Quantifying the Disease Ecology and Network Connectedness Across Pollinator Communities as a Result of Planted Pollinator Plots

Final report for GS19-215

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Project Information

Summary:

As much as 30 percent of the American diet is a direct result of animal pollination, the majority of which is provided by bees. This bee pollination equates to more than $18 billion worth of crops annually in the United States alone. Despite their significant economic value, bees — both honey bees and native bees — are facing severe population pressures from multiple factors including habitat loss, pathogens, pesticides, climate change, and increased monoculture. These pressures can lead to severe population declines. Recently, providing pollinators with augmented habitat as a conservation method has become an increasingly popular trend. Much of this effort has been centered around adding habitat into the agricultural landscape to promote floral resources for beneficial arthropods and pollinators. Building on this trend, the NC Department of Agriculture and Consumer Services (NCDA&CS) has recently implemented an initiative called “Protecting NC Pollinators,” that mandates the planting of pollinator habitat at all Experimental Agricultural Research Stations across the state — which is the focus of this study. Despite the increasing popularity of augmented habitat, there are still many gaps in the empirical research documenting the impact of this tool. This study fills this gap by documenting the bee communities found on NCDA&CS research stations across the state — resulting in the most detailed survey of native bees in the state to date — measuring the pathogen ecology of the bee communities in this habitat to ensure that pollinator health is supported, and finally, measuring the impact habitat has on crop output.

Project Objectives:

- Screen bee samples for pathogens;
- Document pollinator networks at the plots and a nearby crop;
- Measure the impact of the plots on crop output.

Research

Materials and methods:

Site Selection

Disease Ecology

We collected samples from twelve official NCDA&CS research stations from 2017 - 2018, utilizing pollinator habitats that were established in 2016: Border Belt, Caswell, Clinton, Central Crops, Lake Wheeler, Mountain, Mountain Horticulture, Oxford, Peanut Belt, Piedmont, Sandhills, and Upper Piedmont. Collection events occurred once a month for 4 months during peak bloom at each plot, for a total of four sampling events per station per year. Eight different bee species (Apidae: *Apis mellifera, Bombus impatiens, Bombus pensylvanicus, Svastra obliqua, Xylocopa virginica, Xylocopa micans*; Halictidae: *Halictus poeyi/ligatus*; and Megachilidae: *Megachile xylocopoides*) were screened against a panel of 10 different pathogens (Acute Bee Paralysis Virus [ABPV], Black Queen Cell Virus [BQCV], Chronic Bee Paralysis Virus [CBPV], Deformed Wing Virus: Strain A [DWVa], Deformed Wing Virus: Strain B [DWVb], Israeli Acute Paralysis Virus [ABPV], Lake Sanai Virus [LSV], *Trypanosome* Universal primer [*Trypanosome* spp.], *Nosema* universal primer [*Nosema* spp.], and *Nosema ceranae* [*N. ceranae*]) and two reference genes (Apocrita 28s [Apo28s] and Actin.

Pathogen Testing

The samples from three of the bee species (*Apis mellifera, Bombus impatiens,* and *Xylocopa virginica*) were tested individually, and the samples from the remaining species were tested in pools of up to five individuals per sampling event. Samples were crushed using Zirconium beads after which RNA was extracted using TRIzol Reagent and the Zymo Directzol RNA Mini Prep Kit. RNA was then synthesized into cDNA using the BioBasic High Reverse Transcriptase Kit and then subjected to real time PCR using Life Technologies PowerUp SYBER Green chemistry and quantified plasmid standards.

Crop Pollination

Sampling was conducted in 2019, again at established pollinator habitat at NCDA&CS research stations. In total we sampled at eight research stations that represented different ecoregions of the state, had high quality pollinator habitat (for this study high quality habitat meant high seed take and high bloom as well as high floral diversity), and regularly plant soybeans were prioritized: Peanut Belt Research Station (upper coastal), Caswell Research Farm (central coastal), Horticulture Crops Research Station - Clinton (central coastal), Border Belt Tobacco Research Station (lower coastal), Horticulture Crops Research Station - Castle Hayne (lower coastal), Piedmont Research Station (piedmont), Mountain Research Station (mountain), and Mountain Horticulture Crops Research and Extension Center (mountain).

At each of the 8 sites, sampling occurred at 3 fields. The first field was the established pollinator habitat. The second field, the near soybean field, was the closest field as possible to the habitat where soy was to be grown in order to measure the impact the presence of habitat has on yield. And the third field, the far

soybean field, was the furthest field as possible to the habitat where the soy was to be grown in order to act as a control as the presence of the habitat should not directly impact yield. There was variation between sites with how close the near and far fields were to the habitat, but there was no overlap between the near and far field distances between the sites. All near fields were within 270 meters from the habitat, with the closest being 9 meters away. All the far fields were more than 320 meters from the habitat with the furthest being 3700 meters away. All soybean fields selected grew indeterminate plants, although variety varied across the state.

Sampling

We used two sampling methods in all 3 fields, visual surveys and netting surveys. Both survey methods were conducted using haphazard transects through the fields. In all 3 fields, only floral visitors were documented in order to truly document the community of flower visiting pollinators. Any insect found on leaves, the ground, or air was not documented. We spent 30 minutes total in each field, during which time both survey methods were used. We surveyed each field twice per day, once in the morning and once in the afternoon, in order to account for any temporal variation. The order in which we visited each field was randomly determined, for both the morning and afternoon sampling, to make sure the order in which we sampled the fields was not repeated. We sampled the fields 2 – 3 times over the bloom period depending on bloom longevity of the soybean fields (pollinator plot surveys were only conducted during the same day as soybean surveys, so once the soybean had senesced, we stopped sampling). Surveys were conducted when the soybean fields were between the R2 and R5 stages.

Visual Surveys

During the visual surveys one person documented the bee visitors and one person documented all non-bee visitors. Identifications were made down to the family, genus, or species depending on the level of absolute certainty capable for each insect. The plant that each insect visitor was found on was also documented. After 20 minutes, the visual surveyors switched to conducting netting surveys.

Netting Surveys

For the entire 30-minute sampling time, one person collected plant visitors using a hand net in order to have an identification verification collection. This collection also allowed individuals unable to be identified visually in the field to be identified later under a microscope. Each visitor was stored in individual 1.7 ml microcentrifuge tubes and stored on ice. The plant that each sample was collected on was documented. After 20 minutes, the visual surveyors also collected samples by net using the same methods. Once the 30 minutes was up, all samples were stored on dry ice until transported back to the lab where they were stored at -80C.

Harvesting

Plant were collected for yield analysis once they reached R8 and then had sufficient time to dry in the field. Plants were collected as close as possible to when the research stations were harvesting the field in order to have realistic harvest conditions and data. 30 plants from both the near soybean field and the far soybean field were removed by walking a haphazard transect and randomizing the distances between each plant selected. Plants were either processed by hand in the field or brought back to the lab for processing depending on impending weather conditions. To process each plant, each node was removed from the plant individually. The number of pods per node and the number of beans in each pod was documented. Any variation in a particular bean – such as deformity, abortion, herbivory damage, or mold – was documented. Once an entire plant was processed, all of the beans from that plant were weighed together. Thus, for every plant we documented the

total number of beans, total number of pods, number of pods per node, number of nodes, average bean weight, number of deformed beans, number of aborted beans, number of aborted pods, number of beans damaged from herbivory, and number of beans with mold growth. Beans and pods that were aborted or experienced herbivory damage were not included in the total bean or pod count for the plant.

Research results and discussion:

Results

Disease Ecology

(1) Pathogens within Apis mellifera populations
Out of 189 A. mellifera screened, we found a positive detection for every pathogen in our panel except for CBPV. Many individuals were found to be simultaneously infected with multiple pathogens, with two individuals infected with four pathogens. Some individuals that tested positive for Nosema spp. did not also test positive for N. ceranae so was likely infected with a different species of Nosema (presumably N. apis).

From the X2 analysis, we found that infection level across both years and all sampling events was significantly different among stations ($X2 (33) = 91.8$; $p < 0.0001$) and among pathogens ($X2 (27) = 48.7$; $p < 0.01$). We found that across years and stations, infection level was significantly different among sampling events ($X2 (9) = 33.9$; $p < 0.0001$) but not between years ($X2 (3) = 2.22$; $p = 0.53$). Interestingly, there were significantly more individuals with low-level detections overall than medium or high detections ($X2 (3) = 559.8$; $p < 0.005$).

We did not run results from ABPV, CBPV, and IAPV in the ZINB model due to their low detection numbers. We found that BQCV copy number was not significantly influenced by any of the variables in our model ($\log\square = -0.80$; $DF = 20$; all p-values > 0.23). DWVa copy number was significantly highest in Late Summer ($\log\square = -0.13$; $DF = 20$; $p < 0.005$, SE ± 1.30) and was significantly lowest during Late Summer ($\log\square = -0.13$; $DF = 20$; $p < 0.05$, SE ± 1.01). DWVa copy number was not significantly different between years, but it was numerically higher in 2018. Similarly, DWVb copy number was significantly highest during Late Summer ($\log\square = 0.05$; $DF = 16$; $p < 0.005$, SE ± 0.92) but was significantly higher in 2018 ($\log\square = 0.05$; $DF = 16$; $p < 0.0001$, SE ± 0.46). Due to low detection number, plot cover was removed from this specific model. LSV copy number was significantly lowest during Fall ($\log\square = -0.72$; $DF = 20$; $p < 0.0001$, SE ± 1.54) and Plot Cover 3 ($\log\square = -0.72$; $DF = 20$; $p < 0.0001$, SE ± 1.77) but only neared significance between years ($\log\square = -0.72$; $DF = 20$; $p = 0.087$) with lower infection levels detected in 2018. Trypanosome spp. copy number was significantly highest at Plot Cover 5 ($\log\square = -0.29$; $DF = 20$; $p < 0.0005$, SE ± 1.49) and significantly lower in 2018 ($\log\square = -0.29$; $DF = 20$; $p < 0.01$, SE ± 1.45). Trypanosome spp. copy number was not significantly impacted by sampling event ($\log\square = -0.29$; $DF = 20$; all $p > 0.19$). Alternatively, Nosema spp. copy number was significantly higher in 2018 ($\log\square = -0.38$; $DF = 16$; $p < 0.0001$, SE ± 1.13) and was significantly lower during Early Summer ($\log\square = -0.38$; $DF = 16$; $p < 0.0001$, SE ± 1.26). Due to low detection numbers, plot cover was removed from this specific model. Nosema ceranae copy number was significantly lowest in Fall ($\log\square = -0.72$; $DF = 16$; $p < 0.0001$, SE ± 1.54) and Plot Cover 3 ($\log\square = -0.72$; $DF = 16$; $p < 0.0001$, SE ± 1.77), but only neared significance across years ($\log\square = -0.72$; $DF = 16$; $p = 0.087$) where it was lower in 2018. The number of pathogens an individual samples was infected with was significantly higher in 2018 ($\log\square = 16.8$; $DF = 20$; $p < 0.0001$, SE ± 0.20) and highest in Plot Cover 5 ($\log\square = 16.8$; $DF = 20$; $p < 0.0001$, SE ± 0.37). The number of pathogens was not significantly different across sampling events.

(2) Pathogens within Bombus impatiens populations
Out of 201 B. impatiens screened against our panel, we found no positive detections for any of the viruses (ABPV, BQCV, CBPV, DWVa, DWVb, IAPV, LSV; Figure 1). However, many individuals tested positive for gut pathogen. None of the B. impatiens were found to be infected with more than one pathogen simultaneously.

From the X2 analysis, we found that infection level across both years and all sampling events was not significantly different among stations (X2 = (3) = 37.4; p = 0.27). Infection level was significantly different among pathogens (X2 (27) = 215.6; p < 0.0001) with nearly all positive detections of any level found under Trypanosome spp. Infection level was not significantly different among sampling events (X2 (9) = 8.17; p = 0.52) but was significantly different between years (X2 (3) = 14.7; p < 0.005). We found significantly more individuals with medium-level detections overall than medium or high (X2 (3) = 263.2; p < 0.001). Neither the number of honey bees collected during a sampling event nor the number of pathogens with which those honey bees were infected significantly impacted the infection level of B. impatiens (all X2 (3) < 5.00; all p-values > 0.15).

Trypanosome spp. was the only pathogen with high enough detection levels to run in the ZINB. In doing so, we found that when accounting for station, Trypanosome spp. copy number was significantly higher in 2018 (log = 0.29; DF = 21; p < 0.0001, SE ± 0.32) and significantly highest during Late Summer (log = 0.29; DF = 21; p < 0.05, SE± 0.45). Plot cover did not significantly impact Trypanosome spp. copy number (log = 0.29; DF = 21; all p > 0.16). We found that the number of pathogens an individual was infected with was significantly lowest during Fall (log = 11.6; DF = 21; p < 0.0001, SE ± 0.50) but did not significantly change across plot cover or year (log = 11.6; DF = 21; all p > 0.10).

(3) Pathogens among all pollinator populations
We found no positive detections for any virus included in our screening panel among the other native bee species in our study, although many individuals tested positive for the gut pathogens. We found many individuals across these native bee species tested positive for Nosema spp. did not also test positive for N. ceranae.

From the X2 analysis, we found that infection level was not significantly different across stations (X2 (33) = 37.8; p = 0.26), between years (X2 (33) = 3.42; p = 0.33), among sampling events (X2 (33) = 10.2; p = 0.33), or number of individuals infected (X2 (3) = 311.0; all p-values > 0.97). Infection level was significantly different among the gut pathogens (X2 (27) = 80.0; p < 0.0001). Infection level was also significantly different among bee species, with most detections found in samples of B. pensylvanicus overall. Neither the number of honey bees collected during a sampling event nor the number of pathogens those honey bees were infected with significantly impacted the infection level of B. pensylvanicus (all X2 (3) < 4.00; all p-values > 0.14).

Trypanosome spp. was the only pathogen with high enough detection rates to analyze with the ZINB; however, Trypanosome spp. copy number was not significantly impacted by any variable in our model (log = 0.03; DF = 22; all p > 0.11). The number of pathogens infecting a sample was also not impacted by any variable (log = 14.6; DF = 22; all p > 0.20).

Crop Pollination

We documented a total of 7218 bees in our study covering 4 different families, 21 different genera, and at least 53 different species of bees. We found that bee abundance in the crop fields was significantly driven by growth stage in the soybeans ($F_{3,34}$ = 13.4, p < 0.0001), with the highest number of bees found visiting during R2 and quickly dropping off in later stages (R2 = 155.5 ± 13.5 (B), R3 = 94.6

± 19.7 (AB), R4 = 29.6 ± 19.7 (A), R5 = 19.6 ± 24.9 (A)).

(4) Are the pollinator communities in the habitat 'spilling over' into the soybean fields?

Through the NMDS (visualized using Bray-Curtis distance with two dimensions and a 0.13 stress value), we found that the bee communities within the habitat sites all cluster together, separate from the two soybean site types. The adjacent and negative control sites cluster together, although the adjacent site cluster was closer to the habitat cluster than was the negative control site. When analyzing which genera were driving the clustering, we found that *Apis* ($p < 0.001$), *Bombus* ($p < 0.01$), *Svastra* ($p < 0.001$), *Triepeolus* ($p < 0.005$), *Halictus* ($p < 0.001$), and *Megachile* ($p < 0.005$) were all significant. We then ran an NMDS of the species composition and found that *Apis mellifera* ($p < 0.001$), *Bombus impatiens* ($p < 0.005$), *Bombus pensylvanicus* ($p < 0.05$), *Svastra aegis* ($p < 0.05$), *Svastra obliqua* ($p < 0.01$), *Triepeolus concavus* ($p < 0.05$), *Halictus poeyi/ligatus* ($p < 0.001$), *Megachile frigida* ($p < 0.05$), *Megachile lippiae* ($p < 0.005$), and *Megachile mendica* ($p < 0.005$) were influencing the differences in site community compositions the most, with *Apis mellifera, Bombus impatiens,* and most *Megachile* species driving the two soybean site types to be more similar to each other than the habitat. Alternatively, *Halictus poeyi/ligatus* and *Svastra obliqua* distinguished the habitat from the soybean sites.

(5) How does the presence of the habitat, and resulting pollinator community, impact soybean yield?

Overall, seed quality was found to be higher in the adjacent sites compared to the negative control sites. While we did find 2.50% more seeds per pod in the negative control sites (site-type: $t418 = 2.28$, $p < 0.05$; Shannon's: $t418 = -0.11$, $p = 0.91$), adjacent sites had significantly heavier seeds that weighed 6.52% more per plant on average (site-type: $t418 = 11.7$, $p < 0.001$; Shannon's: $t418 = -2.09$, $p < 0.05$). The total number of seeds per plant (site-type: $t418 = -0.52$, $p = 0.60$; Shannon's: $t418 = 0.81$, $p = 0.42$) and the number of deformed seeds per plant (site-type: $z = 0.03$, $p = 0.98$; Shannon's: $z = -1.99$, $p < 0.05$) were not significantly different between soybean sites in our models.

Discussion

Apis mellifera was the only pollinator species to be infected with any of the viruses included in our pathogen panel. These results suggest that even though large abundances of bees across a wide range of species are attracted to augmented pollinator habitat, interspecific co-occurrence of pathogens is not occurring. This could be due to the fact that even though shared flowers have been documented as a source of spread for some pathogens, the occurrence may actually be rather rare and its success depends on the bee and flower species in question. It has also been suggested that non-host bees can reduce infection levels through the dilution effect.

Within honey bees, there were more pathogens detected and higher infection levels of some of those pathogens (DWVa, DWVb, and Nosema spp.) in 2018 compared to 2017. While the limits of this study prevent us from investigating this further, it is possible that as time progresses and bees continue to utilize these habitats, the pathogens pressures will intensify. Further long-term testing will be necessary to evaluate this possibility. Several samples that tested positive to the universal gut primer for Nosema spp. did not test positive for N. ceranae. This could be due to different bee species acting as incompetent hosts for these gut pathogens and so not supporting pathogen replication, or that these species face their own specific species of gut parasites that we have not tested for. Gut parasites are currently considered a serious threat to several bee species, especially bumble bees; of particular concern in the eastern United States is the American Bumble Bee (B.

pensylvanicus). In our study, B. pensylvanicus had the greatest positive detections of gut parasites out of all the native bee species tested, supporting the hypothesis that gut parasites pose a threat to their populations. Further studies on the prevalence and impacts of these pathogens should be conducted across a broad range of native bee species in order to support native bee health. However, it should also be noted that detecting a pathogen neither equates to infection nor demonstrates any health impacts of the pathogen. It has been suggested that the presence of N. ceranae in B. terrestris may be due to ingested spores passing through the gut rather than true infection. Future research should prioritize evaluating the true infectivity and health impacts of these pathogens on native bee species.

Many studies have previously found the presence of what are traditionally called 'honey bee' viruses in various native bee species, something this study does not confirm. Given other recently published papers also documented fewer detections than previous research, the unexpected results require speculation as to why. One factor driving lower detections could be that the infection levels found in the foraging honey bees in this study are noticeably lower than what has been documented nationally, perhaps indicating that the bees sampled in our system did not have high enough infection levels to spread these pathogens. Indeed, unlike most other studies, we collected these honey bee samples as individual foragers rather than groups from nest entrances or even inside managed beehives, which may explain discrepancies in the relative levels of various pathogens (e.g., heavily infected bees may not live long enough to forage). Floral diversity was also found by Daughenbaugh et al. (2021) to be an important factor for pathogen sharing and especially honey bee infection levels. Thus, plant diversity could potentially be used as a tool to intentionally limit pathogen sharing between honey bees and native bees at these planted habitats. This is something that should be investigated further in future research and taken into consideration when establishing new pollinator habitat.

Another factor to consider when comparing the results from this study to previously published work is the techniques used to screen for pathogens. Many previous papers evaluating co-occurrence of pathogens between honey bees and native bees have used traditional PCR or ran PCR reactions at high cycle numbers (summarized in Table 2). However, these results are could be due to spurious PCR amplification, which is known to occur at 30 cycles and above. When our RT-qPCR results were re-scored at 35 cycles rather than the cycle number recorded from the serially diluted standards, we saw an 85.1% increase in positive detections across all targets and all bee species. Similarly, we saw a 270.3% increase in positive detections when our samples were re-scored at 40 cycles. Within our standardized results, we saw no detection of CBPV in any bee species and only one individual each infected with ABPV and IAPV. When scoring at 35 and 40 cycles, however, all three of these pathogens were detected at significantly higher levels. While we believe these detections to be spurious, if they are true detections it begs the question of biological relevance when pathogen infections are present at such low levels. Comparing across studies, therefore, should be done with caution, because the advancement of technology and their application make direct comparisons difficult.

As planted habitat for pollinators will likely continue to be used as a tool in pollinator conservation, we should take care to establish this habitat with plant species that provide floral resources while limiting pathogen transmission. We should also prioritize conducting long-term monitoring of the bees within these habitats to ensure it continues to protect pollinator populations and their health over time.

The presence of pollinator habitat was found to positively impact some measures of

soybean yield quality and quantity, more specifically leading to heavier seeds. This suggests that having habitat near soybean fields results in more pollinator visits and better pollination services, a finding that is supported by a recent global meta-analysis by Albrecht et al. (2020) that includes data from over 10 different crops. We found numerically more seeds per plant in the adjacent sites and more deformed seeds per plant in the negative control sites, although due to the limitations of our data we were unable to explore these measures further. These results, however, highlight factors—including pollinator visitation, pollinator community diversity, and pollinator functional traits—that future research should address. These factors are known to be important in many crops deemed to be pollinator dependent, but their importance in pollinator-independent crops is less understood. The impacts of planted habitat on pollinator dependent crops have been investigated in past research showing 12.2% increase in seed set in blueberries, 55% increase in production in mangos, and 150% increase in fruit set in sweet cherries, to name a few. Previous studies evaluating this impact in soybeans have also found yield increases, at times of more than 100%. Increased soybean yield in our study system, which compares to previous research, further highlights the importance of evaluating plant-pollinator interactions in these crops. However, it will be important to consider the implications of different crop varieties, different growth behaviors (i.e. indeterminate vs determinate soybeans), and different growing conditions in future research as there is already evidence that this can affect both yield and pollinator attractiveness in soybeans. Additionally, this study is limited in that yield was evaluated on a per-plant basis from a small subset of the larger crop fields; the impact of habitat on soybeans at larger field scales should be addressed in future research. A preliminary analysis of the influence of landscape factors on the bee community and soybean yield in this study was inconclusive and did not find any significant associations (unpublished data). Previous literature has found differing impacts of landscape variables on pollinators and crop yield, as such this is an area that would benefit from further exploration. As pollinator-independent crops constitute the majority of the world’s caloric intake and global agricultural acreage, our results show that plant-pollinator interactions within these systems should not be overlooked.

Participation Summary

8 Farmers participating in research

Educational & Outreach Activities

5 Webinars / talks / presentations

1 Workshop field days

PARTICIPATION SUMMARY:

20 Farmers

10 Ag professionals participated

Education/outreach description:

The presentations counted above include 1 presentation to a local garden club, 1 presentation during a pollinator conference at Montgomery Community College, 2 presentation at the annual national Entomological Society of America conference, and 1 presentation at a local scientific conference (Southern Appalachian Honey bee Research Consortium). The preliminary data on pollinators in soybeans was very well received and sparked a lot of interest. Conversations started by these presentations have resulted in Hannah Levenson, the graduate student on this project, developing a "pollinator in soybean network" with other scientists across 4 different states. Hannah recently worked with two of the scientists in this unofficial network to organize a new symposium focused on pollinators in soybean at the 2020 ESA conference.

Hannah also participated in a Pollinator Field Day that was coordinated by the North Carolina Pollinator Conservation Alliance. At this field day she ran a station where she talked about her research to attendees and demonstrated how to survey bees in the field. Attendees also learned a few way to ID different species of bees on the wing.

Currently, Hannah and David Tarpy are in the process of submitting two different papers for publication (one on pathogen ecology and one on soybean pollination in relation to the presence of pollinator habitat).

Project Outcomes

3 New working collaborations

Project outcomes:

As we are just now about to submit this work for publication, I think in the future it will contribute to agriculture sustainability. In this project we highlight that soybeans are a resource regularly used by multiple different bee species, that bee visitation can benefit soybean yield, and that there are particular times of the soybean growth period where the most bees visit. Additionally, we found that adding habitat into the agricultural system does not harm bee health (across multiple species) and that planting habitat nearby soybean fields supports pollination services provided to those fields. All of these could directly advise and impact current management of soybeans and provides very concrete changes to implement.

Knowledge Gained:

During the course of this project my advisor and I had to become more acquainted with the IPM side of agriculture than before. While pollinator research in general easily and readily relates to agriculture, we do not as regularly deal with IPM. Since part of the work under this project was measuring yield of soybeans, we had many conversations with other researchers about the soybean agroecosystem, the IPM of soybeans, and how to sustainably fit pollinators into this system.

Recommendations:

Future studies should expand investigating bees in soybean to more varieties, different growing characteristics, and different abiotic factors such as nutrients and soil type. Additionally, long term monitoring of the disease ecology of pollinators at pollinator habitat should be conducted in the future as we saw evidence that pathogens may build up over time. If this does occur, the likelihood of those

pathogens spreading between bee species could increase.

Sustainable Agriculture Research & Education US Department of Agriculture

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