AmNat table removals

Table A2.6: Gamma GLMM (glmer lme4) for proportions of flowers visited including Microsite \* RTU interaction to test for differences in RTU response to microsite.

|  |  |  |  |  |
| --- | --- | --- | --- | --- |
|  | Estimate | Std Error | Z | P |
| Microsite | -0.2956 | 0.1499 | -1.973 | 0.04852 |
| RTU.Bombylid | -0.3373 | 0.1226 | -2.752 | 0.00592 |
| RTU.Honeybee | 0.3531 | 0.2415 | 1.462 | 0.14375 |
| RTU.Lep | -0.4734 | 0.1472 | -3.215 | 0.00131 |
| RTU.Other | -0.4738 | 0.1117 | -4.243 | 2.2e-05 |
| RTU.Syrphid | -0.3421 | 0.1079 | -3.172 | 0.00152 |
| Microsite \* RTU.Bombylid | 0.2888 | 0.1717 | 1.682 | 0.09253 |
| Microsite \* RTU.Lep | 0.2057 | 0.2111 | 0.974 | 0.32988 |
| Microsite \* RTU.Other | 0.2655 | 0.1486 | 1.787 | 0.07399 |
| Microsite \* Syrphid | 0.3527 | 0.1410 | 2.502 | 0.01235 |

Table A2.7: Post-hoc constrast (lsmeans) on significant interaction from Table A6.

|  |  |  |  |  |
| --- | --- | --- | --- | --- |
|  | Proportion of flowers visited | | | |
| Contrast | **Estimate** | **SE** | **t.ratio** | **p** |
| Open, bee – shrub, bee | 0.2956276573 | 0.14985202 | 1.973 | 0.7122 |
| Open, bombylid – shrub, bombylid | 0.0067785545 | 0.12221348 | 0.055 | 1.0000 |
| Open, honeybee – shrub, honeybee | nonEst | NA | NA | **NA** |
| Open, lep – Shrub, lep | 0.0899409512 | 0.17203545 | 0.523 | 1.0000 |
| Open, other – Shrub, other | 0.0301074801 | 0.08727658 | 0.345 | 1.0000 |
| Open, syrphid – shrub, syrphid | -0.0570436624 | 0.08160285 | -0.699 | 0.9999 |

|  |  |  |  |  |  |  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- |
|  | Insect abundance (Melyridae: excluded) | | | Arthropod Species Richness | | | Bee abundance | | | Bee richness | | |
|  | **Coef** | **χ**2 | p | **Coef** | **χ**2 | p | **Coef** | **χ**2 | p | Coef | **χ**2 | p |
| Microsite | 0.406 | 15.49 | **<0.0001** | 0.1454 | 6.62 | **0.01** | 0.058 | 0.079 | 0.778 | -0.065 | 0.125 | 0.724 |
| Blooming | -0.396 | 13.59 | **0.00023** | -0.254 | 25.6 | **<0.0001** | -0.08 | 0.21 | 0.646 | -0.056 | 0.094 | 0.759 |
| Microsite \* Blooming | -0.277 | 3.455 | 0.063 | NA | NA | NA | NA | NA | NA | NA | NA | NA |
|  | **Percent cover** | | | **Annual Richness** | | | **Annual Bloom Density** | | | **Blooming shrub density within 2 m** | | |
|  | **Coef** | **χ**2 | p | **Coef** | **χ**2 | p | **Coef** | **χ**2 | p | **Coef** | **χ**2 | p |
| Microsite | 1.7599 | 165.4 | **<0.0001** | 0.0719 | 0.707 | 0.40 | -0.28 | 0.601 | 0.438 | 0.366 | 4.083 | **0.04331** |
| Blooming | -0.793 | 34.18 | **<0.0001** | 0.1407 | 2.701 | 0.10 | -1.36 | 13.36 | **0.0003** | 1.67 | 149.7 | **<0.0001** |
| Microsite \* blooming | 0.794 | 22.81 | **<0.0001** | NA | NA | NA | NA | NA | NA | NA | NA | NA |

Table 2.5: Results from GLMM testing for differences in arthropod, bee and plant communities in response to response to microsite (shrub and open) and blooming stage (full bloom and pre-blooming). 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 all models to account for the repeated measures study design. Significance was denoted at α = 0.05 and shown in bold.

Redundancy analysis was used to test for the influence of microsite and associated annual communities on insect community composition (RDA, vegan). Arthropod abundances were Hellinger transformed to lower the weight of rare RTU (Legendre and Gallagher 2001). Microsite, percent annual cover, annual richness and heterospecific annual bloom density were used as constraining variables in the ordination.

In order to examine the change in interaction between the vegetation factors and arthropod communities with the phenological shift, rather than the effect of blooming itself, the dataset was split into pre-blooming and blooming, and analyses were run separately on each subset. In order to test for the significance of the constraining variables in explaining the variation, a permutation-like ANOVA was used on each RDA (anova.cca, vegan).

Table 2.6: Permutation test ANOVA on RDA testing for changes in influence of shrub microsite and understory annual vegetation on arthropod community composition with phenological shift into flowering of *Larrea tridentata*. The constraining variables of the pre-blooming RDA explained 12.5% of the total variation and the blooming RDA explained 4%.

|  |  |  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- | --- | --- |
|  | Pre-blooming | | | | Blooming | | | |
|  | **Df** | **Variance** | **F** | **p** | **Df** | **Variance** | **F** | **p** |
| Microsite | 1 | 0.04396 | 9.5687 | **0.001** | 1 | 0.01074 | 2.0561 | **0.005** |
| Percent cover | 1 | 0.00688 | 1.4983 | 0.087 | 1 | 0.00507 | 0.9700 | 0.471 |
| Annual richness | 1 | 0.00443 | 0.9653 | 0.449 | 1 | 0.00701 | 1.3421 | 0.119 |
| Annual bloom density | 1 | 0.00619 | 1.3470 | 0.131 | 1 | 0.00197 | 0.3765 | 0.995 |

Arthropod community composition was significantly influenced by microsite for both blooming treatments (Table 2.6). There was no significant effect of the annual understory. The constraining variables of the pre-blooming RDA explained more variation (12.5%) than blooming (4%). Only the pre-blooming RDA was significant (pre: F = 3.3448, df = 4, p = 0.001, blooming: F = 1.1862, df = 4, p = 0.118).

Solitary bees and ‘other’ RTUs were subsetted to fit linear mixed models for both RTU using log-transformed foraging duration as the response variable.

Foraging duration

This was driven by visitors in the ‘other’ category (Figure 2.2, Est: -1.0703, χ2: 12.274, t: -3.503, p = 0.000605). There was no difference in solitary bee foraging duration between blooming treatments (Est: -0.9341, χ2: 1.9017, t: -1.379, p = 0.208).

but there were no RTU specific response to blooming or microsite (Table A2.5, A2.6).

Table 2.3: Results from Gamma GLMM (lme4, glmer.nb) testing for differences foraging 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.

|  |  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- | --- |
|  | Foraging duration | | | | Proportion of flowers visited | | |
|  | **Coef** | | **χ2 value** | **p – value** | **Coef** | **χ2 value** | **p – value** |
| Microsite (shrub) | -0.047260 | 0.0464 | | 0.8295 | -0.03538 | 1.0051 | 0.46515 |
| Blooming (bloom) | -0.777931 | | 23.1788 | **<0.0001** | 0.0805 | 0.5335 | 0.31609 |
| Microsite \* Blooming | NA | | NA | NA | -0.20443 | 7.0691 | **0.00784** |

Table A5: Gamma GLMM (glmer lme4) models for proportions of flowers visited including Blooming \* RTU interaction to test for differences in RTU response to blooming stage.

|  |  |  |  |  |
| --- | --- | --- | --- | --- |
|  | Estimate | Std Error | Z | P |
| Blooming | -0.116064 | 0.140156 | -0.828 | 0.40761 |
| RTU.Bombylid | -0.247470 | 0.112323 | -2.203 | 0.02758 |
| RTU.Honeybee | 0.186243 | 0.240711 | 0.774 | 0.43910 |
| RTU.Lep | -0.329590 | 0.262264 | -1.257 | 0.20886 |
| RTU.Other | -0.300436 | 0.095633 | -3.142 | 0.00168 |
| RTU.Syrphid | -0.173276 | 0.085192 | -2.034 | 0.04196 |
| Blooming \* RTU.Bombylid | 0.202234 | 0.174650 | 1.158 | 0.24689 |
| Blooming\* RTU.Lep | 0.069411 | 0.297303 | 0.233 | 0.81540 |
| Blooming \* RTU.Other | 0.033465 | 0.153065 | 0.219 | 0.82693 |

|  |  |  |  |  |
| --- | --- | --- | --- | --- |
| Blooming \* Syrphid | 0.006737 | 0.171338 | 0.039 | 0.96863 |

Table 2.4: Results from quasi-Poisson GLMM (MASS, glmmPQL) testing for the influence of *L. tridentata*, and two metrics of conspecific density on conspecific and heterospecific pollen deposition. Flower ID nested within plant was used as a random effect to account for multiple samples coming from individual plants. Significance was denoted at α = 0.05 and shown in bold.

|  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- |
|  | Conspecific Pollen Deposition | | | Heterospecific Pollen Deposition | | |
|  | **Coef** | **χ2** | **p** | **Coef** | **χ2** | **p** |
| Distance to *L. tridentata* | 0.0002 | 0.4686 | 0.4936 | 0.0013 | 6.7835 | **0.0092** |
| Distance to *M. glabrata* | 0.0019 | 2.4188 | 0.1199 | -0.0009 | 0.2256 | 0.6348 |
| *M. glabrata* floral number | 0.0076 | 0.6184 | 0.4316 | -0.0201 | 1.6668 | 0.1967 |

(χ2= 1.6668, p = 0.1967)

Table A6: Results from post-hoc test (lsmeans, Tukey’s) for the Gamma generalized linear mixed model on significant interaction for proportion of flowers visited. Significance was denoted at α = 0.05 and shown in bold.

|  |  |  |  |  |
| --- | --- | --- | --- | --- |
|  | Proportion of flowers visited | | | |
| Contrast | Estimate | SE | t.ratio | p |
| pre,open - post,open | 0.03537548 | 0.04843350 | 0.730 | 0.8849 |
| pre,open - pre,shrub | -0.08050042 | 0.08029773 | -1.003 | 0.7479 |
| pre,open - post,shrub | 0.15930471 | 0.08775466 | 1.815 | 0.2660 |
| post,open - pre,shrub | -0.11587589 | 0.08384195 | -1.382 | 0.5106 |
| post,open - post,shrub | 0.12392924 | 0.09113159 | 1.360 | 0.5247 |
| pre,shrub - post,shrub | 0.23980513 | 0.05952906 | 4.028 | 0.0003 |

|  |  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- | --- |
|  | Total flower visits | | |  | Foraging instances | | |
|  | 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 | 0.04354 |
| RTU\*blooming | NA | 70.0222 | <0.0001 |  | NA | 70.35 | <0.0001 |