Designing farms that support wild bees

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Project Objectives:
To develop clear guidelines that farmers can use to design optimal pollinator habitat, we selected 33 sites in the greater Ithaca region, New York across forest, agricultural, wetland, successional, and developed habitat typical of Northeast US agricultural landscapes. Within each of these sites, we will complete Objectives 1-3.

1. **Assess plant species abundance and richness (to be completed with existing data from collaborators)**
2. **Document bee species abundance and richness.**
3. **Measure soil moisture, fertility, and organic matter content.**

Using the data from these objectives, we will complete the following analytical objectives:

4. **Determine relationships among local abiotic factors, including soil moisture, fertility, and proximity to water, and plant and wild bee abundance and richness.** *Expected Outcome:* Plant and wild bee communities will be more diverse at sites close to water features, and sites with more spatially variable soil moisture, and lower soil fertility (as these sites are less likely to be dominated by a few very competitive plant species).
5. **Determine the relative contribution and interactions among local abiotic factors, plant diversity, landscape heterogeneity, and connectivity in explaining wild bee diversity and abundance.** *Expected Outcome:* Local abiotic factors will interact with landscape heterogeneity and connectivity, so that there is a minimum amount of habitat necessary to support wild bees, but plant diversity and abiotic factors will significantly influence bee community diversity above this threshold.

Materials and methods:

Objective 1: Plant species richness, abundance, and floral area was measured by Iverson et al (in preparation) in the greater Ithaca region, New York in 2015 and 2016.

Objective 2: We measured bee species richness and abundance using 12oz. Solo polystyrene plastic cups as bee bowls according to the protocol of a long-term bee monitoring program in our region. We filled fluorescent blue, fluorescent yellow, and white bee bowls with 50:50 mix of propylene glycol and water and placed them at the height of dominant vegetation for 7-14 days of sampling. We arranged bee bowls in 100m transects in visible areas, alternating bowl color with 10 meters between each bowl, for a total of 9 bowls per site. We sampled wild bees at 33 field sites of 7 habitat types (forest, forest edge, floodplain forest, old field, roadside ditch, mixed vegetable farm, and apple orchard) that span a range of semi-natural to agricultural land use. From Iverson et al. plant sampling locations, we selected bee sampling sites based on landowner willingness to participate in our study and distance between sites. To ensure we were sampling independent bee communities at each site, we chose sampling locations that were at least 1km from all other sites, a distance greater than the mean foraging range of a typical mid-Atlantic wild bee community (Kammerer et al 2016). We sampled bees in late April and again in mid-July, guided by peak floral abundance in forest, wetland, and successional habitat. After collection, bee specimens were stored in 70% ethyl alcohol solution until pinning and sorting. After the field season ended, we washed and pinned all specimens, and began identifying bee specimens to genus, or species, when possible,

with taxonomic assistance from collaborators within the PSU Center for Pollinator Research, including Dr. David Biddinger, and Sam Droege at the USGS Bee Inventory and Monitoring Lab.

Figure 1: Left, a yellow bee bowl sampling bees at an organic vegetable farm. Center, wild bees captured in bee bowl surrounded with spring ephemeral flowers at a floodplain forest site. Right, spring beauty (a spring ephemeral flower visited by a specialist wild bee, *Andrena erigeniae*) flowering at a forested patch within a crop farm.

Objective 3: In May 2018, we collected soils at each of the bee sampling sites. Along the bee sampling transect, we collected five soil samples with a bucket auger to a depth of 9-18 cm, depending on rock and moisture content of subsoil. Shallower soil cores (9-12cm) were taken at sites with very rocky or wet (floodplain habitat) subsoil due to sampling constraints. Also, wild bee nesting would likely be inhibited by very high rock content or completely saturated subsoils, so we considered the shallower sampling depth representative of the most favorable zone for soil nesting wild bees. At two locations along the bee transect, we collected three undisturbed soil cores (0-3 cm, 4-6 cm, and 7-9cm deep) with a slide hammer soil core sampler (Soilmoisture Equipment Corp, Goleta, CA) to quantify bulk density. Due to above described sampling constraints, we were only able to sample 2 bulk density soil cores deep at some locations, but the number of cores was recorded for each sample. Bulk density cores at all depths were combined for processing and analysis.

Figure 2: Kammerer Allen collecting a soil core to measure bulk density in an apple orchard near Geneva, NY.

After collection, we measured the wet mass of all soil samples, then dried them at 60 degrees C for five days, or until the mass did not decrease. We sent the bucket auger samples to the Penn State Agricultural Analytics lab and they measured pH, P, K, Mg, Ca, Zn, Cu, S, total nitrogen by combustion, percent organic matter, and percentage sand, silt, and clay via standard laboratory methods (https://agsci.psu.edu/aasl/soil-testing/soil-methods). We calculated soil bulk density of each sample as the total dry mass of bulk density cores divided by the volume of the sampling cylinder multiplied by the number of cores. To identify patterns across the 14 soil characteristics we measured, we used a principal components analysis. We conducted the analysis using the *prcomp* function in R on centered and scaled soil variables.

Objective 4: Following the Kammerer et al [15] analytical approach, I plan to use statistical models to quantify the relationship between plant richness and local soil moisture, fertility, organic matter content, proximity to water features, and landscape heterogeneity and connectivity at each site. I will calculate proximity to water features using ArcMap GIS software version 10.5 and a dataset of water features from the Tompkins County GIS office. Landscape heterogeneity will be represented with two metrics, the percent of perennial habitat land cover, and diversity of land cover types in the landscape. Landscape heterogeneity and connectivity metrics will be calculated from the 2016 USDA National Crop Data Layer using FRAGSTATS landscape analysis software and geospatial tools in the R statistical computing language. All landscape metrics will be computed at 3 scales (500m, 1000m, and 1500m) centered around each plant sampling site.

For statistical analyses, I will use generalized additive models, and specify a habitat random effect to account for variance due to habitat specific variables that were not measurable. Statistical model fits will be compared using Akaike information criterion and variance explained values. All analyses will be conducted in the R statistical computing language.

Objective 5: Analyses for this objective will use the same predictor variables and statistical methods as Objective 4, except plant species richness, evenness, and floral area at each site will be included as a predictor of bee richness.

Results and discussion:

In year one of the project, we captured 1677 wild bees and 241 *Apis mellifera.* Surprisingly, we collected more wild bees in the April sample than the July sample. In April, we left the traps out for 14 days instead of 7 because it was very cold during the first week of sampling and there were very few bees in the traps that we inspected after one week. It is possible that this increased sampling time led to higher number of specimens, but we also observed greater diversity of wild bees in April than July. After taxonomic identification is complete, we will verify our field observations by analyzing species richness at each site. We will also adjust the the April and July samples to a common sampling effort using species rarefaction curves (*iNEXT* package in R statistical computing language). In the field, we observed that, in April, the old fields and floodplain forests had the most bees, while the roadside ditches yielded the greatest number in July. As we expected, the floodplain forest, forest, and forest edge sites had many more bees in late April than July, as the latter sample occurred after the forest canopy closed and traps were shaded. Surprisingly, the old field sites had more bees in late-April than July, even though the diversity of flowering plants at these sites was much higher later in the season.

We found significant variation in soil characteristics between the site and habitat types we sampled. There were two main gradients in our soil dataset revealed by the principal components analysis (Figure 1). Explaining 27.5% of the variation in our soil data, the first principal component was correlated with soil texture (percent sand, silt, and clay). Roadside ditches had sandier soil than any of the other habitat types, except some floodplain forest samples. All the other habitat types

had loam to silt-loam soil. Interestingly, soil texture was highly variable between floodplain forests, with soil texture in this habitat encompassing the full range of texture classes represented at all other sites. The second principal component explained 19.5% of the variation in soil characteristics and was associated with several soil fertility variables. Specifically, some vegetable farm and orchard samples had much higher potassium, phosphorus, copper, and zinc content than the other habitats, likely due to fertilizer or manure application to support crop growth. Forested sites were most highly correlated with higher total nitrogen in the soil, probably due to high organic matter content from leaf litter accumulation. In future analyses, we will analyze if and how these patterns in soil characteristics explain patterns in plant and bee abundance and species richness.

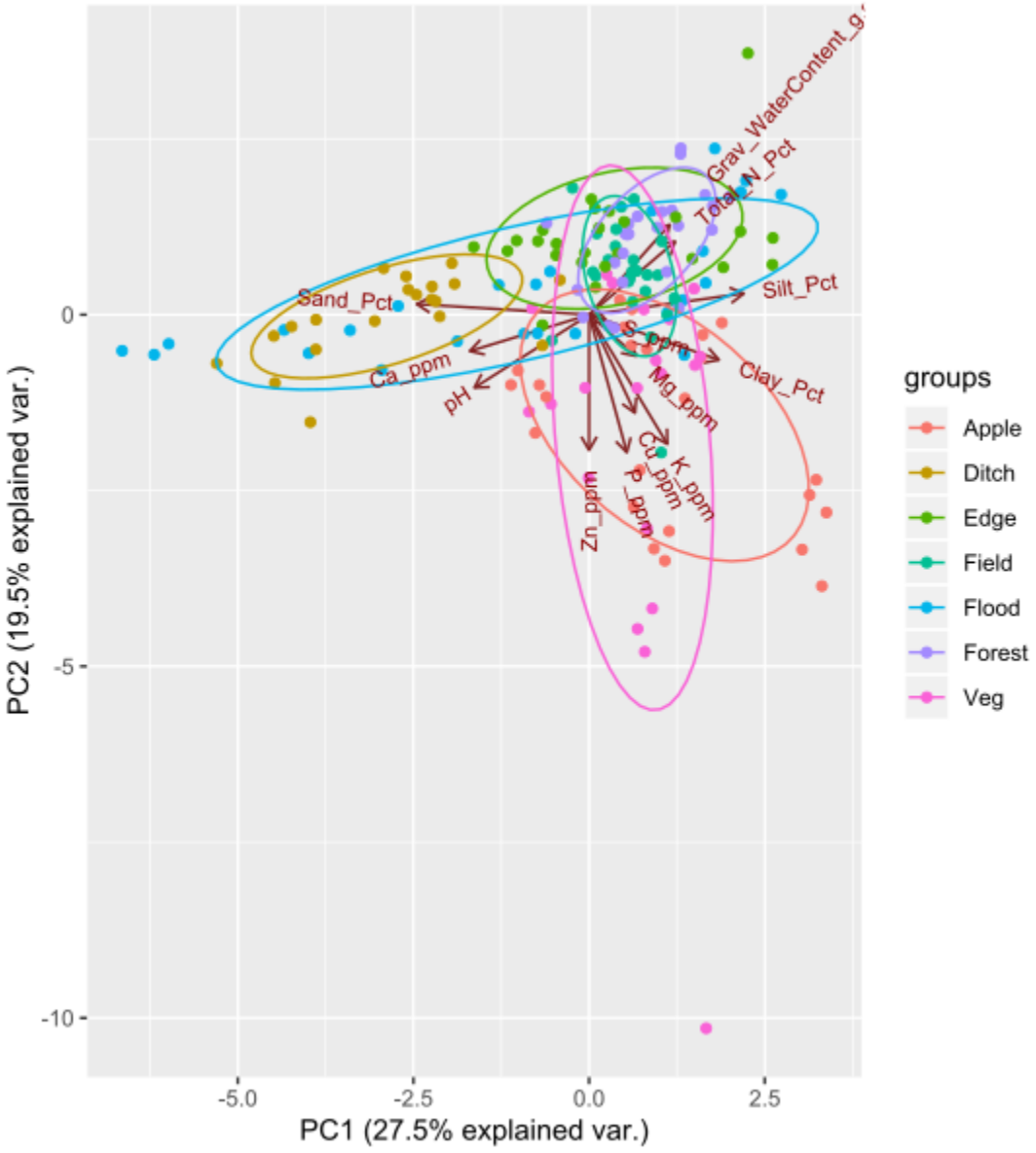

Figure 3: Principle components ordination plot of soil characteristics at 33 sites in the Finger Lakes region, NY. Sample colors correspond to the following habitat types: 'apple'= apple orchard, 'ditch' = roadside ditch, 'edge' = forest edge, 'field' = old field, 'flood' = floodplain forest, 'forest' = mesic upland remnant forest, and 'veg' = mixed vegetable farm.