

APPENDIX

1. Supplementary Methods

1.1. Mantel tests

We performed simple Mantel tests to determine the area over which landscape composition best explained the abundance of bees, wasps and enemies. We used Bray-Curtis dissimilarities for the percentage cover of the seven landscape categories at a distance of 100, 200, 300, 400 and 500 m and the abundance of the trap-nest community members, and performed 10,000 permutations (Goslee & Urban 2007).

In accordance with Gathmann and Tschardt (2002), measurements at a radius of 500 m best explained species abundances in the trap nests ($r = 0.37$, $P = 0.02$).

1.2. Food web metrics

Quantitative, weighted measures of link density, generality, vulnerability, interaction diversity and compartment diversity based on Shannon's entropy were calculated following Bersier *et al.* (2002), Tylianakis *et al.* (2007) and Dormann *et al.* (2008). Quantitative metrics are weighted to incorporate the total inflow and outflow (based on frequency of interactions) of individuals per species. Diversity of hosts ($H_{N,k}$) and diversity of consumers ($H_{P,k}$), were calculated for each species k as:

$$H_{N,k} = - \sum_{i=1}^s \frac{b_{ik}}{b_{\cdot k}} \log_2 \frac{b_{ik}}{b_{\cdot k}} \quad H_{P,k} = - \sum_{j=1}^s \frac{b_{kj}}{b_{k\cdot}} \log_2 \frac{b_{kj}}{b_{k\cdot}}$$

The sum of column $b_{\cdot k}$ is the number of individuals attacked by taxon k and the sum of row $b_{k\cdot}$ is the number of individuals attacking taxon k . The frequency of interactions from taxon i to taxon k , and from taxon k to taxon j , is represented as b_{ik} and b_{kj} , respectively.

The "reciprocals" of the diversities ($n_{N,k}$ - effective number of hosts and $n_{P,k}$ - effective number of consumers) give the theoretical number of species interacting in equal proportion that would yield the same value of H :

$$n_{P,k} = \begin{cases} 2^{H_{P,k}} \\ 0 \end{cases} \quad \text{if } b_{k\cdot} = 0. \quad n_{N,k} = \begin{cases} 2^{H_{N,k}} \\ 0 \end{cases} \quad \text{if } b_{\cdot k} = 0$$

Generality (G_q), the weighted average effective number of host species per consumer, and **vulnerability** (V_q), the weighted average effective number of consumer species per host, were calculated as:

$$G_q = \sum_{k=1}^s \frac{b_{\cdot k}}{b_{\cdot\cdot}} n_{N,k} \quad V_q = \sum_{k=1}^s \frac{b_{k\cdot}}{b_{\cdot\cdot}} n_{P,k}$$

where $b_{\cdot\cdot}$ is the total number of attacked individuals.

Link density (LD_q) is the number of links per species, calculated as the arithmetic mean of generality and vulnerability:

$$LD_q = \frac{1}{2} \left(\sum_{k=1}^s \frac{b_{k\cdot}}{b_{\cdot\cdot}} 2^{H_{P,k}} + \sum_{k=1}^s \frac{b_{\cdot k}}{b_{\cdot\cdot}} 2^{H_{N,k}} \right).$$

Interaction Diversity (ID_q) was calculated as:

$$ID_q = - \sum_{i=1}^s \sum_{j=1}^s p_{ij} \ln(p_{ij})$$

where p_{ij} is the number of cells of host i attacked by enemy j , divided by the grand sum of the number of attacked cells. It uses Shannon's diversity index with links rather than individuals as the basis of measurement.

Compartment diversity (CD_q) was calculated as:

$$CD_q = \exp \left(- \sum_{i=1}^n p_i \ln(p_i) \right)$$

where p_i is the fraction of all species in the i th of n compartments. The number of compartments in a web is defined as the number of sub webs with no link to any other sub web (Tylianakis, Tscharntke & Lewis 2007).

2. Supplementary Tables

Table S1. Means \pm standard errors, minimum and maximum values of each variable across the 10 strips.

	Mean \pm SE	Min	Max
Species richness			
total community	40.8 \pm 3.1	29	54
all hosts	26.6 \pm 1.7	19	35
bees	9.9 \pm 0.9	5	15
wasps	14.7 \pm 1.4	9	22
aphid predators	4.3 \pm 0.7	2	8
other herbivore predators	6.5 \pm 0.7	4	10
spider predators	3.1 \pm 0.3	2	4
enemies	12.7 \pm 1.3	8	19
Abundance (number of cells)			
average number of brood cells per trap	124.7 \pm 16.8	29.1	193.3
bee cells	86.2 \pm 13.9	7.5	144.1
wasp cells	34.8 \pm 6.4	16.0	70.1
aphid predators	2.5 \pm 0.7	0.2	7.4
other herbivore predators	18.0 \pm 4.3	6.0	54.6
spider predators	13.9 \pm 5.3	0.9	44.2
cells parasitized	23.1 \pm 17.4	4.3	58.4
Food web metrics			
vulnerability	1.7 \pm 0.2	1.2	3.2
generality	2.3 \pm 0.2	1.2	3.9
link density	2.0 \pm 0.2	1.2	2.9
interaction diversity	2.1 \pm 0.2	1.5	2.8
compartment diversity	2.6 \pm 0.5	1.0	6.3
Average abundance in D-vac samples			
arthropods	103.1 \pm 10.1	63.7	175.0
aphids	48.3 \pm 7.5	28.7	103.6
other herbivores	10.1 \pm 1.5	3.1	16.2
spiders	42.4 \pm 6.6	15.3	86.9
Vegetation measurements			
Plant species richness	39.6 \pm 2.1	30	50
Plant biomass (g/m ²)	522.9 \pm 28.6	379.6	686.2
Landscape cover (%)			
Agricultural fields	75.0 \pm 3.1	58.4	90.5
Forest	6.3 \pm 2.1	0.0	17.0
Orchards, hedges, extensive meadows	9.7 \pm 2.1	2.8	19.6
Wildflower strips	0.6 \pm 0.2	0.0	1.7
Water bodies	0.2 \pm 0.1	0.0	1.3
Roads and houses	8.0 \pm 1.2	3.6	16.3
Landscape heterogeneity	2.4 \pm 0.2	1.5	3.6
Distance to closest wildflower strip (m)	291.0 \pm 72.2	118	777
Distance to closest forest (m)	291.4 \pm 87.4	20	861

Table S2. Trap-nesting host Hymenoptera in the 10 experimental wildflower strips. Species codes are used in Fig. 1. Larval food: p/n = pollen and nectar; a = aphids; h = other herbivores; s = spiders. The species groups used in the analyses are defined as follows: "bees" = Apidae; "wasps" = Eumenidae, Sphecidae, Pompilidae; the three subgroups for wasps (aphid-, other herbivore- and spider-predating wasps) are defined according to their larval food.

Nesting species	# brood cells	Larval food	Code	Nesting species	# brood cells	Larval food	Code
Apidae				Sphecidae			
<i>Hylaeus communis</i>	58	p/n	1	<i>Ectemius continuus</i>	1	h	31
<i>H. difformis</i>	7	p/n	2	<i>Isodontia mexicana</i>	31	h	32
<i>Hylaeus</i> sp.	301	p/n	3	<i>Nitela</i> sp.	5	h	33
<i>Chelostoma florissomne</i>	124	p/n	4	Sphecidae sp.	27	h	34
<i>Heriades truncorum</i>	1819	p/n	5	<i>Passaloecus borealis</i>	73	a	35
<i>Megachile centuncularis</i>	138	p/n	6	<i>P. gracilis</i>	62	a	36
<i>M. ericetorum</i>	53	p/n	7	<i>P. insignis</i>	43	a	37
<i>M. versicolor</i>	219	p/n	8	<i>P. corniger</i>	11	a	38
<i>Megachile</i> sp.	250	p/n	9	<i>P. vandeli</i>	3	a	39
<i>Osmia adunca</i>	119	p/n	10	<i>Passaloecus</i> sp.	83	a	40
<i>O. bicornis</i>	7980	p/n	11	<i>Pemphredon lugubris</i>	20	a	41
<i>O. brevicornis</i>	21	p/n	12	<i>Pemphredon</i> sp.	20	a	42
<i>O. caerulescens</i>	362	p/n	13	<i>Psenulus pallipes</i>	22	a	43
<i>O. gallarum</i>	4	p/n	14	<i>Psenulus</i> sp.	2	a	44
<i>O. caerulescens/gallarum</i>	87	p/n	15	<i>Trypoxylon figulus</i>	1823	s	45
<i>O. cornuta</i>	12	p/n	16	<i>Trypoxylon</i> sp.	73	s	46
<i>Osmia</i> sp.	13	p/n	17	Pompilidae			
Apidae sp.	413	p/n	18	<i>Agenioides cinctellus</i>	27	s	47
Eumenidae				<i>Auplopus carbonarius</i>	9	s	48
<i>Alastor atrops</i>	1	h	19	<i>Dipogon subintermedius</i>	5	s	50
<i>Allodynerus rossii</i>	55	h	20	<i>Dipogon</i> sp.	6	s	49
<i>Ancistrocerus antillope</i>	61	h	21	Others			
<i>A. gazella</i>	498	h	22	Symphyta sp.	6	-	52
<i>A. nigricornis</i>	1253	h	23	undetermined hosts	512	-	55
<i>A. parietinus</i>	11	h	24	Host Braconidae 1	12	-	56
<i>Ancistrocerus</i> sp.	16	h	25	Host Braconidae 2	17	-	57
<i>Euodynerus notatus</i>	5	h	26				
<i>Gymnomerus laevipes</i>	34	h	27				
<i>Microdynerus timidus</i>	74	h	28				
<i>Symmorphus gracilis</i>	18	h	29				
Eumenidae sp.	344	h	30				
Total number of brood cells					17 243		

Table S3. Higher trophic level ("enemy") species in the 10 experimental wildflower strips. Species codes are used in Fig. 1. Host group: B = bees; W = wasps; G = bees and wasps; O = enemies of undetermined hosts. *Morphospecies.

Enemy species	# Cells attacked	Host group	Code
Hymenoptera			
Apidae			
<i>Coelioxys inermis</i>	4	B	59
<i>C. mandibularis</i>	4	B	60
<i>C. inermis/mandibularis</i>	3	B	58
<i>Stelis breviscula</i>	61	B	61
Chrysididae			
<i>Chrysis cyanea</i>	22	G	62
<i>C. ignita</i>	3	O	63
<i>Omalus auratus</i>	5	W	64
Chrysididae sp.	7	W	65
Eulophidae			
<i>Mellitobia acasta</i>	596	G	66
Ichneumonidae			
<i>Ephialtes manifestator</i>	45	G	67
Ichneumonidae spp. 1-5*	17	O	68-72
Cryptinae sp.	1	W	73
<i>Lissonota</i> sp.	2	W	74
Tryphoninae sp.	1	O	75
Campopleginae sp.	1	W	76
<i>Ophion</i> sp.	5	O	77
Gasteruptiidae			
<i>Gasteruption assectator</i>	2	B	78
Sapygidae			
<i>Sapyga decemguttata</i>	16	B	79
<i>S. quinquepunctata</i>	127	G	80
Sapygidae sp.	7	G	81
Pteromalidae			
Pteromalidae sp.	3	W	82
Toryminae			
<i>Monodontomerus obsoletus</i>	15	B	83
Braconidae			
Braconidae spp. 1-6*	77	O	84-89
<i>Isodontia</i> parasites	3	W	90
Coleoptera			
<i>Trichodes alvearius</i>	407	G	91
<i>Megatoma undata</i>	108	G	92
Diptera			
<i>Anthrax anthrax</i>	13	B	93
<i>Cacoxenus indagator</i>	1544	B	94
Diptera larvae	2	W	95
Acari			
<i>Chaetodactylus osmiaae</i>	106	B	96
undetermined			
Species 1	1	W	97
Total	3208		

Table S4. Correlations among variables. Cell entries are Pearson's correlation coefficient, n=10. ***P<0.001, **P<0.01, *P<0.05, †P<0.1

		Cover (%)						landscape heterogeneity	Distance (m) to next		Vegetation	
		forest	extensive meadows	gardens, hedges & orchards	wildflower strips	roads & houses	water bodies		wildflower strip	forest	species richness	biomass
Cover (%)	agricultural fields	-0.61 †	-0.80 **	-0.78 *	-0.07	-0.12	0.29	-0.98 ***	0.20	0.81 **	-0.23	-0.07
	forest		0.12	0.12	0.11	-0.43	0.14	0.56	-0.19	-0.74 *	0.02	-0.25
	extensive meadows			0.92 ***	0.08	0.16	-0.25	0.86 ***	-0.26	-0.51	0.18	0.29
	gardens, hedges & orchards				0.28	0.07	-0.40	0.86 ***	-0.52	-0.46	0.02	0.42
	wildflower strips					-0.44	-0.39	0.17	-0.72 *	0.22	-0.67 *	0.40
	roads & houses						-0.47	0.01	0.65 †	0.06	0.51	-0.06
	water bodies							-0.27	0.12	-0.10	-0.12	-0.36
	landscape heterogeneity							-0.33	-0.75 *	0.17	0.11	
Distance (m) to next	wildflower strip								0.03	0.60 †	-0.57	
	forest									-0.17	0.04	
Vegetation	species richness										-0.57	

3. Supplementary Figures

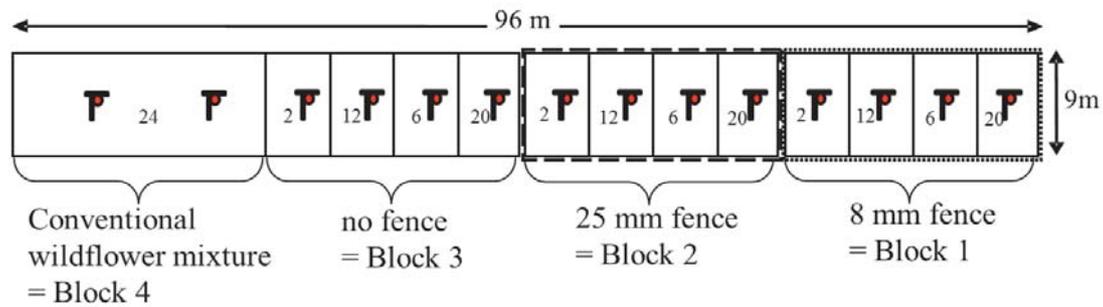


Fig. S1. Arrangement of the 14 trap-nests (red circles) within subplots in the experimental wildflower strips. Numbers indicate sown plant species richness. Strips were divided into four blocks of equal size: 1. fence with 8 mm mesh (dotted-line), 2. fence with 25 mm mesh (dashed-line), 3. no fence, and 4. conventional wildflower mixture without fence. Note that fencing had no effect on the trap-nest community, and the effects of the plant diversity treatments are discussed elsewhere (Fabian 2013).

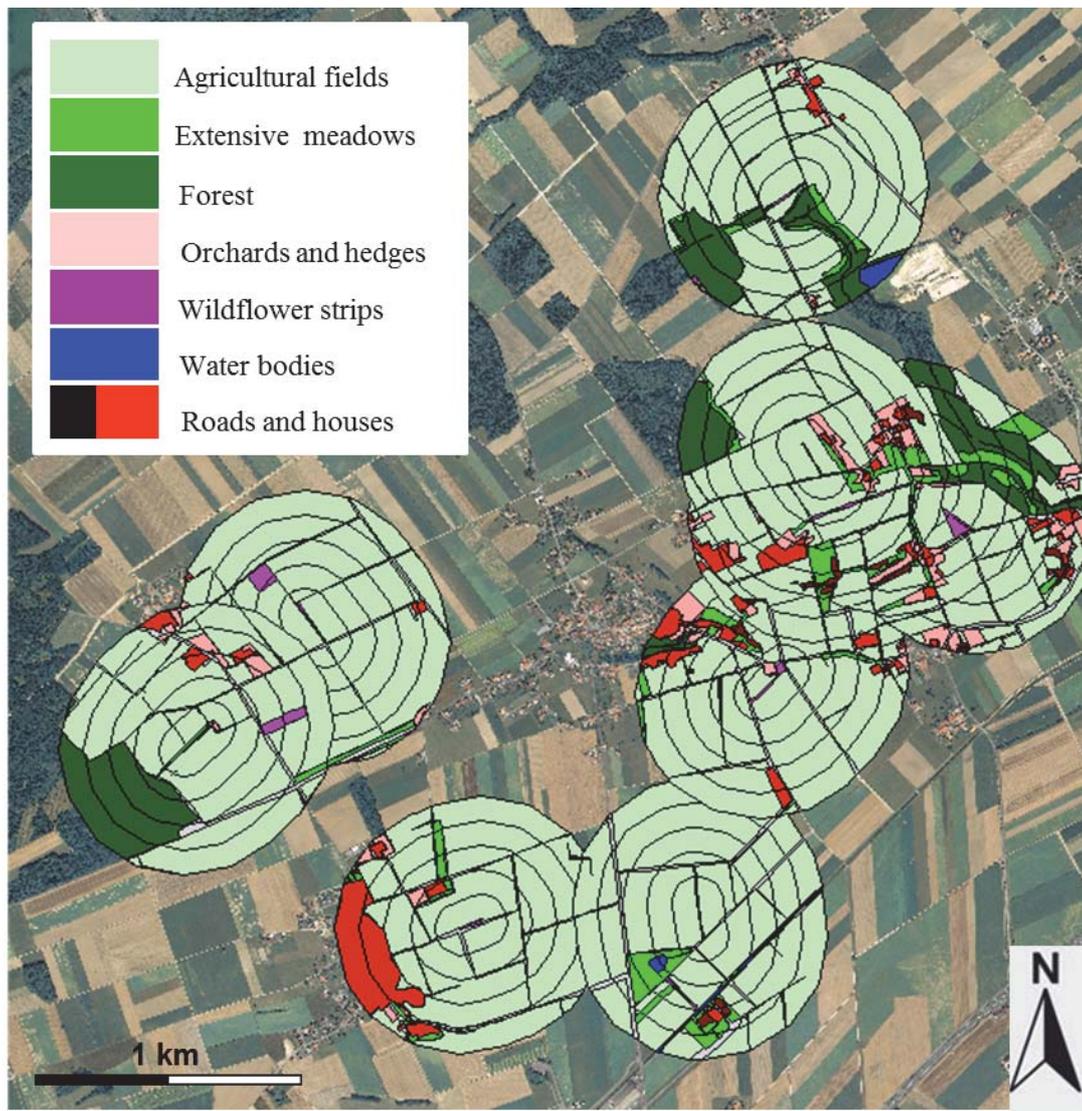


Fig. S2. Aerial photo of the study area. The 10 experimental wildflower strips are surrounded by ellipsoids of 500 m radius in which land use was measured. The colours depict landscape composition.



Fig. S3. Trap nests for solitary bees and wasps. Photographs show a single trap and its placement in a wildflower strip in an agricultural landscape. Photographs by N. Sandau

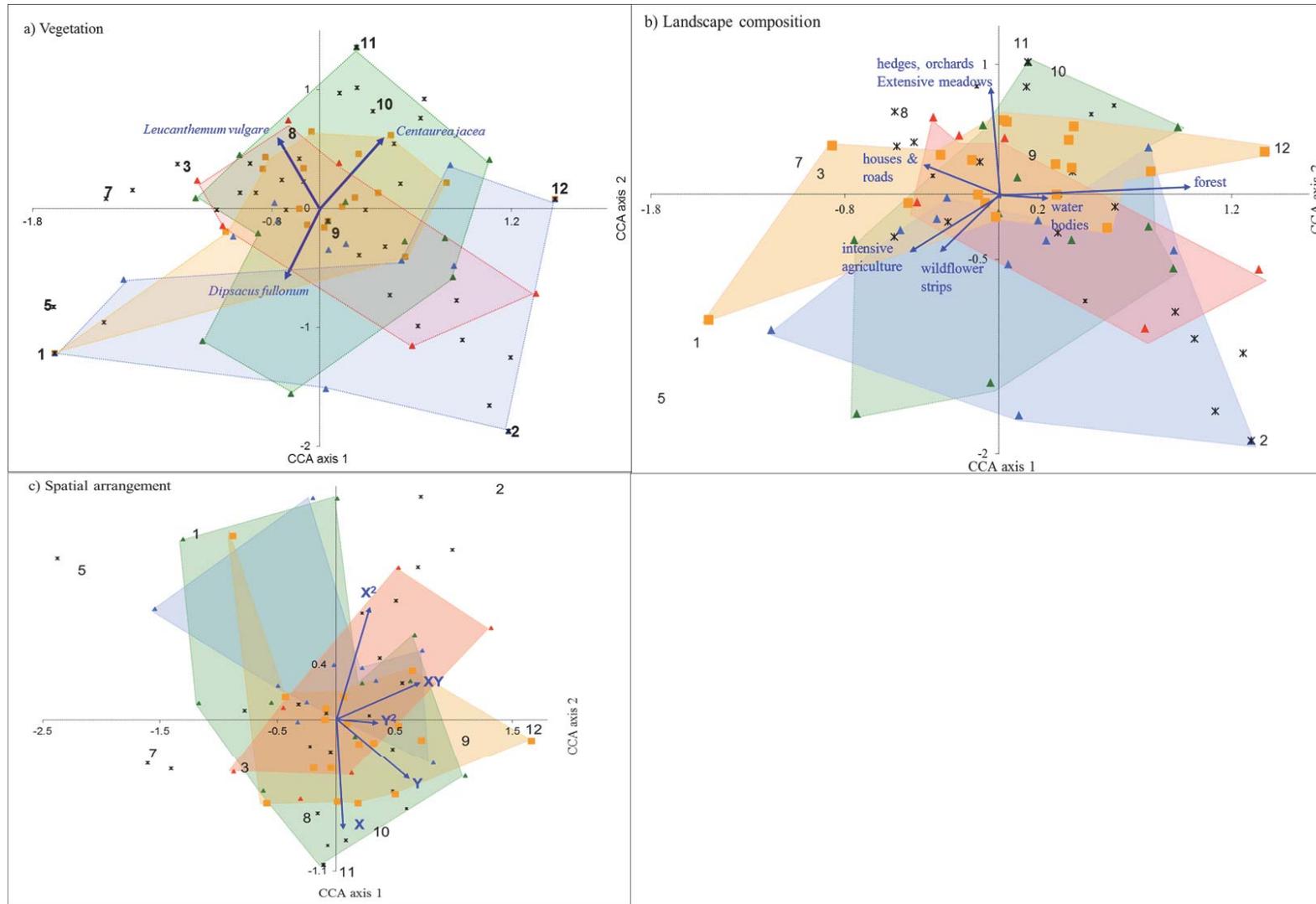


Fig. S4. Relationship between the three sets of environmental descriptors and the trap-nest community in canonical correspondence analyses. The host functional groups are shown as coloured areas: bees = orange squares, aphid predators = green triangles, other herbivore predators = blue triangles, spider predators = red triangles; enemies are shown with black stars. Only the most important among the 30 most abundant plant species are shown. Black numbers indicate the identity of the wildflower strips.

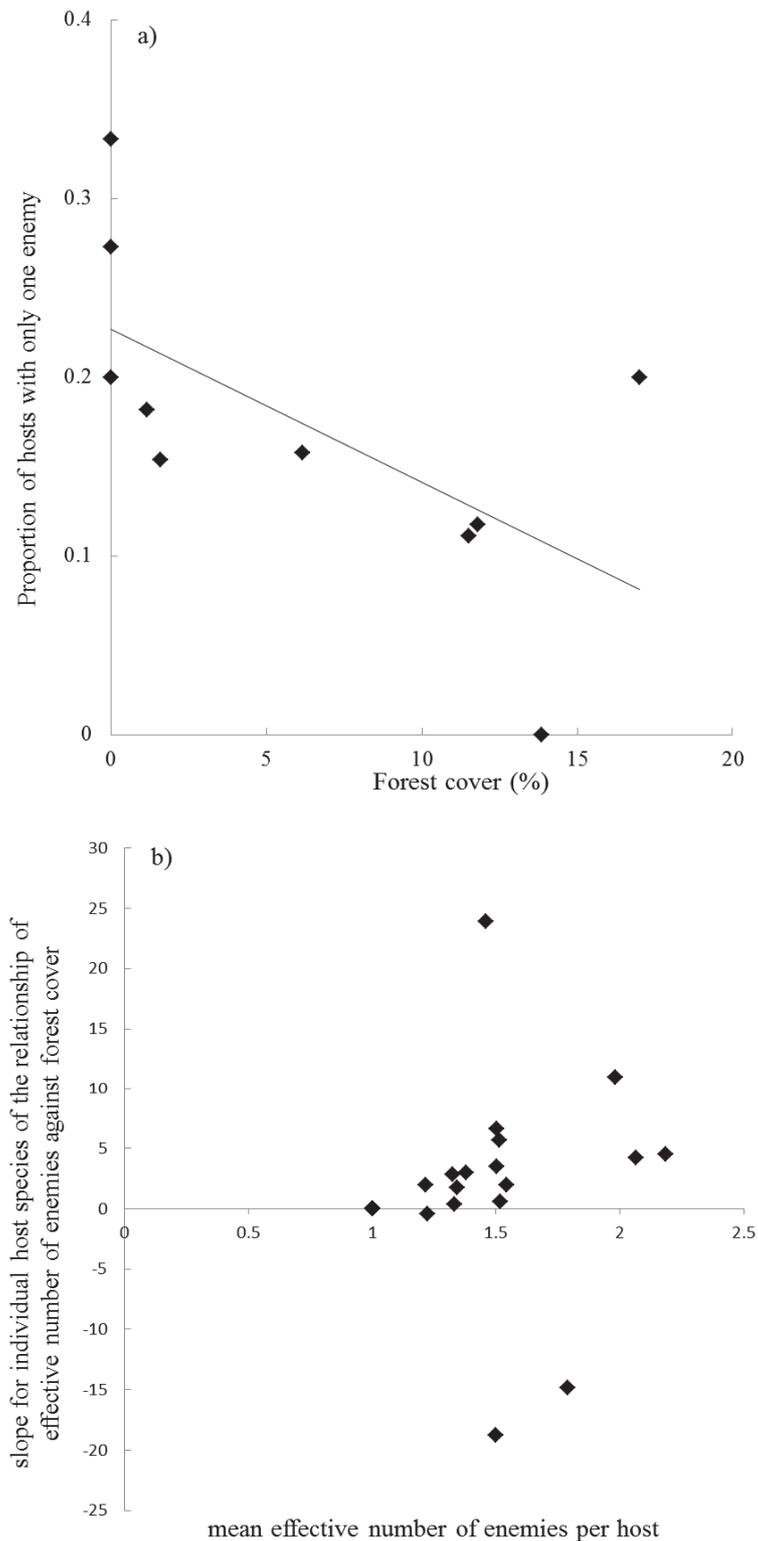


Fig. S5. Potential explanations for the relationship between forest cover and vulnerability. The relationship between a) the proportion of hosts that have only a single enemy and forest cover, and b) values of the slopes for individual host species in the effective number of enemies regressed against forest cover and their mean effective number of enemies over all 10 strips. It shows that most host species interact with more enemies in strips with greater forest cover.

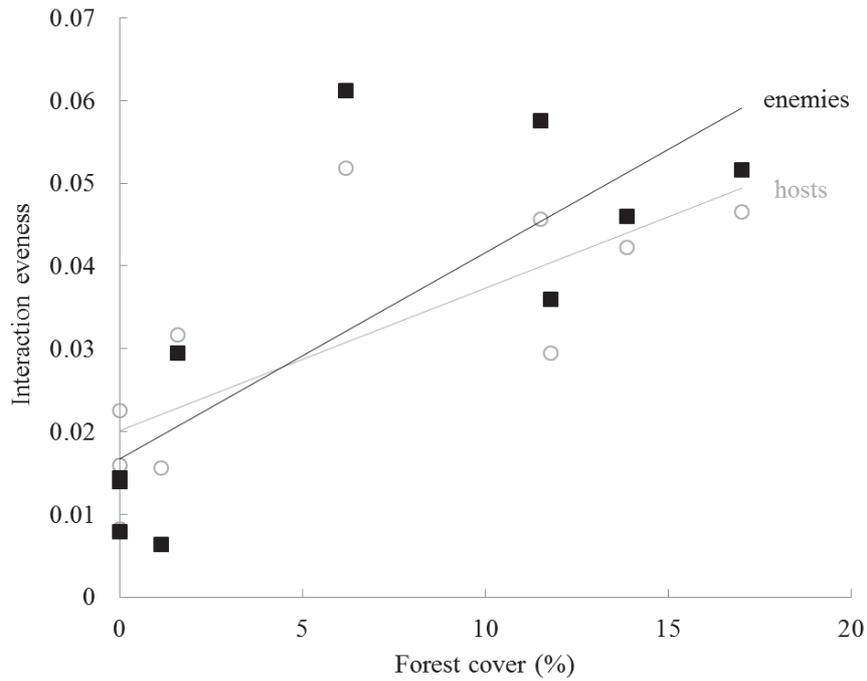


Fig. S6. Potential explanations for the relationship between forest cover and generality/vulnerability: the average interaction evenness of all hosts (grey circles) and enemies (black squares) in each strip as a function of forest cover. Evenness for a given host is measured as the ratio of the Shannon index for the frequencies of interactions with its enemies, over the maximum value of this index (the log of its number of enemies). Evenness for enemies is measured similarly, but based on interactions with hosts. Values given here are averages for each food web.

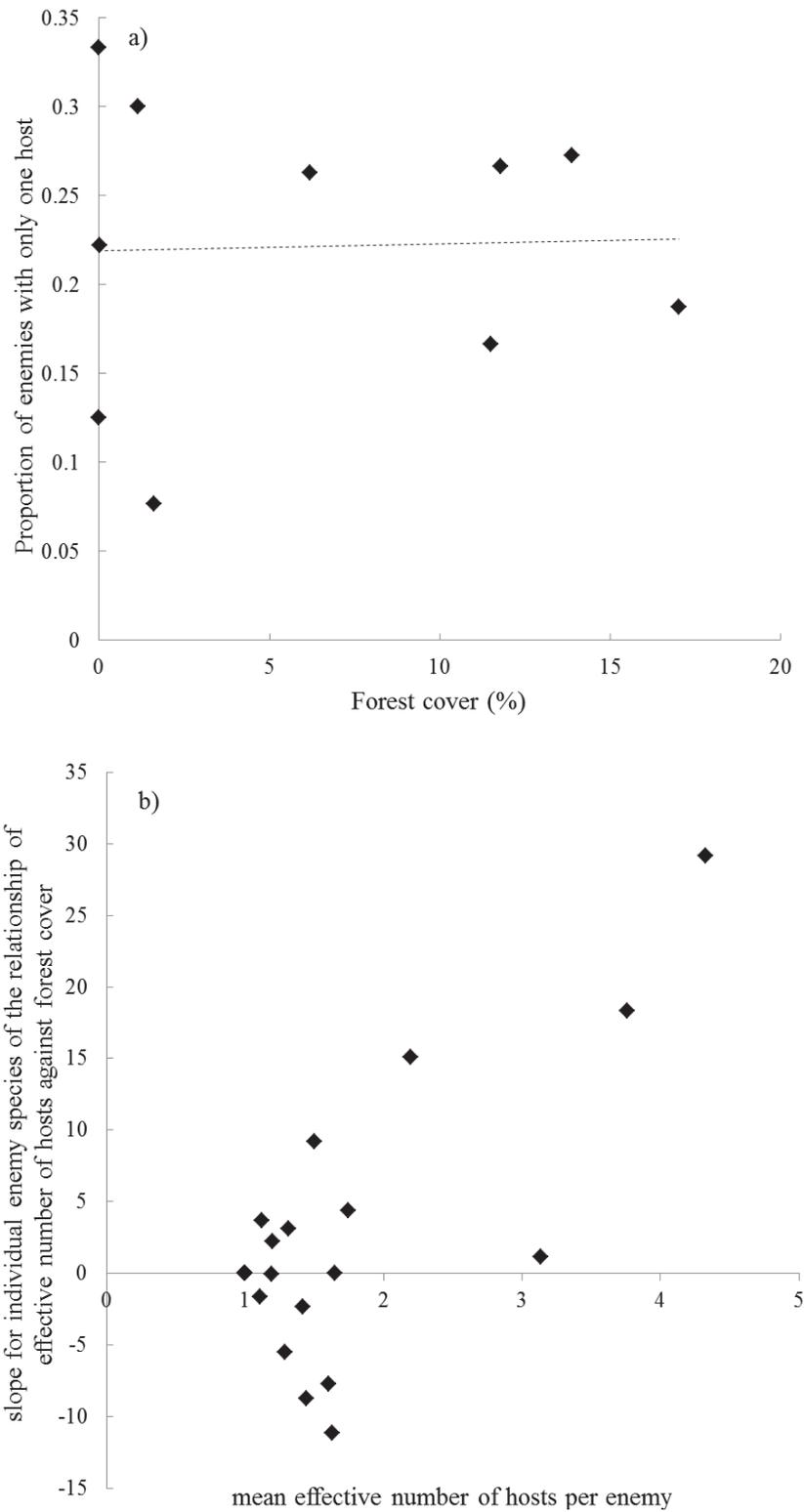


Fig. S7. Potential explanations for the relationship between forest cover and generality. The relationship between a) the proportion of enemies that have only a single host and forest cover, and b) the values of the slopes for individual enemy species in the effective number of hosts regressed against forest cover and their mean effective number of prey over all 10 strips. Enemies with the highest number of hosts are also those showing the strongest positive effect of forest cover.

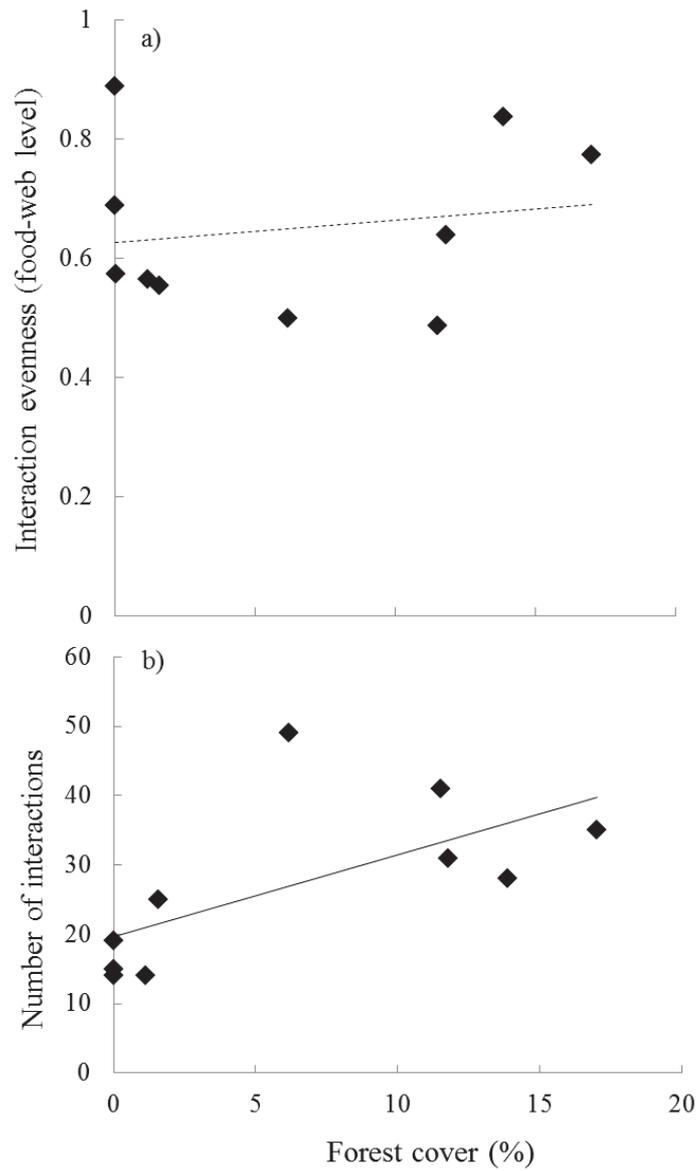


Fig. S8. Potential explanations for the relationship between forest cover and interaction diversity: a) the total interaction evenness for each food web as a function of forest cover and b) the total number of interactions of each food web as a function of forest cover.

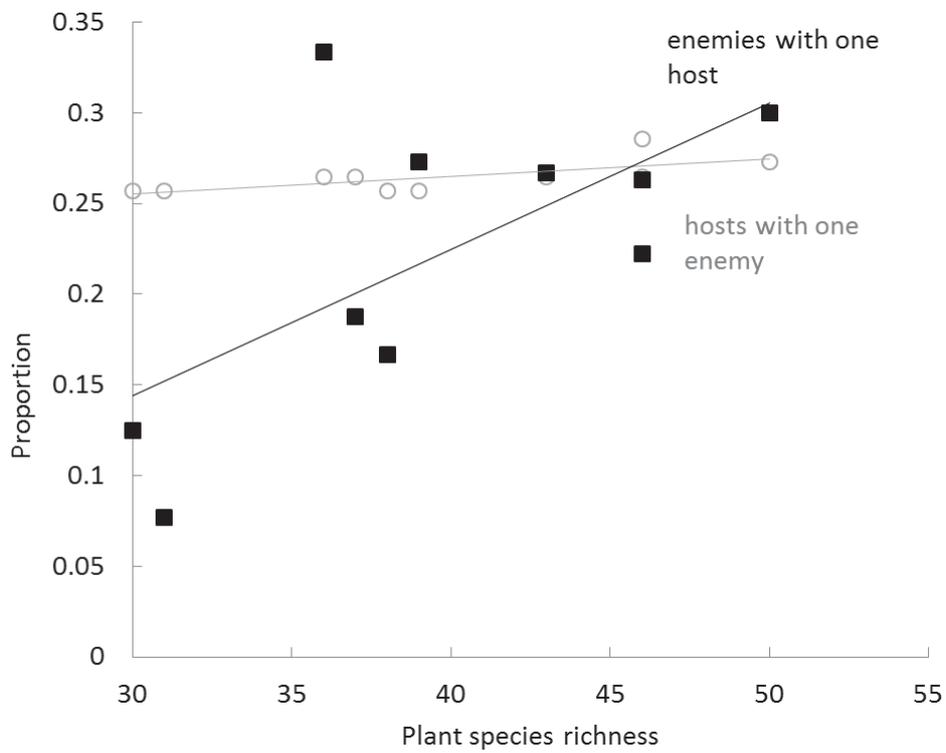


Fig. S9. A potential explanation for the relationship between plant species richness and compartmentalisation: the proportion of “specialist” hosts with only one enemy (grey circles) and of specialist enemies with only one host (black squares) both increase significantly with plant species richness.

4. Supplementary References

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