

Appendix S2

Manuscript title: Habitat Quality Influences Pollinator Pathogen Prevalence Through Both Habitat–Disease and Biodiversity–Disease Pathways

Authors: Michelle L. Fearon, Chelsea L. Wood, Elizabeth A. Tibbetts

Journal: Ecology

Section S1: Additional details about the main path model

All analyses were performed in R version 4.1.1 (R Core Team 2021) and models were fit and evaluated with the *piecewiseSEM* package (Lefcheck 2016). All habitat and pollinator community variables were scaled and centered, pollinator species richness and *E. pruinosa* abundance were square root transformed, and proportion of natural area was arcsine square root transformed (details in **Appendix S2: Table S1**). All other species-specific abundances were normally distributed without transformation. The main path model is presented in **Figure 1b** and **Appendix S2: Table S3** and included combined *A. mellifera* and *B. impatiens* abundance (hereafter called the ‘main path model’).

The models also included correlated errors between pollinator species richness and abundance to control for the positive correlation between these factors, and among the three viruses since presence of one virus in a host could impact the likelihood of infection with another virus.

We evaluated all component models for their model assumptions (*olsrr* package, Hebbali 2020). All main factors in the models had Variance Inflation Factors <4.5 and Pearson’s correlations <0.75, indicating that there were acceptable levels of collinearity among factors in the model (Dormann et al. 2013; **Appendix S2: Table S4**). None of the component GLMMs were overdispersed. None of the component models showed evidence of spatial autocorrelation in model residuals (Moran’s I test, *ape* and *DHARMA* packages; **Appendix S2: Table S5**) (Paradis and Schliep 2018, Hartig 2020).

The viral prevalence GLMMs include the prevalence of all four host species combined, with host species and visit to each site nested within site as random effects. In some models, the nested random effects of visit within site were singular, indicating that the random effect did not explain any variation in the model. However, we left all the random effects in the model to account for bees that were collected at the same time and from the same sites that may have more similar viral prevalence to each other. These models will capture overall patterns of habitat and pollinator community effects on BQCV, DWV, and SBV prevalence within the communities, while also accounting differences in viral prevalence based on host species, as we previously found in Fearon and Tibbetts 2021.

Since the main path model was completely saturated (included all possible links), we could not assess the goodness of fit ($\chi^2=0$, $p=1$) nor conduct tests of directed separation for the full model. To better assess the goodness of fit for the model, we used model simplification where we

removed select paths that had little support in the model with p-values greater than 0.8, following (Grace 2020), to produce a similar model to the main model that was no longer fully saturated. The χ^2 test of goodness of fit determines whether the hypothesized relationships in the model deviate substantially from the relationships found in the data. Therefore, a high p-value for the χ^2 statistic indicates that the data fits the model-implied relationships (H_0), while a low p-value suggests that a different model structure would be better (H_1). The tests of directed separation evaluate whether there are any significant paths that are missing from the model, where missing paths with a significant path coefficient would produce a low p-value for the Fisher's C statistic. In the main model, two paths were temporarily removed (proportion of natural area on DWV prevalence, $p=0.858$, and landscape richness on SBV prevalence, $p=0.912$), which produced Chi-squared and direction of separation test statistics that indicated that the data fits the model well with p-values well above the 0.05 threshold ($\chi^2=0.044$, $p=0.978$; Fisher's C=0.489; $p=0.975$). Furthermore, the topography of significant paths and their relative magnitudes did not change in the simplified model. All paths are included in the main path model that is presented in the main text.

Section S2: Parallel path model with estimated species richness

Though our main analyses utilize observed pollinator species richness, we also conducted a parallel analysis with estimated species richness because it is rare to reach an asymptote when sampling invertebrate communities (Novotný and Basset 2000, Gotelli and Colwell 2001). We generated individual-based rarefaction curves (*iNext* package, Hsieh et al. 2016) and determined that estimated species richness for the average number of pollinators captured at each site (mean = 338 across all 13 field sites; rarefaction curves previously published in appendices of Fearon and Tibbetts 2021). This estimates species richness at a consistent number of individuals sampled for each site. Then we ran a parallel path model as described in the main text with estimated species richness instead of observed species richness.

The estimated species richness path model was completely saturated; therefore, we could not test model fit with d-separation or Chi-squared tests. However, we conducted a similar temporary model simplification procedure as described above for the main model and removed selected paths that had p-values greater than 0.7 to assess goodness of fit. Here we used a lower p-value threshold for removing paths because there were not any paths that had a p-value over 0.8. Three paths were removed (proportion of natural area on DWV prevalence, $p=0.729$, landscape richness and floral richness on SBV prevalence, $p=0.715$ and $p=0.747$, respectively), which produced test statistics that indicated good model fit with the data ($\chi^2=0.373$, $p=0.946$; Fisher's C=1.984; $p=0.921$). We did not remove the total density on *Apis* and *Bombus* abundance pathway even though the p-value was > 0.7 because the d-separation test indicated that path needed to be included in the model.

We found that the topography of significant pathways in the estimated richness path model varied slightly from main path model presented with the lowest AIC but was overall consistent with the results from the other versions of the main path model described above. Additionally, the estimated richness path model had a Δ AIC of 9.11 higher than the model with the lowest AIC, therefore our results were robust to our choice of species richness measurement (**Appendix S2: Table S11**).

Section S3: Methods and results for path models with total pollinator abundance or species-specific host abundance instead of combined *A. mellifera* and *B. impatiens* abundance

Overall, path models that included total pollinator abundance or each of the species-specific host abundance had relatively similar topography of significant pathways and directionality to the main path model presented in **Figure 1b**. The model that contained *B. impatiens* abundance was the second-best model based on lowest AIC, followed by the models including total pollinator abundance, *E. pruinosa* abundance, *Lasioglossum* spp. abundance, and *A. mellifera* abundance (**Appendix S2: Table S2**). Most importantly, none of the pollinator abundance terms in any of these models were significantly linked with BQCV, DWV, nor SBV prevalence.

Here, we will mainly focus on the key differences among these models in significant pathways from the main path model presented in **Figure 1b** that included combined *A. mellifera* and *B. impatiens* abundance (hereafter called the ‘main path model’) and refer to the corresponding model output table with additional details for pathway coefficients, p-values, and R^2 . In general, all differences among these models reflect changes in whether a subset of pathways are significant in one model versus another, but none of the significant pathways change in directionality (i.e., a significant positive link does not become a significant negative link in another model). In most cases where a link changes from significant to non-significant (or vice versa), the p-values for the statistically insignificant paths remain < 0.1 .

The model that includes *B. impatiens* abundance has the same topography of significant pathways as the main path model (**Appendix S2: Table S8**). In the total pollinator abundance path model, only major difference from the main path model is that the negative link between pollinator species richness and DWV prevalence is no longer significant (RCF = -0.121 , $p = 0.077$; **Appendix S2: Table S6**). The *A. mellifera* abundance path model does not include the link between proportion of natural area and *A. mellifera* abundance (RCF = 0.341 , $p = 0.5$), nor the link between pollinator species richness and DWV prevalence (RCF = -0.071 , $p = 0.36$). But it does now include a significant positive pathway between floral richness and BQCV prevalence (RCF = -0.086 , $p = 0.046$; **Appendix S2: Table S7**). Similarly, in the *Lasioglossum* spp. abundance path model, proportion of natural area is not significantly linked with *Lasioglossum* spp. abundance (RCF = 0.81 , $p = 0.052$) and pollinator species richness is not correlated with DWV prevalence (RCF = -0.134 , $p = 0.072$; **Appendix S2: Table S9**). Finally, in the *E. pruinosa* abundance path model, proportion of natural area is not significantly linked with *E. pruinosa* abundance (RCF = -0.244 , $p = 0.56$) and pollinator species richness is not correlated with DWV prevalence (RCF = -0.121 , $p = 0.059$). However, floral richness is significantly positively associated with greater BQCV prevalence (RCF = 0.065 , $p = 0.042$; **Appendix S2: Table S10**).

Table S1: Description of variables included in the path models. Table contains the name, type of variable, applied transformations, mean and standard deviation of untransformed values, and a brief description of each variable. DWV, BQCV, and SBV prevalence includes all four host species in the main model, and only a single host species prevalence in the species-specific models. All variables except for viral prevalence were scaled and centered.

| Variable Name | Type | Transformation* | Mean | SD | Description |
|--|-------------|------------------------|-------------|-----------|---|
| DWV | binary | none | na | na | Presence (1) or absence (0) of DWV in individual bees. |
| BQCV | binary | none | na | na | Presence (1) or absence (0) of BQCV in individual bees. |
| SBV | binary | none | na | na | Presence (1) or absence (0) of SBV in individual bees. |
| Species Richness | integer | square root | 28.46 | 13.28 | The number of pollinator host species detected per site. |
| Total Abundance | integer | none | 333.08 | 163.86 | The total number of pollinator individuals detected per site. |
| <i>Apis mellifera</i> Abundance | integer | none | 38.85 | 20.84 | The number of <i>Apis mellifera</i> individuals detected per site. |
| <i>Bombus impatiens</i> Abundance | integer | none | 80.38 | 53.34 | The number of <i>Bombus impatiens</i> individuals detected per site. |
| <i>Apis</i> and <i>Bombus</i> Abundance | integer | none | 119.23 | 63.17 | The number of <i>Apis mellifera</i> and <i>Bombus impatiens</i> individuals detected per site. |
| <i>Lasioglossum</i> spp. Abundance | integer | none | 93.69 | 93.55 | The number of <i>Lasioglossum</i> spp. individuals detected per site. |
| <i>Eucera pruinosa</i> Abundance | integer | square root | 42.85 | 52.62 | The number of <i>Eucera pruinosa</i> individuals detected per site. |
| Landscape Richness | integer | none | 20.15 | 3.46 | The number of different landcover types that occur within a 1000m radius of each site. |
| Natural Area | continuous | arcsine square root | 0.52 | 0.20 | The proportion of area within a 1000m that was classified as ‘Natural Area’ for each site. We classified forest, wetland, meadow landcover types as ‘Natural Area’. Continuous between 0 and 1. |
| Floral Richness | integer | none | 10.69 | 4.80 | The number of different floral species detected at each site. |
| Floral Density (m²) | continuous | none | 32.42 | 23.63 | The density of all flowers per m ² detected at each site. |

Table S2: Comparison of main path model AIC and Δ AIC. All path models have the same topography and model structure, but the pollinator abundance factor varies among the models to include either Total pollinator abundance, *Apis mellifera* abundance, *Bombus impatiens* abundance, combined *Apis* and *Bombus* abundance, *Lasioglossum* spp. abundance, and *Eucera pruinosa* abundance. Different path models are indicated by the type of pollinator abundance included in the model.

| Path Model | AIC | ΔAIC |
|---------------------------------------|------------|-------------------------------|
| <i>Apis</i> + <i>Bombus</i> abundance | 2506.9 | 0 |
| <i>Bombus impatiens</i> abundance | 2507.3 | 0.37 |
| Total pollinator abundance | 2512.4 | 5.48 |
| <i>Eucera pruinosa</i> abundance | 2514.4 | 7.47 |
| <i>Lasioglossum</i> spp. | 2517.0 | 10.14 |
| <i>Apis mellifera</i> abundance | 2519.7 | 12.78 |

Table S3: The full path model statistics for main model shown in **Figure 1B** that had the lowest AIC and included the combined *Apis mellifera* and *Bombus impatiens* abundance. The table shows the unstandardized estimated pathway coefficients, range-standardized estimated coefficients, scale standardized estimated coefficients, standard error, degrees of freedom, critical value, and p-value for each path. R² is shown for each response variable. The last four rows are correlated errors. Significant pathway coefficients and p-values are bolded, with negative coefficients in red and positive coefficients in black.

| Response variable | Predictor variable | Range Std | | Scale Std | | Critical | | R ² | |
|---------------------------------------|---------------------------------------|---------------|---------------|---------------|-----------|----------|--------|----------------------|---------|
| | | Estimate | Estimate | Estimate | Std Error | DF | Value | | P-value |
| Species Richness | Prop. Natural Area 1000m | 0.633 | 0.910 | 0.633 | 0.199 | 8 | 3.173 | 0.013 * | 0.70 |
| | Landscape Richness 1000m | 0.403 | 0.438 | 0.403 | 0.241 | 8 | 1.673 | 0.133 | |
| | Floral Richness | 0.167 | 0.179 | 0.167 | 0.256 | 8 | 0.653 | 0.532 | |
| | Floral Density | -0.236 | -0.209 | -0.236 | 0.278 | 8 | -0.851 | 0.419 | |
| <i>Apis</i> + <i>Bombus</i> Abundance | Prop. Natural Area 1000m | 0.567 | 0.834 | 0.567 | 0.186 | 8 | 3.049 | 0.016 * | 0.71 |
| | Landscape Richness 1000m | 0.439 | 0.488 | 0.439 | 0.225 | 8 | 1.954 | 0.086 | |
| | Floral Richness | -0.094 | -0.103 | -0.094 | 0.239 | 8 | -0.395 | 0.703 | |
| | Floral Density | 0.084 | 0.076 | 0.084 | 0.259 | 8 | 0.323 | 0.755 | |
| DWV | Prop. Natural Area 1000m | -0.042 | -0.017 | -0.020 | 0.234 | 888 | -0.179 | 0.858 | 0.22 |
| | Landscape Richness 1000m | -0.371 | -0.112 | -0.175 | 0.202 | 888 | -1.837 | 0.066 | |
| | Floral Richness | 0.289 | 0.086 | 0.137 | 0.170 | 888 | 1.701 | 0.089 | |
| | Floral Density | -0.130 | -0.032 | -0.061 | 0.188 | 888 | -0.690 | 0.490 | |
| | Species Richness | -0.500 | -0.138 | -0.236 | 0.231 | 888 | -2.165 | 0.030 * | |
| | <i>Apis</i> + <i>Bombus</i> Abundance | 0.352 | 0.095 | 0.167 | 0.246 | 888 | 1.432 | 0.152 | |
| BQCV | Prop. Natural Area 1000m | 0.467 | 0.156 | 0.185 | 0.187 | 888 | 2.497 | 0.013 * | 0.41 |
| | Landscape Richness 1000m | 0.348 | 0.088 | 0.138 | 0.156 | 888 | 2.230 | 0.026 * | |
| | Floral Richness | 0.251 | 0.062 | 0.099 | 0.131 | 888 | 1.916 | 0.055 | |
| | Floral Density | -0.416 | -0.085 | -0.165 | 0.143 | 888 | -2.904 | 0.004 ** | |
| | Species Richness | -0.670 | -0.155 | -0.266 | 0.187 | 888 | -3.587 | <0.001 *** | |
| | <i>Apis</i> + <i>Bombus</i> Abundance | -0.087 | -0.020 | -0.034 | 0.185 | 888 | -0.470 | 0.638 | |
| SBV | Prop. Natural Area 1000m | -0.058 | -0.018 | -0.022 | 0.184 | 888 | -0.314 | 0.753 | 0.38 |
| | Landscape Richness 1000m | -0.019 | -0.005 | -0.007 | 0.175 | 888 | -0.110 | 0.912 | |
| | Floral Richness | 0.051 | 0.012 | 0.019 | 0.135 | 888 | 0.376 | 0.707 | |
| | Floral Density | 0.045 | 0.009 | 0.017 | 0.148 | 888 | 0.304 | 0.761 | |
| | Species Richness | -0.246 | -0.054 | -0.092 | 0.189 | 888 | -1.302 | 0.193 | |
| | <i>Apis</i> + <i>Bombus</i> Abundance | 0.163 | 0.035 | 0.061 | 0.205 | 888 | 0.796 | 0.426 | |
| DWV | BQCV | 0.199 | 0.199 | 0.199 | NA | 888 | 6.048 | <0.001 *** | |
| BQCV | SBV | 0.165 | 0.165 | 0.165 | NA | 888 | 4.965 | <0.001 *** | |
| SBV | DWV | 0.180 | 0.180 | 0.180 | NA | 888 | 5.446 | <0.001 *** | |
| <i>Apis</i> + <i>Bombus</i> Abundance | Species Richness | 0.149 | 0.149 | 0.149 | NA | 13 | 0.475 | 0.323 | |

Table S4: Pearson’s correlation between each continuous variable included in the main path model below the diagonal, with the corresponding p-values above the diagonal. Variables have the same transformations used in the path model. Significant coefficients and p-values are bolded, with negative correlations colored red and positive correlations colored black.

| | DWV | BQCV | SBV | Species Richness | Total Abundance | <i>A. mellifera</i> Abundance | <i>B. impatiens</i> Abundance | <i>Apis + Bombus</i> Abundance | <i>Lasioglossum</i> Abundance | <i>E. pruinosa</i> Abundance | Landscape Richness | Natural Area | Floral Richness | Floral Density |
|--------------------------------|---------------|------------------|------------------|------------------|------------------|-------------------------------|-------------------------------|--------------------------------|-------------------------------|------------------------------|--------------------|------------------|------------------|------------------|
| DWV | -- | <0.001 | <0.001 | <0.001 | 0.001 | 0.556 | <0.001 | 0.002 | 0.024 | 0.605 | <0.001 | 0.001 | 0.616 | 0.184 |
| BQCV | 0.365 | -- | <0.001 | 0.003 | 0.005 | 0.771 | 0.028 | 0.082 | 0.311 | 0.315 | 0.668 | 0.03 | 0.537 | 0.02 |
| SBV | 0.266 | 0.312 | -- | 0.163 | 0.073 | 0.283 | 0.764 | 0.545 | 0.135 | 0.112 | 0.975 | 0.253 | 0.768 | 0.754 |
| Species Richness | -0.181 | -0.101 | -0.047 | -- | <0.001 | 0.228 | <0.001 | <0.001 | <0.001 | <0.001 | <0.001 | <0.001 | <0.001 | <0.001 |
| Abundance | -0.116 | -0.095 | -0.06 | 0.517 | -- | <0.001 | <0.001 | <0.001 | <0.001 | <0.001 | <0.001 | <0.001 | 0.33 | <0.001 |
| <i>A. mellifera</i> Abundance | 0.02 | 0.01 | -0.036 | 0.041 | 0.685 | -- | <0.001 | <0.001 | <0.001 | <0.001 | <0.001 | <0.001 | <0.001 | <0.001 |
| <i>B. impatiens</i> Abundance | -0.13 | -0.074 | -0.01 | 0.815 | 0.726 | 0.348 | -- | <0.001 | <0.001 | <0.001 | <0.001 | <0.001 | <0.001 | <0.001 |
| <i>Apis + Bombus</i> Abundance | -0.102 | -0.058 | -0.02 | 0.695 | 0.833 | 0.621 | 0.951 | -- | <0.001 | <0.001 | <0.001 | <0.001 | <0.001 | <0.001 |
| <i>Lasioglossum</i> Abundance | -0.076 | -0.034 | -0.05 | 0.117 | 0.84 | 0.703 | 0.408 | 0.573 | -- | 0.847 | 0.629 | <0.001 | <0.001 | 0.882 |
| <i>E. pruinosa</i> Abundance | 0.017 | -0.034 | -0.053 | -0.224 | 0.155 | 0.255 | -0.256 | -0.13 | 0.006 | -- | <0.001 | <0.001 | <0.001 | <0.001 |
| Landscape Richness | -0.161 | -0.014 | -0.001 | 0.502 | 0.203 | 0.326 | 0.524 | 0.546 | 0.016 | -0.222 | -- | <0.001 | <0.001 | <0.001 |
| Natural Area | -0.112 | -0.073 | -0.038 | 0.677 | 0.7 | 0.374 | 0.694 | 0.704 | 0.512 | -0.131 | 0.182 | -- | <0.001 | <0.001 |
| Floral Richness | 0.017 | -0.021 | 0.01 | 0.33 | 0.033 | 0.161 | 0.24 | 0.253 | -0.258 | 0.141 | 0.333 | 0.253 | -- | <0.001 |
| Floral Density | -0.045 | -0.078 | 0.011 | 0.2 | 0.329 | 0.41 | 0.315 | 0.398 | 0.005 | 0.434 | 0.455 | 0.255 | 0.526 | -- |

Table S5: Moran's I spatial autocorrelation model output for each of the component models in the main path model.

| Model Response Variable | Observed | Expected | SD | P-value |
|---|-----------------|-----------------|-----------|----------------|
| Species Richness | -0.140 | -0.083 | 0.060 | 0.35 |
| Abundance | -0.079 | -0.083 | 0.060 | 0.95 |
| <i>A. mellifera</i> Abundance | -0.075 | -0.083 | 0.060 | 0.89 |
| <i>B. impatiens</i> Abundance | -0.088 | -0.083 | 0.059 | 0.94 |
| <i>A. mellifera</i> and <i>B. impatiens</i> Abundance | -0.086 | -0.083 | 0.058 | 0.97 |
| <i>Lasioglossum</i> spp. Abundance | -0.083 | -0.083 | 0.060 | 0.996 |
| <i>E. pruinosa</i> Abundance | -0.068 | -0.083 | 0.060 | 0.79 |
| DWV | -0.119 | -0.083 | 0.060 | 0.56 |
| BQCV | -0.154 | -0.083 | 0.059 | 0.23 |
| SBV | -0.037 | -0.083 | 0.060 | 0.44 |

Table S6: The full path model statistics for the path model that included the total pollinator abundance. The table shows the unstandardized estimated pathway coefficients, range-standardized estimated coefficients, standard error, degrees of freedom, critical value, and p-value for each path. R² is shown for each response variable. The last four rows are correlated errors. Significant pathway coefficients and p-values are bolded, with negative coefficients in red and positive coefficients in black.

| Response variable | Predictor variable | Range Std | | Std Error | DF | Critical | | R ² |
|----------------------------|----------------------------|---------------|---------------|-----------|-----|----------|----------------------|----------------|
| | | Estimate | Estimate | | | Value | P-value | |
| Species Richness | Prop. Natural Area 1000m | 0.633 | 0.910 | 0.199 | 8 | 3.173 | 0.013 * | 0.70 |
| | Landscape Richness 1000m | 0.403 | 0.438 | 0.241 | 8 | 1.673 | 0.133 | |
| | Floral Richness | 0.167 | 0.179 | 0.256 | 8 | 0.653 | 0.532 | |
| | Floral Density | -0.236 | -0.209 | 0.278 | 8 | -0.851 | 0.419 | |
| Total Pollinator Abundance | Prop. Natural Area 1000m | 0.682 | 0.741 | 0.210 | 8 | 3.255 | 0.012 * | 0.65 |
| | Landscape Richness 1000m | 0.021 | 0.017 | 0.253 | 8 | 0.084 | 0.935 | |
| | Floral Richness | -0.282 | -0.228 | 0.269 | 8 | -1.047 | 0.326 | |
| | Floral Density | 0.305 | 0.203 | 0.292 | 8 | 1.044 | 0.327 | |
| DWV | Prop. Natural Area 1000m | 0.140 | 0.056 | 0.258 | 888 | 0.540 | 0.589 | 0.22 |
| | Landscape Richness 1000m | -0.240 | -0.072 | 0.195 | 888 | -1.229 | 0.219 | |
| | Floral Richness | 0.238 | 0.071 | 0.197 | 888 | 1.207 | 0.227 | |
| | Floral Density | -0.082 | -0.020 | 0.215 | 888 | -0.382 | 0.703 | |
| | Species Richness | -0.438 | -0.121 | 0.248 | 888 | -1.769 | 0.077 | |
| | Total Pollinator Abundance | -0.016 | -0.006 | 0.236 | 888 | -0.069 | 0.945 | |
| BQCV | Prop. Natural Area 1000m | 0.476 | 0.159 | 0.185 | 888 | 2.566 | 0.010 * | 0.41 |
| | Landscape Richness 1000m | 0.313 | 0.079 | 0.141 | 888 | 2.220 | 0.026 * | |
| | Floral Richness | 0.229 | 0.057 | 0.138 | 888 | 1.664 | 0.096 | |
| | Floral Density | -0.393 | -0.080 | 0.151 | 888 | -2.609 | 0.009 ** | |
| | Species Richness | -0.663 | -0.154 | 0.185 | 888 | -3.596 | <0.001 *** | |
| | Total Pollinator Abundance | -0.100 | -0.031 | 0.161 | 888 | -0.618 | 0.536 | |
| SBV | Prop. Natural Area 1000m | 0.032 | 0.010 | 0.181 | 888 | 0.177 | 0.860 | 0.38 |
| | Landscape Richness 1000m | 0.047 | 0.011 | 0.148 | 888 | 0.318 | 0.750 | |
| | Floral Richness | 0.029 | 0.007 | 0.139 | 888 | 0.206 | 0.837 | |
| | Floral Density | 0.071 | 0.014 | 0.151 | 888 | 0.468 | 0.640 | |
| | Species Richness | -0.213 | -0.047 | 0.182 | 888 | -1.174 | 0.240 | |
| | Total Pollinator Abundance | -0.032 | -0.009 | 0.174 | 888 | -0.187 | 0.852 | |
| DWV | BQCV | 0.199 | 0.199 | NA | 888 | 6.030 | <0.001 *** | |
| BQCV | SBV | 0.163 | 0.163 | NA | 888 | 4.910 | <0.001 *** | |
| SBV | DWV | 0.181 | 0.181 | NA | 888 | 5.472 | <0.001 *** | |
| Total Pollinator Abundance | Species Richness | 0.095 | 0.095 | NA | 13 | 0.301 | 0.385 | |

Table S7: The full path model statistics for the path model that included *Apis mellifera* abundance. The table shows the unstandardized estimated pathway coefficients, range-standardized estimated coefficients, standard error, degrees of freedom, critical value, and p-value for each path. R² is shown for each response variable. The last four rows are correlated errors. Significant pathway coefficients and p-values are bolded, with negative coefficients in red and positive coefficients in black.

| Response variable | Predictor variable | Range Std | | Std Error | DF | Critical | | R ² |
|---------------------------------|---------------------------------|---------------|---------------|-----------|-----|----------|----------------------|----------------|
| | | Estimate | Estimate | | | Value | P-value | |
| Species Richness | Prop. Natural Area 1000m | 0.633 | 0.910 | 0.199 | 8 | 3.173 | 0.013 * | 0.70 |
| | Landscape Richness 1000m | 0.403 | 0.438 | 0.241 | 8 | 1.673 | 0.133 | |
| | Floral Richness | 0.167 | 0.179 | 0.256 | 8 | 0.653 | 0.532 | |
| | Floral Density | -0.236 | -0.209 | 0.278 | 8 | -0.851 | 0.419 | |
| <i>Apis mellifera</i> Abundance | Prop. Natural Area 1000m | 0.213 | 0.341 | 0.302 | 8 | 0.705 | 0.501 | 0.25 |
| | Landscape Richness 1000m | 0.238 | 0.289 | 0.364 | 8 | 0.654 | 0.532 | |
| | Floral Richness | -0.172 | -0.206 | 0.387 | 8 | -0.445 | 0.668 | |
| | Floral Density | 0.311 | 0.305 | 0.421 | 8 | 0.738 | 0.481 | |
| DWV | Prop. Natural Area 1000m | -0.044 | -0.018 | 0.253 | 888 | -0.176 | 0.860 | 0.22 |
| | Landscape Richness 1000m | -0.366 | -0.110 | 0.213 | 888 | -1.720 | 0.085 | |
| | Floral Richness | 0.255 | 0.076 | 0.172 | 888 | 1.487 | 0.137 | |
| | Floral Density | -0.115 | -0.028 | 0.191 | 888 | -0.601 | 0.548 | |
| | Species Richness | -0.255 | -0.071 | 0.280 | 888 | -0.911 | 0.362 | |
| | <i>Apis mellifera</i> Abundance | 0.228 | 0.057 | 0.192 | 888 | 1.189 | 0.234 | |
| BQCV | Prop. Natural Area 1000m | 0.471 | 0.157 | 0.196 | 888 | 2.399 | 0.016 * | 0.41 |
| | Landscape Richness 1000m | 0.349 | 0.088 | 0.161 | 888 | 2.164 | 0.030 * | |
| | Floral Richness | 0.259 | 0.064 | 0.130 | 888 | 1.992 | 0.046 * | |
| | Floral Density | -0.420 | -0.086 | 0.143 | 888 | -2.940 | 0.003 ** | |
| | Species Richness | -0.732 | -0.170 | 0.210 | 888 | -3.483 | <0.001 *** | |
| | <i>Apis mellifera</i> Abundance | -0.058 | -0.012 | 0.141 | 888 | -0.411 | 0.681 | |
| SBV | Prop. Natural Area 1000m | 0.118 | 0.037 | 0.173 | 888 | 0.681 | 0.496 | 0.38 |
| | Landscape Richness 1000m | 0.140 | 0.033 | 0.158 | 888 | 0.886 | 0.376 | |
| | Floral Richness | 0.043 | 0.010 | 0.121 | 888 | 0.353 | 0.724 | |
| | Floral Density | 0.074 | 0.014 | 0.133 | 888 | 0.559 | 0.576 | |
| | Species Richness | -0.344 | -0.075 | 0.200 | 888 | -1.725 | 0.085 | |
| | <i>Apis mellifera</i> Abundance | -0.152 | -0.030 | 0.137 | 888 | -1.107 | 0.268 | |
| DWV | BQCV | 0.199 | 0.199 | NA | 888 | 6.047 | <0.001 *** | |
| BQCV | SBV | 0.161 | 0.161 | NA | 888 | 4.856 | <0.001 *** | |
| SBV | DWV | 0.182 | 0.182 | NA | 888 | 5.504 | <0.001 *** | |
| <i>Apis mellifera</i> Abundance | Species Richness | -0.564 | -0.564 | NA | 13 | -2.158 | 0.028 * | |

Table S8: The full path model statistics for the path model that included *Bombus impatiens* abundance. The table shows the unstandardized estimated pathway coefficients, range-standardized estimated coefficients, standard error, degrees of freedom, critical value, and p-value for each path. R² is shown for each response variable. The last four rows are correlated errors. Significant pathway coefficients and p-values are bolded, with negative coefficients in red and positive coefficients in black.

| Response variable | Predictor variable | Range Std | | Std Error | DF | Critical | | R ² |
|-----------------------------------|-----------------------------------|---------------|---------------|-----------|-----|----------|----------------------|----------------|
| | | Estimate | Estimate | | | Value | P-value | |
| Species Richness | Prop. Natural Area 1000m | 0.633 | 0.910 | 0.199 | 8 | 3.173 | 0.013 * | 0.70 |
| | Landscape Richness 1000m | 0.403 | 0.438 | 0.241 | 8 | 1.673 | 0.133 | |
| | Floral Richness | 0.167 | 0.179 | 0.256 | 8 | 0.653 | 0.532 | |
| | Floral Density | -0.236 | -0.209 | 0.278 | 8 | -0.851 | 0.419 | |
| <i>Bombus impatiens</i> Abundance | Prop. Natural Area 1000m | 0.594 | 0.913 | 0.196 | 8 | 3.025 | 0.016 * | 0.69 |
| | Landscape Richness 1000m | 0.431 | 0.501 | 0.237 | 8 | 1.817 | 0.107 | |
| | Floral Richness | -0.045 | -0.051 | 0.252 | 8 | -0.178 | 0.863 | |
| | Floral Density | -0.022 | -0.021 | 0.274 | 8 | -0.081 | 0.937 | |
| DWV | Prop. Natural Area 1000m | 0.043 | 0.017 | 0.219 | 888 | 0.196 | 0.844 | 0.22 |
| | Landscape Richness 1000m | -0.310 | -0.093 | 0.195 | 888 | -1.589 | 0.112 | |
| | Floral Richness | 0.285 | 0.084 | 0.175 | 888 | 1.621 | 0.105 | |
| | Floral Density | -0.117 | -0.029 | 0.192 | 888 | -0.609 | 0.543 | |
| | Species Richness | -0.602 | -0.167 | 0.273 | 888 | -2.206 | 0.027 * | |
| | <i>Bombus impatiens</i> Abundance | 0.310 | 0.080 | 0.273 | 888 | 1.136 | 0.256 | |
| BQCV | Prop. Natural Area 1000m | 0.449 | 0.150 | 0.176 | 888 | 2.551 | 0.011 * | 0.41 |
| | Landscape Richness 1000m | 0.334 | 0.084 | 0.149 | 888 | 2.247 | 0.025 * | |
| | Floral Richness | 0.250 | 0.062 | 0.132 | 888 | 1.897 | 0.058 | |
| | Floral Density | -0.421 | -0.086 | 0.143 | 888 | -2.942 | 0.003 ** | |
| | Species Richness | -0.647 | -0.150 | 0.214 | 888 | -3.022 | 0.003 ** | |
| | <i>Bombus impatiens</i> Abundance | -0.076 | -0.017 | 0.202 | 888 | -0.376 | 0.707 | |
| SBV | Prop. Natural Area 1000m | -0.068 | -0.021 | 0.165 | 888 | -0.410 | 0.682 | 0.38 |
| | Landscape Richness 1000m | -0.028 | -0.007 | 0.160 | 888 | -0.176 | 0.860 | |
| | Floral Richness | 0.071 | 0.017 | 0.132 | 888 | 0.541 | 0.589 | |
| | Floral Density | 0.033 | 0.006 | 0.145 | 888 | 0.229 | 0.819 | |
| | Species Richness | -0.391 | -0.086 | 0.211 | 888 | -1.854 | 0.064 | |
| | <i>Bombus impatiens</i> Abundance | 0.321 | 0.066 | 0.211 | 888 | 1.518 | 0.129 | |
| DWV | BQCV | 0.199 | 0.199 | NA | 888 | 6.036 | <0.001 *** | |
| BQCV | SBV | 0.165 | 0.165 | NA | 888 | 4.971 | <0.001 *** | |
| SBV | DWV | 0.180 | 0.180 | NA | 888 | 5.432 | <0.001 *** | |
| <i>Bombus impatiens</i> Abundance | Species Richness | 0.510 | 0.510 | NA | 13 | 1.875 | 0.045 * | |

Table S9: The full path model statistics for the path model that included *Lasioglossum* spp. abundance. The table shows the unstandardized estimated pathway coefficients, range-standardized estimated coefficients, standard error, degrees of freedom, critical value, and p-value for each path. R² is shown for each response variable. The last four rows are correlated errors. Significant pathway coefficients and p-values are bolded, with negative coefficients in red and positive coefficients in black.

| Response variable | Predictor variable | Range Std | | Std Error | DF | Critical | | R ² |
|------------------------------------|------------------------------------|---------------|---------------|-----------|-----|----------|----------------------|----------------|
| | | Estimate | Estimate | | | Value | P-value | |
| Species Richness | Prop. Natural Area 1000m | 0.633 | 0.910 | 0.199 | 8 | 3.173 | 0.013 * | 0.70 |
| | Landscape Richness 1000m | 0.403 | 0.438 | 0.241 | 8 | 1.673 | 0.133 | |
| | Floral Richness | 0.167 | 0.179 | 0.256 | 8 | 0.653 | 0.532 | |
| | Floral Density | -0.236 | -0.209 | 0.278 | 8 | -0.851 | 0.419 | |
| <i>Lasioglossum</i> spp. Abundance | Prop. Natural Area 1000m | 0.579 | 0.818 | 0.254 | 8 | 2.277 | 0.052 | 0.43 |
| | Landscape Richness 1000m | 0.020 | 0.021 | 0.307 | 8 | 0.064 | 0.950 | |
| | Floral Richness | -0.447 | -0.471 | 0.326 | 8 | -1.370 | 0.208 | |
| | Floral Density | 0.103 | 0.090 | 0.354 | 8 | 0.292 | 0.778 | |
| DWV | Prop. Natural Area 1000m | 0.205 | 0.082 | 0.290 | 888 | 0.706 | 0.480 | 0.22 |
| | Landscape Richness 1000m | -0.221 | -0.066 | 0.201 | 888 | -1.100 | 0.272 | |
| | Floral Richness | 0.213 | 0.063 | 0.198 | 888 | 1.071 | 0.284 | |
| | Floral Density | -0.089 | -0.022 | 0.199 | 888 | -0.449 | 0.653 | |
| | Species Richness | -0.484 | -0.134 | 0.269 | 888 | -1.797 | 0.072 | |
| | <i>Lasioglossum</i> spp. Abundance | -0.081 | -0.023 | 0.213 | 888 | -0.381 | 0.703 | |
| BQCV | Prop. Natural Area 1000m | 0.513 | 0.171 | 0.202 | 888 | 2.540 | 0.011 * | 0.41 |
| | Landscape Richness 1000m | 0.340 | 0.086 | 0.142 | 888 | 2.390 | 0.017 * | |
| | Floral Richness | 0.220 | 0.055 | 0.137 | 888 | 1.604 | 0.109 | |
| | Floral Density | -0.429 | -0.088 | 0.137 | 888 | -3.131 | 0.002 ** | |
| | Species Richness | -0.732 | -0.170 | 0.188 | 888 | -3.887 | <0.001 *** | |
| | <i>Lasioglossum</i> spp. Abundance | -0.113 | -0.027 | 0.144 | 888 | -0.781 | 0.435 | |
| SBV | Prop. Natural Area 1000m | 0.046 | 0.015 | 0.204 | 888 | 0.227 | 0.821 | 0.38 |
| | Landscape Richness 1000m | 0.057 | 0.014 | 0.154 | 888 | 0.369 | 0.712 | |
| | Floral Richness | 0.025 | 0.006 | 0.140 | 888 | 0.180 | 0.857 | |
| | Floral Density | 0.058 | 0.011 | 0.142 | 888 | 0.412 | 0.680 | |
| | Species Richness | -0.237 | -0.052 | 0.197 | 888 | -1.205 | 0.228 | |
| | <i>Lasioglossum</i> spp. Abundance | -0.037 | -0.008 | 0.156 | 888 | -0.239 | 0.811 | |
| DWV | BQCV | 0.199 | 0.199 | NA | 888 | 6.027 | <0.001 *** | |
| BQCV | SBV | 0.163 | 0.163 | NA | 888 | 4.899 | <0.001 *** | |
| SBV | DWV | 0.181 | 0.181 | NA | 888 | 5.468 | <0.001 *** | |
| <i>Lasioglossum</i> spp. Abundance | Species Richness | -0.435 | -0.435 | NA | 13 | -1.530 | 0.079 | |

Table S10: The full path model statistics for the path model that included *Eucera pruinosa* abundance. The table shows the unstandardized estimated pathway coefficients, range-standardized estimated coefficients, standard error, degrees of freedom, critical value, and p-value for each path. R² is shown for each response variable. The last four rows are correlated errors. Significant pathway coefficients and p-values are bolded, with negative coefficients in red and positive coefficients in black.

| Response variable | Predictor variable | Range Std | | Std Error | DF | Critical | | R ² |
|----------------------------------|----------------------------------|---------------|---------------|-----------|-----|----------|----------------------|----------------|
| | | Estimate | Estimate | | | Value | P-value | |
| Species Richness | Prop. Natural Area 1000m | 0.633 | 0.910 | 0.199 | 8 | 3.173 | 0.013 * | 0.70 |
| | Landscape Richness 1000m | 0.403 | 0.438 | 0.241 | 8 | 1.673 | 0.133 | |
| | Floral Richness | 0.167 | 0.179 | 0.256 | 8 | 0.653 | 0.532 | |
| | Floral Density | -0.236 | -0.209 | 0.278 | 8 | -0.851 | 0.419 | |
| <i>Eucera pruinosa</i> Abundance | Prop. Natural Area 1000m | -0.164 | -0.244 | 0.274 | 8 | -0.600 | 0.565 | 0.41 |
| | Landscape Richness 1000m | -0.552 | -0.619 | 0.331 | 8 | -1.667 | 0.134 | |
| | Floral Richness | 0.082 | 0.091 | 0.352 | 8 | 0.233 | 0.821 | |
| | Floral Density | 0.731 | 0.664 | 0.382 | 8 | 1.911 | 0.092 | |
| DWV | Prop. Natural Area 1000m | 0.093 | 0.037 | 0.207 | 888 | 0.448 | 0.654 | 0.22 |
| | Landscape Richness 1000m | -0.348 | -0.105 | 0.208 | 888 | -1.672 | 0.094 | |
| | Floral Richness | 0.253 | 0.075 | 0.172 | 888 | 1.468 | 0.142 | |
| | Floral Density | 0.055 | 0.013 | 0.228 | 888 | 0.241 | 0.810 | |
| | Species Richness | -0.438 | -0.121 | 0.232 | 888 | -1.886 | 0.059 | |
| | <i>Eucera pruinosa</i> Abundance | -0.198 | -0.053 | 0.176 | 888 | -1.126 | 0.260 | |
| BQCV | Prop. Natural Area 1000m | 0.463 | 0.154 | 0.170 | 888 | 2.722 | 0.006 ** | 0.41 |
| | Landscape Richness 1000m | 0.399 | 0.101 | 0.162 | 888 | 2.458 | 0.014 * | |
| | Floral Richness | 0.263 | 0.065 | 0.129 | 888 | 2.037 | 0.042 * | |
| | Floral Density | -0.539 | -0.110 | 0.174 | 888 | -3.099 | 0.002 ** | |
| | Species Richness | -0.703 | -0.163 | 0.181 | 888 | -3.875 | <0.001 *** | |
| | <i>Eucera pruinosa</i> Abundance | 0.151 | 0.034 | 0.141 | 888 | 1.067 | 0.286 | |
| SBV | Prop. Natural Area 1000m | -0.038 | -0.012 | 0.144 | 888 | -0.261 | 0.794 | 0.38 |
| | Landscape Richness 1000m | -0.058 | -0.014 | 0.150 | 888 | -0.386 | 0.700 | |
| | Floral Richness | 0.040 | 0.009 | 0.118 | 888 | 0.335 | 0.738 | |
| | Floral Density | 0.222 | 0.043 | 0.163 | 888 | 1.362 | 0.173 | |
| | Species Richness | -0.219 | -0.048 | 0.164 | 888 | -1.337 | 0.181 | |
| | <i>Eucera pruinosa</i> Abundance | -0.234 | -0.050 | 0.127 | 888 | -1.835 | 0.067 | |
| DWV | BQCV | 0.201 | 0.201 | NA | 888 | 6.097 | <0.001 *** | |
| BQCV | SBV | 0.166 | 0.166 | NA | 888 | 5.016 | <0.001 *** | |
| SBV | DWV | 0.176 | 0.176 | NA | 888 | 5.319 | <0.001 *** | |
| <i>Eucera pruinosa</i> Abundance | Species Richness | -0.037 | -0.037 | NA | 13 | -0.117 | 0.454 | |

Table S11: The path model with estimated species richness replacing the observed species richness. In this model, species richness was estimated for each site based on a rarefaction curve at the average number of individuals collected across all sites (338 individuals). The unstandardized estimated pathway coefficients, range standardized estimated pathway coefficients, standard error, degrees of freedom, critical value, and p-value for each path. R² for each component model. The last four rows are correlated errors included in the model. Significant pathway coefficients and p-values are bolded, with negative coefficients in red and positive coefficients in black. Model AIC was 2516.01, with a Δ AIC of 9.11 compared to the lowest AIC model in **Appendix S2: Table S2**.

| Response variable | Predictor variable | Estimate | Range Std | | DF | Critical | | R ² |
|--------------------------------|--------------------------------|---------------|---------------|-----------|-----|----------|----------------------|----------------|
| | | | Estimate | Std Error | | Value | P-value | |
| Estimated Species Richness | Prop. Natural Area 1000m | 0.547 | 0.799 | 0.230 | 8 | 2.382 | 0.044 * | 0.63 |
| | Landscape Richness 1000m | 0.335 | 0.370 | 0.278 | 8 | 1.207 | 0.262 | |
| | Floral Richness | 0.343 | 0.373 | 0.295 | 8 | 1.162 | 0.279 | |
| | Floral Density | -0.251 | -0.224 | 0.320 | 8 | -0.783 | 0.456 | |
| <i>Apis + Bombus</i> Abundance | Prop. Natural Area 1000m | 0.567 | 0.834 | 0.186 | 8 | 3.049 | 0.016 * | 0.71 |
| | Landscape Richness 1000m | 0.439 | 0.488 | 0.225 | 8 | 1.954 | 0.086 | |
| | Floral Richness | -0.094 | -0.103 | 0.239 | 8 | -0.395 | 0.703 | |
| | Floral Density | 0.084 | 0.076 | 0.259 | 8 | 0.323 | 0.755 | |
| DWV | Prop. Natural Area 1000m | -0.087 | -0.034 | 0.250 | 888 | -0.347 | 0.729 | 0.22 |
| | Landscape Richness 1000m | -0.389 | -0.117 | 0.218 | 888 | -1.787 | 0.074 | |
| | Floral Richness | 0.315 | 0.094 | 0.189 | 888 | 1.670 | 0.095 | |
| | Floral Density | -0.091 | -0.022 | 0.197 | 888 | -0.463 | 0.644 | |
| | Estimated Species Richness | -0.358 | -0.098 | 0.213 | 888 | -1.683 | 0.092 | |
| | <i>Apis + Bombus</i> Abundance | 0.212 | 0.058 | 0.260 | 888 | 0.816 | 0.414 | |
| BQCV | Prop. Natural Area 1000m | 0.464 | 0.155 | 0.201 | 888 | 2.315 | 0.021 * | 0.42 |
| | Landscape Richness 1000m | 0.344 | 0.087 | 0.170 | 888 | 2.021 | 0.043 * | |
| | Floral Richness | 0.287 | 0.072 | 0.145 | 888 | 1.983 | 0.047 * | |
| | Floral Density | -0.369 | -0.076 | 0.150 | 888 | -2.457 | 0.014 * | |
| | Estimated Species Richness | -0.532 | -0.122 | 0.173 | 888 | -3.075 | 0.002 ** | |
| | <i>Apis + Bombus</i> Abundance | -0.291 | -0.066 | 0.196 | 888 | -1.483 | 0.138 | |
| SBV | Prop. Natural Area 1000m | -0.111 | -0.035 | 0.195 | 888 | -0.568 | 0.570 | 0.39 |
| | Landscape Richness 1000m | -0.067 | -0.016 | 0.183 | 888 | -0.365 | 0.715 | |
| | Floral Richness | 0.047 | 0.011 | 0.146 | 888 | 0.322 | 0.747 | |
| | Floral Density | 0.083 | 0.016 | 0.152 | 888 | 0.543 | 0.587 | |
| | Estimated Species Richness | -0.121 | -0.026 | 0.172 | 888 | -0.704 | 0.481 | |
| | <i>Apis + Bombus</i> Abundance | 0.115 | 0.025 | 0.213 | 888 | 0.540 | 0.589 | |
| DWV | BQCV | 0.200 | 0.200 | NA | 888 | 6.074 | <0.001 *** | |
| BQCV | SBV | 0.168 | 0.168 | NA | 888 | 5.059 | <0.001 *** | |
| SBV | DWV | 0.181 | 0.181 | NA | 888 | 5.486 | <0.001 *** | |
| <i>Apis + Bombus</i> Abundance | Estimated Species Richness | -0.141 | -0.141 | NA | 13 | -0.449 | 0.331 | |

References

- Dormann, C. F., J. Elith, S. Bacher, C. Buchmann, G. Carl, G. Carré, J. R. García Márquez, B. Gruber, B. Lafourcade, P. J. Leitão, T. Münkemüller, C. McClean, P. E. Osborne, B. Reineking, B. Schröder, A. K. Skidmore, D. Zurell, and S. Lautenbach. 2013. Collinearity: a review of methods to deal with it and a simulation study evaluating their performance. *Ecography* 36:27–46.
- Fearon, M. L., and E. A. Tibbetts. 2021. Pollinator community species richness dilutes prevalence of multiple viruses within multiple host species. *Ecology* 102:e03305.
- Gotelli, N. J., and R. K. Colwell. 2001. Quantifying biodiversity: Procedures and pitfalls in the measurement and comparison of species richness. *Ecology Letters* 4:379–391.
- Grace, J. B. 2020. A “weight of evidence” approach to evaluating structural equation models. *One Ecosystem* 5:e50452.
- Hartig, F. 2020. DHARMA: Residual Diagnostics for Hierarchical (Multi-Level/Mixed) Regression Models. <https://cran.r-project.org/package=DHARMA>.
- Hebbali, A. 2020. olsrr: Tools for Building OLS Regression Models.
- Hsieh, T. C., K. H. Ma, and A. Chao. 2016. iNEXT: an R package for rarefaction and extrapolation of species diversity (Hill numbers). *Methods in Ecology and Evolution* 7:1451–1456.
- Lefcheck, J. S. 2016. PIECEWISE SEM: Piecewise structural equation modelling in R for ecology, evolution, and systematics. *Methods in Ecology and Evolution* 7:573–579.
- Novotný, V., and Y. Basset. 2000. Rare species in communities of tropical insect herbivores: Pondering the mystery of singletons. *Oikos* 89:564–572.
- Paradis, E., and K. Schliep. 2018. ape 5.0: an environment for modern phylogenetics and evolutionary analyses in R. *Bioinformatics* 35:526–528.
- R Core Team. 2021. R: A language and environment for statistical computing. R Foundation for Statistical Computing, Vienna, Austria.