Tables and Figures

Table 1: Results from negative binomial generalized linear mixed models (lme4, glmer.nb) testing for differences in the frequency of pollinator floral visits and foraging bouts in response to microsite (shrub and open) and blooming stage (pre-blooming and full bloom). Conspecific floral density was included as a predictor and the log-transformed length of video was used as an offset as a measure of exposure. The repID (shrub ID + microsite) was used a random effect in both models to account for the repeated measures study design. Significance was denoted at α = 0.05 and shown in bold. Non-significant interactions were excluded from all models.

|  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- |
|  | Total flower visits | | | Foraging bouts | | |
|  | **Coeff** | **χ2** | **p** | **Coeff** | **χ2** | **p** |
| Microsite (shrub) | -0.3493 | 4.4979 | **0.03396** | -0.3258 | 5.1183 | **0.0237** |
| Blooming (bloom) | -1.2473 | 61.52 | **<0.0001** | -1.2513 | 76.883 | **<0.0001** |
| Flowers.pot | 0.0694 | 6.9013 | **0.0086** | 0.0474 | 4.1109 | **0.0426** |
| Microsite \* Blooming | NA | NA | NA | NA | NA | NA |

Table 2: Results from negative binomial GLMM (glmmTMB) testing for the influence of heterospecific annual floral density and shrub blooming density on the frequency of pollinator floral visits and foraging bouts. Each variable was added to the base model that includes microsite (shrub and open), blooming stage (pre-blooming and full bloom) and conspecific floral density was as predictors. The log-transformed length of video was used as an offset as a measure of exposure. The repID (shrub ID + microsite) was used a random effect in both models to account for the repeated measures study design. Significance was denoted at α = 0.05 and shown in bold.

|  |  |  |  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- | --- | --- | --- |
|  | Total flower visits | | | |  | Plant visits | | | |
|  | **Coeff** | **SE** | **z** | **p** |  | **Coeff** | **SE** | **z** | **p** |
| Microsite (shrub) | -0.3660 | 0.16944 | -2.160 | **0.03077** |  | -0.33019 | 0.14706 | -2.245 | **0.02475** |
| Blooming (bloom) | -1.2396 | 0.16353 | -7.581 | **<0.0001** |  | -1.24571 | 0.14513 | -8.584 | **<0.0001** |
| Flowers.pot | 0.08084 | 0.02711 | 2.981 | **0.00287** |  | 0.05943 | 0.02374 | 2.503 | **0.01230** |
| Heterospecific  annual bloom  density | 0.04013 | 0.02342 | 1.713 | 0.08664 |  | 0.04086 | 0.01984 | 2.059 | **0.03950** |
| Microsite (shrub) | -0.3289 | 0.16998 | -1.935 | **0.05301** |  | -0.31539 | 0.14829 | -2.127 | **0.033435** |
| Blooming (bloom) | -1.1662 | 0.18601 | -6.269 | **<0.0001** |  | -1.20875 | 0.16707 | -7.235 | **<0.0001** |
| Flowers.pot | 0.07598 | 0.02703 | 2.811 | **0.00494** |  | 0.05296 | 0.02376 | 2.229 | **0.025799** |
| Heterospecific  blooming shrub  density | -0.0494 | 0.04093 | -1.207 | 0.22744 |  | 0.03124 | 0.03744 | -0.835 | 0.403997 |

Table 3: Results from quasi-poisson generalized linear mixed models (MASS, glmmPQL) testing for RTU specific interactions with blooming stage. The interaction term was added to the base model that includes microsite (shrub and open), blooming stage (pre-blooming and full bloom) and conspecific floral density was as predictors. The log-transformed length of video was used as an offset as a measure of exposure. The repID (shrub ID + microsite) was used a random effect to account for the repeated measures study design. Significance was denoted at α = 0.05 and shown in bold.

|  |  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- | --- |
|  | Total flower visits | | |  | Plant visits | | |
|  | **Coeff** | **χ2** | **p** |  | **Coeff** | **χ2** | **p** |
| Microsite (shrub) | -0.337480 | 4.1903 | **0.040655** |  | -0.311383 | 4.6322 | **0.03137** |
| Blooming (bloom) | -1.729417 | 15.4730 | **< 0.0001** |  | -1.683054 | 12.2157 | **0.0004739** |
| RTU | NA | 197.0575 | **<0.0001** |  | NA | 217.5031 | **<0.00001** |
| Flowers.pot | 0.064325 | 7.8743 | **0.005014** |  | 0.042763 | 4.0741 | 0.4354 |
| RTU\*blooming | NA | 70.0222 | **<0.0001** |  | NA | 70.35 | **<0.0001** |

Table 4: Results from post-hoc test (lsmeans, Tukey’s) for the quasipoisson GLMM , contrasting RTU specific responses between pre-blooming and blooming. Significance was denoted at α = 0.05 and shown in bold.

|  |  |  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- | --- | --- |
|  | Floral Visits | | | | Plant Visits | | | |
| RTU | **Estimate** | **SE** | **t.ratio** | **p** | **estimate** | **SE** | **t.ratio** | **p** |
| Solitary bee | 1.7294 | .4419 | 3.914 | **0.0001** | 1.6831 | .4840 | 3.478 | **0.0005** |
| Bombyliidae | 0.04603 | .3886 | 0.118 | 0.9057 | 0.3956 | .3.5568 | 1.112 | 0.2662 |
| Honeybee | 24.9969 | 77838 | 0.000 | 0.9997 | 24.3349 | 65302.3 | 0.000 | 0.9997 |
| Lepidoptera | -2.4017 | 1.28900 | -1.862 | 0.0629 | -2.0771 | 1.0625 | -1.955 | 0.0508 |
| Other | -0.0197 | .2403 | -0.082 | 0.9347 | 0.1341 | .2065 | 0.64 | 0.5163 |
| Syrphid | 3.0563 | .3347 | 8.813 | **<0.0001** | 3.1228 | .3404 | 9.173 | **<0.0001** |

Table 5: Results from Gamma generalized linear mixed models (lme4, glmer.nb) testing for differences visit duration and the proportion of flowers visited per visit in response to microsite (shrub and open) and blooming stage (pre-blooming and full bloom). The repID (shrub ID + microsite) was used a random effect in both models to account for the repeated measures study design. Significance was denoted at α = 0.05 and shown in bold. Non-significant interactions were excluded from all models.

|  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- |
|  | Visit duration | | | Proportion of flowers visited | | |
|  | **Coef** | **χ2 value** | **p – value** | **Coef** | **χ2 value** | **p – value** |
| Microsite | -0.047260 | 0.0464 | 0.8295 | -0.03538 | 1.0051 | 0.46515 |
| Blooming | -0.777931 | 23.1788 | **<0.0001** | 0.08050 | 0.5335 | 0.31609 |
| Microsite \* Blooming | NA | NA | NA | -0.20443 | 7.0691 | **0.00784** |

Table 6: Results from quasipoisson GLMM (MASS, glmmPQL) testing for the influence of L. tridentata, and two metrics of conspecific density on conspecific and heterospecific pollen deposition. Sample nested in flower nested in plant were used as a random effect to account for samples coming from same plant. Significance was denoted at α = 0.05 and shown in bold.

|  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- |
|  | Conspecific Pollen Deposition | | | Heterospecific Pollen Deposition | | |
|  | **Coef** | **χ2 value** | **p – value** | **Coef** | **χ2 value** | **p – value** |
| Distance to *L.tridentata* | 0.0002 | 0.8803 | 0.3533 | 0.00130 | 23.7883 | **<0.0001** |
| Distance to *M.glabrata* | 0.0015 | 3.8146 | 0.0541 | -0.0014 | 2.1656 | 0.1411 |
| *M. glabrata* floral number | 0.0089 | 2.0027 | 0.1620 | -0.0122 | 2.3713 | 0.1236 |

Table 7: Results from negative binomial generalized linear mixed models (lme4, glmer.nb) testing for differences in arthropod abundance in response to microsite (shrub and open) and blooming stage (pre-blooming and full bloom). Melyridae beetles comprised 1217/3384 individuals, models were fit with them excluded, included and individually. The repID (shrub ID + microsite) was used a random effect in both models to account for the repeated measures study design. Significance was denoted at α = 0.05 and shown in bold.

|  |  |  |  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- | --- | --- | --- |
|  | Insect abundance (Melyridae: excluded) | | | Insect abundance (Melyridae: included) | | | Melyridae: abundance only | | |
|  | **Coef** | **χ**2 value | p – value | **Coef** | **χ**2 value | p – value | **Coef** | **χ**2 value | p – value |
| Microsite  (shrub) | 0.40610 | 15.4926 | **<0.0001** | -0.09872 | 1.808 | 0.1787 | -1.1920 | 38.0394 | **0<0.0001** |
| Blooming  (in bloom) | -0.39624 | 13.5868 | **0.000228** | -0.39280 | 33.553 | **<0.00001** | -0.2989 | 3.3485 | 0.067267 |
| Microsite \* Blooming | -0.27673 | 3.4553 | 0.063049 | NA | NA | NA | 0.6521 | 7.1290 | **0.007585** |

Table 8: Results from poisson generalized linear mixed models (lme4, glmer.nb) testing for differences in bee abundance and arthropod species richness in response to microsite (shrub and open) and blooming stage (pre-blooming and full bloom). The repID (shrub ID + microsite) was used a random effect in both models to account for the repeated measures study design. Significance was denoted at α = 0.05 and shown in bold. Non-significant interactions were excluded from all models.

|  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- |
|  |  | Species Richness | | Bee abundance | | |
|  | **Coef** | **χ**2 value | p – value | **Coef** | **χ**2 value | p – value |
| Microsite | 0.14541 | 6.6289 | 0.01 | 0.05766 | 0.0792 | 0.778323 |
| Blooming | -0.25442 | 25.6295 | **<0.0001** | -0.0787 | 0.2104 | 0.646419 |
| Microsite \* Blooming | NA | NA | NA | NA | NA | NA |

|  |  |  |  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- | --- | --- | --- |
|  | **Percent cover** | | | **Annual Richness** | | | **Annual Bloom Density** | | |
|  | **Coef** | **χ**2 | p | **Coef** | **χ**2 | p | **Coef** | **χ**2 | p |
| **Microsite** | **2.14420** | 165.399 | **<0.0001** | 0.07186 | 0.7071 | 0.40 |  |  | 0.438 |
| **Blooming** |  | 34.180 | **<0.0001** | 0.14068 | 2.7010 | 0.10 |  |  | **0.0003** |
| **Microsite \* blooming** |  | 22.806 | **<0.0001** | NA | NA | NA |  |  | NA |

Table 9: Results from negative binomial generalized linear mixed models (lme4, glmer.nb) testing for differences in annual percent cover, annual species richness and annual blooming density in response to microsite (shrub and open) and blooming stage (pre-blooming and full bloom). The repID (shrub ID + microsite) was used a random effect in both models to account for the repeated measures study design. Significance was denoted at α = 0.05 and shown in bold. Non-significant interactions were excluded from all models.