**Figure S1: Initial belowground plant model**

The four Soil factors are combined measures of 12 soil parameters obtained by a PCA (see Table S4 above). "Soil Het." is the soil heterogeneity factor 5 (from PCA on within-plot CV in soil parameters), which was found to be significant in the general linear model for belowground biomass (see main text). The "Div*Het Interaction" is the interaction of interest between diversity and soil heterogeneity. Plant composition 1 and 2 are the NMDS axes from the species composition ordinations in Supplementary Results 3 above.

| Parameters | Cmin | AIC | BCC |
|---|---|---|---|
| 45 | 37.136 | 127.136 | 268.565 |

**Final belowground plant model (Fig. 3 A)**

| Parameters | Cmin | AIC | BCC |
|---|---|---|---|
| 34 | 43.869 | 111.869 | 218.726 |
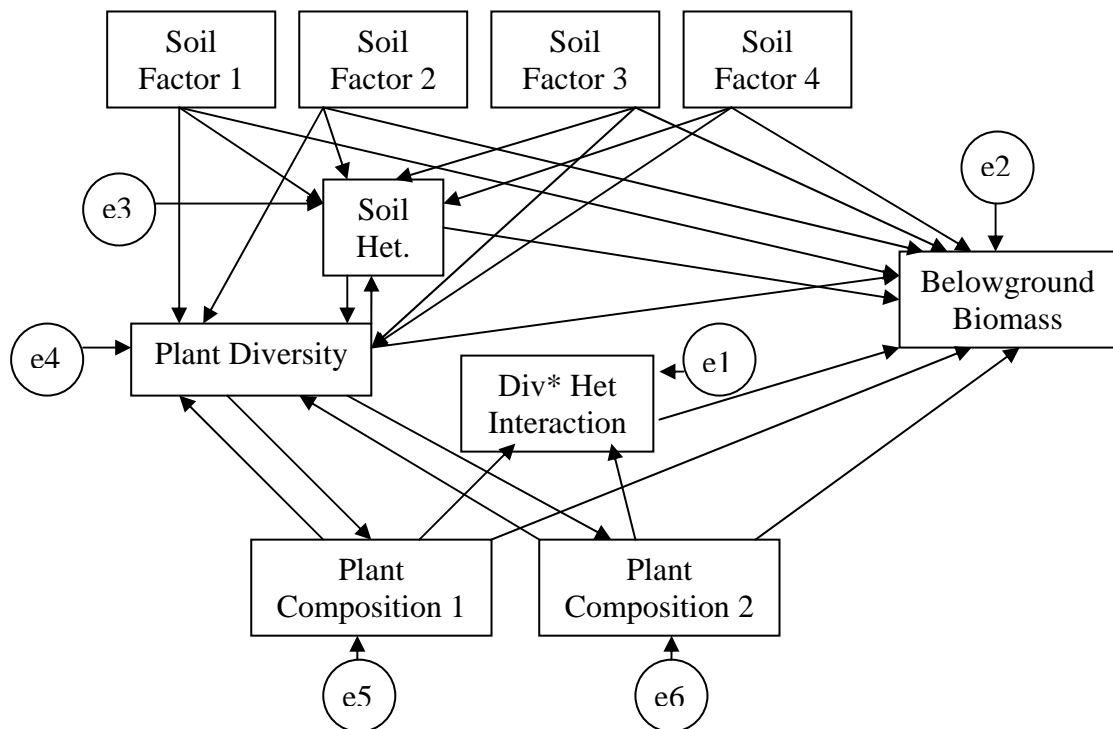
**Figure S2: Initial aboveground plant model**

| Parameters | Cmin | AIC | BCC |
|---|---|---|---|
| 45 | 37.140 | 127.140 | 268.568 |

**Final aboveground plant model (Fig. 3 B)**

| Parameters | Cmin | AIC | BCC |
|---|---|---|---|
| 29 | 52.647 | 110.647 | 201.790 |

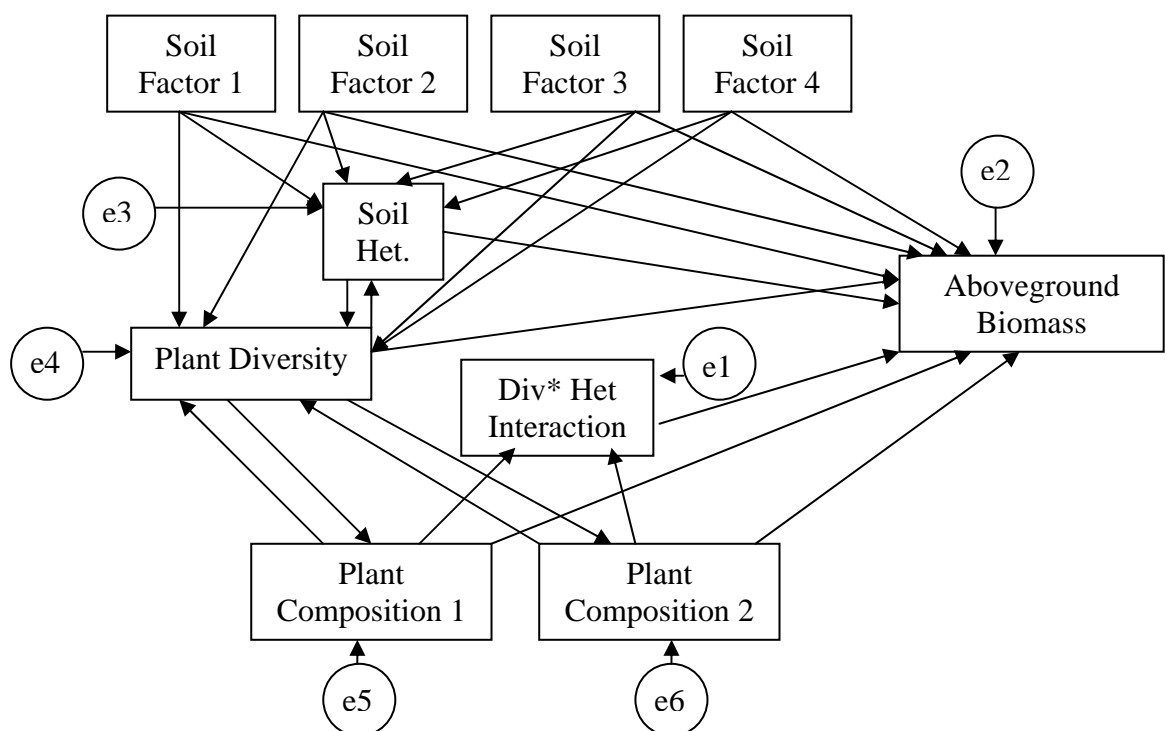Note: model was unstable

**Initial Model:**

**Figure S3: Initial parasitoid model**
"Host Het." is the heterogeneity in host abundance (within-plot CV in abundance).
The "Div*Het Interaction" is the interaction of interest between parasitoid diversity
and heterogeneity in host abundance. Plant composition 1 and 2 are the NMDS axes
from the species composition ordinations in Supplementary Results 3 above. The
proportion parasitized is arcsin square root transformed, as in the GLM in the main
text.


Minimisation was unsuccessful, reliable parameter estimates could not be obtained.

**Final parasitoid model (Fig. 3 C)**

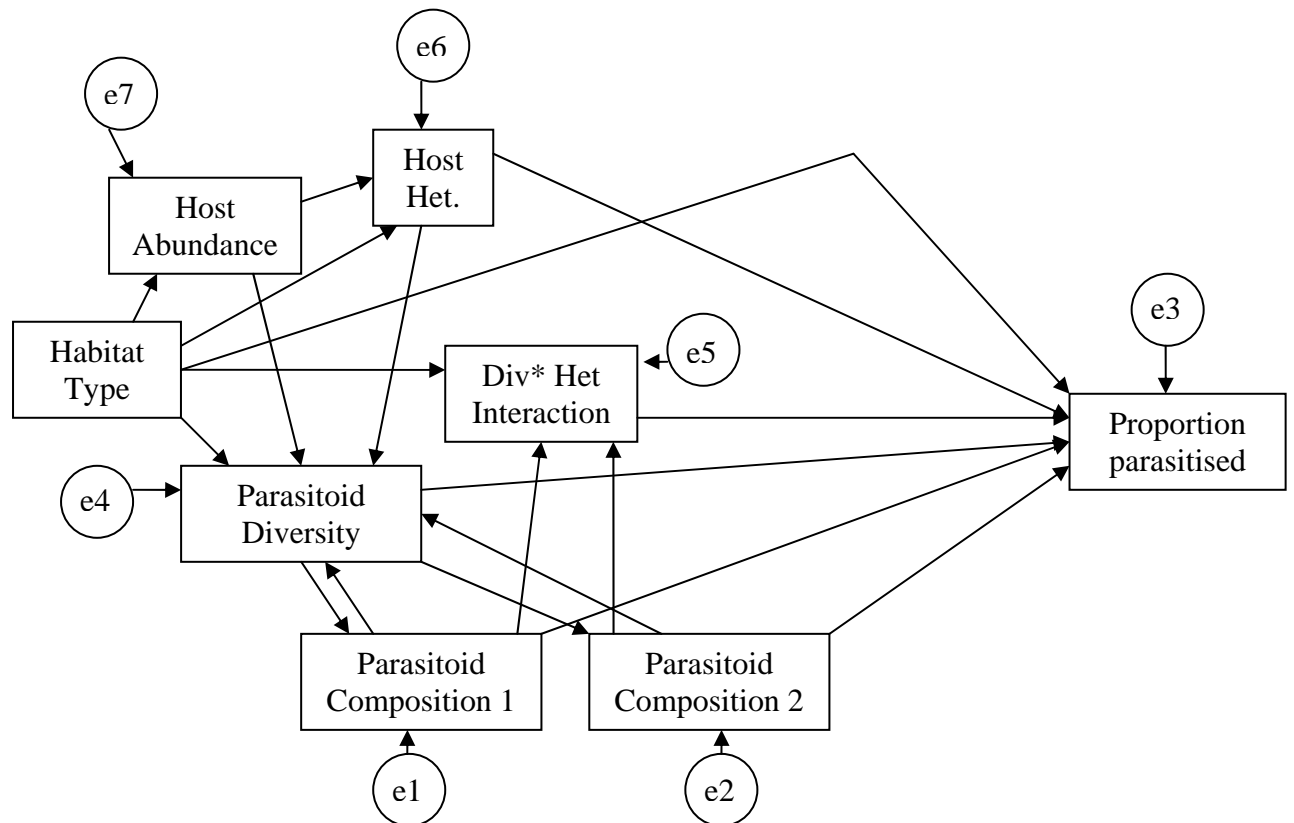| Parameters | Cmin | AIC | BCC |
|---|---|---|---|
| 24 | 48.707 | 96.707 | 108.076 |


**Initial Model:**

**Figure S4: Initial pollinator model**
 "Flower Het." is the heterogeneity in abundance of coffee flowers (between-shrub
CV in abundance). The "Div*Het Interaction" is the interaction of interest between
pollinator diversity and heterogeneity in flower abundance. Pollinator composition 1-
3 are the NMDS axes from the species composition ordinations in Supplementary
Results 3 above. "Pollination benefit" was quantified as the proportion of flowers that
set fruit from the open pollination treatment, minus the proportion that set fruit in the
bagged control treatment (as in the GLM in the main text).

| Parameters | Cmin | AIC | BCC |
|---|---|---|---|
| 36 | 753.599 | 825.599 | 871.885 |

**Final pollinator model (Fig. 3 D)**

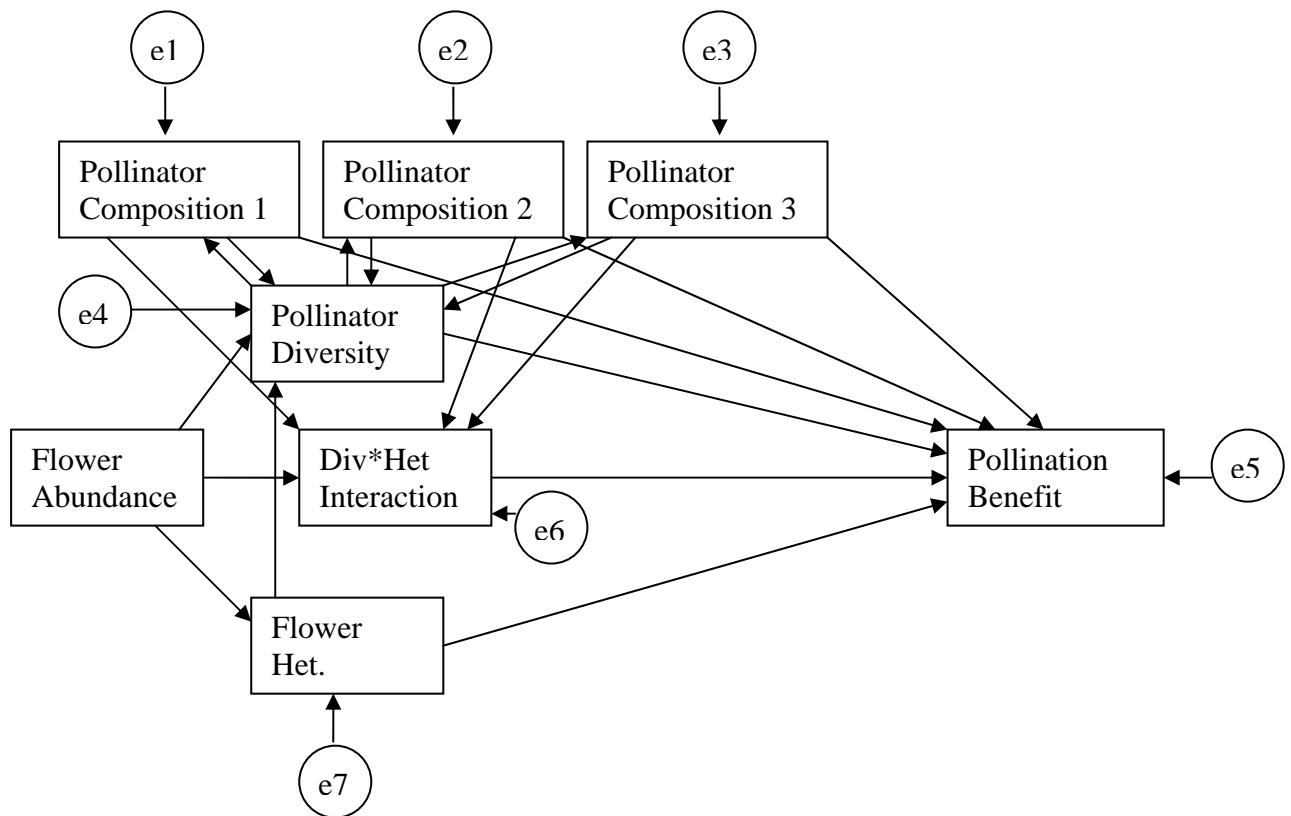| Parameters | Cmin | AIC | BCC |
|---|---|---|---|
| 22 | 768.347 | 812.347 | 840.633 |

**Initial Model:**

**Table S1: PCA statistics.** 12 factors that explained all of the variance in heterogeneity of the original 12 soil parameters. Only factors 1-5 (in bold) were included in further analyses, as they had eigenvalues greater than 1 (i.e., the factor explained more variance than any one of the soil parameters). Heterogeneity of the soil variables was defined as the within-site coefficient of variation in the value/concentration of the variable.

| Factor number | Eigenvalue | % Total variance | Cumulative eigenvalue | Cumulative % variance |
|---|---|---|---|---|
| **1** | **3.294631** | **27.45526** | **3.29463** | **27.4553** |
| **2** | **2.210440** | **18.42034** | **5.50507** | **45.8756** |
| **3** | **1.724824** | **14.37353** | **7.22990** | **60.2491** |
| **4** | **1.432895** | **11.94079** | **8.66279** | **72.1899** |
| **5** | **1.048067** | **8.73389** | **9.71086** | **80.9238** |
| 6 | 0.687185 | 5.72654 | 10.39804 | 86.6504 |
| 7 | 0.669933 | 5.58278 | 11.06798 | 92.2331 |
| 8 | 0.444657 | 3.70547 | 11.51263 | 95.9386 |
| 9 | 0.370145 | 3.08454 | 11.88278 | 99.0231 |
| 10 | 0.087127 | 0.72606 | 11.96990 | 99.7492 |
| 11 | 0.022787 | 0.18989 | 11.99269 | 99.9391 |
| 12 | 0.007310 | 0.06091 | 12.00000 | 100.0000 |

**Table S10: Total effects for final parasitoid model**

| | Host Abundance | Parasitoid composition 2 | Parasitoid diversity | Parasitoid composition 1 | Div*Het. interaction |
|---|---|---|---|---|---|
| Host Abundance | .000 | .000 | .000 | .000 | .000 |
| Parasitoid composition 2 | .000 | .000 | .000 | .000 | .000 |
| Parasitoid diversity | .002 | .000 | .000 | .000 | .000 |
| Parasitoid composition 1 | .001 | .000 | .543 | .000 | .000 |
| Div*Het. interaction | .000 | .000 | -.097 | -.179 | .000 |
| Proportion Parasitised | .000 | .073 | .091 | .123 | .082 |

**Table S11: Standardized total effects for final parasitoid model**

|  | Host Abundance | Parasitoid composition 2 | Parasitoid diversity | Parasitoid composition 1 | Div*Het. interaction |
|---|---|---|---|---|---|
| Host Abundance | .000 | .000 | .000 | .000 | .000 |
| Parasitoid composition 2 | .000 | .000 | .000 | .000 | .000 |
| Parasitoid diversity | .368 | .000 | .000 | .000 | .000 |
| Parasitoid composition 1 | .218 | .000 | .593 | .000 | .000 |
| Div*Het. interaction | -.088 | .000 | -.240 | -.405 | .000 |
| Proportion Parasitised | -.410 | .443 | .523 | .649 | .192 |

**Table S12: Total effects for final pollinator model**

| | Flower Abundance | Pollinator Diversity | Pollinator Composition 3 | Div*Het Interaction |
|---|---|---|---|---|
| Flower Het. | .366 | .000 | .000 | .000 |
| Pollinator Diversity | .000 | .000 | -2.951 | .000 |
| Pollinator Composition 3 | .000 | .000 | .000 | .000 |
| Div*Het Interaction | .000 | .000 | .000 | .000 |
| Pollination Benefit | .000 | .883 | -2.606 | .068 |

**Table S13: Standardized total effects for final pollinator model**

|  | Flower Abundance | Pollinator Diversity | Pollinator Composition 3 | Div*Het Interaction |
|---|---|---|---|---|
| Flower Het. | .386 | .000 | .000 | .000 |
| Pollinator Diversity | .000 | .000 | -.582 | .000 |
| Pollinator Composition 3 | .000 | .000 | .000 | .000 |
| Div*Het Interaction | .000 | .000 | .000 | .000 |
| Pollination Benefit | .000 | .327 | -.190 | .553 |

**Table S2: PCA factor loadings.** Correlation between the 5 PCA factors used in analyses and the original soil heterogeneity variables. Heterogeneity of the soil variables was defined as the within-site coefficient of variation (CV) in the value/concentration of the variable.

| Variable | Factor 1 | Factor 2 | Factor 3 | Factor 4 | Factor 5 |
|---|---|---|---|---|---|
| **CV(pH (H$_2$O))** | -0.673946 | -0.010276 | -0.395666 | -0.114985 | 0.070111 |
| **CV(NO$_3$)** | 0.083850 | 0.052005 | -0.608923 | 0.324529 | 0.680187 |
| **CV(NH$_4$)** | -0.031314 | -0.857229 | 0.282664 | 0.313409 | -0.199787 |
| **CV(Nmin)** | -0.037389 | -0.892460 | 0.179104 | 0.266419 | 0.137947 |
| **CV(N)** | -0.786310 | -0.015380 | 0.505209 | -0.215345 | 0.222465 |
| **CV(C)** | -0.432143 | 0.243452 | 0.690046 | -0.234347 | 0.440702 |
| **CV(C:N ratio)** | -0.773682 | -0.397617 | -0.208118 | -0.121152 | -0.084274 |
| **CV(Ca)** | -0.693500 | -0.154505 | -0.418682 | 0.145306 | -0.027421 |
| **CV(K)** | -0.523453 | 0.075792 | 0.095347 | 0.484505 | 0.180250 |
| **CV(Mg)** | -0.596703 | 0.026154 | -0.295180 | -0.415063 | -0.205115 |
| **CV(Na)** | 0.203792 | -0.459922 | -0.177725 | -0.667821 | 0.062921 |
| **CV(P)** | 0.524283 | -0.465695 | -0.087705 | -0.393777 | 0.437571 |

**Table S3:** Correlation coefficient (*r*) and significance level (*p*) for Pearson correlations between soil parameters and significant soil heterogeneity factor 5.

|  | pH (H$_2$O) | NO$_3$ | NH$_4$ | Nmin | N | C | C:N ratio | Ca | K | Mg | Na | P |
|---|---|---|---|---|---|---|---|---|---|---|---|---|
| *r* | .3904 | .1505 | -.0895 | .0184 | -.5151 | -.5812 | -.6534 | .0810 | -.0100 | .4629 | -.2069 | .6079 |
| *p* | p=.210 | p=.641 | p=.782 | p=.955 | p=.087 | p=.047 | p=.021 | p=.802 | p=.975 | p=.130 | p=.519 | p=.036 |

**Table S4: PCA statistics.** 12 factors that explained all of the variance in the absolute values of the 12 soil parameters (i.e., not variability as in Tables S1 and S2). Only factors 1-4 (in bold) were included in further analyses, as they had eigenvalues greater than 1 (i.e., the factor explained more variance than any one of the soil parameters).

| Factor number | Eigenvalue | % Total variance | Cumulative eigenvalue | Cumulative % variance |
|---|---|---|---|---|
| **1** | **4.513576** | **37.61313** | **4.51358** | **37.6131** |
| **2** | **2.021481** | **16.84567** | **6.53506** | **54.4588** |
| **3** | **1.653362** | **13.77801** | **8.18842** | **68.2368** |
| **4** | **1.558421** | **12.98685** | **9.74684** | **81.2237** |
| 5 | 0.837959 | 6.98299 | 10.58480 | 88.2067 |
| 6 | 0.554984 | 4.62487 | 11.13978 | 92.8315 |
| 7 | 0.469333 | 3.91111 | 11.60912 | 96.7426 |
| 8 | 0.261408 | 2.17840 | 11.87052 | 98.9210 |
| 9 | 0.088922 | 0.74102 | 11.95945 | 99.6621 |
| 10 | 0.037927 | 0.31606 | 11.99737 | 99.9781 |
| 11 | 0.001882 | 0.01569 | 11.99926 | 99.9938 |
| 12 | 0.000744 | 0.00620 | 12.00000 | 100.0000 |

**Table S5: PCA factor loadings.** Correlation between the 4 PCA factors used in SEM analyses and the original soil variables.

| Variable | Factor 1 | Factor 2 | Factor 3 | Factor 4 |
|---|---|---|---|---|
| pH (H2O) | 0.914468 | -0.013510 | -0.061760 | 0.041953 |
| NO3 | 0.452826 | -0.323251 | 0.384014 | 0.535364 |
| NH4 | 0.601412 | -0.449081 | -0.178362 | -0.552145 |
| Nmin | 0.729474 | -0.506839 | 0.068598 | -0.315550 |
| N | -0.551019 | -0.736764 | 0.057245 | 0.279442 |
| C | -0.611417 | -0.748733 | 0.180451 | 0.065063 |
| CN | -0.389071 | -0.357785 | 0.431301 | -0.525761 |
| Ca | 0.772261 | -0.245772 | -0.010219 | 0.128659 |
| K | 0.141837 | 0.273902 | 0.819518 | -0.278131 |
| Mg | 0.867384 | -0.201753 | -0.316961 | 0.127179 |
| Na | -0.468694 | -0.220543 | -0.427736 | 0.272155 |
| P | 0.401348 | 0.045245 | 0.537183 | 0.568078 |

**Table S6: Total effects for final belowground plant model**

| | Soil Factor 4 | Soil Factor 2 | Soil Factor 1 | Plant composition 2 | Plant composition 1 | Plant diversity | Soil Het. | Div.*Het. Interaction |
|---|---|---|---|---|---|---|---|---|
| Plant composition 1 | .439 | .301 | .682 | .000 | -.888 | -.014 | -.215 | .000 |
| Plant diversity | -1.088 | -.745 | -1.691 | .000 | 2.202 | -.965 | .533 | .000 |
| Soil Het. | .157 | .108 | .245 | .000 | -.319 | -.005 | -.077 | .000 |
| Div.*Het. Interaction | .000 | .000 | .000 | -2.789 | .000 | .000 | .000 | .000 |
| Belowground Biomass | -106.59 | -12.93 | -181.00 | 58.925 | 38.197 | .605 | 257.24 | 59.005 |

**Table S7: Standardized total effects for final belowground plant model**

|  | Soil Factor 4 | Soil Factor 2 | Soil Factor 1 | Plant composition 2 | Plant composition 1 | Plant diversity | Soil Het. | Div.*Het. Interaction |
|---|---|---|---|---|---|---|---|---|
| Plant composition 1 | .456 | .313 | .709 | .000 | -.888 | -.061 | -.226 | .000 |
| Plant diversity | -.260 | -.178 | -.404 | .000 | .506 | -.965 | .129 | .000 |
| Soil Het. | .156 | .107 | .243 | .000 | -.304 | -.021 | -.077 | .000 |
| Div.*Het. Interaction | .000 | .000 | .000 | -.420 | .000 | .000 | .000 | .000 |
| Belowground Biomass | -.273 | -.033 | -.464 | .078 | .094 | .006 | .666 | .518 |

**Table S8: Total effects for final aboveground plant model**

| | Soil Factor 4 | Soil Factor 2 | Soil Factor 1 | Plant composition 2 | Plant composition 1 | Plant diversity | Soil Het. |
|---|---|---|---|---|---|---|---|
| Plant composition 1 | .439 | .301 | .682 | .000 | -.888 | -.014 | -.215 |
| Plant diversity | -1.088 | -.745 | -1.691 | .000 | 2.202 | -.965 | .533 |
| Soil Het. | .157 | .108 | .245 | .000 | -.319 | -.005 | -.077 |
| Div.*Het. Interaction | .000 | .000 | .000 | -2.789 | .000 | .000 | .000 |
| Aboveground biomass | 64.055 | 43.888 | 99.545 | .000 | 16.358 | -2.053 | -31.393 |

**Table S9: Standardized total effects for final aboveground plant model**

| | Soil Factor 4 | Soil Factor 2 | Soil Factor 1 | Plant composition 2 | Plant composition 1 | Plant diversity | Soil Het. |
|---|---|---|---|---|---|---|---|
| Plant composition 1 | .456 | .313 | .709 | .000 | -.888 | -.061 | -.226 |
| Plant diversity | -.260 | -.178 | -.404 | .000 | .506 | -.965 | .129 |
| Soil Het. | .156 | .107 | .243 | .000 | -.304 | -.021 | -.077 |
| Div.*Het. Interaction | .000 | .000 | .000 | -.420 | .000 | .000 | .000 |
| Aboveground biomass | .398 | .273 | .618 | .000 | .098 | -.053 | -.197 |

## Text S1:
### 1A) Belowground biomass:
<u>Maximal model</u> (containing plant diversity, five soil heterogeneity factors from PCA, and interactions between plant diversity and heterogeneity factors as predictors).

```
Coefficients:
                           Estimate Std. Error t value Pr(>|t|)
(Intercept)               1.986e+02  3.667e+02   0.542   0.6049
plant.divers              6.027e+01  3.240e+01   1.860   0.1052
soil.het1                -6.056e+02  4.522e+02  -1.339   0.2223
soil.het2                 6.676e+02  3.299e+02   2.024   0.0827
soil.het3                -2.591e+01  3.562e+02  -0.073   0.9440
soil.het4                -3.169e+01  2.094e+02  -0.151   0.8840
soil.het5                -1.139e+03  6.583e+02  -1.731   0.1271
plant.divers:soil.het1    3.116e+01  2.278e+01   1.368   0.2137
plant.divers:soil.het2   -5.152e+01  2.407e+01  -2.141   0.0696
plant.divers:soil.het3   -3.795e-02  2.851e+01  -0.001   0.9990
plant.divers:soil.het4    1.267e+01  1.529e+01   0.829   0.4346
plant.divers:soil.het5    9.770e+01  5.547e+01   1.761   0.1216
---
Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05

Residual standard error: 200.9 on 7 degrees of freedom
Multiple R-Squared: 0.745,      Adjusted R-squared: 0.3444
F-statistic:  1.86 on 11 and 7 DF,  p-value: 0.2104
```

<u>Minimal adequate model:</u>

```
Coefficients:
                         Estimate Std. Error t value Pr(>|t|)
(Intercept)               125.15     226.69   0.552  0.58902
plant.divers               54.05      18.04   2.996  0.00904 **
soil.het5                -616.34     235.27  -2.620  0.01933 *
plant.divers:soil.het5     60.69      20.81   2.916  0.01064 *
---
Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

Residual standard error: 207.8 on 15 degrees of freedom
Multiple R-Squared: 0.4156,      Adjusted R-squared: 0.2987
F-statistic: 3.555 on 3 and 15 DF,  p-value: 0.04009
```

## 1B) Aboveground biomass:

<u>Maximal model</u> (containing plant diversity, five soil heterogeneity factors from PCA, and interactions between plant diversity and heterogeneity factors as predictors).

```
Coefficients:
                          Estimate Std. Error t value Pr(>|t|)
(Intercept)               535.3830   336.6722   1.590    0.156
plant.divers               -4.7591    29.7479  -0.160    0.877
soil.het1                 170.0041   415.1191   0.410    0.694
soil.het2                 196.9513   302.8702   0.650    0.536
soil.het3                 482.6106   326.9768   1.476    0.183
soil.het4                  31.9617   192.2193   0.166    0.873
soil.het5                 395.7568   604.3784   0.655    0.534
plant.divers:soil.het1     -3.8456    20.9169  -0.184    0.859
plant.divers:soil.het2    -10.0107    22.0969  -0.453    0.664
plant.divers:soil.het3    -38.4684    26.1745  -1.470    0.185
plant.divers:soil.het4     -0.9989    14.0416  -0.071    0.945
plant.divers:soil.het5    -25.6033    50.9290  -0.503    0.631


Residual standard error: 184.5 on 7 degrees of freedom
Multiple R-Squared: 0.4251,      Adjusted R-squared: -0.4782
F-statistic: 0.4706 on 11 and 7 DF,  p-value: 0.873
```

<u>Minimal adequate model:</u> (Lowest AIC score, but remained non-significant)

```
Coefficients:
             Estimate Std. Error t value Pr(>|t|)
(Intercept)   631.572    123.840   5.100  8.9e-05 ***
plant.effdiv   -8.933      8.749  -1.021    0.322
---
Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

Residual standard error: 151.5 on 17 degrees of freedom
Multiple R-Squared: 0.05778,     Adjusted R-squared: 0.00236
F-statistic: 1.043 on 1 and 17 DF,  p-value: 0.3215
```

## 1C) Parasitoid model:
```
Analysis of Variance Table

Response: proportion parasitised
                              Df   Sum Sq  Mean Sq F value    Pr(>F)
Habitat type                   4 0.055273 0.013818  2.4107    0.0719 .
Parasitoid diversity           1 0.087968 0.087968 15.3470    0.0005***
Host heterogeneity             1 0.008009 0.008009  1.3973    0.2468
Diversity*heterogeneity        1 0.029809 0.029809  5.2004    0.0301*
Habitat*diversity*heterogeneity 4 0.022755 0.005689  0.9925    0.4273
Residuals                     29 0.166227 0.005732
---
Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

## 1D) Pollinator model:

```
Analysis of Variance Table

Response: Fruit set change
                        Df  Sum Sq Mean Sq F value    Pr(>F)
Pollinator diversity     1  666.66  666.66  8.9482 0.007215 **
Flower heterogeneity     1   75.94   75.94  1.0193 0.324737
Diversity*heterogeneity  1  701.58  701.58  9.4170 0.006059 **
Residuals               20 1490.04   74.50
---
```
Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

**Text S2: Soil heterogeneity and nutrient availability**
Previous studies (see main text for citations) have shown that nutrient availability can affect the diversity-productivity relationship. This may lead to the reasonable contention that the relationships with soil heterogeneity we present are in fact due to positive or negative correlations between soil heterogeneity and the availability of certain nutrients. To test this possibility, we used a Pearson's correlation analysis to test for correlations between the significant soil heterogeneity PCA factor 5 and each of the 12 soil variables (raw values/concentrations, not heterogeneity). We found no significant correlations at a Bonferroni corrected alpha of 0.00416. Although Bonferroni corrections have been criticised (Moran 2003), the probability of two variables out of 12 having $p$ values below 0.047 (see C and P in Table S3) can be calculated using a Bernoulli process (Moran 2003, see also main text), and in our case this probability was 0.09 – still higher than the alpha of 0.05 conventionally used in scientific studies.

Nevertheless, resource abundance in general may be a confounding factor in any field study of the BDEF relationship, therefore it was included as an exogenous variable in the SEM analyses below (Text S4). Resource abundance was easily measured for the parasitoid-host system in Ecuador (abundance of host larvae) and the pollinator-plant system in Indonesia (abundance of coffee flowers). However, in the German grasslands, a variety of nutrients are present, and the 'abundance' (concentration) of different nutrients may be intercorrelated. Therefore, to take into account this intercorrelation and reduce the number of variables for analysis, we conducted another PCA as above, but using the concentrations of each soil variable, rather than their within-site variability. This allowed us to reduce the 12 soil variables to 4 orthogonal factors that cumulatively explained over 81% of the variance in the soil variables (Tables S4 and S5). These factors were used in the SEM analyses below (Text S4).

**Reference:**
Moran, M.D. 2003. Arguments for rejecting the sequential Bonferroni in ecological studies. Oikos 100, 403-405.

**Text S3: Community composition analyses**

In real-world ecosystems, extinctions of species are non-random. This was not a problem for BDEF experiments, as diversity treatments were created using random assemblages of species. In real-world studies, however, habitats that differ in their diversity, may also differ in the species that comprise that diversity, and this change in composition must be controlled for in any assessment of diversity effects on ecosystem functioning.

To analyse compositional differences among plants/parasitoids/pollinators, we applied non-metric multidimensional scaling (NMDS) ordination techniques using the program PC-ORD version 4.25 (McCune & Mefford 1997). NMDS is an iterative search for ranking and placement of n entities (samples) in k dimensions (ordination axes) that minimizes the stress of the k-dimensional configuration. The ''stress'' value is a measure of departure from monotonicity in the relationship between the dissimilarity (distance) in the original p-dimensional space and in the reduced k-dimensional ordination space (Clarke 1993). NMDS is therefore used to find a configuration in a given number of dimensions, which preserves rank-order dissimilarities in species composition as closely as possible, such that distance along a NMDS axis corresponds to relative difference in community composition. As distance measure, the Bray-Curtis coefficient was used (also known as Sørensen or Czekanowski coefficient), which is one of the most robust measures for this purpose (Faith et al. 1987).

We then tested for correlations between NMDS axes and diversity in each of our systems, to determine whether species composition correlates with diversity in our sites:

**Plants (Germany)**
Number of axes: 2
Number of iterations: 43
Stress for 2-dimensional solution: axis 1= 20.08, axis 2= 12.45 (final stress value: 12.45)

|                | NMDS axis 1 | NMDS axis 2 | Plant diversity |
|----------------|-------------|-------------|-----------------|
| NMDS axis 1    | 1           |             |                 |
| NMDS axis 2    | **0.528***  | 1           |                 |
| Plant diversity| -0.349      | -0.301      | 1               |

Correlations from Pearson, N = 19. * = significant at 0.05, ** = significant at 0.01

**Parasitoids (Ecuador)**
Number of axes: 2
Number of iterations: 400
Stress for 2-dimensional solution: axis 1= 27.91 , axis 2= 12.58 (final stress value: 12.58)

|                     | NMDS axis 1 | NMDS axis 2 | Parasitoid richness |
|---------------------|-------------|-------------|---------------------|
| NMDS axis 1         | 1           |             |                     |
| NMDS axis 2         | -0.035      | 1           |                     |
| Parasitoid richness | **0.644**** | 0.036       | 1                   |

Correlations from Pearson, N = 41. * = significant at 0.05, ** = significant at 0.01

**Pollinators (Indonesia)**
Number of axes: 3
Number of iterations: 196
Stress for 2-dimensional solution: axis 1= 26.49, axis 2= 13.52, axis 3= 7.92 (final stress value: 8.14)

|  | NMDS axis 1 | NMDS axis 2 | NMDS axis 3 | Pollinator richness |
|---|---|---|---|---|
| NMDS axis 1 | 1 |  |  |  |
| NMDS axis 2 | 0.099 | 1 |  |  |
| NMDS axis 3 | 0.002 | 0.215 | 1 |  |
| Pollinator richness | 0.256 | -0.183 | **-0.615\*\*** | 1 |

Correlations from Pearson, N = 24. * = significant at 0.05, ** = significant at 0.01

Diversity did not correlate with composition in the plant communities, however, parasitoid diversity was significantly correlated with NMDS axis 1, and pollinator diversity was significantly correlated with NMDS axis 3.

**References:**
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Faith, D. P., Minchin, P. R. and Belbin, L. 1987. Compositional dissimilarity as a robust measure of ecological distance. Vegetatio 69, 7–68.
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**Text S4 Structural Equation Modelling (SEM)**

In a field study such as ours, diversity may be a predictor of function, but it may also respond to another variable that also has an effect on function. Furthermore, resource abundance may have complex indirect effects, possibly mediated through diversity, which was also correlated with species composition in the parasitoid and pollinator communities (quantified using the NMDS axes in Text S3). Therefore, the apparent effect of diversity could in fact be due to shifts in species composition, and the effects of diversity and the diversity*heterogeneity interaction may not be significant after controlling for all of these different confounding variables.

To distinguish between these potential causal pathways and control for these possible confounding variables, we used SEM, performed in Amos v.16.0.1 (Amos Development Corporation http://amosdevelopment.com). For each system we constructed an initial model (presented below) with a variety of pathways allowing resource abundance and heterogeneity to affect diversity. We also included pathways from diversity to species composition to function, allowing for the effect of diversity to be mediated via shifts in composition, rather than diversity per se. The interaction term was derived by cross-multiplying "centred" (deviation) scores of the main effects (Kline & Dunn 2000). We allowed for species composition, resource abundance, and habitat type (parasitoid model only) to affect this interaction term of interest. All paths in the original model were treated as optional, and were thus able to be removed during model simplification. We used the specification search function, to test all subsets of our initial model using maximum likelihood estimation. As a final model we selected the model with a subset of the parameters in the initial model that included at least one predictor of function (plant biomass, parasitism or pollination respectively), and had the lowest AIC (Akaike Information Criterion) score. When multiple models did not differ significantly in AIC (less than 2 units difference), we selected the most parsimonious model (fewest parameters). Below we present the diagram for the initial model, and present the final most parsimonious model in main text Fig. 3. Values adjacent to paths indicate unstandardized direct effects, with significance indicated by * = P< 0.05, ** = P<0.01, ***=P<0.001. For each model we present the number of distinct parameters being estimated, Cmin (the minimum value of the discrepancy *C*), AIC score and BCC (the Browne-Cudeck Criterion, which was developed specifically for analysis of moment structures and gives a slightly greater penalty for model complexity than AIC). Unstandardized (absolute) and standardized (accounting for different unit sizes in different predictors) total effects (direct and indirect combined) are presented in tables below each final model. In the total effects tables, the column variable is explaining the row variable.

**Reference:**

Kline T.J.B. and Dunn, B. (2000) Analysis of interaction terms in structural equation models: a non-technical demonstration using the deviation score approach. Can. J. Behav. Sci. 32, 127-132.