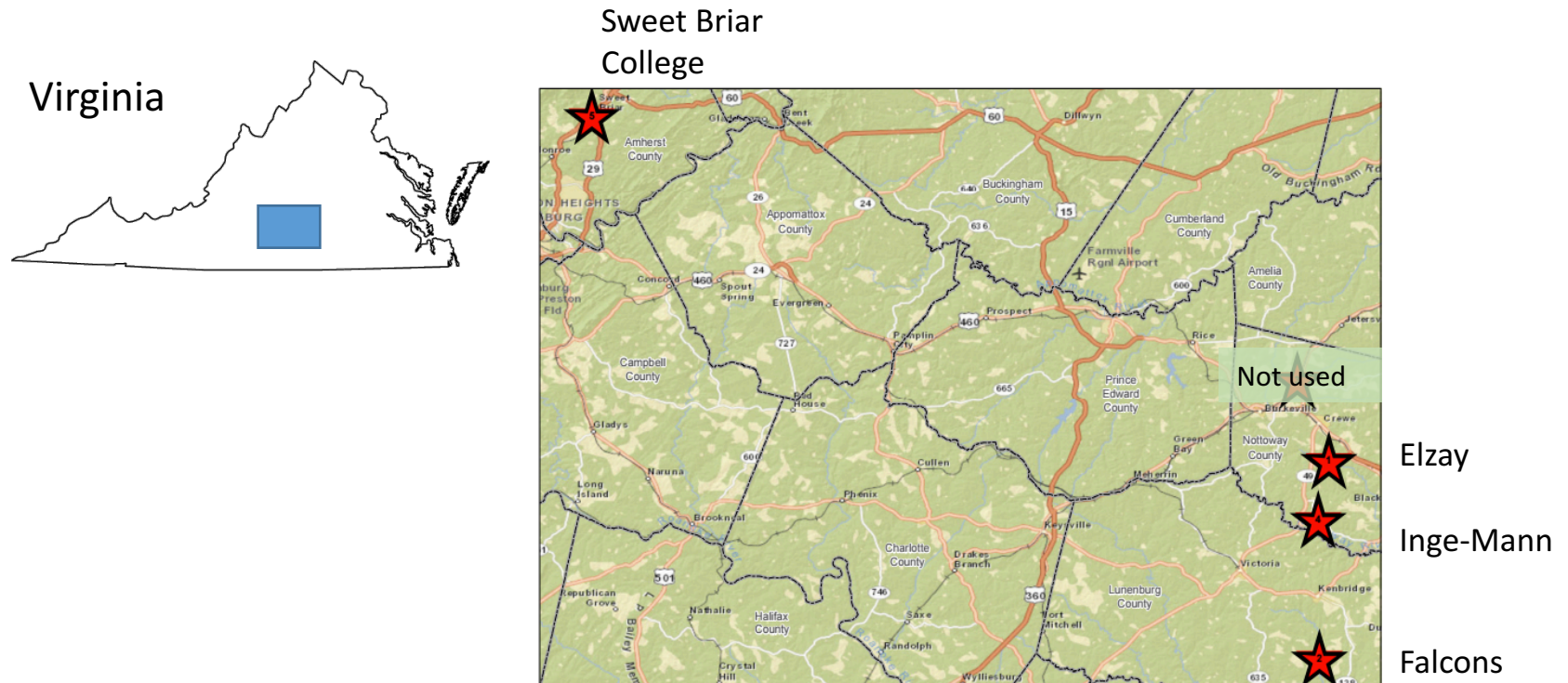


Figure 9: NMDS ordination of bee species community composition (based on Square Root transformed abundance data, Bray-Curtis distances). Here we can see the significant site effect as the fields from Elzay, Inge-Mann, Sweet Briar and Falcons fall in distinctly separate regions of the ordination. Groupings of treatments (filled points) also cluster near each other, with Control fields (open points) at the outsides of the plots.

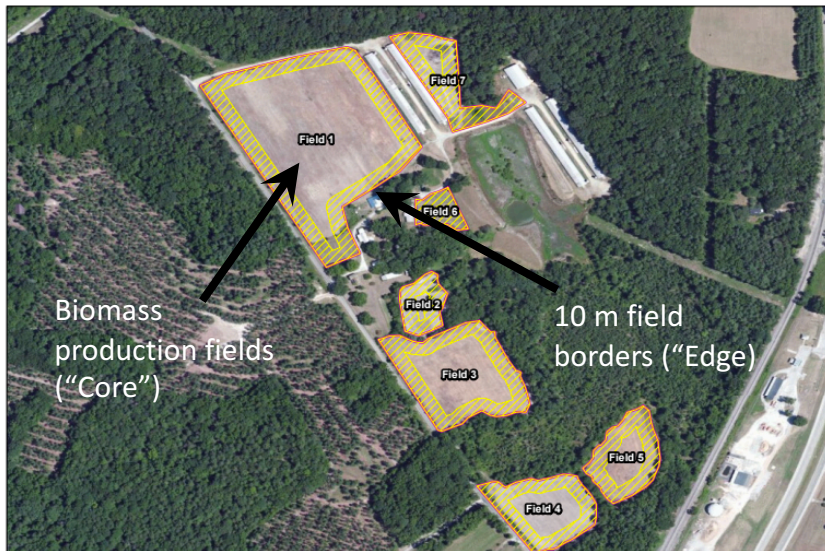


Appendix 1: Location of sites in south-central Virginia used as study areas for experimental pollinator border plantings and bee sampling. Elzay, Falcons, Inge-Mann, Sweet Briar College.

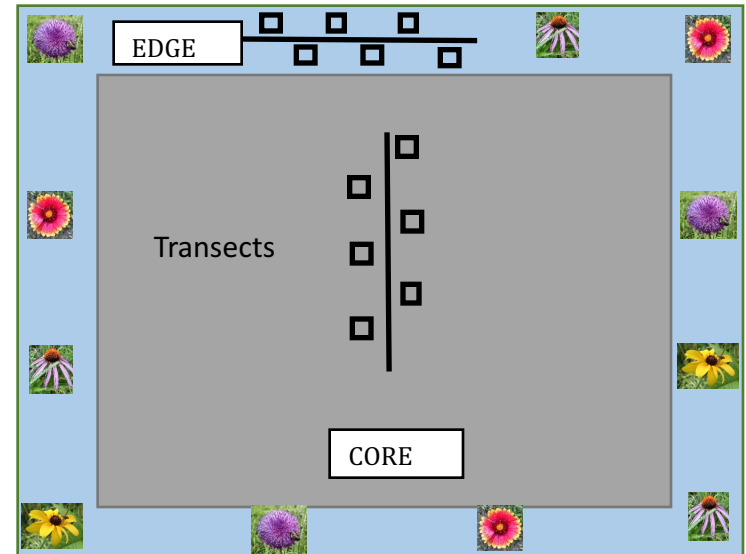


Appendix 2: (A) Example of 10 m field borders (yellow hatched areas) surrounding switchgrass plots at study site. **(B)** Two transects were present in each field. The “Edge” transect was placed down the central corridor of the wildflower border and the “Core” transect was placed perpendicular to the border within the bioenergy crop. **(C)** Each 50 m sampling transect included 6 stations, placed 10 m apart. At each station, a 2x2 m quadrat was used to measure the plant community and pan trap arrays were distributed evenly to catch bees. Each pan trap array included a florescent blue, yellow, and white colored cup containing a diluted soap-water mixture.

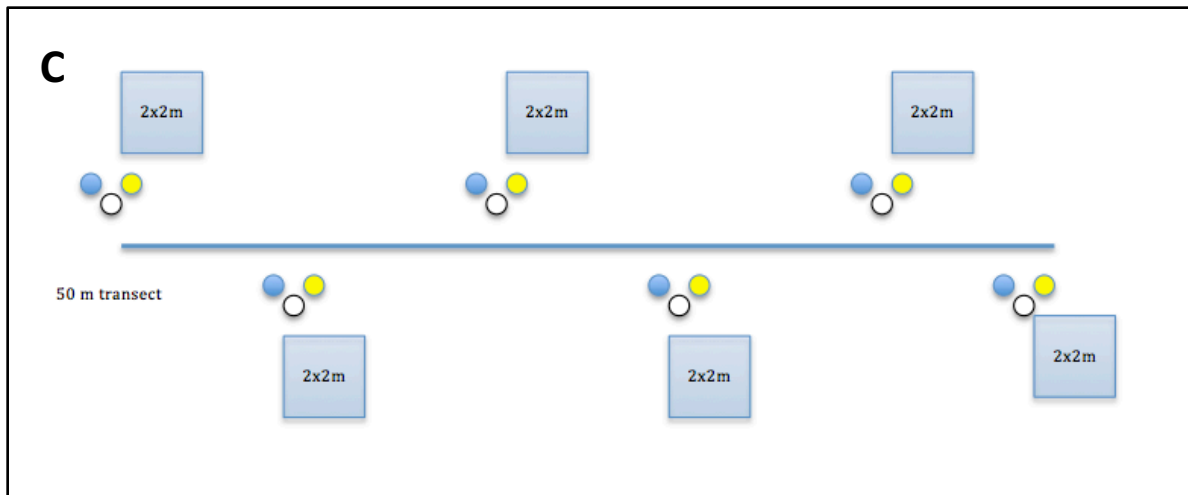
A



B



C

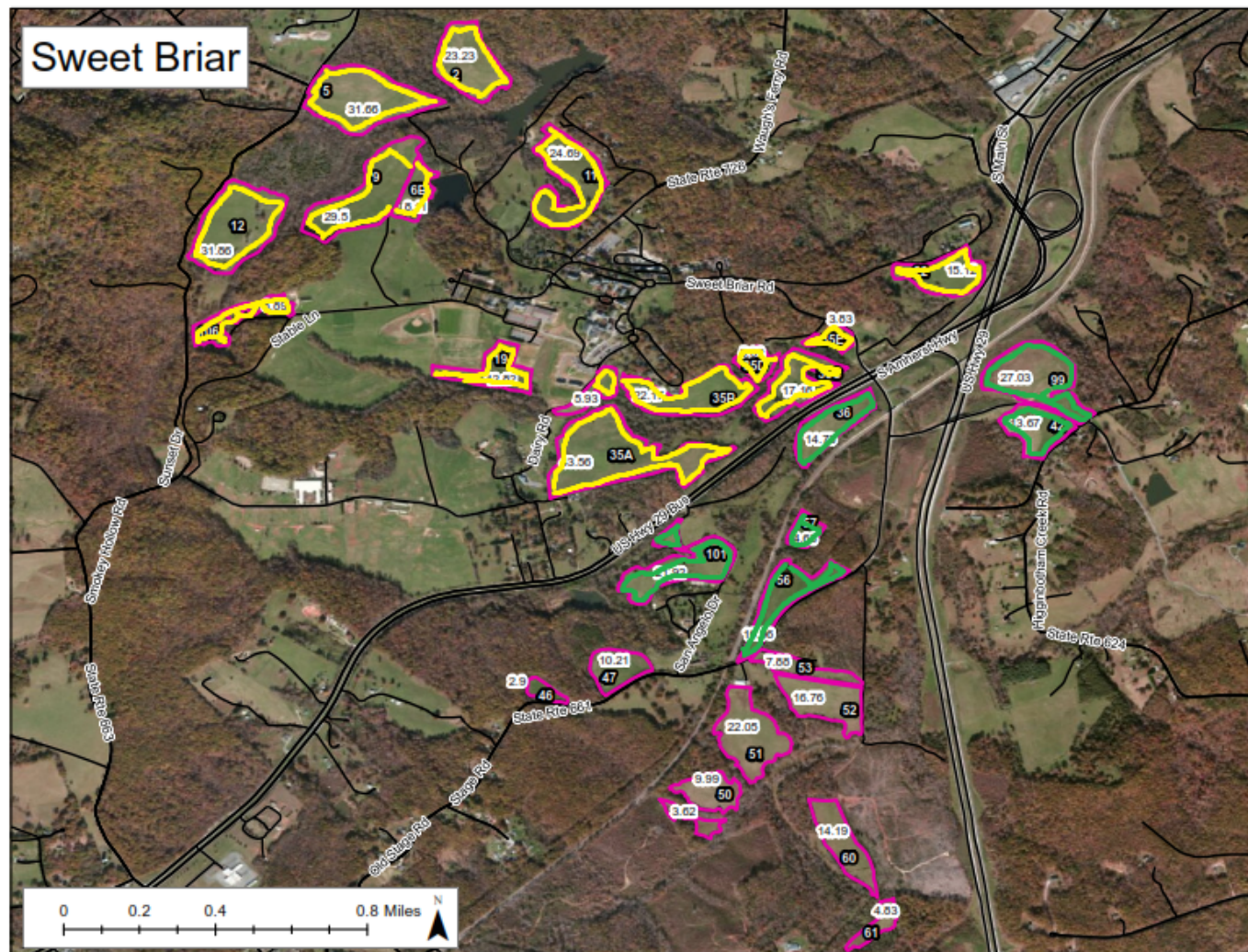


Appendix 3: List of plant species used in seed mixes for the Low (9 spp) and High (49 spp) diversity plant treatments planted in 2014 in field borders around biomass grassland sites in Virginia (USA) sites.

Scientific Name	Common Name	Low Diversity mix	High Diversity Mix
<i>Achillea millefolium</i>	Common Yarrow	X	X
<i>Allium canadense</i>	Wild Garlic		X
<i>Allium cernuum</i>	Wild Onion		X
<i>Artemisia ludoviciana</i>	Cudweed Sagewort or Prairie Sage		X
<i>Asclepias syriaca</i>	Common Milkweed	X	X
<i>Asclepias tuberosa</i>	Butterfly Milkweed	X	X
<i>Aster novae-angliae</i>	New England Aster	X	X
<i>Aster oolentangiensis</i> or <i>azureus</i>	Azure or Sky Blue Aster		X
<i>Baptisa australis</i>	Plains False Indigo		X
<i>Bidens aristosa</i>	Tickseed Sunflower		X
<i>Chamaecrista fasciculata</i>	Showy Partridgepea		X
<i>Coreopsis grandiflora</i>	Large flowered Coreopsis		X
<i>Coreopsis lanceolata</i>	Lanceleaf Coreopsis		X
<i>Coreopsis tinctoria</i>	Plains Coreopsis	X	X
<i>Coreopsis verticillata</i>	Whorled Tickseed		X
<i>Dalea purpurea</i>	Purple Prairieclover		X
<i>Desmodium canadense</i>	Canada or Showy Tick-trefoil		X
<i>Desmodium paniculatum</i>	Panicked Tick-trefoil		X
<i>Echinacea purpurea</i>	Purple Coneflower		X
<i>Eupatorium coelestinum</i>	Mistflower	X	X
<i>Eupatorium perfoliatum</i>	Boneset		X
<i>Gaillardia pulchella</i>	Blanketflower (Indian Blanket)		X
<i>Helianthus giganteus</i>	Giant Sunflower		X
<i>Helianthus grosseserratus</i>	Sawtooth Sunflower		X
<i>Helianthus mollis</i>	Ashy Sunflower		X
<i>Lespedeza capitata</i>	Roundhead Lespedeza		X
<i>Lespedeza virginica</i>	Slender Lespedeza	X	X
<i>Liatris pycnostachya</i>	Thickspike Gayfeather		X
<i>Liatris squarrosa</i>	Scaly Blazingstar		X
<i>Lotus corniculatus</i>	Birdsfoot Trefoil		X
<i>Ludwigia alternifolia</i>	Seed Box		X
<i>Medicago spp.</i>	Alfalfa		X
<i>Monarda citriodora</i>	Lemon Mint or Lemon Bee		X

	Balm		
<i>Monarda fistulosa</i>	Wild Bergamot		X
<i>Monarda punctata</i>	Dotted Bee Balm		X
<i>Oenothera biennis</i>	Common Evening Primrose		X
<i>Parthenium integrifolium</i>	Wild Quinine		X
<i>Penstemon digitalis</i>	Foxglove Beardstongue	X	X
<i>Penstemon laevigatus</i>	Appalachian Beardstongue		X
<i>Pycnanthemum virginianum</i>	Virginia Mountain Mint		X
<i>Rudbeckia hirta</i>	Blackeyed Susan		X
<i>Rudbeckia laciniata</i>	Cutleaf Coneflower or Golden Glow		X
<i>Silphium astericus</i>	Whorled Rosinweed		X
<i>Solidago nemoralis</i>	Gray Goldenrod		X
<i>Solidago rigida</i>	Stiff Goldenrod		X
<i>Tradescantia ohiensis</i>	Ohio Spiderwort	X	X
<i>Trifolium incarnetum</i>	Crimson Clover		X
<i>Trifolium pratense</i>	Red Clover		X
<i>Verbena hastata</i>	Blue Vervain		X

Appendix 4: Images of selected field sites at the four locations (Elzay, Sweet Briar College, Inge-Mann, Falcons). Areas outlined in pink and red only are Control treatment borders. Areas outlined in pink and green are Low diversity treatment borders. Areas outlined in pink and yellow are High diversity treatment borders.

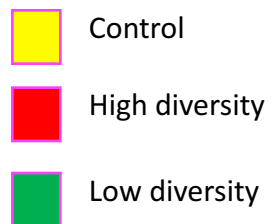


Appendix 4: continued.



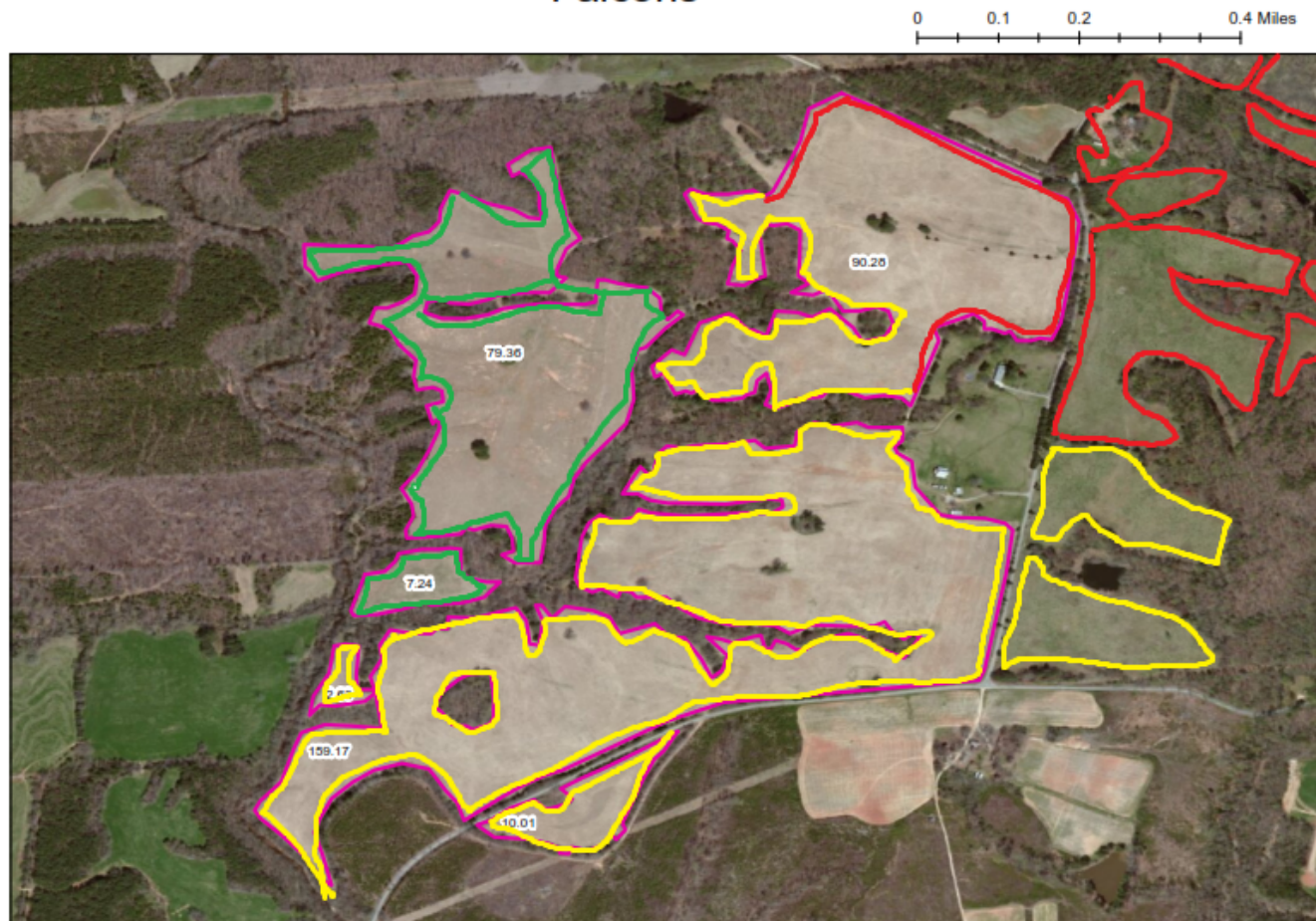
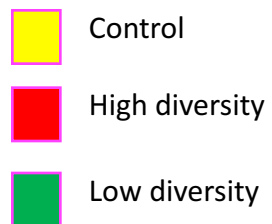
Appendix 4: continued.

Inge/Mann



Appendix 4: continued.

Falcons



Appendix 5: Bee species and total species abundances collected in Virginia throughout three sampling sessions (June, July, and August 2015).

<i>Species Identification</i>	<i>Total Abundance</i>
<i>Lasioglossum imitatum</i>	1,701
<i>Lasioglossum pilosum</i>	394
<i>Halictus poeyi/ligatus</i>	382
<i>Agapostemon virescens</i>	317
<i>Lasioglossum hitchensi</i>	297
<i>Lasioglossum bruneri</i>	224
<i>Lasioglossum versatum</i>	182
<i>Lasioglossum zephyrum</i>	174
<i>Augochlora pura</i>	144
<i>Lasioglossum callidum</i>	128
<i>Bombus impatiens</i>	105
<i>Melissodes bimaculatus</i>	98
<i>Ceratina calcarata</i>	81
<i>Hylaeus affinis</i>	80
<i>Lasioglossum gotham</i>	67
<i>Apis mellifera</i>	65
<i>Hylaeus modestus</i>	51
<i>Bombus griseocollis</i>	46
<i>Lasioglossum weemsi</i>	45
<i>Lasioglossum pectorale</i>	37
<i>Lasioglossum paradmirationum</i>	35
<i>Lasioglossum trigeminum</i>	30
<i>Agapostemon sericeus</i>	27
<i>Lasioglossum tegulare</i>	26
<i>Melitoma taurea</i>	26
<i>Ceratina dupla</i>	25
<i>Bombus vagans</i>	22
<i>Lasioglossum cressonii</i>	22
<i>Lasioglossum coreopsis</i>	20
<i>Xylocopa virginica</i>	18
<i>Lasioglossum weemsi/hitchensi</i>	17

<i>Hylaeus mesillae</i>	16
<i>Lasioglossum coeruleum</i>	16
<i>Dieunomia heteropoda</i>	15
<i>Bombus bimaculatus</i>	13
<i>Lasioglossum illinoense</i>	13
<i>Lasioglossum oblongum</i>	13
<i>Bombus citrinus/variabilis</i>	11
<i>Lasioglossum quebecense</i>	10
<i>Svastra obliqua</i>	10
<i>Peponapis pruinosa</i>	8
<i>Ceratina strenua</i>	6
<i>Sphecodes mandibularis</i>	6
<i>Lasioglossum cinctipes</i>	5
<i>Lasioglossum obscurum</i>	5
<i>Megachile sculpturalis</i>	5
<i>Halictus confusus</i>	4
<i>Lasioglossum coriaceum</i>	4
<i>Melissodes comptoides</i>	4
<i>Bombus fervidus</i>	3
<i>Bombus terricola</i>	3
<i>Ceratina mikmaqi</i>	3
<i>Lasioglossum fuscipenne</i>	3
<i>Lasioglossum lustrans</i>	3
<i>Augochloropsis metallica</i>	2
<i>Halictus rubicundus</i>	2
<i>Heriades variolosa</i>	2
<i>Lasioglossum lionotum</i>	2
<i>Lasioglossum nigroviride</i>	2
<i>Lasioglossum rozeni</i>	2
<i>Lasioglossum simplex</i>	2
<i>Sphecodes pimpinellae</i>	2
<i>Bombus auricomus</i>	1
<i>Bombus citrinus</i>	1
<i>Ceratina calcorata</i>	1
<i>Coelioxys germana</i>	1
<i>Halictus illinoense</i>	1

<i>Lasioglossum admirandum</i>	1
<i>Lasioglossum ellisiae</i>	1
<i>Lasioglossum leurozonium</i>	1
<i>Lasioglossum subviridatum</i>	1
<i>Megachile gemula</i>	1
<i>Megachile rotunda</i>	1
<i>Megachile rubi</i>	1
<i>Osmia georgica</i>	1
<i>Sphecodes dichrous</i>	1
Total Abundance	5,095