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# Supplementary Materials for

## Interactive effects of climate and land use on pollinator diversity differ among taxa and scales

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## Supplementary Text

### *Effectivity of Malaise traps for catching flower-visiting insects*

Apart from estimating the proportion of pollinator taxa caught with Malaise traps (see Results), we compared the richness obtained with our Malaise traps with other studies from Bavaria that used methods more targeted to specific insect groups.

For instance, one study caught a total of 87 bee species in grasslands in and in the vicinity of the National Park Berchtesgaden with sweep netting, finding between 6 and 24 species per site (***81***). In our only grassland plot in the vicinity of Berchtesgaden, we found 38 wild bee species: Andrena carantonica, A. fucata, A. minutula, A. ovatula, B. campestris, B. hortorum, B. pascuorum, B. sylvestris, Hylaeus communis, H. gredleri, H. punctatus, H. sinuatus, Halictus rubicundus, H. tumulorum, Lasioglossum calceatum, L. fulvicorne, L. laticeps, L. leucopus, L. leucozonium, L. morio, L. nitidulum, L. pauxillum, L. villosulum, L. zonulum, Sphecodes crassus, S. gibbus, S. hyalinatus, S. longulus, S. monilicornis, S. pellucidus, S. reticulatus, S. scabriocollis, Anthidiellum strigatum, Anthidium oblongatum, Hoplitis leucomelana, Megachile centuncularis, M. ligniseca, M. nigriventris. This high diversity could be attributed to the long exposure of Malaise traps (active all-day long for six weeks), which are more likely to catch less abundant species (***82***).

We also compared our data with a study that used several different methods to analyze 12 taxonomic groups in different agri-environmental schemes and calcareous grasslands in the north-west of Bavaria (***61***). This study found in their 27 plots: 143 bee species (transect walks + pan traps), 91 flower visiting beetles (pan traps), 56 butterfly species and 120 moth species (transect walks + light traps), and 66 syrphids (Malaise traps and DNA metabarcoding). While our study covers a larger area, this previous study captured insects in calcareous grasslands, which are considered biodiversity hotspots in Europe. Since they used the same method to survey the syrphid taxa, we can use the difference in syrphid catches as a baseline to compare both studies. While they got 70% of the number of syrphid taxa we caught, the combination of pan traps and sweep netting used by (***61***) was effective for bees (74% of our catches), while they got 24% of the number of butterflies and moths and 35% of the flower-visiting beetles. This means that, although the combination of pan traps and sweep netting is likely the best to survey wild bees, Malaise traps are also an effective and much more representative method across pollinator taxa.

| | Pollinators | Bees | Hymenoptera | Syrphids | Diptera | Butterflies | Moths | Beetles |
|---|---|---|---|---|---|---|---|---|
| **Species** | 3218 | 194 | 869 | 95 | 1060 | 96 | 646 | 258 |
| **Genera** | 1452 | 31 | 435 | 47 | 459 | 58 | 314 | 108 |
| **Families** | 136 | 6 | 34 | 1 | 47 | 10 | 18 | 20 |

**Table S1. Total number of species, genera and families found from each pollinator taxon (n samples = 534, n sites = 179).** ‘Butterflies’ includes all butterflies plus the moth families in which all species are known to be diurnal (Choreutidae, Micropterigidae, Scythrydidae, Sesiidae and Zygaenidae).

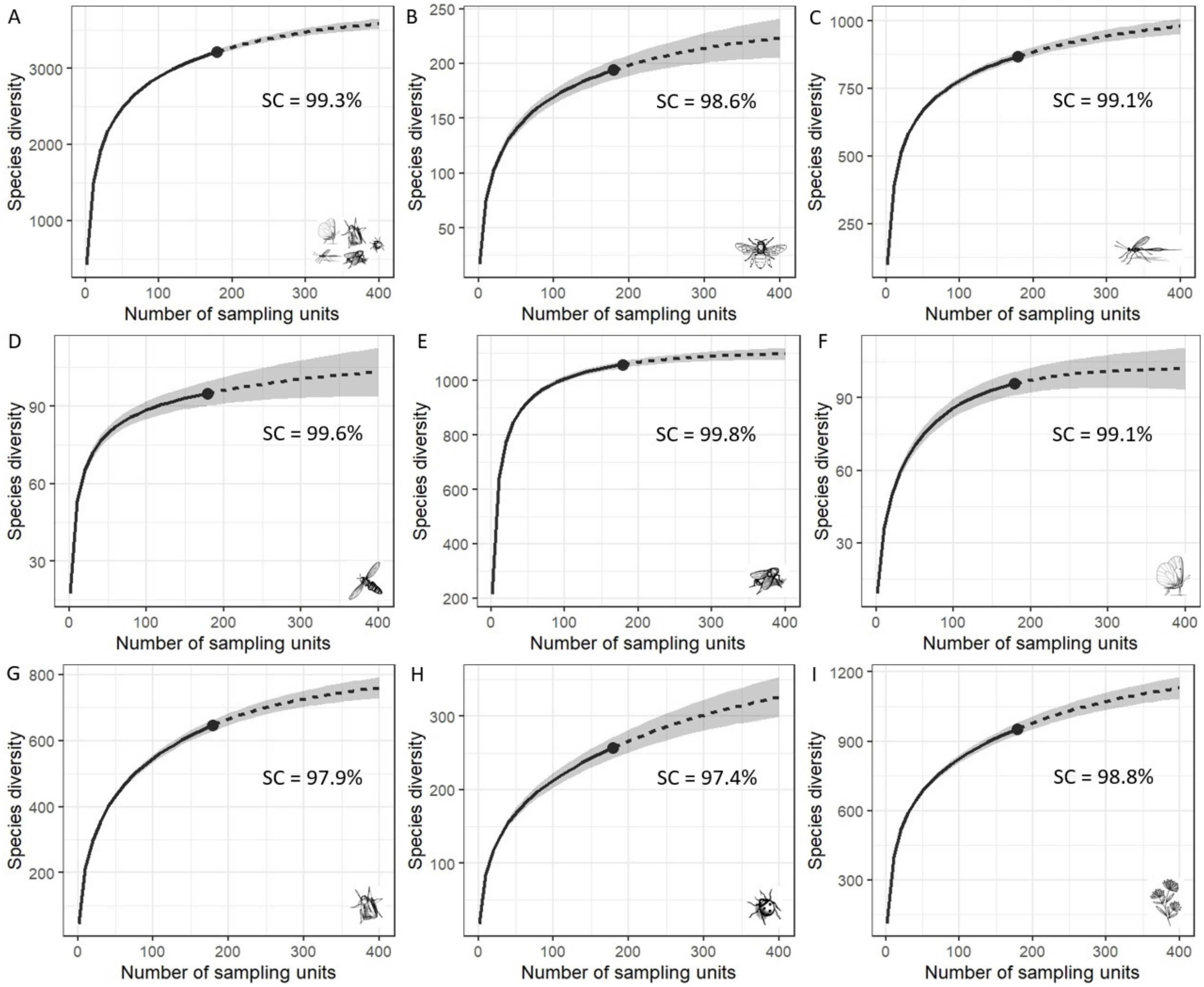

**Fig. S1. Rarefaction interpolation curves for the different pollinator communities and flowering plants.** We compared diversity estimates for our study plots with rarefaction and extrapolation sampling curves of Hill numbers (i.e. the effective number of species; q = 0, species richness) via the iNEXT function (iNEXT package (***83***)). Continuous lines indicate interpolated data and dashed lines extrapolated data. The sample completeness percentage (SC) is indicated in the panels. The different panels show: **(A)** whole pollinator community, **(B)** bees, **(C)** non-bee Hymenoptera, **(D)** syrphids, **(E)** non-syrphid Diptera, **(F)** butterflies, **(G)** moths, **(H)** beetles, **(I)** flowering plants.

**Response: Community composition - whole pollinator community**

| | Df | SumsOfSqs | MeanSqs | F.Model | R2 | Pr(>F) |
|---|---|---|---|---|---|---|
| RLU | 2 | 0.573 | 0.287 | 1.627 | 0.051 | 0.002 ** |
| MAT | 1 | 0.687 | 0.687 | 3.904 | 0.061 | 0.001 *** |
| RLU:MAT | 2 | 0.456 | 0.228 | 1.296 | 0.041 | 0.015 * |
| Residuals | 54 | 9.507 | 0.176 | | 0.847 | |
| Total | 59 | 11.224 | | | 1.000 | |

**Response: Community composition - bee community**

| | Df | SumsOfSqs | MeanSqs | F.Model | R2 | Pr(>F) |
|---|---|---|---|---|---|---|
| RLU | 2 | 0.631 | 0.315 | 1.670 | 0.051 | 0.043 * |
| MAT | 1 | 0.747 | 0.747 | 3.956 | 0.060 | 0.001 *** |
| RLU:MAT | 2 | 0.819 | 0.409 | 2.168 | 0.066 | 0.003 ** |
| Residuals | 54 | 10.197 | 0.189 | | 0.823 | |
| Total | 59 | 12.394 | | | 1.000 | |

**Response: Community composition - Hymenoptera community**

| | Df | SumsOfSqs | MeanSqs | F.Model | R2 | Pr(>F) |
|---|---|---|---|---|---|---|
| RLU | 2 | 0.606 | 0.303 | 1.555 | 0.049 | 0.003 ** |
| MAT | 1 | 0.588 | 0.588 | 3.016 | 0.048 | 0.001 *** |
| RLU:MAT | 2 | 0.591 | 0.296 | 1.516 | 0.048 | 0.006 ** |
| Residuals | 54 | 10.529 | 0.195 | | 0.855 | |
| Total | 59 | 12.314 | | | 1.000 | |

**Response: Community composition - syrphid community**

| | Df | SumsOfSqs | MeanSqs | F.Model | R2 | Pr(>F) |
|---|---|---|---|---|---|---|
| RLU | 2 | 0.428 | 0.214 | 1.645 | 0.049 | 0.075 . |
| MAT | 1 | 0.615 | 0.615 | 4.731 | 0.070 | 0.001 *** |
| RLU:MAT | 2 | 0.673 | 0.337 | 2.588 | 0.077 | 0.008 ** |
| Residuals | 54 | 7.024 | 0.130 | | 0.804 | |
| Total | 59 | 8.740 | | | 1.000 | |

**Response: Community composition - Diptera community**

| | Df | SumsOfSqs | MeanSqs | F.Model | R2 | Pr(>F) |
|---|---|---|---|---|---|---|
| RLU | 2 | 0.467 | 0.233 | 1.766 | 0.054 | 0.004 ** |
| MAT | 1 | 0.615 | 0.615 | 4.651 | 0.071 | 0.001 *** |
| RLU:MAT | 2 | 0.396 | 0.198 | 1.497 | 0.046 | 0.011 * |
| Residuals | 54 | 7.138 | 0.132 | | 0.829 | |
| Total | 59 | 8.615 | | | 1.000 | |

**Response: Community composition - butterfly community**

| | Df | SumsOfSqs | MeanSqs | F.Model | R2 | Pr(>F) |
|---|---|---|---|---|---|---|
| RLU | 2 | 0.491 | 0.245 | 1.576 | 0.048 | 0.122 |
| MAT | 1 | 0.410 | 0.410 | 2.630 | 0.040 | 0.022 * |
| RLU:MAT | 2 | 0.952 | 0.476 | 3.057 | 0.093 | 0.002 ** |
| Residuals | 54 | 8.411 | 0.156 | | 0.819 | |
| Total | 59 | 10.264 | | | 1.000 | |

**Response: Community composition - moth community**

| | Df | SumsOfSqs | MeanSqs | F.Model | R2 | Pr(>F) |
|---|---|---|---|---|---|---|
| RLU | 2 | 0.688 | 0.344 | 1.581 | 0.050 | 0.016 * |
| MAT | 1 | 0.746 | 0.746 | 3.428 | 0.054 | 0.001 *** |
| RLU:MAT | 2 | 0.699 | 0.349 | 1.606 | 0.050 | 0.007 ** |
| Residuals | 54 | 11.748 | 0.218 | | 0.846 | |
| Total | 59 | 13.880 | | | 1.000 | |

**Response: Community composition - beetle community**

| | Df | SumsOfSqs | MeanSqs | F.Model | R2 | Pr(>F) |
|---|---|---|---|---|---|---|
| RLU | 2 | 0.622 | 0.311 | 1.590 | 0.048 | 0.040 * |
| MAT | 1 | 0.877 | 0.877 | 4.488 | 0.068 | 0.001 *** |
| RLU:MAT | 2 | 0.841 | 0.420 | 2.150 | 0.065 | 0.005 ** |
| Residuals | 54 | 10.557 | 0.196 | | 0.819 | |
| Total | 59 | 12.897 | | | 1.000 | |

**Response: Community composition - flowering plant community**

| | Df | SumsOfSqs | MeanSqs | F.Model | R2 | Pr(>F) |
|---|---|---|---|---|---|---|
| RLU | 2 | 0.703 | 0.351 | 2.115 | 0.064 | 0.001 *** |
| MAT | 1 | 0.700 | 0.700 | 4.213 | 0.064 | 0.001 *** |
| RLU:MAT | 2 | 0.601 | 0.301 | 1.809 | 0.055 | 0.003 ** |
| Residuals | 54 | 8.970 | 0.166 | | 0.817 | |
| Total | 59 | 10.973 | | | 1.000 | |

**Table S2. The community composition of most pollinator taxa and flowering-plant species changed significantly across land-use intensity and temperature gradients, and with the interaction between both gradients.** Shown are results of permutational multivariate analyses of variance (PERMANOVA), performed with the adonis function (vegan package **(***72***)**), using Jaccard distances and the standard number of permutations (n = 999).

**Response: Distances (whole pollinator community)**

| | Df | Sum Sq | Mean Sq | F value | Pr (>F) |
|---|---|---|---|---|---|
| Groups | 2 | 0.00 | 0.00 | 0.43 | 0.652 |
| Residuals | 57 | 0.04 | 0.00 | | |

**Response: Distances (bee community)**

| | Df | Sum Sq | Mean Sq | F value | Pr (>F) |
|---|---|---|---|---|---|
| Groups | 2 | 0.03 | 0.02 | 1.35 | 0.268 |
| Residuals | 57 | 0.64 | 0.01 | | |

**Response: Distances (non-bee Hymenoptera community)**

| | Df | Sum Sq | Mean Sq | F value | Pr (>F) |
|---|---|---|---|---|---|
| Groups | 2 | 0.00 | 0.00 | 0.14 | 0.866 |
| Residuals | 57 | 0.11 | 0.00 | | |

**Response: Distances (syrphid community)**

| | Df | Sum Sq | Mean Sq | F value | Pr (>F) |
|---|---|---|---|---|---|
| Groups | 2 | 0.03 | 0.01 | 1.22 | 0.301 |
| Residuals | 57 | 0.61 | 0.01 | | |

**Response: Distances (non-syrphid Diptera community)**

| | Df | Sum Sq | Mean Sq | F value | Pr (>F) |
|---|---|---|---|---|---|
| Groups | 2 | 0.00 | 0.00 | 0.03 | 0.970 |
| Residuals | 57 | 0.06 | 0.00 | | |

**Response: Distances (butterfly community)**

| | Df | Sum Sq | Mean Sq | F value | Pr (>F) |
|---|---|---|---|---|---|
| Groups | 2 | 0.02 | 0.01 | 0.75 | 0.476 |
| Residuals | 57 | 0.97 | 0.02 | | |

**Response: Distances (moth community)**

| | Df | Sum Sq | Mean Sq | F value | Pr (>F) |
|---|---|---|---|---|---|
| Groups | 2 | 0.00 | 0.00 | 0.06 | 0.944 |
| Residuals | 57 | 0.19 | 0.00 | | |

**Response: Distances (beetle community)**

| | Df | Sum Sq | Mean Sq | F value | Pr (>F) |
|---|---|---|---|---|---|
| Groups | 2 | 0.02 | 0.01 | 0.89 | 0.416 |
| Residuals | 57 | 0.61 | 0.01 | | |

**Response: Distances (flowering plant community)**

| | Df | Sum Sq | Mean Sq | F value | Pr (>F) |
|---|---|---|---|---|---|
| Groups | 2 | 0.00 | 0.00 | 0.82 | 0.446 |
| Residuals | 57 | 0.11 | 0.00 | | |

**Table S3. Different regional land-use types have a similar compositional variance of the different pollinator taxa.** Shown are ANOVA tables displaying the non-significant results of the betadisper function models for the three regional land uses (semi-natural, agricultural, urban).

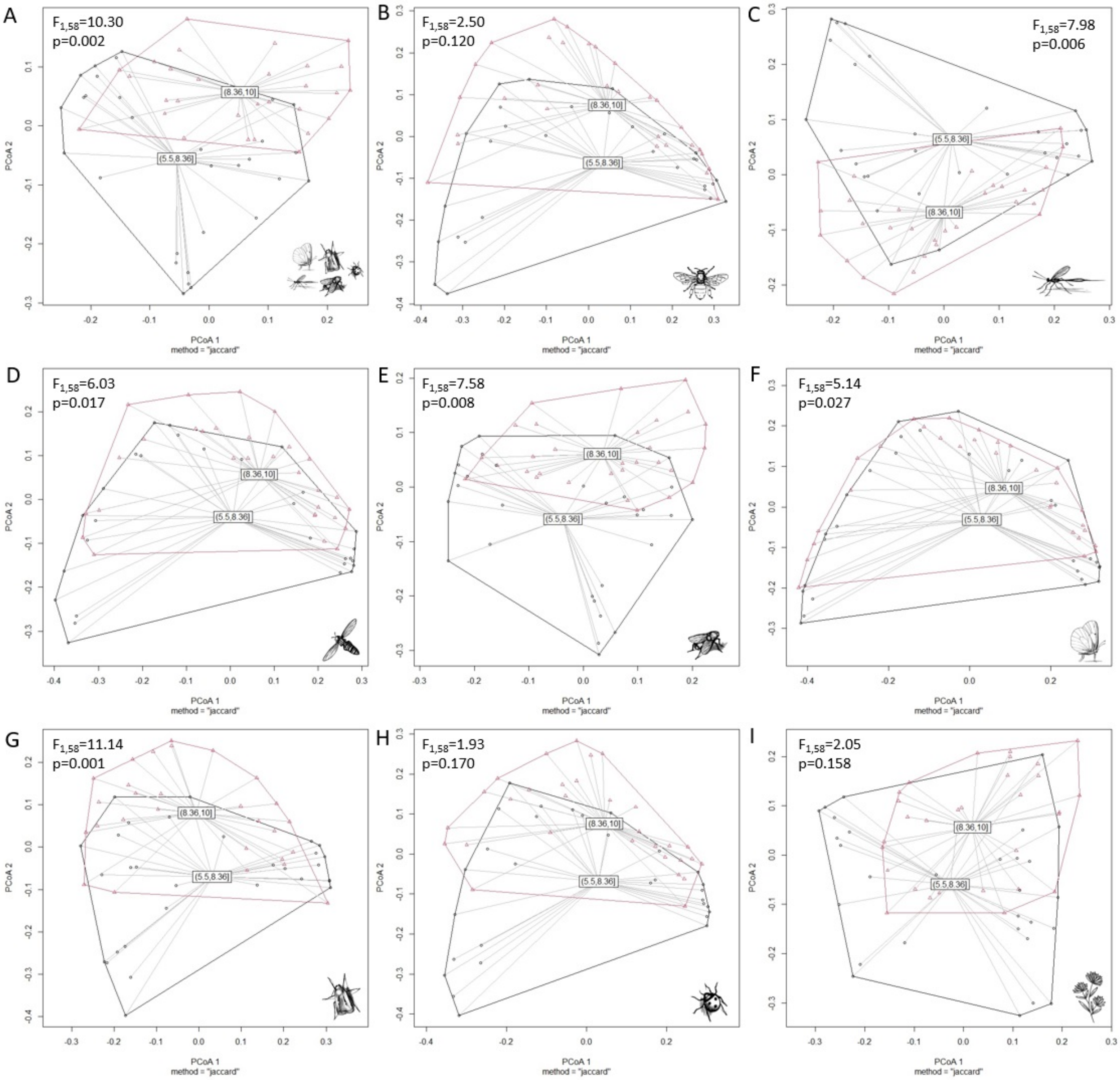

**Fig. S2. Difference in compositional variance (inter-regional dissimilarity) between cooler and warmer regions for the different pollinator taxa.** Ordinations (NMDS, Jaccards' method) show the homogeneity of dispersion of the different pollinator taxa in cooler (multi-annual mean temperature between 5.6 and 8.4 °C) versus warmer (multi-annual mean temperature between 8.4 and 9.8 °C) regions. The position of regions (dots) in the NMDS space represents the similarity in pollinator community composition in relation to other regions: the closer the dots, the higher the proportion of species shared. Rectangles represent centroids of the two temperature regimes; polygons delimit the NMDS space occupied by regions with the same temperature category. The different panels show: **(A)** whole pollinator community, **(B)** bees, **(C)** non-bee Hymenoptera, **(D)** syrphids, **(E)** non-syrphid Diptera, **(F)** butterflies, **(G)** moths, **(H)** beetles, **(I)** flowering plants. Results from betadisper function models (F and p values from ANOVA) indicating whether the compositional variance of the different pollinator taxa is significantly different between temperature regimes are indicated in the upper corner of each panel.

**Response: Distances (whole pollinator community)**

| | Df | Sum Sq | Mean Sq | F value | Pr (>F) |
|---|---|---|---|---|---|
| Groups | 5 | 0.01 | 0.00 | 1.79 | 0.131 |
| Residuals | 54 | 0.03 | 0.00 | | |

**Response: Distances (bee community)**

| | Df | Sum Sq | Mean Sq | F value | Pr (>F) |
|---|---|---|---|---|---|
| Groups | 5 | 0.07 | 0.01 | 1.26 | 0.296 |
| Residuals | 54 | 0.61 | 0.01 | | |

**Response: Distances (non-bee Hymenoptera community)**

| | Df | Sum Sq | Mean Sq | F value | Pr (>F) |
|---|---|---|---|---|---|
| Groups | 5 | 0.02 | 0.00 | 1.97 | 0.098 . |
| Residuals | 54 | 0.12 | 0.00 | | |

**Response: Distances (syrphid community)**

| | Df | Sum Sq | Mean Sq | F value | Pr (>F) |
|---|---|---|---|---|---|
| Groups | 5 | 0.10 | 0.02 | 1.65 | 0.164 |
| Residuals | 54 | 0.64 | 0.01 | | |

**Response: Distances (non-syrphid Diptera community)**

| | Df | Sum Sq | Mean Sq | F value | Pr (>F) |
|---|---|---|---|---|---|
| Groups | 5 | 0.01 | 0.00 | 1.17 | 0.337 |
| Residuals | 54 | 0.05 | 0.00 | | |

**Response: Distances (butterfly community)**

| | Df | Sum Sq | Mean Sq | F value | Pr (>F) |
|---|---|---|---|---|---|
| Groups | 5 | 0.13 | 0.03 | 1.38 | 0.247 |
| Residuals | 54 | 1.04 | 0.02 | | |

**Response: Distances (moth community)**

| | Df | Sum Sq | Mean Sq | F value | Pr (>F) |
|---|---|---|---|---|---|
| Groups | 5 | 0.03 | 0.01 | 1.70 | 0.150 |
| Residuals | 54 | 0.18 | 0.00 | | |

**Response: Distances (beetle community)**

| | Df | Sum Sq | Mean Sq | F value | Pr (>F) |
|---|---|---|---|---|---|
| Groups | 5 | 0.05 | 0.01 | 0.95 | 0.455 |
| Residuals | 54 | 0.57 | 0.01 | | |

**Response: Distances (flowering plant community)**

| | Df | Sum Sq | Mean Sq | F value | Pr (>F) |
|---|---|---|---|---|---|
| Groups | 5 | 0.01 | 0.00 | 0.77 | 0.573 |
| Residuals | 54 | 0.10 | 0.00 | | |

**Table S4. The interaction between land-use intensity and temperature does not affect the compositional variance of the different pollinator taxa across regions.** Shown are ANOVA tables displaying the non-significant results of the betadisper function models for the interaction between regional land-use types and temperature.

**Response: Pollinator Gamma diversity**

| | Estimate | Std. Error | Z value | Pseudo-$R^2$ | AIC | $\Delta\mathrm{AIC}_{\mathrm{null}}$ |
|---|---|---|---|---|---|---|
| (Intercept) | 6.687 | 0.013 | 531.84 | 0.132 | 699.0 | 3.3 |
| $\mathrm{For}_{\mathrm{Region}}$ | 0.030 | 0.013 | 2.37 | | | |

**Response: Bee Gamma diversity**

| | Estimate | Std. Error | Z value | Pseudo-$R^2$ | AIC | $\Delta\mathrm{AIC}_{\mathrm{null}}$ |
|---|---|---|---|---|---|---|
| (Intercept) | 3.476 | 0.042 | 83.73 | 0.611 | 451.1 | 25.5 |
| MAT | 0.201 | 0.044 | 4.52 | | | |
| MAP | -0.014 | 0.048 | -0.30 | | | |
| MAT:MAP | -0.134 | 0.036 | -3.71 | | | |

**Response: Hymenoptera Gamma diversity**

| | Estimate | Std. Error | Z value | Pseudo-$R^2$ | AIC | $\Delta\mathrm{AIC}_{\mathrm{null}}$ |
|---|---|---|---|---|---|---|
| (Intercept) | 5.310 | 0.020 | 266.41 | 0.131 | 588.5 | 3.2 |
| $\mathrm{For}_{\mathrm{Region}}$ | 0.047 | 0.020 | 2.36 | | | |

**Response: Syrphid Gamma diversity**

| | Estimate | Std. Error | Z value | Pseudo-$R^2$ | AIC | $\Delta\mathrm{AIC}_{\mathrm{null}}$ |
|---|---|---|---|---|---|---|
| (Intercept) | 3.429 | 0.023 | 147.26 | 0.299 | 374.7 | 11.7 |
| MAP | 0.083 | 0.022 | 3.78 | | | |

**Response: Diptera Gamma diversity**

| | Estimate | Std. Error | Z value | Pseudo-$R^2$ | AIC | $\Delta\mathrm{AIC}_{\mathrm{null}}$ |
|---|---|---|---|---|---|---|
| (Intercept) | 5.939 | 0.012 | 494.99 | 0.322 | 603.8 | 12.0 |
| MAP | 0.048 | 0.012 | 3.98 | | | |

**Response: Butterfly Gamma diversity**

| | Estimate | Std. Error | Z value | Pseudo-$R^2$ | AIC | $\Delta\mathrm{AIC}_{\mathrm{null}}$ |
|---|---|---|---|---|---|---|
| (Intercept) | 2.815 | 0.043 | 66.11 | 0.395 | 370.3 | 7.8 |
| MAT | -0.009 | 0.044 | -0.20 | | | |
| MAP | -0.097 | 0.050 | -1.93 | | | |
| $\mathrm{For}_{\mathrm{Region}}$ | -0.006 | 0.038 | -0.14 | | | |
| MAT:MAP | -0.180 | 0.052 | -3.43 | | | |
| MAT:$\mathrm{For}_{\mathrm{Region}}$ | 0.215 | 0.051 | 4.24 | | | |

**Response: Moth Gamma diversity**

| | Estimate | Std. Error | Z value | Pseudo-$R^2$ | AIC | $\Delta\mathrm{AIC}_{\mathrm{null}}$ |
|---|---|---|---|---|---|---|
| (Intercept) | 4.574 | 0.023 | 203.24 | 0.340 | 514.1 | 13.0 |
| MAP | -0.096 | 0.023 | -4.14 | | | |

**Response: Beetle Gamma diversity**

| | Estimate | Std. Error | Z value | Pseudo-$R^2$ | AIC | $\Delta\mathrm{AIC}_{\mathrm{null}}$ |
|---|---|---|---|---|---|---|
| (Intercept) | 3.644 | 0.024 | 152.22 | 0.307 | 412.0 | 9.2 |
| MAT | 0.066 | 0.025 | 2.66 | | | |
| $\mathrm{For}_{\mathrm{Region}}$ | 0.079 | 0.024 | 3.25 | | | |

**Table S5. Summary tables of the best gamma diversity models (n = 60).** Gamma diversity models were analyzed with generalized linear models (GLMs) with a Poisson or a negative binomial error distribution when Poisson models showed overdispersion. $\Delta\mathrm{AIC}_{\mathrm{null}}$ indicate the difference in AIC between the best model and the null model.

**Response: Pollinator Beta diversity**

| | Estimate | Std. Error | t value | $R^2$/adj. $R^2$ | AIC | $\Delta AIC_{null}$ |
|---|---|---|---|---|---|---|
| (Intercept) | 0.707 | 0.005 | 156.66 | 0.418/0.364 | -239.3 | 22.5 |
| MAT | -0.009 | 0.005 | -1.79 | | | |
| MAP | 0.003 | 0.005 | 0.50 | | | |
| $For_{Region}$ | 0.009 | 0.004 | 2.18 | | | |
| Flower β | 0.017 | 0.004 | 4.12 | | | |
| MAT:MAP | 0.019 | 0.004 | 4.49 | | | |

**Response: Bee Beta diversity**

| | Estimate | Std. Error | t value | $R^2$/adj. $R^2$ | AIC | $\Delta AIC_{null}$ |
|---|---|---|---|---|---|---|
| (Intercept) | 0.800 | 0.009 | 88.800 | 0.297/0.259 | -153.7 | 15.1 |
| MAT | -0.017 | 0.009 | -1.83 | | | |
| $Urb_{Region}$ | 0.009 | 0.013 | 0.70 | | | |
| $MAT:Urb_{Region}$ | -0.038 | 0.011 | -3.39 | | | |

**Response: Hymenoptera Beta diversity**

| | Estimate | Std. Error | t value | $R^2$/adj. $R^2$ | AIC | $\Delta AIC_{null}$ |
|---|---|---|---|---|---|---|
| (Intercept) | 0.775 | 0.005 | 152.51 | 0.243/0.216 | -213.0 | 12.7 |
| MAT | -0.018 | 0.005 | -3.57 | | | |
| Flower β | 0.012 | 0.005 | 2.29 | | | |

**Response: Syrphid Beta diversity**

| | Estimate | Std. Error | t value | $R^2$/adj. $R^2$ | AIC | $\Delta AIC_{null}$ |
|---|---|---|---|---|---|---|
| (Intercept) | 0.628 | 0.009 | 70.33 | 0.205/0.178 | -145.3 | 9.8 |
| MAT | 0.025 | 0.009 | 2.81 | | | |
| Flower β | 0.023 | 0.009 | 2.52 | | | |

**Response: Diptera Beta diversity**

| | Estimate | Std. Error | t value | $R^2$/adj. $R^2$ | AIC | $\Delta AIC_{null}$ |
|---|---|---|---|---|---|---|
| (Intercept) | 0.639 | 0.005 | 123.86 | 0.376/0.319 | -223.1 | 18.3 |
| MAT | -0.007 | 0.005 | -1.34 | | | |
| MAP | 0.009 | 0.006 | 1.53 | | | |
| $For_{Region}$ | 0.011 | 0.005 | 2.21 | | | |
| Flower β | 0.020 | 0.005 | 4.14 | | | |
| MAT:MAP | 0.016 | 0.005 | 3.40 | | | |

**Response: Butterfly Beta diversity**

| | Estimate | Std. Error | t value | $R^2$/adj. $R^2$ | AIC | $\Delta AIC_{null}$ |
|---|---|---|---|---|---|---|
| (Intercept) | 0.7546 | 0.013 | 58.81 | 0.289/0.251 | -100.9 | 14.5 |
| MAT | -0.038 | 0.013 | -2.85 | | | |
| $Agr_{Region}$ | -0.036 | 0.013 | -2.72 | | | |
| Flower β | 0.026 | 0.013 | 2.00 | | | |

**Response: Moth Beta diversity**

| | Estimate | Std. Error | t value | $R^2$/adj. $R^2$ | AIC | $\Delta AIC_{null}$ |
|---|---|---|---|---|---|---|
| (Intercept) | 0.788 | 0.005 | 145.25 | 0.467/0.417 | -217.1 | 27.7 |
| MAT | -0.014 | 0.006 | -2.42 | | | |
| MAP | 0.014 | 0.007 | 2.00 | | | |
| $Agr_{Region}$ | 0.012 | 0.006 | -2.16 | | | |
| Flower β | 0.018 | 0.005 | 3.69 | | | |
| MAT:MAP | 0.013 | 0.005 | 2.63 | | | |

**Response: Beetle Beta diversity**

| | Estimate | Std. Error | t value | $R^2$/adj. $R^2$ | AIC | $\Delta AIC_{null}$ |
|---|---|---|---|---|---|---|
| (Intercept) | 0.792 | 0.008 | 103.02 | 0.299/0.248 | -163.5 | 13.3 |
| MAT | -0.006 | 0.008 | -0.76 | | | |
| $For_{Region}$ | 0.012 | 0.008 | 1.46 | | | |
| Flower β | 0.028 | 0.008 | 3.62 | | | |
| $MAT:For_{Region}$ | 0.020 | 0.007 | 2.77 | | | |

**Table S6. Summary tables of the best intra-regional beta diversity models (n = 60).** Beta diversity models were analyzed with simple linear models (LMs). $\Delta AIC_{null}$ indicate the difference in AIC between the best model and the null model.

**Response: Pollinator Alpha diversity**

| | Estimate | Std. Error | Z value | Marg./Cond. $R^2$ | AIC | $\Delta\mathrm{AIC}_{\mathrm{null}}$ |
|---|---|---|---|---|---|---|
| (Intercept) | 6.204 | 0.026 | 237.49 | 0.335/0.403 | 2022.1 | 62.1 |
| $\mathrm{HabGra}_{\mathrm{Local}}$ | -0.220 | 0.036 | -6.07 | | | |
| $\mathrm{HabAgr}_{\mathrm{Local}}$ | -0.329 | 0.037 | -8.93 | | | |
| $\mathrm{HabUrb}_{\mathrm{Local}}$ | -0.216 | 0.047 | -4.55 | | | |
| Flower α | 0.063 | 0.017 | 3.67 | | | |

**Response: Bee Alpha diversity**

| | Estimate | Std. Error | Z value | Marg./Cond. $R^2$ | AIC | $\Delta\mathrm{AIC}_{\mathrm{null}}$ |
|---|---|---|---|---|---|---|
| (Intercept) | 3.369 | 0.081 | 41.46 | 0.370/0.487 | 1345.8 | 59.8 |
| $\mathrm{T}_{\mathrm{Local}}$ | 0.162 | 0.051 | 3.21 | | | |
| $\mathrm{HabGra}_{\mathrm{Local}}$ | -0.413 | 0.109 | -3.77 | | | |
| $\mathrm{HabAgr}_{\mathrm{Local}}$ | -0.636 | 0.114 | -5.57 | | | |
| $\mathrm{HabUrb}_{\mathrm{Local}}$ | -0.316 | 0.162 | -1.95 | | | |
| $\mathrm{Urb}_{\mathrm{Landsc}}$ | 0.154 | 0.055 | 2.81 | | | |
| Flower α | 0.173 | 0.056 | 3.12 | | | |

**Response: Hymenoptera Alpha diversity**

| | Estimate | Std. Error | Z value | Marg./Cond. $R^2$ | AIC | $\Delta\mathrm{AIC}_{\mathrm{null}}$ |
|---|---|---|---|---|---|---|
| (Intercept) | 4.817 | 0.040 | 120.09 | 0.301/0.399 | 1653.0 | 54.8 |
| $\mathrm{HabGra}_{\mathrm{Local}}$ | -0.362 | 0.055 | -6.61 | | | |
| $\mathrm{HabAgr}_{\mathrm{Local}}$ | -0.450 | 0.056 | -8.05 | | | |
| $\mathrm{HabUrb}_{\mathrm{Local}}$ | -0.329 | 0.073 | -4.53 | | | |
| Flower α | 0.083 | 0.027 | 3.12 | | | |

**Response: Syrphid Alpha diversity**

| | Estimate | Std. Error | Z value | Marg./Cond. $R^2$ | AIC | $\Delta\mathrm{AIC}_{\mathrm{null}}$ |
|---|---|---|---|---|---|---|
| (Intercept) | 2.994 | 0.040 | 73.96 | 0.175/0.254 | 1072.4 | 22.8 |
| $\mathrm{T}_{\mathrm{Local}}$ | -0.059 | 0.025 | -2.33 | | | |
| $\mathrm{HabGra}_{\mathrm{Local}}$ | -0.193 | 0.057 | -3.40 | | | |
| $\mathrm{HabAgr}_{\mathrm{Local}}$ | -0.235 | 0.061 | -3.87 | | | |
| $\mathrm{HabUrb}_{\mathrm{Local}}$ | -0.208 | 0.075 | -2.75 | | | |
| Flower α | 0.105 | 0.028 | 3.78 | | | |

**Response: Diptera Alpha diversity**

| | Estimate | Std. Error | Z value | Marg./Cond. $R^2$ | AIC | $\Delta\mathrm{AIC}_{\mathrm{null}}$ |
|---|---|---|---|---|---|---|
| (Intercept) | 5.474 | 0.023 | 235.58 | 0.292/0.329 | 1755.8 | 51.2 |
| $\mathrm{HabGra}_{\mathrm{Local}}$ | -0.141 | 0.033 | -4.28 | | | |
| $\mathrm{HabAgr}_{\mathrm{Local}}$ | -0.231 | 0.038 | -6.15 | | | |
| $\mathrm{HabUrb}_{\mathrm{Local}}$ | -0.094 | 0.036 | -2.58 | | | |
| $\mathrm{Agr}_{\mathrm{Landsc}}$ | -0.034 | 0.015 | -2.34 | | | |

**Response: Butterfly Alpha diversity**

| | Estimate | Std. Error | Z value | Marg./Cond. $R^2$ | AIC | $\Delta\mathrm{AIC}_{\mathrm{null}}$ |
|---|---|---|---|---|---|---|
| (Intercept) | 2.126 | 0.050 | 42.84 | 0.073/0.517 | 1021.0 | 14.5 |
| $\mathrm{EdgeD}_{\mathrm{Landsc}}$ | 0.069 | 0.031 | 2.27 | | | |
| Flower α | 0.102 | 0.031 | 3.26 | | | |

**Response: Moth Alpha diversity**

| | Estimate | Std. Error | Z value | Marg./Cond. $R^2$ | AIC | $\Delta\mathrm{AIC}_{\mathrm{null}}$ |
|---|---|---|---|---|---|---|
| (Intercept) | 4.052 | 0.045 | 89.95 | 0.248/0.396 | 1419.0 | 38.8 |
| $\mathrm{T}_{\mathrm{Local}}$ | 0.065 | 0.028 | 2.31 | | | |
| $\mathrm{HabGra}_{\mathrm{Local}}$ | -0.147 | 0.065 | -2.29 | | | |
| $\mathrm{HabAgr}_{\mathrm{Local}}$ | -0.395 | 0.064 | -6.21 | | | |
| $\mathrm{HabUrb}_{\mathrm{Local}}$ | -0.315 | 0.079 | -4.01 | | | |
| $\mathrm{Gra}_{\mathrm{Landsc}}$ | -0.351 | 0.161 | -2.19 | | | |
| Flower α | 0.062 | 0.030 | 2.11 | | | |

**Response: Beetle Alpha diversity**

| | Estimate | Std. Error | Z value | Marg./Cond. $R^2$ | AIC | $\Delta\mathrm{AIC}_{\mathrm{null}}$ |
|---|---|---|---|---|---|---|
| (Intercept) | 3.078 | 0.046 | 67.08 | 0.187/0.327 | 1114.7 | 30.2 |
| $\mathrm{HabGra}_{\mathrm{Local}}$ | -0.294 | 0.063 | -4.64 | | | |

| | | | |
|---|---|---|---|
| HabAgr$_{Local}$ | -0.386 | 0.066 | -5.86 |
| HabUrb$_{Local}$ | -0.316 | 0.084 | -3.76 |
| Flower α | 0.088 | 0.031 | 2.81 |

**Table S7. Summary tables of the best alpha diversity models (n = 175).** Alpha diversity models were analyzed with generalized linear mixed models (GLMMs, glmmTMB function **(*73*)**), with a Poisson or a negative binomial error distribution and the term ‘region’ included as random effect. $\Delta AIC_{null}$ indicate the difference in AIC between the best model and the null model.

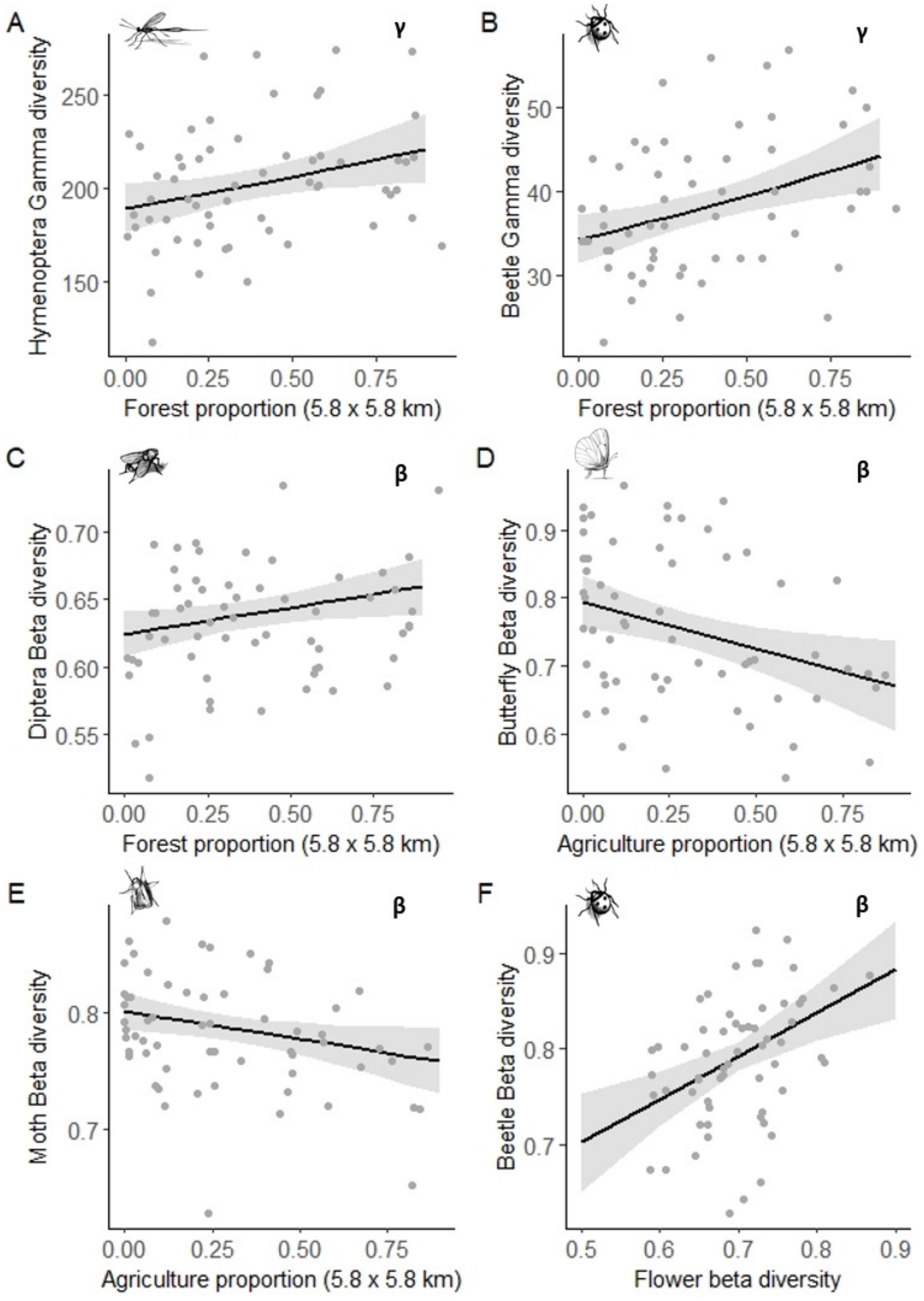

**Fig. S3. Response of the gamma and beta diversity of different pollinator taxa to land-use variables**. Graphs show predictions of the relationships selected in the best models between gamma diversity (n = 60) and **(A, B)** the proportion of forest in the region, and between beta diversity (n = 60) and **(C)** the proportion of forest and **(D, E)** agriculture in the region, and **(F)** flowering-plant beta diversity.

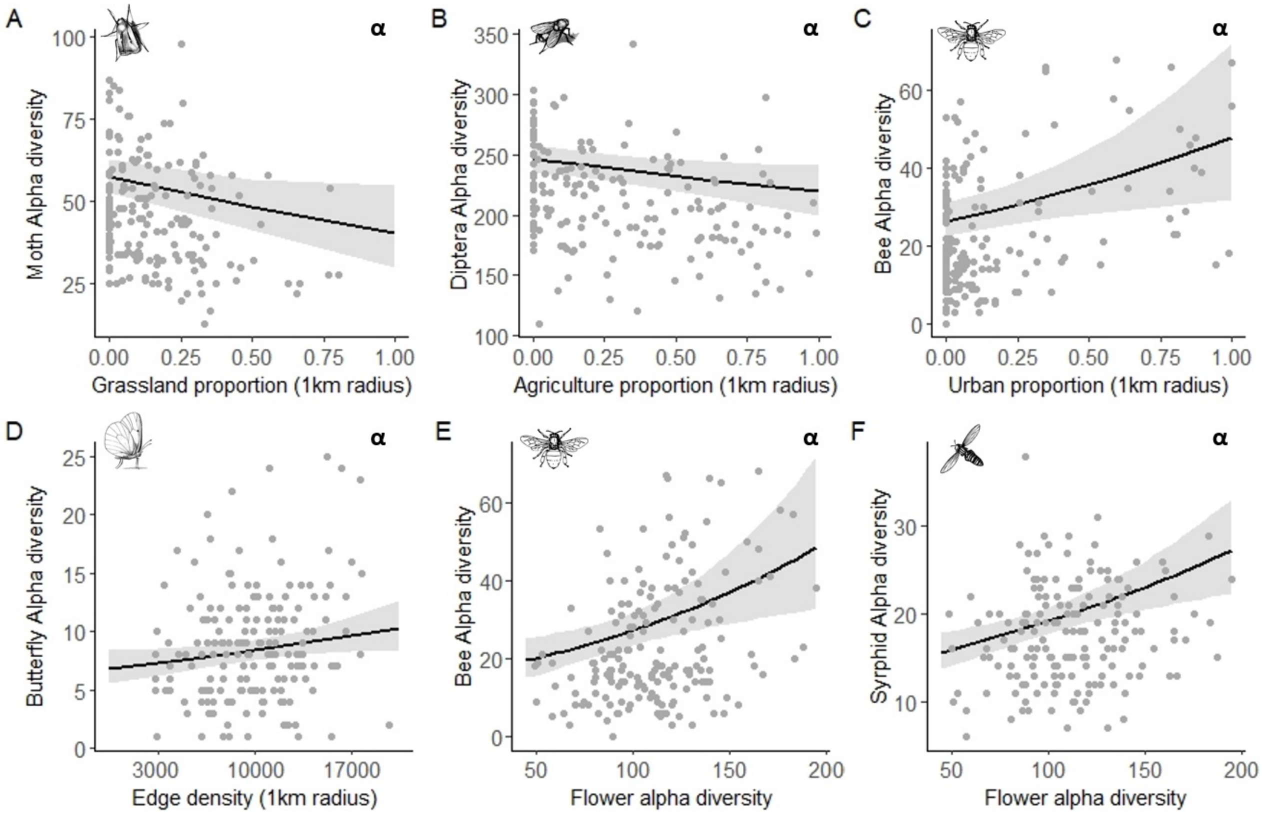

**Fig. S4. Response of the alpha diversity of different pollinator taxa to land-use variables.** Graphs show predictions of the relationships selected in the best models between alpha diversity (n = 175) and **(A)** the proportion of grassland**, (B)** agriculture and **(C)** urban in the landscape, **(D)** edge density, and **(E, F)** flowering-plant alpha diversity.

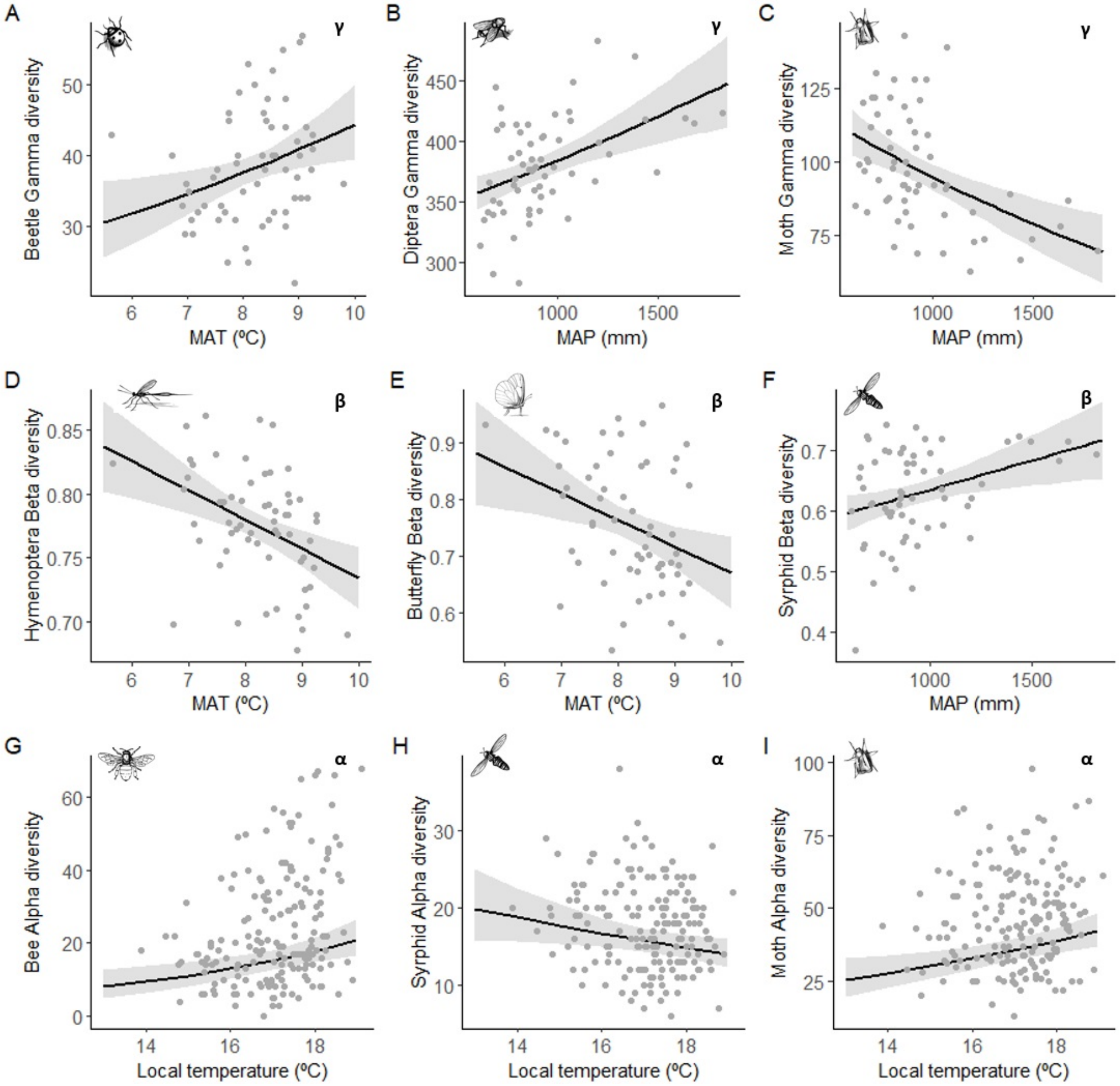

**Fig. S5. Response of the gamma, beta and alpha diversity of different pollinator taxa to climate variables.** Graphs show predictions of the relationships selected in the best models between gamma diversity (n = 60) and **(A)** multi-annual mean temperature and **(B, C)** precipitation, between beta diversity (n = 60) and **(D, E)** multi-annual mean temperature and **(F)** precipitation, and between alpha diversity (n = 175) and **(G-I)** local temperature.

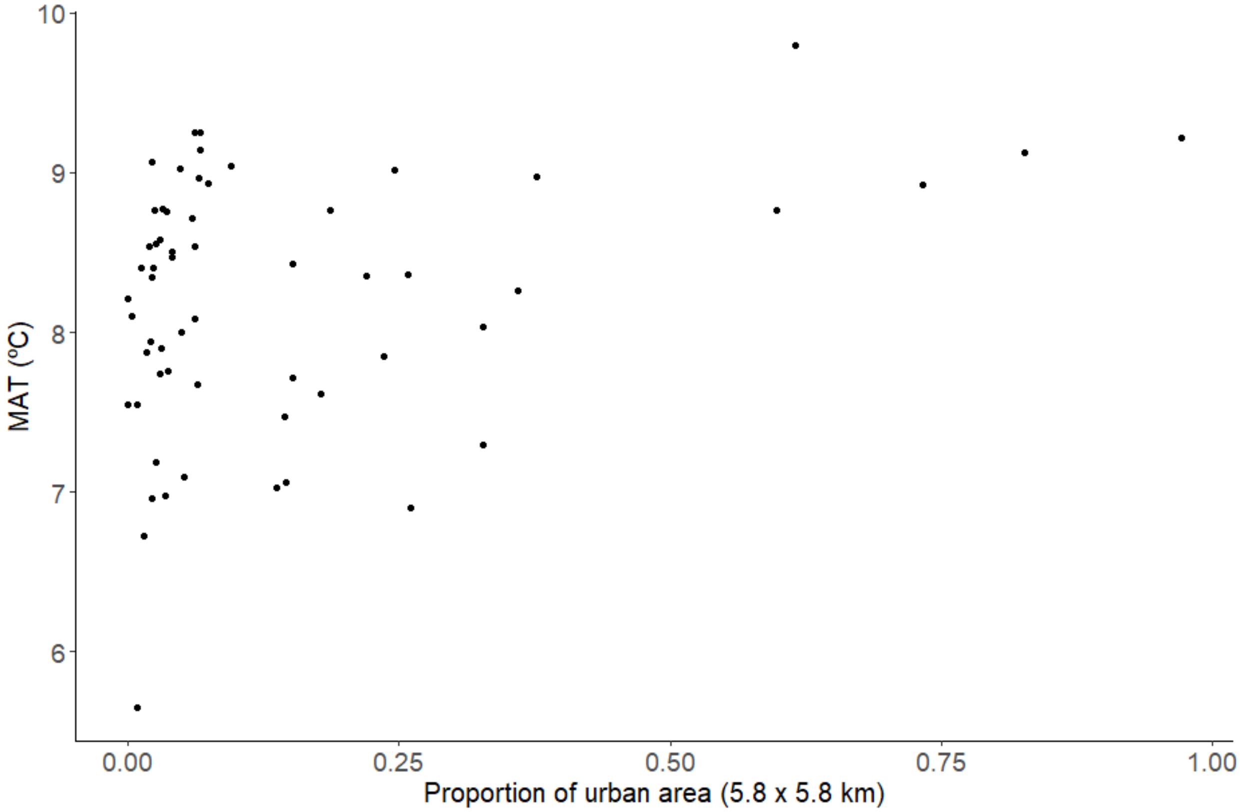

**Fig. S6. Relationship between multi-annual mean temperature (MAT) and the proportion of urban area in the region (n = 60).** Since we are lacking regions with a high proportion of urban and low temperatures, we must be careful with the interpretation of the interaction between multi-annual mean temperature and the proportion of urban area. If only the proportion of urban area is included in the model, highly urbanized regions show more homogeneous communities (LM, $F_{1,58} = 9.30$, p = 0.003).

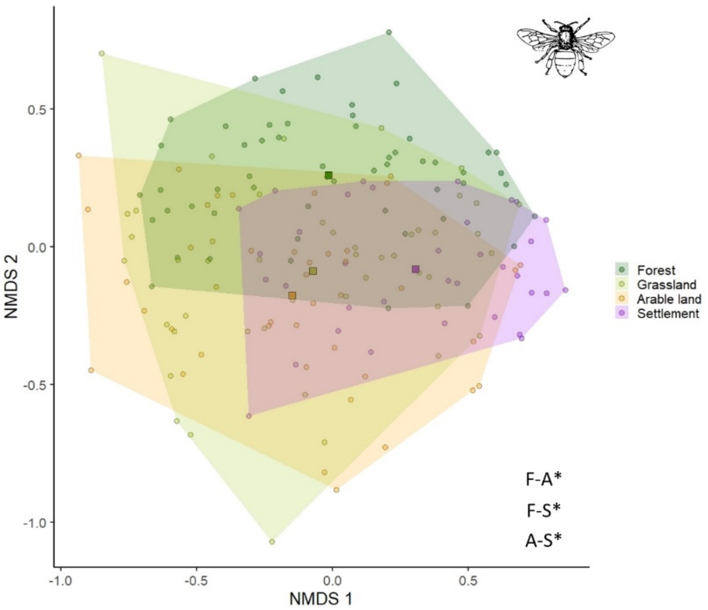

**Fig. S7. Overlap in bee species composition among the four habitat types.** The ordination diagram is based on non-metric multidimensional scaling (NMDS) of Jaccards dissimilarity matrices. The position of plots (dots, n = 179) in the NMDS space represents the similarity in bee community composition in relation to other plots: the closer the dots, the higher the proportion of species shared. Squares represent centroids of the four habitat types and polygons delimit the NMDS space occupied by plots with the same local habitat type. Significant differences in species composition between habitat types based on permutational multivariance analysis of variance (adonis function in the vegan package **(*72*)**) are shown in the downer right corner. Forest: n = 54, grassland: n = 46, arable land: n = 41, settlement: n = 34. Significance levels: ***p < 0.001, **p < 0.01, *p < 0.05. The diagram shows a big overlap of grassland communities with the communities of other habitat types, especially forest habitats (see Table S8). This is not surprising, since all our plots were located on grassy strips. The high bee richness found in forest habitats can be explained by the fact that forest clearings may offer resources that are typical for both forest and grassland habitats: bee communities in forest habitats have most species in common with grasslands, and fewer with arable land and settlements; and more importantly, they have a higher number of non-overlapping plots compared to the other habitat types, which highlights the singularity of some bee communities of forest habitats.

**Response: Bee species composition in forest and grassland habitats**

| | Df | SumsOfSqs | MeanSqs | F.Model | R2 | Pr (>F) |
|---|---|---|---|---|---|---|
| Habitat_FG | 1 | 0.329 | 0.329 | 1.633 | 0.016 | 0.119 |
| Residuals | 99 | 19.923 | 0.201 | | 0.984 | |
| Total | 100 | 20.251 | | | 1.000 | |

**Response: Bee species composition in forest and arable habitats**

| | Df | SumsOfSqs | MeanSqs | F.Model | R2 | Pr (>F) |
|---|---|---|---|---|---|---|
| Habitat_FA | 1 | 0.556 | 0.556 | 2.818 | 0.029 | 0.015 * |
| Residuals | 96 | 18.938 | 0.197 | | 0.971 | |
| Total | 97 | 19.494 | | | 1.000 | |

**Response: Bee species composition in grassland and arable habitats**

| | Df | SumsOfSqs | MeanSqs | F.Model | R2 | Pr (>F) |
|---|---|---|---|---|---|---|
| Habitat_GA | 1 | 0.357 | 0.357 | 1.753 | 0.020 | 0.082 |
| Residuals | 87 | 17.699 | 0.203 | | 0.980 | |
| Total | 88 | 18.056 | | | 1.000 | |

**Response: Bee species composition in settlements and forest habitats**

| | Df | SumsOfSqs | MeanSqs | F.Model | R2 | Pr (>F) |
|---|---|---|---|---|---|---|
| Habitat_SF | 1 | 0.498 | 0.498 | 2.466 | 0.027 | 0.028 * |
| Residuals | 88 | 17.768 | 0.202 | | 0.973 | |
| Total | 89 | 18.266 | | | 1.000 | |

**Response: Bee species composition in settlements and grassland habitats**

| | Df | SumsOfSqs | MeanSqs | F.Model | R2 | Pr (>F) |
|---|---|---|---|---|---|---|
| Habitat_SG | 1 | 0.413 | 0.412 | 1.946 | 0.024 | 0.054 |
| Residuals | 79 | 16.721 | 0.212 | | 0.976 | |
| Total | 80 | 17.133 | | | 1.000 | |

**Response: Bee species composition in settlements and arable habitats**

| | Df | SumsOfSqs | MeanSqs | F.Model | R2 | Pr (>F) |
|---|---|---|---|---|---|---|
| Habitat_SA | 1 | 0.565 | 0.565 | 2.730 | 0.035 | 0.014 * |
| Residuals | 76 | 15.729 | 0.207 | | 0.9653 | |
| Total | 77 | 16.294 | | | 1.000 | |

**Table S8. Results of permutational multivariate analysis of variance (PERMANOVA) to analyse the difference in bee species composition among habitat types.** PERMANOVAs where performed with the adonis function (vegan package **(*72*)**), using Jaccard distances and the standard number of permutations (n = 999). Prior to analysis, we checked the homogeneity of variance among habitat types with the betadisper function (F = 0.22, P = 0.881).

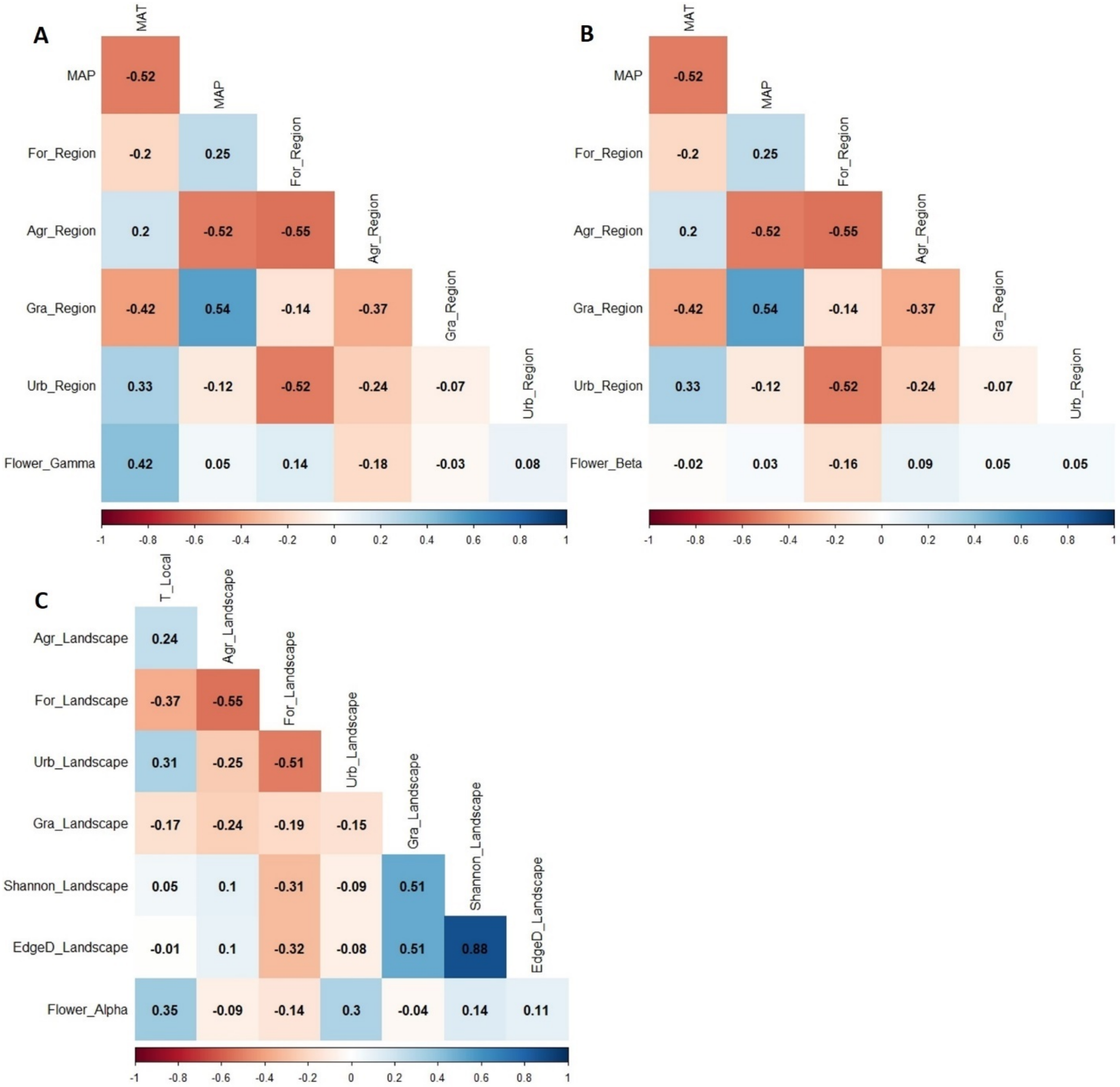

**Fig. S8. Correlation plots of the variables used in (A) gamma, (B) beta, and (C) alpha diversity models.** Positive correlations are displayed in blue and negative correlations in red. Color intensity is proportional to the correlation coefficients. Figures are produced with the corrplot package (***84***).

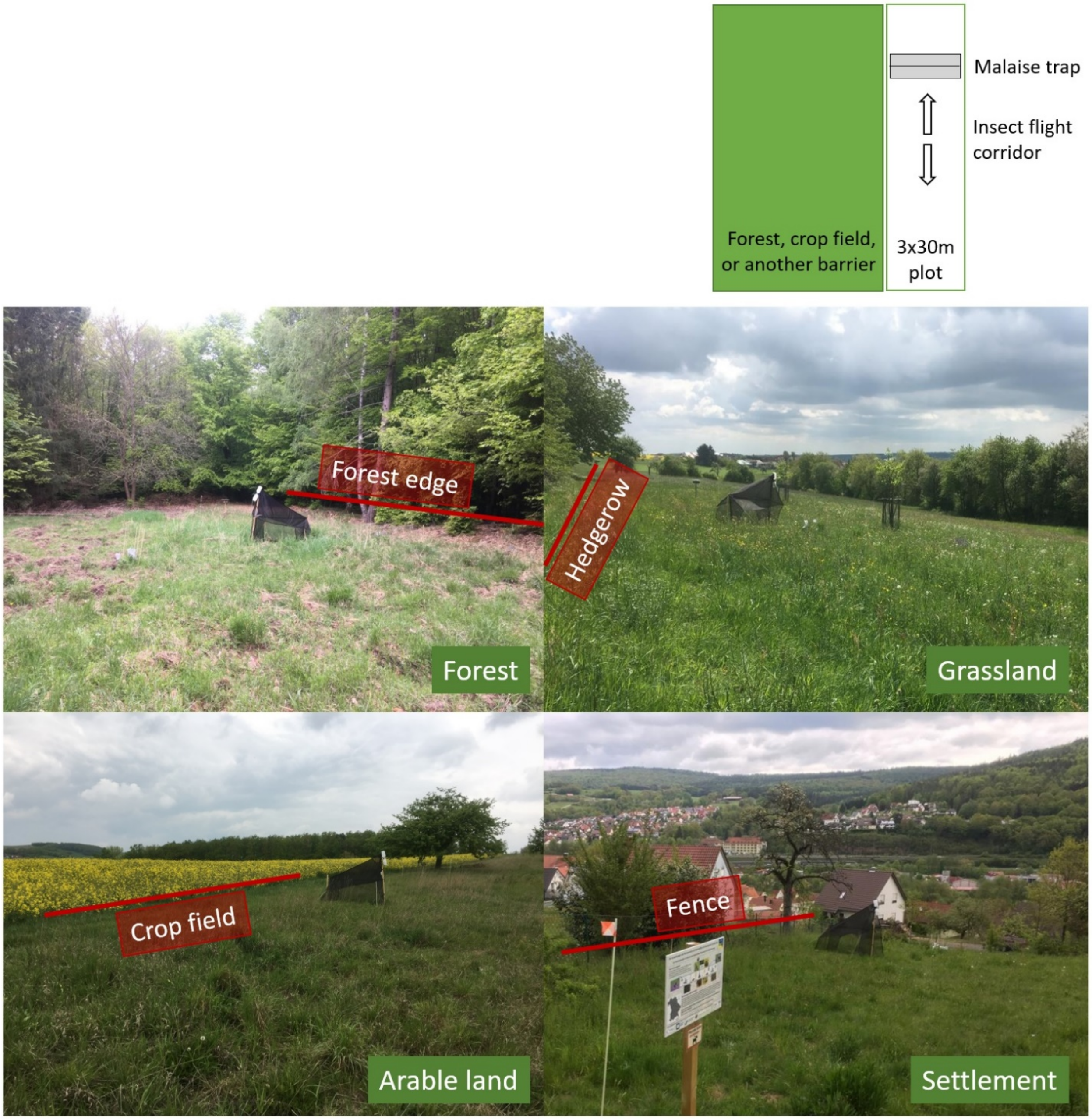

**Fig. S9. Malaise trap placement within study plots.** To ensure the maximum catchability of the traps in the different habitat types, we oriented traps toward insect corridors, i.e. perpendicular to barriers such as forest edges, hedgerows, crop fields, fences, or walls. When no barrier was present, traps were placed randomly, but in protected places rather than in open and windy areas (***85***). When establishing the traps, we made sure that the lowest part of the net touched the ground, to prevent low-flying insects escaping the trap, and we maintained the surrounding vegetation regularly to ensure that the entrance was not blocked by grass.

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