**Supporting Information for**

**Forest structure and heterogeneity increase diversity and alter composition of host-parasitoid networks**

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**Supplementary methods**

a) Remotely sensed environmental variables

The stand structural complexity index (SSCI) is derived from the points on a terrestrially laser scanned vertical scanline of the whole plot. Points on this line are then connected to a polygon which creates a ration of area to perimeter. The SSCI gains especially high values if vegetation or large objects are recorded close to the scanner. Therefore, open stands with many strata occupied by vegetation, and structures such as deadwood and hanging branches gain the highest values (Ehbrecht et al. 2019). The effective number of layers (ENL) is the number of 1 m forest strata occupied by vegetation measured by filled voxels. A high value of the ENL indicates many forest strata occupied by vegetation, a more evenly layered and diverse stand. The ENL reaches high scores if the forest is high with an even distribution of plant material along the vertical axis. Extreme values of ENL are reached in high forests where crown space is densely occupied (Ehbrecht et al. 2016). While the ENL is representing the layering as well as the stand height, the SSCI is capturing the structural heterogeneity and overall shape complexity.

b) Insect collection, identification, and categorisation

Trap nests were constructed by filling ~150 20 cm long reed (*Phragmites australis* Cav.) internodes into an 11 cm diameter PVC plastic tubes. This results in ~150 ± 11 SD cavities exposed per side. Cavity diameters ranged between 1 ± 0.3 to 10 ± 1.1 mm in diameter, to attract nesting females of as many species as possible (Krombein 1967). After filling tubes until no more internodes could fit inside, cavity entrances were wire brushed to improve suitability for bee and wasp nest building. Traps were secured in pairs to each of two wooden poles of ~2 m height approximately halfway between plot centres and the NW and SE corners, with each trap oriented to expose reed cavities in the NW and SE directions, to standardise sampling of communities. Traps were collected following ~7 months of exposure time (March-October 2020) to allow ample time for nest building. Following retrieval from plots, traps were immediately stored in a cool and dry basement room to prevent early emergence of nested individuals. Traps were gradually inspected, with nests found and transferred to a 4 oC cooling chamber.

During refrigeration, nests were opened with razor blades so that identifications could be made (when possible), and the abundance of hosts and parasitoids quantified. Families and genera, (and often species) can be identified by their nest structure, resources provisioned and materials used (Gathmann and Tscharntke, 1999). Refrigeration duration to simulate winter diapause varied between taxa, as several require longer durations to complete development, but was at minimum 8 weeks. Duration of refrigeration has little influence on hatching of individuals, provided that a minimum time (~6 weeks) is met and an extended time (e.g. 32 weeks) is not exceeded. After rewarming, adults hatched, were collected, and then prepared according to entomological standards so that species could be identified (Table S2).

Following morphological identification, host and parasitoid species were categorised according to forest specialisation (forest and non-forest specialists) and host-specificity (general and specific) respectively. Categorisation was done by cross-referencing the relevant literature and habitat description for host species, and examining the range of hosts for parasitoids in our data.

When a host species’ habitat description exclusively included terms such as “forest”, “forest margins”, “woodland”, “open forest” or “forest clearing”, it was considered a forest specialist. When the habitat description of a species included other habitat types, or the previously mentioned forest types in combination with terms such as “heathland”, “sand dunes” or “meadows”, that species was considered a non-forest specialist. For example, *Hylaeus difformis* is a species of cavity-nesting mask bee. According to Westrich et al., (2018), this species’ preferred habitat is described as “open forest areas, forest edges and forest clearings”, and it was therefore classified as a forest specialist (Table S7). When a parasitoid species utilised hosts from species within only one genus, it was considered host-specific. When a parasitoid utilised hosts species from multiple genera, but > 95% of host species were within one genus, it was considered host-specific. When a parasitoid utilised hosts from multiple genera, with no clear preference for one genus it was considered host-general (Table S7).

c) Bipartite network description

Bipartite networks represent a one-way interaction between two sets of nodes, in this case parasitoids in the higher and their hosts in the lower trophic levels (Fig 4). Networks can be constructed according to temporal or (as in the case of our data) spatial scales. Numerous indices can be calculated at network level to allow the comparison between networks (Dormann et al. 2009, Almende et al. 2021), and to test if network properties are related to the environment where the interactions were observed. In our data, connectance and linkage density were chosen to measure network strength while link diversity and specialisation (H2’) were chosen to measure diversity and network specialisation.

Connectance is defined as the linkage density divided by the number of species in the network, and infers the interactivity of species. Linkage density is defined as the marginal totals-weighted diversity of interactions per species. Together they inform about the number and frequency of interactions, and can be used to infer the potential stability of host populations and thus of the entire network (Brown 2022).

Link diversity is the Shannon entropy for all interactions in a given network. Specialisation (H2’) is a measure of discrimination, or how distinct interactions or groups of interactions become in a given network. High values of link diversity indicate potentially high specialisation in networks. High values of specialisation indicate unique and distinct sets of interactions, comprised of species that have a restricted range of hosts.

d) Metanetwork core description

The core of the metanetwork was identified by examining the degree values of interactions to infer centrality. Interactions with degree values within three standard deviations of the maximum value were considered most central and thus forming the metanetwork core. The host-parasitoid interaction pairs forming the metanetwork core and their corresponding degree values were: *Trypoxylon figulus-Trichrysis cyanea* (117), *Ancistrocerus trifasciatus-Chrysis solida* (107), *T. figulus-Melittobia acasta* (100), *T. figulus-Nematopodius debilis* (87), *Deuteragenia subintermedia-M. acasta* (79), *Passaloecus insignis-Omalus aeneus* (76), *P. insignis-Omalus puncticollis* (73), *Symmorphus gracilis-Chrysis corusca* (73), *Trypoxylon clavicerum-N. debilis* (64).



**Figure. S1**. Map of the 134 ConFoBi research plots sampled in the southern Black Forest, Baden-Württemberg, Germany. Green points correspond to plot geolocations (latitude and longitude of plot centres). Figure credit: Julian Frey.

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**Figure S2**. Species accumulation curves of: a) cavity-nesting bees and wasps and b) their associated parasitoids, collected using 4 trap-nests on each of 127 plots. Plots missing remotely sensed variables (7) were excluded prior to analyses. Observed cumulative species richness is represented in each figure by solid lines, with 95% CI of accumulation curves shown as grey polygons. Total species richness (extrapolated) based on jackknife1 estimators is represented by horizontal lines (solid) with 95% CI (dashed lines). In total, 57 species (86% of expected total richness) of cavity-nesting Hymenoptera and 39 species (85 % of expected total richness) of parasitoids were collected.

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**Figure S3.** Host-parasitoid interaction accumulation curve, displaying cumulative parasitism events (one species parasitising another) per each of 115 sampled plots where parasitism was observed. Observed cumulative interactions is represented by solid lines, with 95% CI accumulation curves shown in grey. Total interactions possible (extrapolated) based on jackknife1 estimators is represented by horizontal lines (solid) with 95% CI (dashed lines). In total, 139 interactions (72% of expected total interactions) were observed.

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**Figure S4.** Abundance (parasitised brood cells) (a), diversity (b) and species richness (c) of parasitoids of cavity-nesting bees and wasps and host abundance. Host abundance was log-transformed (log(x+1, 10)) prior to plotting in each figure. Trend lines are depicted for negative binomial generalised linear models (a and c) and a linear model (b), with 95 % confidence intervals coloured in grey.

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**Figure S5.** NMDS (‘metaMDS’, permutations=1,000) of a) cavity nesting bees and wasps and b) their parasitoid species matrices using Bray-Curtis dissimilarities on 3 axes at 0.191 and 0.164 stress respectively. Forest variables were correlated with the scores of each NMDS using the ‘envfit’ function (permutations=1,000, p<0.05). Plots where only one or no individuals were collected were omitted prior to ordination, resulting in 122 plots used for cavity-nesting Hymenoptera and 97 for their parasitoids respectively.

**Table S1.** Spearman correlation coefficients (*ρ*) for all pairwise comparisons of environmental variables. Abbreviations are as follows: DBH, diameter at breast height; ENL, effective number of layers or 1-meter forest strata; SSCI, stand structural complexity index.

|  |  |  |  |  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- |
|  | Canopy cover (%) | Deadwood DBH (lying) | Deadwood DBH (standing) | Deciduous tree share (%) | ENL | Elevation | Forest cover | Herb cover (%) | SSCI | Understorey species richness |
| Canopy cover (%) | 1 | -0.38 |  0.05 |  0.25 | -0.11 | -0.34 | <-0.01 | -0.24 |  0.03 | -0.11 |
| Deadwood DBH (lying) |  | 1 | <0.01 |  0.25 |  0.05 |  0.09 |  0.15 |  0.12 |  0.05 |  0.12 |
| Deadwood DBH (standing) |  |  | 1 | -0.10 | -0.07 |  0.09 |  0.10 | -0.12 | -0.01 |  0.03 |
| Deciduous tree share (%) |  |  |  | 1 | -0.32 | -0.28 |  0.08 | -0.29 |  0.29 |  0.03 |
| ENL |  |  |  |  | 1 |  0.02 |  0.04 |  0.41 | -0.19 |  0.12 |
| Elevation |  |  |  |  |  | 1 |  0.13 |  0.21 | -0.02 | -0.18 |
| Forest cover |  |  |  |  |  |  | 1 | -0.16 | <-0.01 | -0.22 |
| Herb cover (%) |  |  |  |  |  |  |  | 1 | -0.19 |  0.20 |
| SSCI |  |  |  |  |  |  |  |  | 1 |  0.05 |
| Understorey species richness |  |  |  |  |  |  |  |  |  | 1 |

**Table S2.** Parasitoid (including klepto-parasitic) species collected between March-October of 2020 using trap nests, deployed on 134 plots. The total number of nests, genera and host species parasitised are listed for each parasitoid species. The total abundance (number of parasitised brood cells) is listed for each species. The relevant literature used for identification is listed for each species.

|  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- |
| Species | Nests parasitised | Genera parasitised | Host species parasitised | Abundance | Identificationliterature |
| *Anthrax* *anthrax* | 6 | 3 | 4 | 7 | (Oosterbroek 2006, Schaefer 2018) |
| *Ammobia* *signata* | 38 | 5 | 7 | 84 |  |
| *Coelioxys* *alata* | 2 | 1 | 1 | 4 | (Amiet et al. 2004, Westrich 2018) |
|  *inermis* | 4 | 1 | 1 | 7 |  |
| *Chrysis angustula* | 29 | 2 | 5 | 45 | (Paukkunen et al. 2015, Wiesbauer et al. 2020) |
|  *corusca* | 32 | 2 | 6 | 58 |  |
|  *fulgida* | 30 | 2 | 5 | 41 |  |
|  *ignita* | 43 | 2 | 5 | 62 |  |
|  *impressa* | 10 | 2 | 4 | 13 |  |
|  *leptomandibularis* | 1 | 1 | 1 | 1 |  |
|  *ruddii* | 2 | 1 | 1 | 2 |  |
|  *schencki* | 1 | 1 | 1 | 1 |  |
|  *solida* | 78 | 2 | 4 | 118 |  |
|  *terminata* | 2 | 1 | 1 | 4 |  |
|  *vanlithi* | 7 | 2 | 4 | 12 |  |
| *Coelopencyrtus* *arenarius* | 8 | 1 | 2 | 23 | (Westrich 2018) |
| *Ephialtes* *manifestator* | 18 | 7 | 9 | 25 | (Fitton et al. 1988, Horstmann, 1989, Broad et al. 2018, Riedel et al. 2021) |
| *Gasteruption* *assectator* | 23 | 1 | 3 | 33 | (Bogusch, 2021) |
|  *boreale* | 14 | 1 | 3 | 15 |  |
|  *jaculator* | 21 | 1 | 2 | 21 |  |
|  *nigritarse* | 13 | 1 | 2 | 23 |  |
|  *undulatum* | 4 | 1 | 2 | 5 |  |
| *Lochetica* *westoni* | 3 | 1 | 1 | 6 | (Fitton et al. 1988, Horstmann, 1989, Broad et al. 2018, Riedel et al. 2021) |
| *Melittobia* *acasta* | 320 | 14 | 24 | 815 | (Gathmann and Tscharntke, 1999) |
| *Nematopodius* *debilis* | 144 | 2 | 6 | 189 | (Fitton et al. 1988, Horstmann, 1989, Broad et al. 2018, Riedel et al. 2021) |
|  *formosus* | 8 | 1 | 3 | 11 |  |
| *Omalus* *aeneus* | 61 | 1 | 3 | 73 | (Paukkunen et al. 2015, Wiesbauer et al. 2020) |
|  *puncticollis* | 37 | 1 | 3 | 51 |  |
| *Perithous* *divinator* | 8 | 1 | 2 | 11 | (Fitton et al. 1988, Horstmann, 1989, Broad et al. 2018, Riedel et al. 2021) |
|  *scurra* | 1 | 1 | 1 | 1 |  |
| *Picardiella* *melanoleuca* | 1 | 1 | 1 | 1 |  |
| *Poemenia* *brachyura* | 7 | 2 | 3 | 26 |  |
|  *collaris* | 11 | 2 | 3 | 14 |  |
|  *notata* | 13 | 1 | 1 | 16 |  |
| *Pseudomalus* *auratus* | 13 | 1 | 1 | 15 | (Paukkunen et al. 2015, Wiesbauer et al. 2020) |
|  *pusillus* | 5 | 1 | 2 | 5 |  |
|  *triangulifer* | 3 | 1 | 1 | 4 |  |
|  *violaceus* | 2 | 1 | 1 | 2 |  |
| *Trichrysis* *cyanea* | 313 | 3 | 10 | 371 |  |

**Table S3.** Results of Procrustes comparison of 3 to 2 axes ordinations for both host and parasitoid species composition. Procrustes sum of squares is represented as m2.Significant p-values (listed in bold) indicate correlation between ordinations.

|  |  |  |
| --- | --- | --- |
|  | m2 | p-value |
| Host composition | **<0.001** | **0.001** |
| Parasitoid composition | **<0.001** | **0.001** |

**Table S4.** Regression coefficients of models of parasitoid abundance (negative binomial), parasitism rate (binomial), parasitoid species richness (negative binomial) and parasitoid diversity (normal) sampled on 127 plots. Each model included all environmental variables listed in Table 1, with log-transformed host abundance at plot-level included as a covariate. Significant coefficients are displayed in bold. Conditional and marginal R2 valuesare listed in parentheses for models of diversity and parasitism rate, while McFadden’s pseudo R2 is listed for models of abundance and parasitoid species richness.

|  |  |  |  |  |
| --- | --- | --- | --- | --- |
|  | Parasitism rate(R2c=0.17, R2m=0.91) | Parasitoid abundance(R2=0.14) | Parasitoid diversity(R2c=0.52, R2m=0.47) | Parasitoid richness(R2=0.20) |
|  | Est. z-value±SE p-value | Est. z-value±SE p-value | Est. t-value±SE p-value | Est. z-value±SE p-value |
| Canopy cover | - 0.031 - 0.301 0.102 0.763 | - 0.061 - 0.767 0.079 0.443 | - 0.048 - 0.898 0.053 0.371 | - 0.056 - 0.991 0.057 0.322 |
| Deadwood DBH sum (lying) | - 0.075 - 0.735 0.102 0.462 | - 0.056 - 0.717 0.079 0.473 | - 0.046 - 0.906 0.051 0.367 | - 0.039 - 0.631 0.062 0.528 |
| Deadwood DBH sum (standing) |  **0.266 2.998** **0.089 < 0.001** |  **0.232 3.368** **0.069 < 0.001** |  0.042 0.945 0.045 0.347 |  0.026 0.478 0.055 0.633 |
| Deciduous tree share (%) |  0.065 0.636 0.103 0.525 |  0.035 0.427 0.082 0.669 | - 0.018 - 0.325 0.054 0.745 |  0.006 0.103 0.061 0.918 |
| ENL |  -0.004 - 0.042 0.091 0.966 |  -0.015 - 0.209 0.072 0.835 |  0.044 0.903 0.048 0.368 |  0.039 0.697 0.055 0.486 |
| Elevation |  -0.038 - 0.311 0.119 0.756 |  -0.060 - 0.647 0.093 0.518 | - 0.093 - 1.566 0.059 0.120 | - 0.050 - 0.682 0.071 0.495 |
| Forest cover (%) | -0.107 - 1.317 0.081 0.188 | -0.082 - 1.300 0.064 0.194 | - 0.045 -1.005 0.045 0.317 | - 0.064 - 1.449 0.044 0.147 |
| Herb cover (%) | -0.034 - 0.346 0.098 0.729 | -0.027 - 0.345 0.077 0.730 |  0.009 0.182 0.051 0.856 | - 0.036 - 0.632 0.057 0.527 |
| Host abundance |  0.089 0.649 0.137 0.517 |  **1.029 - 9.832** **0.105 < 0.001** |  **0.376 6.640** **0.057 < 0.001** |  **0.671 8.680** **0.077 < 0.001** |
| SSCI |  0.145 1.646 0.088 0.099 |  **0.139 2.036** **0.069 0.042** |  **0.105 2.284** **0.046 0.024** |  0.031 0.617 0.050 0.537 |
| Understorey species richness | -0.067 - 0.815 0.083 0.415 | -0.078 - 1.181 0.066 0.237 | - 0.069 - 1.503 0.046 0.135 | - 0.061 - 1.252 0.049 0.211 |

**Table S5.** Summary results from permutation tests fitting environmental variables to host species NMDS (“metaMDS, 1,000 permutations) using “envfit” function with 1,000 permutations. Significant correlations (p<0.05) are displayed in bold.

|  |  |  |  |  |
| --- | --- | --- | --- | --- |
| **Forest variable** | **NMDS1** | **NMDS2** |  **r2** | **p** |
| **Canopy cover** | **-0.990** | **-0.135** | **0.157** | **<0.001** |
| Deadwood DBH (lying) |  0.999 | -0.009 | 0.012 |  0.474 |
| Deadwood DBH (standing) |  0.879 | -0.476 | 0.005 |  0.776 |
| Deciduous tree share (%) |  0.183 |  0.983 | 0.013 |  0.471 |
| ENL |  0.824 | -0.566 | 0.001 |  0.914 |
| **Elevation** | **-0.759** | **-0.650** | **0.064** |  **0.021** |
| Forest cover (%) | -0.934 | -0.356 | 0.031 |  0.145 |
| **Herb cover (%)** |  **0.967** | **-0.255** | **0.065** |  **0.015** |
| **SSCI** |  **0.803** |  **0.595** | **0.071** |  **0.001** |
| **Understorey species richness** |  **0.999** | **-0.047** | **0.063** |  **0.019** |

|  |  |  |  |  |
| --- | --- | --- | --- | --- |
| **Forest variable** | **NMDS1** |  **NMDS2** |  **r2** | **p** |
| **Canopy cover** |  **0.872** |  **0.489** |  **0.080** | **0.026** |
| Deadwood DBH (lying) | -0.899 | -0.437 |  0.041 | 0.129 |
| Deadwood DBH (standing) | -0.584 | -0.812 |  0.047 | 0.091 |
| Deciduous tree share (%) |  0.077 | -0.997 |  0.003 | 0.893 |
| ENL |  0.025 |  0.999 |  0.021 | 0.375 |
| Elevation | -0.806 |  0.592 |  0.007 | 0.716 |
| Forest cover (%) | -0.051 |  0.999 |  0.020 | 0.389 |
| Herb cover (%) | -0.422 | -0.907 |  0.014 | 0.519 |
| **Host abundance** | **-0.547** | **-0.837** |  **0.094** | **0.015** |
| SSCI | -0.579 | -0.815 |  0.024 | 0.307 |
| Understorey species richness |  0.400 | -0.916 |  0.007 | 0.728 |

**Table S6.** Summary results from permutation tests fitting environmental variables to parasitoid species NMDS (“metaMDS, 1,000 permutations) using “envfit” function with 1, 000 permutations. Significant correlations (p<0.05) are displayed in bold.

**Table S7.** Parasitoid interactions (parasitoids, corresponding hosts and number of parasitised brood cells) from 115 plots where parasitism was sampled. Corresponding bipartite network numbers for parasitoids and their hosts are listed in parentheses. Corresponding habitat specialisation of hosts and specificity (restriction in host acceptance) of parasitoids are included for each interaction.

|  |  |  |  |  |
| --- | --- | --- | --- | --- |
| **Parasitoid** | **Parasitoid specificity** | **Host** | **Host habitat specialisation** | **Cells parasitised** |
| *Anthrax anthrax* (1) | General | *Megachile* *lapponica* (19) *versicolor* (21)*Symmorphus* *crassicornis* (9)*Trypoxylon* *clavicerum* (32) | ForestForest | 411 |
| *Ammobia signata* (2) | General | *Ancistrocerus* *trifasciatus* (5)*Deuteragenia* *subintermedia* (14)*Symmorphus* *allobrogus* (7) *bifasciatus* (13) *gracilis* (10)*Passaloecus* *corniger* (25)*Trypoxylon* *figulus* (34) | ForestForestForestForestForestForestNon-forest | 3951141420 |
| *Coelioxys alata* (3) | Specific | *Megachile* *ligniseca* (20) | Forest | 4 |
| *Coelioxys inermis* (4) | Specific | *Megachile* *lapponica* *versicolor* | ForestForest | 52 |
| *Coelopencyrtus arenarius* (5) | Specific | *Hylaeus* *confusus* (17) *difformis* (18) | ForestForest | 221 |
| *Chrysis angustula* (6) | General | Ancistrocerus trifasciatus (5)Symmorphus allobrogus (7) bifasciatus (8) crassicornis (9) gracilis (10) | ForestForestForestForestForest | 1361681 |
| *Chrysis corusca* (7) | Specific | *Ancistrocerus* *trifasciatus* (5)*Symmorphus* *allobrogus* (7) *bifasciatus* (8) *crassicornis* (9) *gracilis* (10) *murarius* (11) | ForestForestForestForestForestNon-forest | 2523442 |
| *Chrysis fulgida* (8) | Specific | *Ancistrocerus* *trifasciatus* (5)*Symmorphus* *allobrogus* (7) *bifasciatus* (8) *crassicornis* (9) *murarius* (11) | ForestForestForestForestNon-forest | 141897 |
| *Chrysis ignita* (9) | General | *Ancistrocerus* *trifasciatus* (5)*Symmorphus* *allobrogus* (7) *bifasciatus* (8) *crassicornis* (9) *murarius* (11) | ForestForestForestForestNon-forest | 2867151 |
| *Chrysis impressa* (10) | Specific | *Ancistrocerus* *claripennis* (2) *trifasciatus* (5)*Symmorphus* *allobrogus* (7) *bifasciatus* (8) | ForestForestForestForest | 7411 |
| *Chrysis leptomandibularis* (11) | Specific | *Ancistrocerus* *trifasciatus* (5) | Forest | 1 |
| *Chrysis ruddii* (12) | Specific | *Ancistrocerus* *scoticus* (4) | Forest | 2 |
| *Chrysis schencki* (13) | Specific | *Ancistrocerus* *trifasciatus* (5) | Forest | 1 |
| *Chrysis solida* (14) | Specific | *Ancistrocerus* *claripennis* (14)*Ancistrocerus* *trifasciatus* (5)*Symmorphus* *bifasciatus* (8) *crassicornis* (9) | ForestForestForestForest | 211411 |
| *Chrysis terminata* (15) | Specific | *Ancistrocerus* *nigricornis* (3) | Non-forest | 4 |
| *Chrysis vanlithi* (16) | Specific | *Ancistrocerus* *nigricornis* (3) *scoticus* (4) *trifasciatus* (5)*Symmorphus* *bifasciatus* (8) | Non-forestForestForestForest | 1182 |
| *Ephialtes manifestator* (24) | General | *Ancistrocerus* *trifasciatus* (5)*Symmorphus* *bifasciatus* (8) *crassicornis* (9) *gracilis* (10)*Deuteragenia* *subintermedia* (14)*Megachile* *versicolor* (21)*Passaloecus* *insignis* (27)*Pemphredon* lugens (28)*Trypoxylon* *figulus* (34) | ForestForestForestForestForestForestForestForestNon-forest | 211311392 |
| *Gasteruption assectator* (35) | Specific | *Hylaeus* *communis* (16) *confusus* (17) *difformis* (18) | Non-forestForestForest | 9616 |
| *Gasteruption boreale* (36) | Specific | *Hylaeus* *communis* (16) *confusus* (17) *difformis* (18) | Non-forestForestForest | 917 |
| *Gasteruption jaculator* (37) | Specific | *Hylaeus* *communis* (16) *difformis* (18) | Non-forestForest | 120 |
| *Gasteruption nigritarse* (38) | Specific | *Hylaeus* *communis* (16) *difformis* (18) | Non-forestForest | 815 |
| *Gasteruption undulatum* (39) | Specific | *Hylaeus* *confusus* (17) *difformis* (18) | ForestForest | 32 |
| *Lochetica westoni* (25) | Specific | *Passaloecus* *insignis* (27) | Forest | 6 |
| *Melittobia acasta* (34) | General | *Ampulex* *fasciata* (1)*Ancistrocerus* *claripennis* (2) *trifasciatus* (5)*Auplopus* *carbonarius* (12)*Deuteragenia* *bifasciata* (13) *subintermedia* (14) *variegata* (15)*Discoelius* z*onalis* (6)*Hylaeus* *communis* (16)*Megachile* *lapponica* (19) *versicolor* (21)*Nitela* *borealis* *spinolae**Osmia* *leaiana* (22)*Passaloecus* *corniger* (25) *insignis* (27)*Pemphredon* *lugens* (28)*Rhopalum* *clavipes* (30)*Symmorphus* *allobrogus* (7) *gracilis* (10)*Trypoxylon* *clavicerum* (32) *figulus* (34) *kolazyi* (35) *kostylevi* (36) | ForestForestForestForestForestForestForestForestNon-forestForestForestForestForestNon-forestForestForestForestForestForestForestForestNon-forestNon-forestNon-forest | 31825131462532749182232505131345919 |
| *Nematopodius debilis* (26) | Specific | *Deuteragenia* *subintermedia* (14)*Trypoxylon* *beaumonti* (31) *clavicerum* (32) *figulus* (34) *kolazyi* (35) *kostylevi* (36) | ForestNon-forestForestNon-forestNon-forestNon-forest | 22908342 |
| *Nematopodius formosus* (27) | Specific | *Trypoxylon* *beaumonti* (31) *deceptorium* (33) *figulus* (34) | Non-forestNon-forestNon-forest | 117 |
| *Omalus aeneus* (17) | Specific | *Passaloecus* *corniger* (25) *insignis* (27) | ForestForest | 566 |
| *Omalus puncticollis* (18) | Specific | *Passaloecus* *corniger* (25) *eremita* (26) *insignis* (27) | Non-forestForestForest | 6342 |
| *Perithous divinator* (30) | Specific | *Pemphredon* *lugens* (28) *lugubris* (29) | ForestForest | 92 |
| *Perithous scurra* (33) | Specific | *Symmorphus* *murarius* (11) | Non-forest | 1 |
| *Picardiella melanoleuca* (31) | Specific | *Auplopus* *carbonarius* (12) | Forest | 1 |
| *Poemenia brachyura* (28) | Specific | *Passaloecus* *corniger* (25) *insignis* (27)*Pemphredon* *lugens* (28) | ForestForestForest | 4211 |
| *Poemenia collaris* (29) | Specific | *Symmorphus* *gracilis* (10)*Passaloecus* *corniger* (25) *insignis* (27) | ForestForestForest | 148 |
| *Poemenia notata* (32) | Specific | *Passaloecus* *corniger* (25) | Forest | 16 |
| *Pseudomalus auratus* (19) | Specific | *Pemphredon* *lugens* (28) | Forest | 15 |
| *Pseudomalus pusillus* (20) | Specific | *Passaloecus* *corniger* (25) *insignis* (27) | ForestForest | 23 |
| *Pseudomalus triangulifer* (21) | Specific | *Passaloecus* *insignis* (27) | Forest | 4 |
| *Pseudomalus violaceus* (22) | Specific | *Passaloecus* *insignis* (27) | Forest | 2 |
| *Trichrysis cyanea* (23) | Specific | *Auplopus* c*arbonarius* (12)*Deuteragenia* *bifasciata* (13) *subintermedia* (14) *variegata* (15)*Trypoxylon* *beaumonti* (31) *clavicerum* (32) *figulus* (34) *kolazyi* (35) *kostylevi* (36) *minus* (37) | ForestForestForestForestNon-forestForestNon-forestNon-forestNon-forestForest | 36142515306212 |

**Table S8.** Regression coefficients of models using bipartite network indices as response variables, excluding networks with single links for which no indices could be calculated, resulting in values from 90 networks being analysed. Models included all environmental variables listed in Table 1 as fixed-effects and log-transformed host abundance at plot-level as a covariate. Weighted connectance (linear), link density (linear) linkage diversity (linear) and network specialisation (linear) were analysed. Number of interactions (parasitised brood cells) among modelled networks ranged from 3-105 (23 ± 20). Conditional and marginal R2 values are listed in parentheses for each model.

|  |  |  |  |  |
| --- | --- | --- | --- | --- |
|  | Connectance(weighted)(R2c=0.50, R2m=0.43) | Linkage density(R2c=0.28, R2m=0.18) | Link diversity(R2c=0.41, R2m=0.32) | Specialisation(H2’)(R2c=0.14, R2m=0.02) |
|  |  Est. t-value ±SE p-value |  Est. t-value ±SE p-value |  Est. t-value ±SE p-value |  Est. t-value ±SE p-value |
| Canopy cover |  - 0.003 - 0.346 0.007 0.731 |  **- 0.093 - 2.467** **0.038 0.016** |  **- 0.112 - 2.093** **0.053 0.039** |  0.066 1.951 0.034 0.054 |
| Deadwood DBH sum (lying) |  0.004 0.629 0.007 0.531 |  0.039 1.084 0.036 0.281 |  - 0.008 - 0.162 0.050 0.872 |  0.021 0.662 0.032 0.510 |
| Deadwood DBH sum (standing) |  **0.015 2.116** **0.007 0.038** |  0.030 0.835 0.036 0.406 |  - 0.006 - 0.114 0.051 0.909 |  **- 0.074 - 2.277** **0.033 0.026** |
| Deciduous tree share (%) |  - 0.002 - 0.179 0.009 0.858 |  0.008 0.177 0.044 0.860 |  - 0.007 - 0.116 0.062 0.908 |  0.058 - 1.474 0.039 0.144 |
| ENL |  - 0.007 - 0.946 0.007 0.347 |  - 0.055 - 1.470 0.038 0.157 |  0.031 0.602 0.053 0.549 |  0.005 0.146 0.034 0.885 |
| Elevation |  - 0.002 0.203 0.009 0.839 |  - 0.005 - 0.095 0.048 0.925 |  - 0.077 - 1.144 0.068 0.256 |  - 0.009 - 0.217 0.043 0.828 |
| Forest cover (%) |  0.006 0.875 0.007 0.384 |  0.012 0.351 0.034 0.727 |  0.007 0.140 0.048 0.889 |  - 0.006 - 0.211 0.031 0.834 |
| Herb cover (%) |  **0.017 2.297** **0.008 0.024** |  0.016 0.416 0.038 0.679 |  - 0.050 0.906 0.054 0.358 |  - 0.031 - 0.896 0.034 0.373 |
| Host abundance |  **- 0.053 - 6.724** **0.008 < 0.001** |  **0.105 2.653** **0.039 0.009** |  **0.259 4.647** **0.056 < 0.001** |  0.019 0.543 0.035 0.589 |
| SSCI |  0.002 0.296 0.007 0.768 |  0.013 0.336 0.038 0.738 |  0.053 0.997 0.053 0.322 |  - 0.015 - 0.457 0.034 0.649 |
| Understorey species richness |  0.007 1.051 0.007 0.297 |  - 0.034 - 0.992 0.034 0.324 |  - 0.075 - 1.557 0.048 0.123 |  - 0.001 - 0.032 0.030 0.974 |

**Table S9.** Regression coefficients of models using bipartite network indices as response variables, and all environmental variables listed in Table 1 as fixed-effects and log-transformed host abundance at plot-level as a covariate. Weighted connectance (linear), link density (linear) linkage diversity (linear) and network specialisation (linear) were analysed. Bipartite networks which were too small (singleton and doubleton), as well as networks with fewer than ten parasitised brood cells were excluded prior to analyses, resulting in values from 68 networks being analysed. Number of interactions (parasitised brood cells) among modelled networks ranged from 10-105 (27 ± 19). Conditional and marginal R2 values are listed in parentheses for each model.

|  |  |  |  |  |
| --- | --- | --- | --- | --- |
|  | Connectance (weighted)(R2c=0.36, R2m=0.19) | Linkage density(R2c=0.22, R2m=0.06) | Link diversity(R2c=0.23, R2m=0.07) | Specialisation (H2’)(R2c=0.12, R2m=-0.05) |
|  |  Est. t-value ±SE p-value |  Est. t-value ±SE p-value |  Est. t-value ±SE p-value |  Est. t-value ±SE p-value |
| Canopy cover |  0.003 0.419 0.008 0.677 |  **- 0.099 - 2.215** **0.045 0.031** |  **- 0.134 - 2.168** **0.062 0.034** |  0.030 0.919 0.031 0.362 |
| Deadwood DBH sum (lying) |  0.004 0.495 0.008 0.622 |  0.047 1.040 0.045 0.303 |  - 0.007 - 0.115 0.062 0.906 |  - 0.014 - 0.409 0.032 0.684 |
| Deadwood DBH sum (standing) |  0.011 1.432 0.008 0.157 |  0.018 -0.396 0.046 0.693 |  - 0.025 - 0.391 0.063 0.697 |  - 0.027 - 0.818 0.035 0.417 |
| Deciduous tree share (%) |  - 0.008 - 0.895 0.009 0.374 |  0.034 0.628 0.054 0.533 |  0.054 0.725 0.074 0.471 |  0.001 0.037 0.039 0.970 |
| ENL |  - 0.013 - 1.743 0.008 0.086 |  - 0.059 - 1.339 0.044 0.186 |  0.068 1.125 0.061 0.265 |  0.031 0.939 0.032 0.352 |
| Elevation |  - 0.002 - 0.237 0.009 0.813 |  0.028 0.519 0.054 0.606 |  - 0.037 - 0.489 0.075 0.627 |  0.003 - 0.077 0.040 0.939 |
| Forest cover (%) |  0.006 0.870 0.007 0.388 |  - 0.018 - 0.448 0.041 0.656 |  - 0.017 - 0.302 0.057 0.764 | <-0.001 - 0.003 0.030 0.998 |
| Herb cover (%) |  0.007 0.866 0.008 0.390 |  0.031 0.684 0.045 0.497 |  - 0.002 0.024 0.061 0.981 |  -0.004 - 0.112 0.032 0.911 |
| Host abundance |  **- 0.026 - 3.407** **0.008 0.001** |  0.039 0.908 0.044 0.368 |  0.105 1.745 0.059 0.087 |  - 0.039 - 1.228 0.032 0.224 |
| SSCI | < 0.001 0.107 0.008 0.916 |  - 0.002 - 0.060 0.044 0.953 |  0.059 0.981 0.061 0.331 |  - 0.019 - 0.605 0.033 0.547 |
| Understorey species richness |  0.004 0.546 0.007 0.587 |  - 0.017 - 0.444 0.039 0.659 |  - 0.043 - 0.788 0.054 0.434 |  - 0.004 - 0.135 0.029 0.893 |

**Table S10.** Regression coefficients of models using indices calculated for each interaction (host parasitised by parasitoid species) throughout metanetwork as response variables. Interaction degree (negative binomial) and interaction closeness (normal) were each modelled with site included as a random term and an offset using the number of observed interactions per site. Indices were calculated for interactions for each site where they were observed. Singleton interactions (those occurring alone at site level) were excluded prior to analyses, resulting in indices calculated from parasitoids collected on 90 plots being modelled. Each model included all environmental variables listed in Table 1, with log-transformed host abundance at plot-level included as a covariate. Conditional and marginal R2 values are listed in parentheses for each model.

|  |  |  |
| --- | --- | --- |
|  | InteractionDegree(R2c=0.08, R2m=0.08) | InteractionCloseness(R2c=0.99, R2m=0.54) |
|  |  Est. z-value ±SE p-value |  Est. t-value ±SE p-value |
| Canopy cover |  0.078 1.910 0.041 0.056 |  **0.048 2.188** **0.022 0.032** |
| Deadwood DBH sum (lying) |  - 0.047 - 1.390 0.034 0.164 | <-0.001 - 0.015 0.016 0.988 |
| Deadwood DBH sum (standing) |  - 0.022 0.630 0.036 0.529 |  - 0.007 - 0.410 0.016 0.682 |
| Deciduous tree share (%) |  - 0.056 -1.271 0.044 0.204 |  - 0.010 - 0.463 0.022 0.645 |
| ENL |  0.013 0.356 0.036 0.722 |  - 0.008 - 0.455 0.017 0.650 |
| Elevation |  -0.026 - 0.573 0.046 0.567 |  0.010 0.465 0.022 0.643 |
| Forest cover (%) |  0.042 1.218 0.035 0.223 |  0.009 0.526 0.017 0.601 |
| Herb cover (%) |  - 0.012 - 0.322 0.036 0.747 |  0.026 1.430 0.018 0.157 |
| Host abundance |  **- 0.184 - 4.856** **0.038 < 0.001** |  **- 0.139 - 7.338** **0.019 < 0.001** |
| SSCI |  0.002 0.061 0.036 0.952 |  0.009 - 0.467 0.019 0.642 |
| Understorey species richness |  0.053 1.549 0.034 0.121 |  0.028 1.684 0.017 0.096 |

**Table S11.** Results of Moran’s I calculations for assessing potential spatial autocorrelation in model residuals. Moran’s I calculations were performed using residuals of bipartite models including and excluding small networks (fewer than 10 parasitised brood cells) separately. Calculations were performed using simulated residuals for mixed-models of interaction degree and closeness. Note: All models’ residuals were tested for spatial-autocorrelation using the “DHARMa” package (Hartig 2022).

|  |  |  |  |  |
| --- | --- | --- | --- | --- |
| **Model** | **Observed Moran’s I** | **Expected Moran’s I** | **Standard deviation** | **P value** |
| Parasitoid abundance | -0.005 | -0.008 |  0.005 |  0.233 |
| Parasitoid diversity | -0.016 | -0.008 |  0.005 |  0.959 |
| Parasitoid richness | -0.009 | -0.008 |  0.005 |  0.609 |
| Parasitism rate |  -0.004 | -0.008 |  0.005 |  0.187 |
| Bipartite connectance (weighted) | -0.006 | -0.011 | 0.007 | 0.239 |
| Bipartite linkage density | -0.011 | -0.011 | 0.007 | 0.482 |
| Bipartite link diversity | -0.009 | -0.011 | 0.007 | 0.357 |
| Bipartite specialisation (H2’) | -0.007 | -0.011 | 0.007 | 0.288 |
| Bipartite connectance (weighted) excluding small networks | -0.008 | -0.015 |  0.010 |  0.245 |
| Bipartite linkage density excluding excluding small networks | -0.009 | -0.015 |  0.010 |  0.262 |
| Bipartite link diversity excluding excluding small networks | -0.007 | -0.015 |  0.010 |  0.198 |
| Bipartite specialisation (H2’) excluding excluding small networks | -0.013 | -0.015 |  0.009 |  0.438 |
| Metanetwork degree | -0.008 | -0.011 |  0.007 |  0.309 |
| Metanetwork closeness | -0.007 | -0.011 |  0.007 |  0.256 |

**Table S12.** Spearman correlation coefficients (*ρ*) for all pairwise comparisons of bipartite (rows) and mean metanetwork interaction (columns) indices. Mean values of Spearman’s correlation coefficients for interaction degree (0.062 ± 0.039) and interaction closeness (0.066 ± 0.024) showed no correlation to bipartite network indices.

|  |  |  |
| --- | --- | --- |
|  | Interaction degree | Interaction closeness |
| Connectance (weighted) |  0.006 |  -0.028 |
| Link density | -0.087 | -0.066 |
| Link diversity (Shannon) | -0.109 | -0.092 |
| Specialisation (H2) | -0.047 | -0.079 |

**Table S13.** Regression coefficients of models of parasitoid abundance (negative binomial), parasitism rate (binomial), parasitoid species richness (negative binomial) and parasitoid diversity (normal) sampled on 127 plots, following removal of the most common parasitoid species *M. Acasta* from the dataset. Each model included all environmental variables listed in Table 1, with log-transformed host abundance at plot-level included as a covariate. Significant coefficients are displayed in bold. Conditional and marginal R2 valuesare listed in parentheses for the models of diversity and parasitism rate, while McFadden’s pseudo R2 is listed for models of abundance and parasitoid species richness.

|  |  |  |  |  |
| --- | --- | --- | --- | --- |
|  | Parasitism rate(R2c=0.17, R2m=0.91) | Parasitoid abundance(R2=0.14) | Parasitoid diversity(R2c=0.50, R2m=0.45) | Parasitoid richness(R2=0.20) |
|  | Est. z-value±SE p-value | Est. z-value±SE p-value | Est. t-value±SE p-value | Est. z-value±SE p-value |
| Canopy cover | - 0.014 - 0.129 0.111 0.897 | -0.065 - 0.738 0.089 0.460 | - 0.045 - 0.795 0.057 0.428 | - 0.060 - 1.017 0.059 0.309 |
| Deadwood DBH sum (lying) | - 0.058 - 0.521 0.111 0.602 | -0.054 - 0.614 0.088 0.539 | - 0.059 - 1.092 0.054 0.277 | - 0.053 - 0.804 0.066 0.422 |
| Deadwood DBH sum (standing) |  **0.312 3.235** **0.097 0.001** |  **0.275 3.595** **0.076 < 0.001** |  0.029 0.621 0.048 0.536 |  0.024 0.419 0.058 0.676 |
| Deciduous tree share (%) |  0.081 0.725 0.111 0.468 |  0.066 0.734 0.090 0.463 | - 0.003 - 0.047 0.058 0.963 |  0.012 - 0.181 0.064 0.856 |
| ENL | -0.020 - 0.203 0.099 0.839 |  0.002 0.025 0.080 0.979 |  0.050 0.967 0.052 0.336 |  0.042 0.716 0.058 0.474 |
| Elevation |  -0.059 - 0.449 0.130 0.653 |  -0.083 - 0.810 0.103 0.418 | - 0.097 - 1.532 0.063 0.128 | - 0.055 - 0.739 0.074 0.460 |
| Forest cover (%) | -0.123 - 1.384 0.089 0.166 | -0.095 - 1.331 0.071 0.183 | - 0.049 - 1.010 0.048 0.315 | - 0.075 - 1.617 0.046 0.106 |
| Herb cover (%) | -0.106 - 0.994 0.107 0.320 | -0.075 - 0.868 0.086 0.385 |  0.019 0.349 0.055 0.728 | - 0.039 - 0.666 0.059 0.505 |
| Host abundance |  0.029 - 0.200 0.148 0.841 |  **0.958 8.362** **0.115 < 0.001** |  **0.322 5.337** **0.060 < 0.001** |  **0.646 8.013** **0.081 < 0.001** |
| SSCI |  0.095 0.986 0.096 0.324 |  0.103 1.341 0.077 0.179 |  0.084 1.709 0.049 0.090 |  0.026 0.491 0.052 0.623 |
| Understorey species richness | -0.053 - 0.590 0.090 0.555 | -0.071 - 0.961 0.074 0.337 | - 0.072 - 1.456 0.049 0.148 | - 0.071 - 1.380 0.051 0.168 |

**Table S14.** Regression coefficients of models of parasitism rate (binomial), sampled on 127 plots. Each model included all environmental variables listed in Table 1, with log-transformed host and nest abundances at plot-level included as covariates. Significant coefficients are displayed in bold. Conditional and marginal R2 valuesare listed in parentheses.

|  |  |
| --- | --- |
|  | Parasitism rate(R2c=0.20, R2m=0.91) |
|  | Est. z-value±SE p-value |
| Canopy cover | - 0.013 - 0.118 0.111 0.906 |
| Deadwood DBH sum (lying) | - 0.062 - 0.562 0.111 0.574 |
| Deadwood DBH sum (standing) |  **0.312 3.232** **0.096 0.001** |
| Deciduous tree share (%) |  0.096 0.851 0.113 0.395 |
| ENL |  -0.032 - 0.317 0.101 0.751 |
| Elevation |  -0.044 - 0.336 0.131 0.737 |
| Forest cover (%) | -0.133 - 1.480 0.089 0.139 |
| Herb cover (%) | -0.115 - 1.069 0.107 0.285 |
| Host abundance |  -0.288 - 0.637 0.453 0.524 |
| Nest abundance |  0.306 - 0.741 0.413 0.459 |
| SSCI |  0.091 0.953 0.096 0.340 |
| Understorey species richness | -0.048 - 0.532 0.091 0.594 |

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