**Abstract:**

These data were collected to assess community diversity in response to the introduction of canola crops as a novel, pulse-blooming resource. This study samples bee communities 3 times per year (pre, peak, and post-canola 13 bloom) at 10 sites along a gradient of canola landscape composition to measure within-year 14 responses in stability and diversity. I show that bee communities were not strongly impacted by canola as expected, which may be due to the high composition of solitary, range-restricted bee species in the Palouse ecosystem.

**Hypothesis:**

Bee communities in more canola-dominated sites will have more variation in community diversity metrics over the course of the three sample periods.

*Bee\_Samples\_2022*

Bee samples collected during the 2022 field season with site and collection info identified to morphogroup, family and genus.

**Methods:**

Bees collected by continuously sweep-netting along both sides of the walking transects for 10 minutes each. This resulted in a total of 20 minutes of sampling per transect. Each 5m interval was sampled for 1 minute to ensure even sampling. Once the first side of a transect was sampled, section A, we placed the bees caught into a gallon Ziplock bag and placed samples on dry ice. We repeated the process for the opposite side of the transect, section B. Each site was sampled for a total of 80 minutes each per sampling period. Bee samples were stored at -20°C in the lab and identified to genus.

Sites: 10 sites: wildflower patches (semi-natural to natural habitat) selected along a gradient of canola field percentage within a 2km buffer. Canola field percentage within 2km ranged from approximately 0-43%. Sites ranged from approximately 11-8100m in distance from canola fields. At each site, we placed four 50m by 7m walking transects with every 5m interval marked. Transects were placed during the first sampling period visit in areas with flowers visibly blooming and remained in place throughout the survey.

**Fields:**

ID: Unique identifier given to each bee at time of sorting

Date: Date sample was collected

Period: Canola-bloom period when sample was collected (Pre-bloom, Bloom, Post-bloom)

Site: Field site where sample was collected

Transect: Transect number within field site where sample was collected

Morphogroup: Identified morphogroup of bee sample (SB = Solitary Bee; OLB = Other Large Bee; GB = Green Bee; HB = Honey Bee; BB = Bumble Bee)

Family: Family of identified bee

Genus: Genus of identified bee

Notes: Notes made during identification process

*AllFloral*

**Methods:**

We conducted plant biodiversity surveys for each site during each of the three sampling periods. At each site, we placed a 1m2 quadrat at the same meter marker within each transect. Placement was changed between periods to avoid re-sampling the same flowers. We recorded all plants in flower within each quadrant.

**Fields:**

SiteSeason: Sites divided by collection period

Site: Field sites

Season: Canola-bloom period when sample was collected (Pre-bloom, Bloom, Post-bloom)

Abundance: Calculated in *FloralStability* script

Richness: Calculated in *FloralStability* script

Shannon\_Diversity: Calculated in *FloralStability* script

*BeesbySeason*

Bee diversity metrics structured by season

*BeesbySite*

Bee diversity metrics structured by site

*BeesbySiteSeason*

Bee diversity metrics structured by each season within site

*CanolaPercentages*

Percentage of canola in buffers of 500m, 1km, and 2km as well as distance to nearest canola site (m).

Data created using GIS. Percentages calculated in excel sheet.

*BeeSiteTukey*

Results of Tukey test. Used for graphing.

*BeeTukey*

Results of Tukey test. Used for graphing.

*BySiteFloral*

Plant abundance, richness, and Shannon diversity by site.

Calculated in FloralDiv2022 script

*CombinedSiteTukey*

Plant and bee diversity and tukey test results by site.

Used for graphing.