

SUPPORTING INFORMATION
Bi-trophic interactions shape biodiversity in space

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SI MATERIALS AND METHODS

S1 Model Description

As described in the main text, simulations are stochastic, in a lottery manner (1). This means that at each generation (=time step), N_p plants (N_a animals) are drawn at random to replace the N_p plants (N_a animals) of the previous generation. A detailed scheme of the spatial organization of the metacommunity can be found in Fig. S1.

The probabilities of this lottery are detailed in the main text. We here provide additional explanations for the choice of seed (egg) production equations. In the mutualistic case, we consider that there is a base seed (egg) production equal to $1 - c_p$ ($1 - c_a$) for plants (animals). For the plants, this base fecundity corresponds to selfing, that we here assume constant among species for simplicity. For the animals, assuming that fecundity is proportional to diet, the base fecundity corresponds to the diet part which is not achieved during the mutualistic interaction with the plants. The additional term corresponds to the part of seed (egg) production which depends on the mutualistic interaction. For the plants, we consider that each animal of species j effectively pollinates a flower of species i at a rate I_{ij} . Hence a flower of species i is pollinated at a total rate equal to $\sum_{j=1}^{S_a} n_j^a I_{ij}$. We further assume that flowers compete to attract animals, so that the pollinator-mediated fecundity of a flower of species i depends on the rate at which the flower is pollinated compared to the rate at which other flowers are pollinated. This leads to the expres-

sion: $c_p \frac{\sum_{j=1}^{S_a} n_j^a I_{ij}}{\sum_{k=1}^{S_p} \left(\frac{n_k^p}{N_p} \sum_{l=1}^{S_a} n_l^a I_{kl} \right)}$. Our formulation implies that a flower will have a fecundity

above (below) 1 if it is more (less) pollinated than an average flower. For the animals, we consider that animals gather resources from the plant at the same rate I_{ij} that they pollinate the plant, and that the plants provide a fixed amount of resources. We assume

1 that animals compete for these resources, so that an animal of species j gathers from a
2 plant of species i an amount of resources equal to $\frac{I_{ij}}{\sum_{k=1}^{S_a} \frac{n_k^a}{N_a} I_{ik}}$. When summing over the
3 relative frequency of the plants, we recover Equation 2. We additionally studied another
4 way to model animal fecundity, and obtained similar results (see *SI Section S2.11.2*). In
5 the antagonistic case, the reasoning is the same, except that plants are negatively affected
6 by the interaction.

7 This model formulation presents several advantages. First, it corresponds to a purely
8 neutral model when removing between groups interactions. Consequently, this model
9 enables to explore the deterministic effect of ecological interactions in a background of
10 demographic and environmental stochasticity as is often the case in nature (2). Second,
11 this model can be quickly simulated by coalescence, so that it is possible to fit this model
12 to real data by Approximate Bayesian Computation (see Methods). Third, by fixing con-
13 stant community sizes, it focuses on community composition by removing the potential
14 confounding influence of variations in community sizes. This constant community size
15 assumption is a good first approximation for plants in many terrestrial systems. Indeed,
16 herbivores generally have a limited feeding effect on plant biomass for various reasons in-
17 cluding the low food quality of many plant parts, and the control of insect herbivores by
18 natural enemies (3). Although it is not the case for insects, their population fluctuations
19 are likely to be mainly driven by factors not related to plants like climate (4). Conse-
20 quently, our fixed community size assumption is a good simplifying assumption which
21 is unlikely to make us miss any retroactions taking place between the plant and insect
22 groups. An alternative approach would have been to use Lotka-Volterra type equations
23 to model the coupled dynamics of plants and animals (5). A drawback of this approach
24 is that it requires a large number of species-specific parameters like intrinsic growth rates
25 and carrying capacities. Such an increase in the number of parameters would prevent

- 1 the model from being fitted to available data, in that we would need much additional
- 2 information on each species or community dynamics.

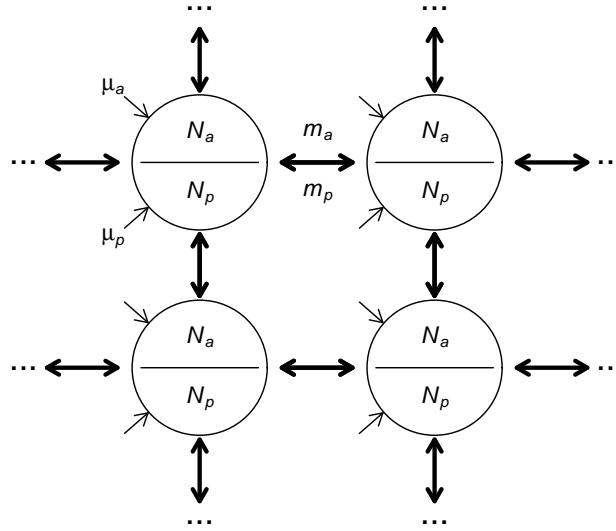


Fig. S1: Model representation. Circles stand for patches, horizontal and vertical arrows represent dispersal between neighboring patches, and oblique arrows indicate dispersal from the species pool. N_p (N_a) is the number of plant (animal) individuals in each patch. m_p (m_a) is the plant (animal) dispersal rate between neighboring patches. μ_p (μ_a) is the plant (animal) dispersal rate from the species pool to each patch.

1 **S2 Model results - impact on the plant set**

2 **S2.1 α diversity of plants**

3 In this section, we detail the results obtained in Fig. 2 of the main text. Let us start by
4 considering nested mutualistic networks produced with a threshold rule (Fig. 2A). For
5 the limiting case of low dispersal rates and weak mutualism (low m_p and c_p), we recover
6 Bastolla et al.'s result (5), namely, that nested networks tend to increase plant local
7 richness (bottom left of Fig. 2A). In this case, bi-trophic interactions have a stabilizing
8 effect (6) induced by the heterogeneity among animals in their plant preferences. Thus,
9 communities tend to gain species with over-dispersed traits during the coupled dynamics
10 (see "Variance Test" in *SI Section S2.5*). This limiting case without dispersal corresponds
11 to the standard network approach.

12 When dispersal rates increase and/or mutualistic interactions become stronger (larger
13 c_p), the positive effect of mutualistic interactions on plant richness decreases and even
14 becomes negative (Fig. 2A). The stabilizing effect of the mutualistic interactions is now
15 counterbalanced by their filtering effect: plants survive only if they encounter a corre-
16 sponding mutualist. We detect this filtering effect by computing the average interaction
17 strength between plant and animal individuals. When mutualistic interactions have a
18 negative impact on plant species richness, the average interaction strength increases com-
19 pared to the neutral case (see "Coupling Test" in *SI Section S2.4*). The surviving plants
20 are those which encounter more mutualists.

21 Similar results are obtained with antagonistic networks (Fig. 2B). In this case, when
22 bi-trophic interactions have a negative impact on plant species richness, the average inter-
23 action strength decreases compared to the neutral case (see "Coupling Test" in *SI Section*
24 *S2.4*). The surviving plants are those which encounter fewer antagonists.

1 Once we have considered nested networks, we now turn our attention to highly spe-
2 cialized networks. We obtained similar results for this type of networks (Fig. 2C-D). The
3 common feature of both nested and specialized networks is their low average degree (i.e.,
4 species interact on average with a low number of species), although the variance in degree
5 distribution is larger in nested networks. This average degree hence appears to play a
6 major role in how network architecture determines the impact of bi-trophic interactions
7 on plant richness.

8 When interactions are generalized both mutualistic and antagonistic networks increase
9 species richness at low dispersal rates and decrease it at high dispersal rates (Fig. 2E-F).
10 At low dispersal rates, local species richness is mainly controlled by local interactions.
11 When they are generalized, the filtering effect of the interactions is low, and the sta-
12 bilizing effect predominates. Equitability in plant abundance is low without bi-trophic
13 interactions and increases in the presence of such interactions. This increase in plant
14 equitability is positively correlated with the variation in plant richness in the presence
15 of interactions (see “Equitability Test” in *SI Section S2.6*). At higher dispersal rates,
16 local species richness increases and becomes more dependent on the recurrent dispersal of
17 locally rare species. When disrupting the fitness equivalence among individuals, interac-
18 tions tend to destabilize this dynamic equilibrium (7). This disruption leads to a reduced
19 equitability in species abundances and, ultimately, in species loss (see “Equitability Test”
20 in *SI Section S2.6*). This result is in agreement with a recent meta-analysis of herbi-
21 vore exclusion experiments showing that herbivory reduced plant species richness when
22 equitability in plant abundances was high, and vice versa (8).

23 Along the second axis of variation, we find that mutualistic interactions have an in-
24 creased negative effect on plant richness for stronger values of coupling c_p (Fig. 2E).
25 This is due to an increase of the filtering effect of the interaction, as encountered earlier

1 for specialized interactions. In contrast, we find the reverse relationship for antagonis-
2 tic interactions: stronger coupling leads to an increased positive effect on plant richness,
3 especially at low dispersal rates (Fig. 2F). Here the stabilizing effect of herbivores ex-
4 ceeds their filtering effect, so that the resulting effect of herbivores on plants is positive.
5 Stronger coupling between plants and herbivores thus increase the magnitude of this pos-
6 itive effect, especially at low dispersal rates for which local interactions have the strongest
7 impact on community dynamics.

8 The balance between the filtering and the stabilizing effects also depends on the species
9 richness of the plant set, both at the local and regional scales. In metacommunities with
10 larger regional species richness, we find a stronger positive effect of both mutualistic and
11 antagonistic interactions on local plant species richness. In contrast, in communities with
12 larger local richness, we observe a stronger negative effect of both interaction types on
13 plant richness, this contrast being stronger for antagonistic interactions (see *SI Section*
14 *2.7*). These results differ from those of Thébault and Fontaine (9) who studied network
15 dynamics in closed communities and found that higher diversity promotes persistence
16 in mutualistic networks and destabilizes it in antagonistic ones. Our current results,
17 therefore, show that local and regional diversity may be associated with different effects
18 of bi-trophic interactions in spatially-extended systems. Another difference is that, as
19 reported here, local and regional richness have a very small correlation with the effect of
20 bi-trophic interactions on plant richness in this spatially extended model ($R^2 = 0.01$).

21 **S2.2 β diversity of plants**

22 Up to here, we have described patterns of local species richness, namely, plant richness
23 at each lattice site. Our framework also enabled us to study the effect of bi-trophic inter-
24 actions on plant richness at the regional scale, i.e., considering the regional abundances

1 across the entire lattice. When interactions have a negative effect on plant local richness,
2 β diversity simultaneously increases (Fig. S2). In 91% (89 %) of the cases for mutual-
3 istic (antagonistic) interactions, the decrease in metacommunity richness is smaller than
4 the decrease in local richness. For the small system size used in the simulations (5×5
5 patches), this increase in β diversity is not always sufficient to make up for decreases in
6 local richness; consequently metacommunity richness can also decrease due to both mutu-
7 alistic and antagonistic interactions. However, as system size increases in the simulations,
8 metacommunity richness becomes less affected by bi-trophic interactions (Fig. S3A). This
9 means that animals do not act to filter the same plant species in every patch, thereby
10 increasing the spatial structure of plant diversity. Indeed, when computing the relative
11 fecundity of plant species in each patch, we find that 63% (56%) of the plant species are
12 positively filtered in at least one patch by the mutualistic (antagonistic) animal group
13 (see *SI Section S2.10*). These results suggest that bi-trophic interactions tend to strongly
14 impact the spatial heterogeneity of plant diversity.

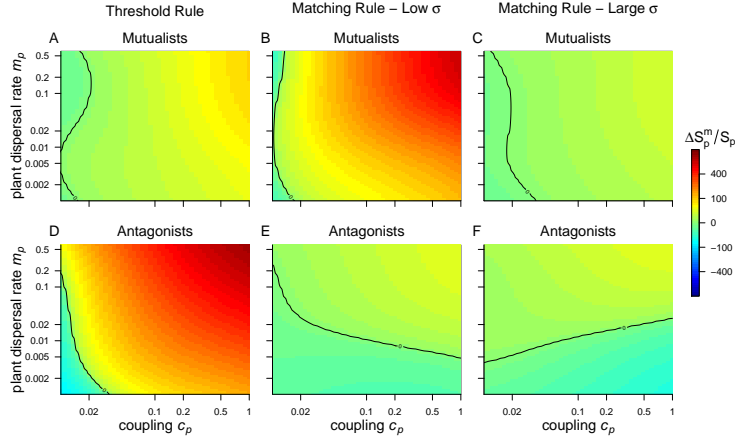


Fig. S2: Relative variation (in %) of plant β diversity between trophically coupled and uncoupled communities. β diversity is measured as the ratio of metacommunity over local plant richness S_p^m/S_p . Panels A and D display a threshold model of interaction with one trait; panels B and E show results for the matching model with one trait and $\sigma = 0.015$; panels C and F are based on a matching model with one trait and $\sigma = 1$. Panels A-C correspond to mutualistic interactions. Panels D-F correspond to antagonistic interactions. Parameter values are $\mu_p = \mu_a = 0.004$, $m_a = 0.625$, $c_a = 0.16$.

1 S2.3 Effects of the model parameters on the impact of bi-trophic 2 interactions

3 As mentioned in the main text, mutualistic and antagonistic interactions can have both
4 positive and negative effects on plant richness S_p , but also on Shannon's diversity H_p .
5 We explore the effects of each model parameter and interaction type by multiple regres-
6 sions (Tables S1-4). In these regressions, the dependent variable is the relative varia-
7 tion in species richness due to the bi-trophic interactions: $\Delta S_p = (S_p^i - S_p^n)/S_p^n$, and
8 $\Delta H_p = (H_p^i - H_p^n)/H_p^n$, where the superscript i means with interaction, and n without
9 interaction.

10 Less diverse, more dispersal-limited, and more strongly impacted plant sets are ex-
11 perienceing a stronger filter from both mutualistic and antagonistic interactions: plant

1 dispersal rates m_p and μ_p are positively correlated with variations in plant Shannon's
2 index ΔH_p , while the interaction impact on plants c_p is negatively correlated with ΔH_p
3 (Tables S3-4). Parameter effects are less straightforward when looking at variation in
4 plant species richness ΔS_p (Tables S1-2), probably because they impact plant diversity
5 patterns at both local and metacommunity scales, and these patterns have contradictory
6 effects on local plant persistence (see below). Parameters of the animal set have overall a
7 lower effect on plant composition.

1 Table S1: Effect of mutualistic interactions on the variation in plant species richness

2 ΔS_p .

3 *the first (second) number is the number of matching (threshold) rules.

4 $R^2 = 0.52$

5

Parameter	Estimate	Standard Error	<i>p</i> -value
Intercept	-0.08	0.002	<2e-16
μ_p	5.06	0.18	<2e-16
μ_a	3.11	0.18	<2e-16
m_p	-0.09	0.001	<2e-16
m_a	-0.03	0.001	<2e-16
c_p	-0.53	0.001	<2e-16
c_a	0.09	0.001	<2e-16
Model_1-0*	-0.12	0.002	<2e-16
Model_0-2*	-0.13	0.002	<2e-16
Model_1-1*	-0.25	0.002	<2e-16
Model_2-0*	-0.19	0.002	<2e-16
Model_1-2*	-0.33	0.002	<2e-16
Model_2-1*	-0.30	0.002	<2e-16
Model_2-2*	-0.37	0.002	<2e-16
σ	0.04	0.0001	<2e-16

6

1 Table S2: Effect of antagonistic interactions on the variation in plant species richness

2 ΔS_p .

3 *the first (second) number is the number of matching (threshold) rules.

4 $R^2 = 0.12$

5

Parameter	Estimate	Standard Error	<i>p</i> -value
Intercept	-0.17	0.007	<2e-16
μ_p	-17.87	0.73	<2e-16
μ_a	9.01	0.73	<2e-16
m_p	-0.38	0.005	<2e-16
m_a	-0.04	0.005	6e-13
c_p	0.09	0.003	<2e-16
c_a	0.14	0.003	<2e-16
Model__1-0*	0.27	0.007	<2e-16
Model__0-2*	-0.43	0.009	<2e-16
Model__1-1*	-0.39	0.007	<2e-16
Model__2-0*	0.14	0.007	<2e-16
Model__1-2*	-0.56	0.007	<2e-16
Model__2-1*	-0.37	0.007	<2e-16
Model__2-2*	-0.51	0.007	<2e-16
σ	0.06	0.0004	<2e-16

6

1 Table S3: Effect of mutualistic interactions on the variation in plant equitability ΔH_p .

2 *the first (second) number is the number of matching (threshold) rules.

3 $R^2 = 0.49$

4

Parameter	Estimate	Standard Error	<i>p</i> -value
Intercept	-0.07	0.002	<2e-16
μ_p	14.15	0.19	<2e-16
μ_a	1.96	0.19	<2e-16
m_p	0.06	0.001	<2e-16
m_a	-0.03	0.001	<2e-16
c_p	-0.47	0.001	<2e-16
c_a	0.08	0.001	<2e-16
Model_1-0*	-0.19	0.002	<2e-16
Model_0-2*	-0.13	0.002	<2e-16
Model_1-1*	-0.30	0.002	<2e-16
Model_2-0*	-0.29	0.002	<2e-16
Model_1-2*	-0.39	0.002	<2e-16
Model_2-1*	-0.38	0.002	<2e-16
Model_2-2*	-0.45	0.002	<2e-16
σ	0.05	0.0001	<2e-16

5

1 Table S4: Effect of antagonistic interactions on the variation in plant equitability ΔH_p .

2 *the first (second) number is the number of matching (threshold) rules.

3 $R^2 = 0.33$

4

Parameter	Estimate	Standard Error	<i>p</i> -value
Intercept	-0.36	0.002	<2e-16
μ_p	18.71	0.23	<2e-16
μ_a	-0.24	0.23	0.31
m_p	0.03	0.002	<2e-16
m_a	-0.03	0.002	<2e-16
c_p	-0.40	0.001	<2e-16
c_a	0.07	0.001	<2e-16
Model_1-0*	0.32	0.002	<2e-16
Model_0-2*	-0.08	0.003	<2e-16
Model_1-1*	-0.07	0.002	<2e-16
Model_2-0*	0.26	0.002	<2e-16
Model_1-2*	-0.08	0.002	<2e-16
Model_2-1*	-0.04	0.002	<2e-16
Model_2-2*	-0.04	0.002	<2e-16
σ	0.01	0.0001	<2e-16

5

1 S2.4 Coupling Test

2 Animals have two opposite effects on plant assemblages. Individually, they have a filtering
3 effect by introducing fitness differences among species. But collectively, they have a sta-
4 bilizing effect by introducing some kind of heterogeneity in resources (6). The emergent
5 effect of the interactions thus depends on the relative importance of these two counter-
6 acting effects.

7 We introduce a statistic (IS) that measures the average interaction strength between
8 plants and animals:

$$IS = \frac{\sum_{i,j} I_{ij}}{S_p S_a}, \quad (S1)$$

9 where I_{ij} indicates the interaction strength between plant i and animal j . Before starting
10 the dynamics with bi-trophic interactions, we compute the initial interaction strength IS^n
11 between plants and animals. To do this, we use plant and animal abundances obtained
12 with neutral assembly and I_{ij} values subsequently used in the dynamics with interactions.
13 At the end of the dynamics with interactions (100 generations forward), we compute the
14 final interaction strength IS^i between plants and animals, using final abundances of plants
15 and animals. We record the variation of the interaction strength $\Delta IS = IS^i - IS^n$ due
16 to the dynamics with bi-trophic interactions. When interactions are mutualistic and
17 their impact on plants is dominated by the filtering effect, plants survive only if they
18 encounter some well-adapted mutualists. Interactions should thus produce an increase of
19 the statistics IS . For antagonistic interactions, on the contrary, plants survive only if they
20 do not encounter well-adapted antagonists, and the statistics IS should then decrease. If
21 our interpretation is correct, then ΔS_p should be negatively (positively) correlated with
22 ΔIS when interactions are mutualistic (resp. antagonistic). This is what we observed

1 ($R^2 = 0.02$ and 0.03 respectively, $p < 0.001$). Note that IS is not correlated with S_p and
2 H_p , hence the correlation observed here is not spurious.

3 **S2.5 Variance Test**

4 To measure the stabilizing effect of the bi-trophic interactions, we use the statistic VT
5 which measures the average variance in trait values among plant individuals, the average
6 being done among the t traits involved in the interactions. The stabilizing effect should
7 produce an increase in VT . If our interpretation is correct, then ΔS_p should be positively
8 correlated with ΔVT . A possible confounding effect, though, is that VT is positively cor-
9 related with S_p and H_p . Hence, this dependence of VT should be taken into account when
10 testing for a correlation between ΔVT and ΔS_p . To do this, we fit a multiple linear regres-
11 sion of VT^n against S_p^n and H_p^n using the simulated non-interacting communities. We then
12 use this fitted regression to predict VT_{fit}^i based on the values of S_p^i and H_p^i observed in the
13 interacting communities. We then define a modified $\Delta VT = (VT_{observed}^i - VT_{fit}^i) / VT_{fit}^i$.
14 Using this conservative statistic, we find a positive correlation between ΔVT and ΔS_p
15 ($R^2 = 0.56$ and 0.10 respectively, $p < 0.001$).

16 **S2.6 Equitability Test**

17 Hillebrand et al. (8) meta-analyzed herbivore exclusion experiments, and found that her-
18 bivory was reducing (increasing) plant species richness when equitability in plant abun-
19 dances (measured by $H' = H/\ln(S)$) was high (low). We found the same negative rela-
20 tionship between the equitability before the interactions $H^n = H_p^n/\ln(S^n)$ and ΔS_p (R^2
21 $= 0.007$ and 0.019 respectively, $p < 0.001$), and this relationship was stronger for antago-
22 nistic and generalized interactions (i.e., matching interaction rule with one or two traits,
23 and $\sigma > 1$, $R^2 = 0.008$ and 0.09 respectively, $p < 0.001$).

1 **S2.7 Effect of network richness on the impact of bi-trophic inter-** 2 **actions**

3 We also investigate the effect of species richness at both the local patch, and the (land-
4 scape) metacommunity on the variation in plant species richness by linear regressions. As
5 mentioned in the main text, larger metacommunity richness is associated with stronger
6 positive effect of both mutualistic and antagonistic interactions on plant species richness,
7 while larger local richness is associated with stronger negative effect of both interaction
8 types ($R^2 = 0.01$, $p < 0.001$).

9 **S2.8 Temporal turnover**

10 As mentioned in the main text, two statistics of temporal turnover in species composition
11 from one generation to the next have been computed for both plants and animals, in
12 both uncoupled and coupled metacommunities. The first statistic is the Jaccard index of
13 similarity J and is computed as follows:

$$J = \frac{\sum_i I(n_i^t > 0) I(n_i^{t-1} > 0)}{\sum_i I(n_i^t + n_i^{t-1} > 0)}, \quad (\text{S2})$$

14 where n_i^t is the number of individuals of species i at generation t , and $I(n > 0)$ equals 1
15 if $n > 0$ and 0 otherwise.

16 The second statistic is an abundance-weighted version of the Jaccard index and is
17 computed as follows:

$$J_q = \frac{\sum_i I(n_i^t > 0) I(n_i^{t-1} > 0) (n_i^t + n_i^{t-1})}{\sum_i (n_i^t + n_i^{t-1})}, \quad (\text{S3})$$

18 Larger J and J_q values indicate a lower temporal turnover.

19 We investigate how variations in community equitability due to bi-trophic interactions

1 are correlated with variations in the temporal turnover of communities due to these same
2 bi-trophic interactions. Temporal turnover is measured with the Jaccard index of similar-
3 ity across time steps (J) and its abundance-weighted version (J_q). Since these statistics
4 are correlated with H_p in non-interacting communities, variations in H_p due to the interac-
5 tions could mechanically cause variations in J and J_q , without any real effect of bi-trophic
6 interactions on the way community composition varies with time. We hence fit two linear
7 regressions of J^n and J_q^n against H_p^n using the simulated non-interacting communities. We
8 then use this fitted regression to predict J_{fit}^i and J_{qfit}^i based on the values of H_p^i observed
9 in the interacting communities. We then define a modified $\Delta J = (J_{observed}^i - J_{fit}^i) / J_{fit}^i$,
10 and a modified $\Delta J_q = (J_{observed}^i - J_{qfit}^i) / J_{qfit}^i$. Using these conservative statistics, we
11 find a positive correlation between ΔJ and ΔH_p for both mutualistic and antagonistic
12 interactions ($R^2 = 0.44$ and 0.35 respectively, $p < 0.001$), and between ΔJ_q and ΔH_p (R^2
13 $= 0.72$ and 0.02 respectively, $p < 0.001$). Since J and J_q measure temporal similarity, this
14 means that in communities experiencing a stronger filter from the bi-trophic interactions
15 (lower ΔH_p), temporal turnover will be larger than expected if bi-trophic interactions
16 were not modifying community dynamics. In such communities, a core of plant species
17 are temporally stabilized by the interactions, while a subset of species become satellites
18 which are temporally unstable (10).

19 **S2.9 Interactions mostly affect rare species**

20 Mutualists and antagonists principally affect the presence and abundance of rare plant
21 species. When comparing coupled and uncoupled plant communities, the abundance-
22 weighted measure of similarity J_q is larger than the unweighted measure J in 97% (resp.
23 95%) of the cases for mutualistic (resp. antagonistic) interactions.

1 **S2.10 Interactions produce a spatially heterogeneous filter**

2 At the end of the coupled metacommunity dynamics, we test whether the filtering effect
3 of the animal set on the plant one is homogeneous across space. To do this, we compute
4 the relative fecundity of each plant species in each patch. The relative fecundity of plant
5 species i equals $f_i^p / \sum_k \frac{n_k^p}{N_p} f_k^p$. For each plant species, we count the number of patches where
6 its relative fecundity is above 1, meaning that it obtains a local competitive advantage
7 due to bi-trophic interactions. We find that 63% (56%) of the plant species are positively
8 filtered in at least one patch due to mutualistic (antagonistic) interactions. To perform
9 this analysis, we used a large grid of 20×20 patches, and a subset of parameter values: μ_p
10 and μ_a in $\{0.0005; 0.004\}$, m_p and m_a in $\{0.005; 0.625\}$, c_p and c_a in $\{0.04; 0.64\}$. We only
11 considered interaction rules with one trait, using either a threshold rule or a matching rule
12 with σ in $\{0.015; 1\}$. We performed 10 replicates per combination of parameters values.

13 **S2.11 Robustness of the results**

14 **S2.11.1 Effect of the number of patches used in the simulations**

15 To perform this computer intensive study, we used a relatively small number of patches:
16 a grid of $l \times l$ patches, with $l = 5$. We performed additional simulations with $l = 10$,
17 and $l = 20$ for a subset of parameter values: $\mu_p = \mu_a = 0.005$, m_p in $\{0.001; 0.005;$
18 $0.025; 0.125; 0.625\}$, m_a in $\{0.005; 0.625\}$, c_p in $\{0.01; 0.04; 0.16; 0.64; 1\}$, and $c_a = 0.01$.
19 For these simulations, we only considered interaction rules with one trait, using either
20 a threshold rule, or a matching rule with σ in $\{0.015; 0.125; 1; 8\}$. We performed 10
21 replicates per combination of parameters values, and computed in each simulation the
22 variation in plant metacommunity richness due to bi-trophic interactions ΔS_p^{met} , and the
23 variation in local plant richness ΔS_p . As the number of patches in the metacommunity
24 increases, the distribution of ΔS_p^{met} converges to zero (Fig. S3A). On the contrary, system

1 size has little impact on the variation in local plant richness due to bi-trophic interactions
2 (Fig. S3B). This means that for large (and realistic) system sizes, bi-trophic interactions
3 have a weak effect on metacommunity richness, but change local richness patterns, and
4 hence the spatial structure of plant diversity.

5 We additionally performed correlations between ΔS_p and ΔH_p in these simulations
6 with larger l , and the statistics ΔS_p , and ΔH_p of the main text. We computed the
7 correlations R^2 , as well as the slopes and intercepts of reduced major axis regressions,
8 using the R package "smatr" (11). Correlations were high ($R \geq 0.91$), intercepts close to
9 0 ($|intercept| \leq 0.062$), and slopes close to 1 ($|slope - 1| \leq 0.081$).

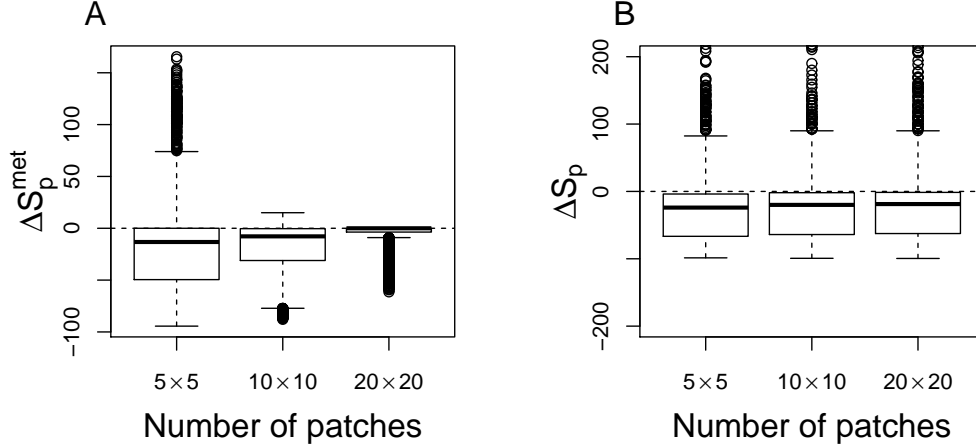


Fig. S3: Effect of system size on bi-trophic impact. Panel A: Distribution of ΔS_p^{met} as a function of the number $l * l$ of patches in the simulations. Panel B: Distribution of ΔS_p as a function of the number $l * l$ of patches in the simulations.

1 S2.11.2 Symmetric model of interaction

2 We evaluated the sensitivity of our results to the way we modeled the plants' impact
 3 on their interactors. We considered alternative models of mutualistic and antagonistic
 4 interactions, replacing Eq. (2) in the main text by:

$$f_i^a = (1 - c_a) + c_a \frac{\sum_{j=1}^{S_p} n_j^p I_{ji}}{\sum_{k=1}^{S_a} \left(\frac{n_k^a}{N_a} \sum_{l=1}^{S_p} n_l^p I_{lk} \right)}. \quad (S4)$$

5 We performed the same simulation analysis of these two models on a subset of the
 6 parameter grid: we used the same subset as for the analysis studying the variation in
 7 number of patches. We computed the same statistics ΔS_p and ΔH_p , which summarize
 8 the way interactions affect community composition. For these calculations, community
 9 statistics were averaged over the 10 simulated replicates. For each of these statistics, we
 10 computed the correlations R^2 between their values in these symmetric models, and
 11 their values in the models reported in the main text, as well as the slopes and intercepts

1 of reduced major axis regressions. Correlations were high ($R \geq 0.95$), intercepts close to
2 0 ($|intercept| \leq 0.062$), and slopes close to 1 ($|slope - 1| \leq 0.051$).

3 **S2.11.3 Variation in community size**

4 We evaluated the robustness of our results to variations in the animal group sizes N_a .
5 We considered the alternative values $N_a = 40$, and $N_a = 1000$. We performed the same
6 simulation analysis as in the main text, on a subset of the parameter grid: we used the
7 same subset as for the analysis studying the variation in number of patches. We computed
8 the same statistics ΔS_p and ΔH_p , which summarize the way interactions affect community
9 composition. For these calculations, community statistics were averaged over the 10
10 simulated replicates. For each of these statistics, we computed the correlations R^2 with
11 the simulations of the main text, as well as the slopes and intercepts of reduced major axis
12 regressions. Correlations were high ($R \geq 0.89$), intercepts close to 0 ($|intercept| \leq 0.072$),
13 and slopes close to 1 ($|slope - 1| \leq 0.124$).

14 **S2.11.4 Variation in boundary conditions**

15 We evaluated the robustness of our results to boundary conditions. We considered two
16 alternative conditions: a reflexive condition, where migrants crossing the boundary return
17 to their patch of origin; and a condition where migrants crossing the boundary are lost. We
18 performed the same simulation analysis as in the main text, on a subset of the parameter
19 grid: we used the same subset as for the analysis studying the variation in number of
20 patches. We computed the two statistics ΔS_p and ΔH_p . For each of these statistics, we
21 computed the correlations R^2 with the simulations of the main text, as well as the slopes
22 and intercepts of reduced major axis regressions. Correlations were high ($R \geq 0.95$),
23 intercepts close to 0 ($|intercept| \leq 0.024$), and slopes close to 1 ($|slope - 1| \leq 0.046$).

1 **S3 Model results - impact on the animal set**

2 We performed similar analyses, focusing this time on the effect of bi-trophic interactions
3 on the animal set. Overall, we found very similar results. The analogue of Fig. 2 for
4 animals is reported in Fig. S4, while the analogue of Fig. S2 is reported in Fig. S5. By
5 comparing Fig. 2 and Fig. S4, one can note that the main differences is that herbivores are
6 more positively impacted than plants by bi-trophic interactions when they are specialized
7 (Panel D in Fig.2, panel E in Fig. S4), while this is the opposite when interactions are
8 generalized (Panels F in the two figures). Indeed, when they are specialized, herbivores
9 feed on different plant species and thereby easily coexist (12), while for plants, another
10 effect is at stake: although herbivore feeding have a stabilizing effect (13), specialized
11 herbivores also induce fitness differences among species, while generalized herbivores have
12 a more equalized effect.

13 The coupling test (see *Section S2.4*) provides coherent results. When animals are neg-
14 atively filtered by bi-trophic interactions, the average interaction strength IS increases
15 for both mutualists and antagonists ($R^2 = 0.07$ and 0.02 respectively, $p < 0.001$): only
16 the more interacting animals are surviving. The variance test (see *Section S2.5*) is also
17 providing coherent results: when animals are positively impacted by bi-trophic interac-
18 tions, their trait variance increase in both mutualistic and antagonistic cases ($R^2 = 0.11$
19 and 0.005 respectively, $p < 0.001$). As for plants, larger animal metacommunity richness is
20 associated with more positive bi-trophic effect, while we observe the opposite correlation
21 with animal local richness in both mutualistic and antagonistic cases ($R^2 = 0.08$ and 0.03
22 respectively, $p < 0.001$, see *Section S2.7*). Temporal similarity in animal composition (mea-
23 sured by J and J_q) is also positively correlated with animal equitability H_a , as we had
24 observed for plants ($R^2 = 0.0001$ and 0.0001 respectively for J and $R^2 = 0.001$ and 0.0001

1 for J_q , $p < 0.001$, see *Section S2.8*). Finally, bi-trophic interactions are also mostly impact-
 2 ing rare animal species: when comparing coupled and uncoupled animal communities, the
 3 abundance-weighted measure of similarity J_q is larger than the unweighted measure J in
 4 97% (92%) of the cases for mutualistic (antagonistic) interactions (see *Section S2.9*).

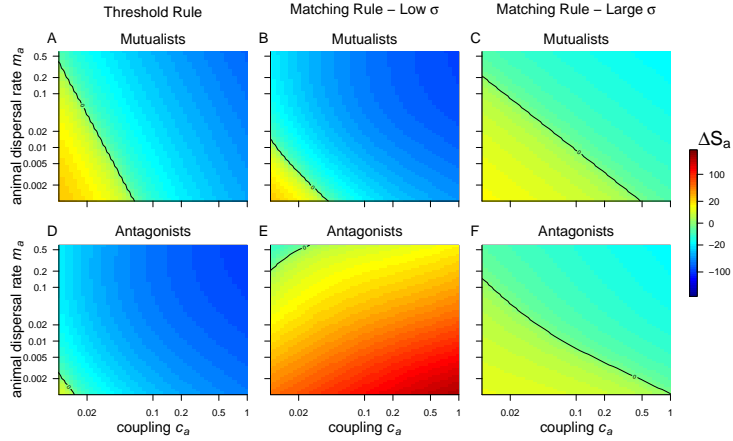


Fig. S4: Relative variation (in %) of animal α diversity between trophically coupled and uncoupled communities. α diversity is measured as the local animal species richness S_a . A positive value means that trophically coupled communities are species-richer than uncoupled ones. Different panels show results for the threshold model with one trait (A and D), the matching model with one trait and $\sigma = 0.015$ (B and E), and the matching model with one trait and $\sigma = 1$ (C and F). Panels A-C correspond to mutualistic interactions, while panels D-F correspond to antagonistic interactions. Parameter values are $\mu_p = \mu_a = 0.004$, $m_p = 0.625$, $c_p = 0.16$.

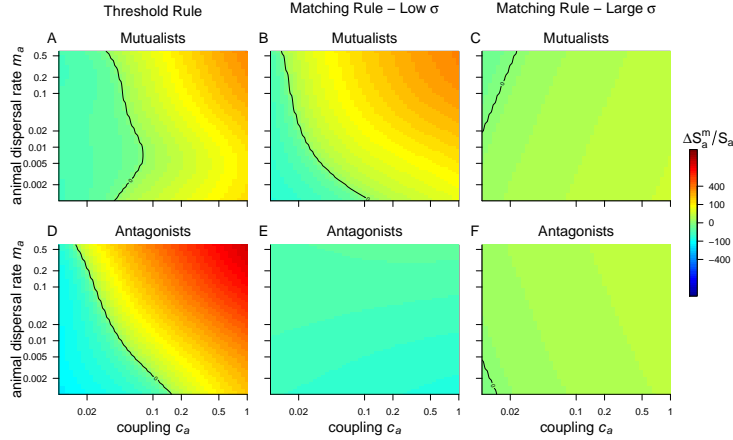


Fig. S5: Relative variation (in %) of animal β diversity between trophically coupled and uncoupled communities. β diversity is measured as the ratio of metacommunity over local animal richness S_a^m/S_a . Panels A and D display a threshold model of interaction with one trait; panels B and E show results for the matching model with one trait and $\sigma = 0.015$; panels C and F are based on a matching model with one trait and $\sigma = 1$. Panels A-C correspond to mutualistic interactions. Panels D-F correspond to antagonistic interactions. Parameter values are $\mu_p = \mu_a = 0.004$, $m_p = 0.625$, $c_p = 0.16$.

1 S4 Application to real datasets

2 S4.1 Approximate Bayesian Computation (ABC) procedure

3 Since the effects of the interactions depend on the interaction rules used (Tables S1-4),
 4 and given that not all interaction rules lead to realistic ecological networks (14), we want
 5 to constrain our simulation results so that they use realistic network structure. To fit
 6 observed networks, we use Approximate Bayesian Computation (15). It consists here in
 7 six steps (see Fig. 1 in the main text).

8 First, we simulate a neutral uncoupled metacommunity of plants and animals to serve
 9 as a benchmark to quantify bi-trophic impact on the plant set, drawing at random all
 10 the model parameters in uniform prior distributions. Prior distributions express our

1 uncertainty on the parameters values before confronting them to real data.

2 Second, starting from this neutral metacommunity, we simulate a coupled dynamics of
3 plants and animals using Eqs. (1) and (2) of main text, choosing one of the 8 interaction
4 rules in turn, and drawing at random all the additional model parameters (linked to the
5 interaction) in uniform prior distributions. The prior distributions were tailored to each
6 dataset so as to reduce computing time. Indeed, only some areas of the parameter space
7 are likely to produce networks similar to the observed ones. The priors used for each
8 dataset are reported in Table S5.

9 Third, at the end of the dynamics, a network of interactions is simulated with the
10 same total number of interactions N_n^{obs} as in the real dataset. N_n^{obs} animals are drawn
11 at random proportionally to their local abundance, and they are simulated to interact
12 with one of the plant species. An animal j interacts with a plant i proportionally to $n_i^p I_{ij}$
13 where I_{ij} is computed with the model parameters used in the simulation.

14 Fourth, four summary statistics of the simulated networks are computed: the plant
15 species richness in the network S_p^s , the animal species richness in the network S_a^s , the
16 nestedness index Ne_p , and the specialization index ϕ .

17 Fifth, the computed network statistics of the simulations are used to select the best-fit
18 simulations. The simulations are retained if both $|S_p^s - S_p^{obs}| \leq 5$ and $|S_a^s - S_a^{obs}| \leq 5$, and
19 the simulation procedure goes on until a total of 2000 such simulations are produced. Out
20 of these 2000 simulations, 200 are retained which statistics ϕ , and Ne_p lead to the smallest
21 Euclidean distance to the observed values (ϕ^{obs}, Ne_p^{obs}) . Each statistic is normalized before
22 performing this selection (15).

23 Sixth, these retained simulations are used to compute the approximate posterior dis-
24 tribution of the statistics ΔS_p , ΔH_p , ΔJ , and ΔJ_q , which describe the impact of the
25 interactions on plant composition and dynamics. A large part of the variation in the pos-

1 terior distribution of these statistics is explained by the variation among the simulations
2 of the two model parameters m_p and c_p . Therefore, approximate posterior distributions
3 are plotted as a function of these two parameters (see the section “Predicted effect of the
4 interactions in real networks based on best-fit simulations” below).

1 Table S5: Priors used for the Approximate Bayesian Computation.

2 $\ln(m_p)$ is always drawn in $[\ln(0.001) ; \ln(0.2)]$. $\ln(c_p)$ is always drawn in $[\ln(0.01) ; \ln(1)]$.

3 $\ln(\sigma)$ is always drawn in $[\ln(0.01) ; \ln(10)]$.

4

Datasets			Priors		
Code	Interaction Type	Citation	$\ln(\mu_p)$	$\ln(\mu_a)$	$\ln(m_a)$
<i>ARIZ</i>	Pollination	Arizmendi and Ornelas (1990)	$[\ln(0.0001) ; \ln(0.02)]$	$[\ln(0.0001) ; \ln(0.011)]$	$[\ln(0.001) ; \ln(0.2)]$
<i>BAHE</i> ♣	Pollination	Barrett and Helenurm (1987)	$[\ln(0.0001) ; \ln(0.02)]$	$[\ln(0.1002) ; \ln(0.5)]$	$[\ln(0.001) ; \ln(0.2)]$
<i>BAUE</i>	Pollination	Bauer (1983)	$[\ln(0.0001) ; \ln(0.02)]$	$[\ln(0.0005) ; \ln(0.02)]$	$[\ln(0.001) ; \ln(0.2)]$
<i>BEZE</i>	Pollination	Bezerra et al. (2009)	$[\ln(0.0001) ; \ln(0.02)]$	$[\ln(0.0001) ; \ln(0.018)]$	$[\ln(0.001) ; \ln(0.2)]$
<i>BRIA</i>	Pollination	Brian (1957)	$[\ln(0.0002) ; \ln(0.02)]$	$[\ln(0.0001) ; \ln(0.01)]$	$[\ln(0.001) ; \ln(0.2)]$
<i>BRHO</i>	Pollination	Brown and Hopkins (1995)	$[\ln(0.0001) ; \ln(0.02)]$	$[\ln(0.0002) ; \ln(0.02)]$	$[\ln(0.001) ; \ln(0.2)]$
<i>DIHI</i> ♣	Pollination	Dicks et al. (2002)	$[\ln(0.0002) ; \ln(0.007)]$	$[\ln(0.01) ; \ln(0.02)]$	$[\ln(0.11) ; \ln(0.2)]$
<i>DISH</i> ♣	Pollination	Dicks et al. (2002)	$[\ln(0.0001) ; \ln(0.02)]$	$[\ln(0.002) ; \ln(0.02)]$	$[\ln(0.11) ; \ln(0.2)]$
<i>ELBE</i> ♣	Pollination	Elberling and Olesen (1999)	$[\ln(0.0015) ; \ln(0.018)]$	$[\ln(0.47) ; \ln(0.6)]$	$[\ln(0.001) ; \ln(0.2)]$
<i>HARD</i>	Pollination	Harder (1985)	$[\ln(0.0001) ; \ln(0.02)]$	$[\ln(0.0001) ; \ln(0.013)]$	$[\ln(0.001) ; \ln(0.2)]$
<i>MACI</i>	Pollination	Macior (1978)	$[\ln(0.0001) ; \ln(0.02)]$	$[\ln(0.0001) ; \ln(0.015)]$	$[\ln(0.001) ; \ln(0.2)]$
<i>MEMM</i> ♣	Pollination	Memmott (1999)	$[\ln(0.0001) ; \ln(0.02)]$	$[\ln(0.0252) ; \ln(0.239)]$	$[\ln(0.001) ; \ln(0.19)]$
<i>OLLE</i> ♣	Pollination	Ollerton et al. (2003)	$[\ln(0.0001) ; \ln(0.013)]$	$[\ln(0.0074) ; \ln(0.02)]$	$[\ln(0.051) ; \ln(0.2)]$
<i>SCHM</i> ♣	Pollination	Schemske (1978)	$[\ln(0.0001) ; \ln(0.02)]$	$[\ln(0.0036) ; \ln(0.02)]$	$[\ln(0.001) ; \ln(0.2)]$
<i>SNOW</i>	Pollination	Snow and Snow (1972)	$[\ln(0.0002) ; \ln(0.02)]$	$[\ln(0.0001) ; \ln(0.012)]$	$[\ln(0.001) ; \ln(0.2)]$
<i>VAZ1</i> ♣	Pollination	Vazquez and Simberloff (2002)	$[\ln(0.0001) ; \ln(0.02)]$	$[\ln(0.0011) ; \ln(0.02)]$	$[\ln(0.001) ; \ln(0.2)]$
<i>VAZ2</i> ♣	Pollination	Vazquez and Simberloff (2002)	$[\ln(0.0001) ; \ln(0.011)]$	$[\ln(0.0018) ; \ln(0.02)]$	$[\ln(0.001) ; \ln(0.2)]$
<i>VAZ3</i> ♣	Pollination	Vazquez and Simberloff (2002)	$[\ln(0.0001) ; \ln(0.02)]$	$[\ln(0.001) ; \ln(0.02)]$	$[\ln(0.001) ; \ln(0.2)]$
<i>VAZ4</i> ♣	Pollination	Vazquez and Simberloff (2002)	$[\ln(0.0001) ; \ln(0.02)]$	$[\ln(0.0017) ; \ln(0.02)]$	$[\ln(0.001) ; \ln(0.2)]$
<i>VAZ5</i> ♣	Pollination	Vazquez and Simberloff (2002)	$[\ln(0.0001) ; \ln(0.02)]$	$[\ln(0.0007) ; \ln(0.02)]$	$[\ln(0.001) ; \ln(0.2)]$
<i>VAZ6</i> ♣	Pollination	Vazquez and Simberloff (2002)	$[\ln(0.0001) ; \ln(0.02)]$	$[\ln(0.001) ; \ln(0.02)]$	$[\ln(0.001) ; \ln(0.2)]$
<i>VAZ7</i> ♣	Pollination	Vazquez and Simberloff (2002)	$[\ln(0.0001) ; \ln(0.02)]$	$[\ln(0.0007) ; \ln(0.02)]$	$[\ln(0.001) ; \ln(0.2)]$
<i>VAZ8</i> ♣	Pollination	Vazquez and Simberloff (2002)	$[\ln(0.0001) ; \ln(0.02)]$	$[\ln(0.0009) ; \ln(0.02)]$	$[\ln(0.001) ; \ln(0.2)]$
<i>HELG</i>	Arbuscular Mycorrhizal Fungi	Helgason et al. (2002)	$[\ln(0.0001) ; \ln(0.02)]$	$[\ln(0.0001) ; \ln(0.02)]$	$[\ln(0.001) ; \ln(0.2)]$
<i>OPIO</i>	Arbuscular Mycorrhizal Fungi	Opik et al. (2008)	$[\ln(0.0001) ; \ln(0.018)]$	$[\ln(0.001) ; \ln(0.02)]$	$[\ln(0.001) ; \ln(0.2)]$
<i>OPIY</i>	Arbuscular Mycorrhizal Fungi	Opik et al. (2008)	$[\ln(0.0001) ; \ln(0.02)]$	$[\ln(0.0008) ; \ln(0.02)]$	$[\ln(0.001) ; \ln(0.2)]$
<i>WU15</i>	Arbuscular Mycorrhizal Fungi	Wu et al. (2007)	$[\ln(0.0001) ; \ln(0.02)]$	$[\ln(0.0001) ; \ln(0.02)]$	$[\ln(0.001) ; \ln(0.2)]$
<i>WU16</i>	Arbuscular Mycorrhizal Fungi	Wu et al. (2007)	$[\ln(0.0001) ; \ln(0.02)]$	$[\ln(0.0001) ; \ln(0.02)]$	$[\ln(0.001) ; \ln(0.2)]$
<i>JOSW</i>	Endophytic Fungi	Joshee et al. (2009)	$[\ln(0.0001) ; \ln(0.01)]$	$[\ln(0.006) ; \ln(0.02)]$	$[\ln(0.01) ; \ln(0.2)]$
<i>JOSS</i>	Endophytic Fungi	Joshee et al. (2009)	$[\ln(0.0001) ; \ln(0.01)]$	$[\ln(0.0014) ; \ln(0.02)]$	$[\ln(0.018) ; \ln(0.2)]$
<i>MUTD</i>	Endophytic Fungi	Murali et al. (2007)	$[\ln(0.0001) ; \ln(0.02)]$	$[\ln(0.0005) ; \ln(0.02)]$	$[\ln(0.001) ; \ln(0.2)]$

<i>MUTW</i>	Endophytic Fungi	Murali et al. (2007)	[ln(0.0001) ; ln(0.02)]	[ln(0.0006) ; ln(0.02)]	[ln(0.001) ; ln(0.2)]
<i>MUDD</i>	Endophytic Fungi	Murali et al. (2007)	[ln(0.0001) ; ln(0.019)]	[ln(0.0009) ; ln(0.02)]	[ln(0.001) ; ln(0.2)]
<i>MUDW</i>	Endophytic Fungi	Murali et al. (2007)	[ln(0.0001) ; ln(0.02)]	[ln(0.0012) ; ln(0.02)]	[ln(0.001) ; ln(0.2)]
<i>PETR</i>	Endophytic Fungi	Petrini (1984)	[ln(0.0001) ; ln(0.02)]	[ln(0.0003) ; ln(0.02)]	[ln(0.001) ; ln(0.2)]
<i>SURB</i>	Endophytic Fungi	Suryanarayanan et al. (2005)	[ln(0.0001) ; ln(0.02)]	[ln(0.0001) ; ln(0.019)]	[ln(0.001) ; ln(0.2)]
<i>SURC</i>	Endophytic Fungi	Suryanarayanan et al. (2005)	[ln(0.0001) ; ln(0.02)]	[ln(0.0001) ; ln(0.019)]	[ln(0.001) ; ln(0.2)]
<i>SURD</i>	Endophytic Fungi	Suryanarayanan et al. (2005)	[ln(0.0001) ; ln(0.02)]	[ln(0.0001) ; ln(0.01)]	[ln(0.001) ; ln(0.2)]
<i>SUTJ</i>	Endophytic Fungi	Sutjaritvorakul et al. (2010)	[ln(0.0001) ; ln(0.02)]	[ln(0.0001) ; ln(0.02)]	[ln(0.001) ; ln(0.2)]
<i>BACH*</i>	Herbivory	Basset and Charles (2000)	[ln(0.0001) ; ln(0.006)]	[ln(0.4001) ; ln(0.6)]	[ln(0.003) ; ln(0.2)]
<i>BASA</i> [◇]	Herbivory	Basset and Samuelson (1996)	[ln(0.0001) ; ln(0.02)]	[ln(0.006) ; ln(0.02)]	[ln(0.035) ; ln(0.2)]
<i>BERK</i>	Herbivory	Berkov and Tavakilian (1999)	[ln(0.0001) ; ln(0.017)]	[ln(0.0015) ; ln(0.02)]	[ln(0.001) ; ln(0.2)]
<i>HANS</i>	Herbivory	Hansen and Ueckert (1970)	[ln(0.0001) ; ln(0.02)]	[ln(0.0001) ; ln(0.014)]	[ln(0.001) ; ln(0.2)]
<i>JANZ</i> [◇]	Herbivory	Janzen (1980)	[ln(0.006) ; ln(0.199)]	[ln(0.1108) ; ln(0.5)]	[ln(0.012) ; ln(0.5)]
<i>JOEA</i> [♣]	Herbivory	Joern (1979)	[ln(0.0002) ; ln(0.02)]	[ln(0.0003) ; ln(0.02)]	[ln(0.001) ; ln(0.2)]
<i>JOEM</i> [♣]	Herbivory	Joern (1979)	[ln(0.0003) ; ln(0.02)]	[ln(0.0007) ; ln(0.02)]	[ln(0.001) ; ln(0.2)]
<i>JOER</i>	Herbivory	Joern (1985)	[ln(0.0004) ; ln(0.02)]	[ln(0.0013) ; ln(0.02)]	[ln(0.001) ; ln(0.2)]
<i>NA96</i> [◇]	Herbivory	Nakagawa et al. (2003)	[ln(0.0001) ; ln(0.02)]	[ln(0.0005) ; ln(0.02)]	[ln(0.001) ; ln(0.2)]
<i>NA98</i> [◇]	Herbivory	Nakagawa et al. (2003)	[ln(0.0001) ; ln(0.02)]	[ln(0.0012) ; ln(0.02)]	[ln(0.001) ; ln(0.2)]
<i>NOMI</i>	Herbivory	Novotny et al.(2005a)	[ln(0.0001) ; ln(0.02)]	[ln(0.0001) ; ln(0.017)]	[ln(0.001) ; ln(0.2)]
<i>NOVO</i> [◇]	Herbivory	Novotny et al.(2005b)	[ln(0.0001) ; ln(0.02)]	[ln(0.0006) ; ln(0.02)]	[ln(0.001) ; ln(0.2)]
<i>OTTE</i>	Herbivory	Otte and Joern (1977)	[ln(0.0001) ; ln(0.02)]	[ln(0.0001) ; ln(0.019)]	[ln(0.001) ; ln(0.2)]
<i>SHEL</i>	Herbivory	Sheldon and Rogers (1978)	[ln(0.0001) ; ln(0.02)]	[ln(0.0001) ; ln(0.014)]	[ln(0.001) ; ln(0.2)]
<i>UECK</i> [◇]	Herbivory	Ueckert and Hansen (1971)	[ln(0.0001) ; ln(0.02)]	[ln(0.0001) ; ln(0.019)]	[ln(0.001) ; ln(0.2)]

1 ♣Datasets found in the Interaction Web Database (<http://www.nceas.ucsb.edu/interactionweb/>).

2 ♠Datasets found in Ref. (16).

3 ◇Datasets found in Ref. (17).

4 *For this dataset, we used in the simulations $J_p=2000$, $J_a=400$ because S_p is larger
5 than 200.

1 S4.2 Predicted effect of the interactions in real networks based 2 on best-fit simulations

3 The information available in the data was not sufficient to fully parameterize our meta-
4 community model, and hence to precisely quantify the effect of bi-trophic interactions on
5 plant and animal richness in these datasets. It was however sufficient to greatly constrain
6 our simulations, so that general trends could be evidenced. We illustrate this with an
7 example dataset (BEZE, see Table S5). This dataset was chosen because it contains the
8 largest number of recorded interactions. The limits of our inference approach that we are
9 pointing here are thus also happening in the other datasets. Thanks to the ABC proce-
10 dure, some parameters are relatively well inferred in that they have a reasonably peaked
11 posterior distribution: μ_p , μ_a and σ (Fig. S6A,B,D). All the interaction rules are rep-
12 resented in the retained simulations (Fig. S6C), which mean that the observed network
13 structure can be reproduced in multiple ways. Note that this explains the presence of two
14 peaks in the posterior distribution of parameter σ : the peak of low σ value is obtained in
15 models without threshold rules, while the other peak is obtained when one or two thresh-
16 old rules are modeled on top of the matching rules. The four remaining parameters m_p ,
17 m_a , c_p and c_a are less well inferred by our procedure in that they have wider posterior
18 distribution hence a large remaining uncertainty on parameters values (Fig. S6E-H). The
19 variance in these parameters values explained a large proportion of the variance of ΔS_p
20 and ΔS_a observed in the simulations. More precisely, variations in m_p and c_p were highly
21 correlated with variations in ΔS_p in the simulations, while variations in m_a and c_a were
22 highly correlated with variations in ΔS_a . This is the reason why we plot our predictions
23 regarding the bi-trophic impact on plants (animals) ΔS_p (ΔS_a) as a function of m_p and
24 c_p (m_a and c_a) in Figs. 2, S2, S4 and S5.

25 We used a kriging technique to interpolate ΔS_p as a function of m_p and c_p (R library

1 "fields", (18)). This interpolation explained on average 70% (64%, 45%) of the variance
2 for plants-pollinators datasets (plant-fungi, plant-insect herbivores). Similarly, the inter-
3 polation of ΔS_a as a function of m_a and c_a explained on average 33% (40%, 30%) for
4 plants-pollinators datasets (plant-fungi, plant-insect herbivores). We represent in Figs.
5 S11- S16 the krigged values of ΔS_p and ΔS_a predicted by the simulations fitted to each
6 dataset. In Fig. 3, these predictions are averaged for each dataset type (plant-pollinators,
7 plants-fungi, and plants-insect herbivores). Similar results for ΔH , ΔJ , ΔJ_q , and $\Delta S^m/S$
8 are reported in Figs. S7- S10. The temporal similarity is expected to decrease for an-
9 tagonistic interactions; the same happens for mutualistic interactions only for realistically
10 strong coupling (c_p and $c_a \geq 0.03$) (Fig. S8). When using the abundance-weighted
11 measure of turnover J_q , the temporal similarity is predicted to be weakly affected by
12 bi-trophic interactions (Fig. S9). Overall, our results hence suggest that the temporal
13 turnover in plant and animal sets should be larger due to bi-trophic interactions, this
14 being due mainly to an increased turnover of rare species.

15 All simulations were performed in C++, and statistical analyses with the R software
16 (R development Core Team 2009).

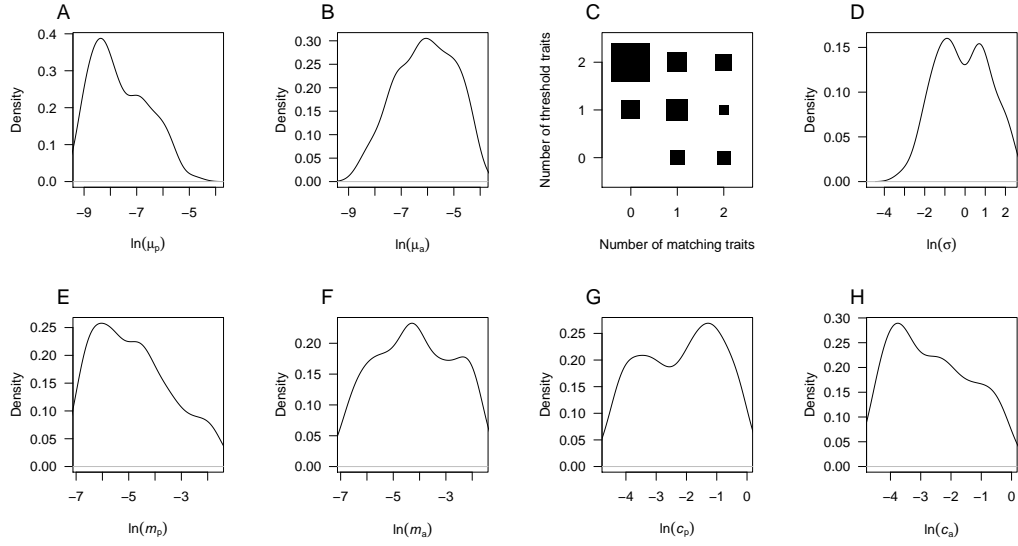


Fig. S6: Approximate posterior distribution of the model parameters. Panels A-B: approximate posterior distribution for parameters μ_p and μ_a . Panel C: posterior weight of the different interaction rules. The length of each square side is proportional to the number of retained simulations with the corresponding number of matching and threshold rules. Panel D: approximate posterior distribution for parameters σ . Panels E-H: approximate posterior distribution for parameters m_p , m_a , c_p and c_a .

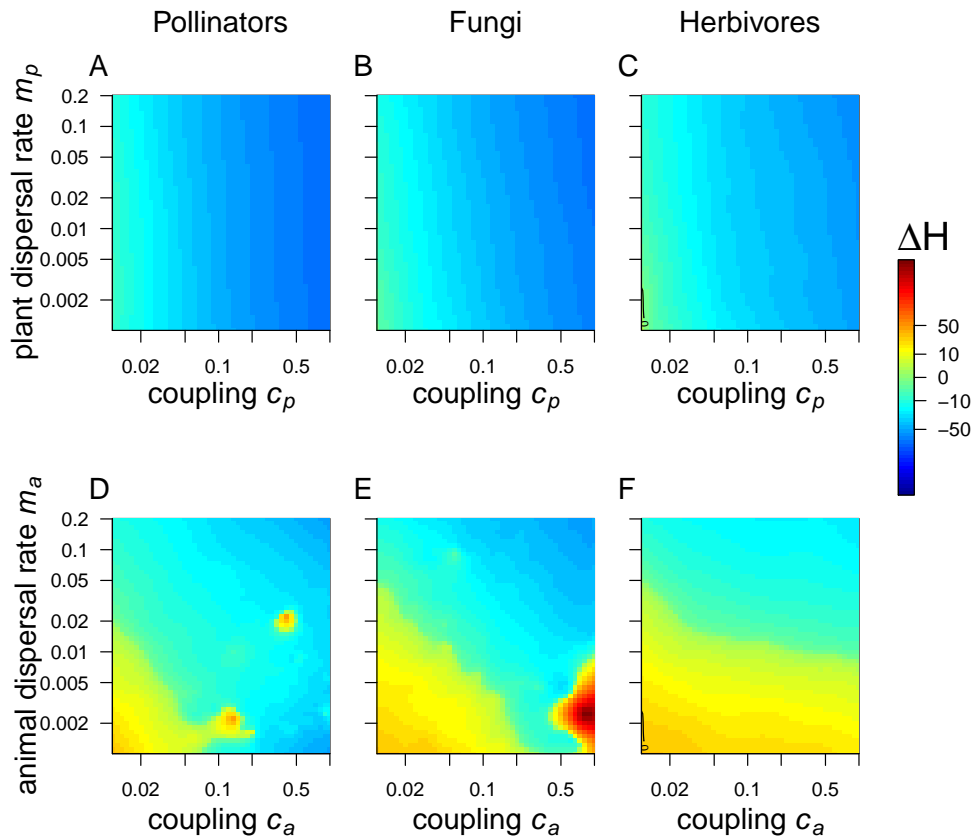


Fig. S7: Relative variation of plant and animal Shannon's index H between coupled and uncoupled communities in simulations which best fit observed network structure in real datasets. Panels A-C: results for plants. Panels D-F: results for animals. Panels A and D: Plant-pollinators datasets ($n=23$). Panels B and E: Plant-fungi datasets ($n=16$). Panels C and F: Plant-insect herbivores datasets ($n=15$). 41% of the variance is explained by the interpolation on average in each dataset.

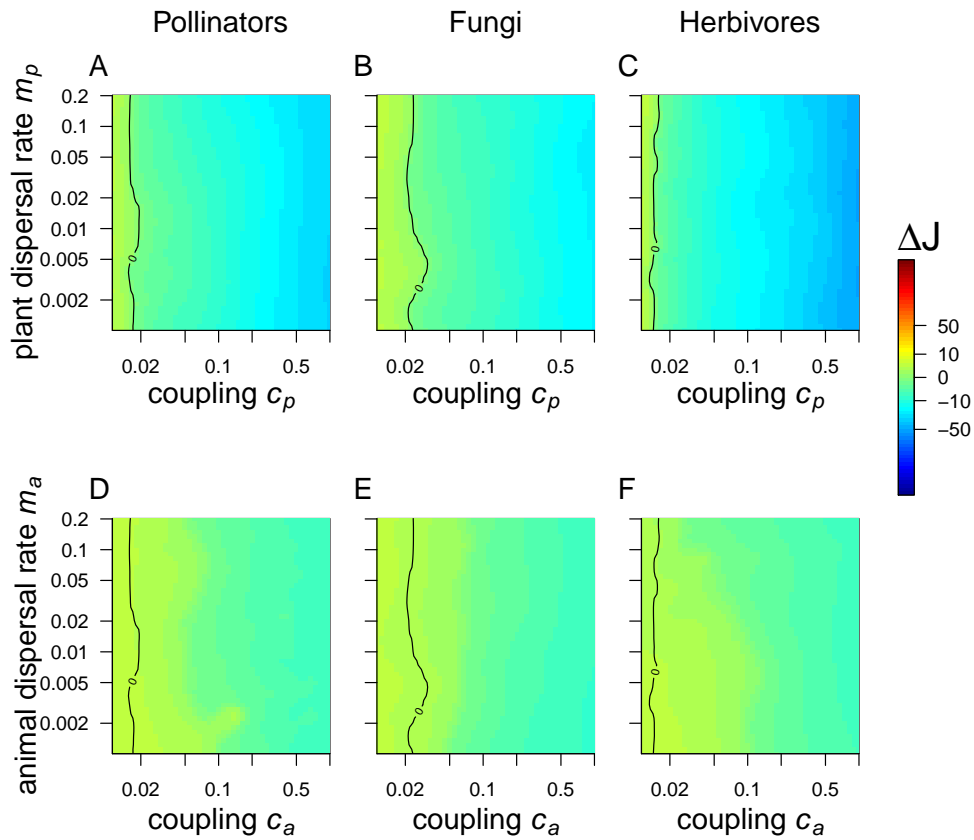


Fig. S8: Relative variation of plant and animal temporal similarity J between coupled and uncoupled communities in simulations which best fit observed network structure in real datasets. Panels A-C: results for plants. Panels D-F: results for animals. Panels A and D: Plant-pollinators datasets ($n=23$). Panels B and E: Plant-fungi datasets ($n=16$). Panels C and F: Plant-insect herbivores datasets ($n=15$). 21% of the variance is explained by the interpolation on average in each dataset.

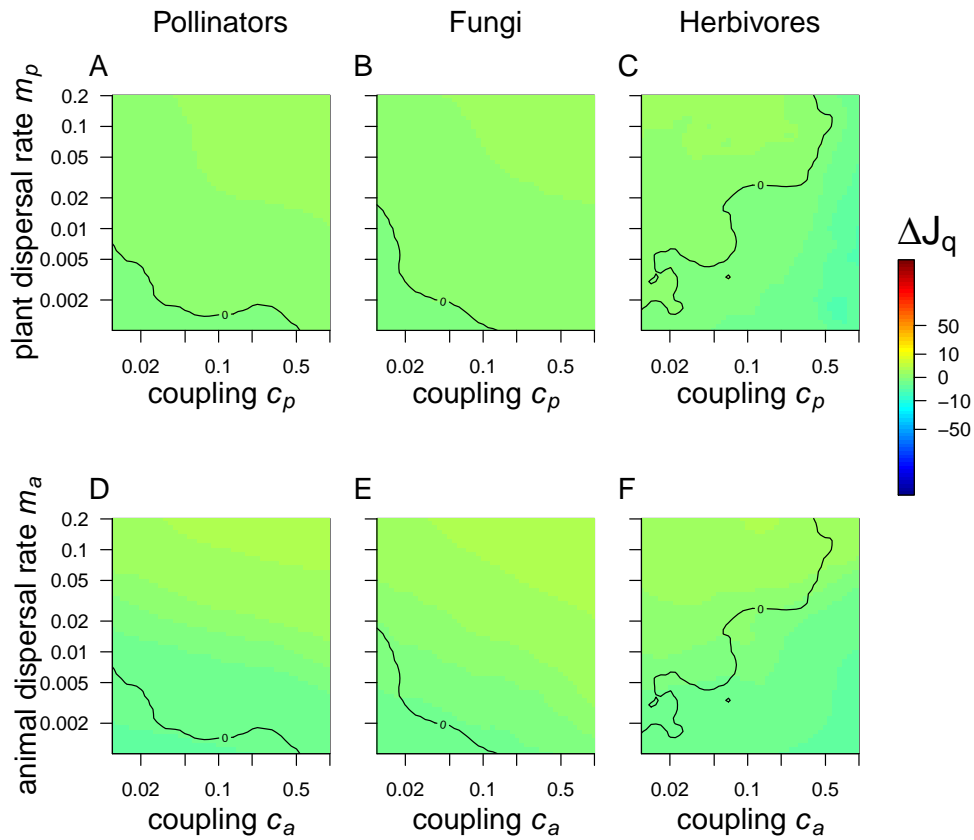


Fig. S9: Relative variation of plant and animal temporal similarity J_q between coupled and uncoupled communities in simulations which best fit observed network structure in real datasets. Panels A-C: results for plants. Panels D-F: results for animals. Panels A and D: Plant-pollinators datasets ($n=23$). Panels B and E: Plant-fungi datasets ($n=16$). Panels C and F: Plant-insect herbivores datasets ($n=15$). 33% of the variance is explained by the interpolation on average in each dataset.

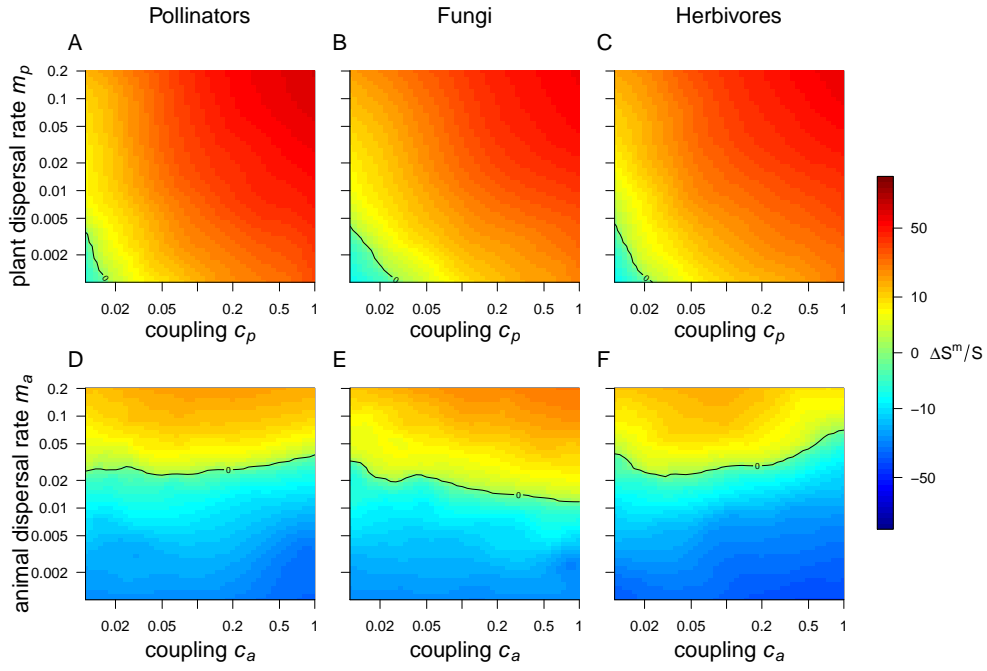


Fig. S10: Relative variation of plant and animal β diversity S^m/S between coupled and uncoupled communities in simulations which best fit observed network structure in real datasets. Panels A-C: results for plants. Panels D-F: results for animals. Panels A and D: Plant-pollinators datasets (n=23). Panels B and E: Plant-fungi datasets (n=16). Panels C and F: Plant-insect herbivores datasets (n=15). 31% of the variance is explained by the interpolation on average in each dataset.

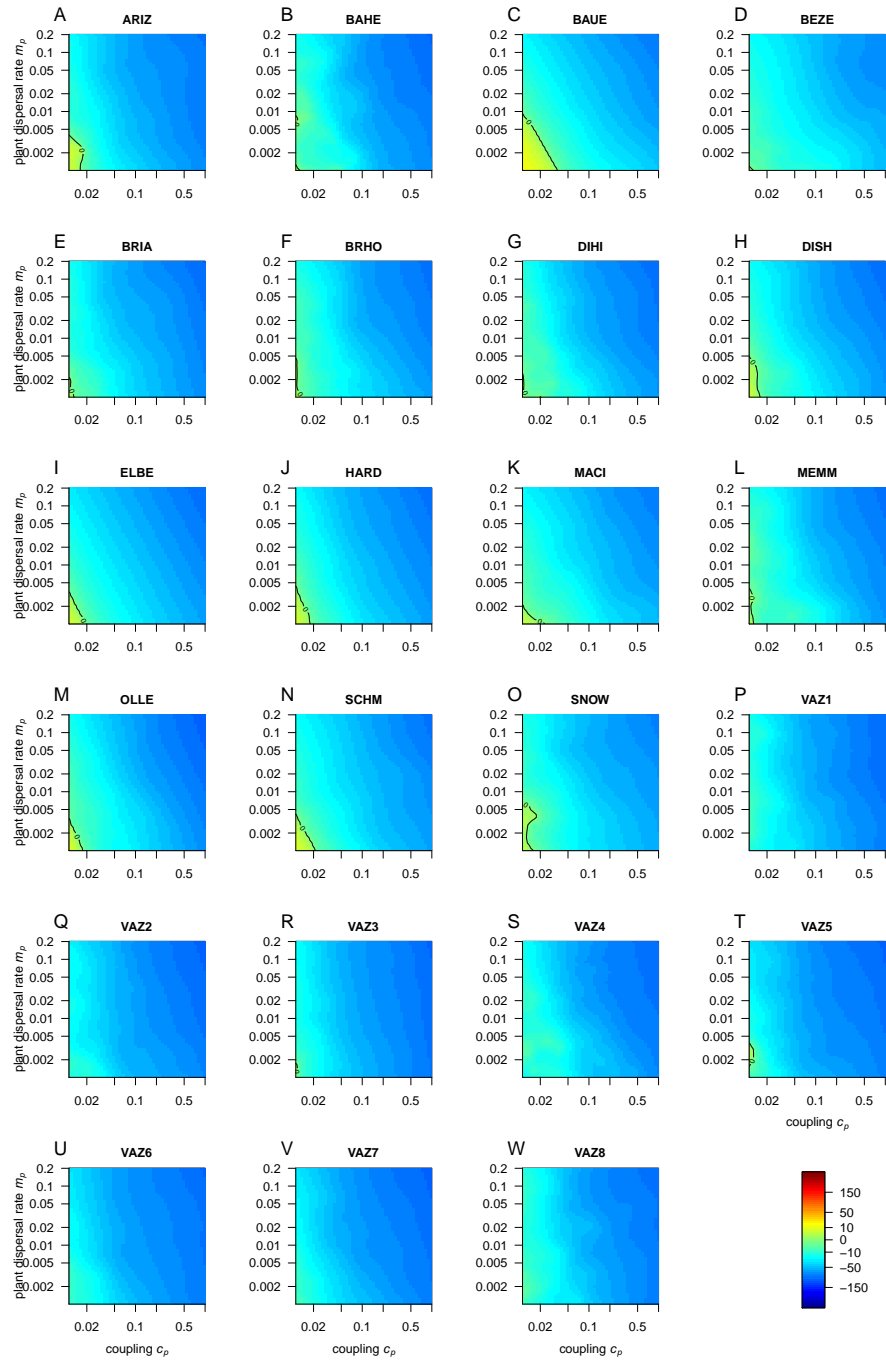


Fig. S11: Relative variation of plant species richness between coupled and uncoupled communities in simulations which best fit observed network structure in real plant-pollinator datasets.

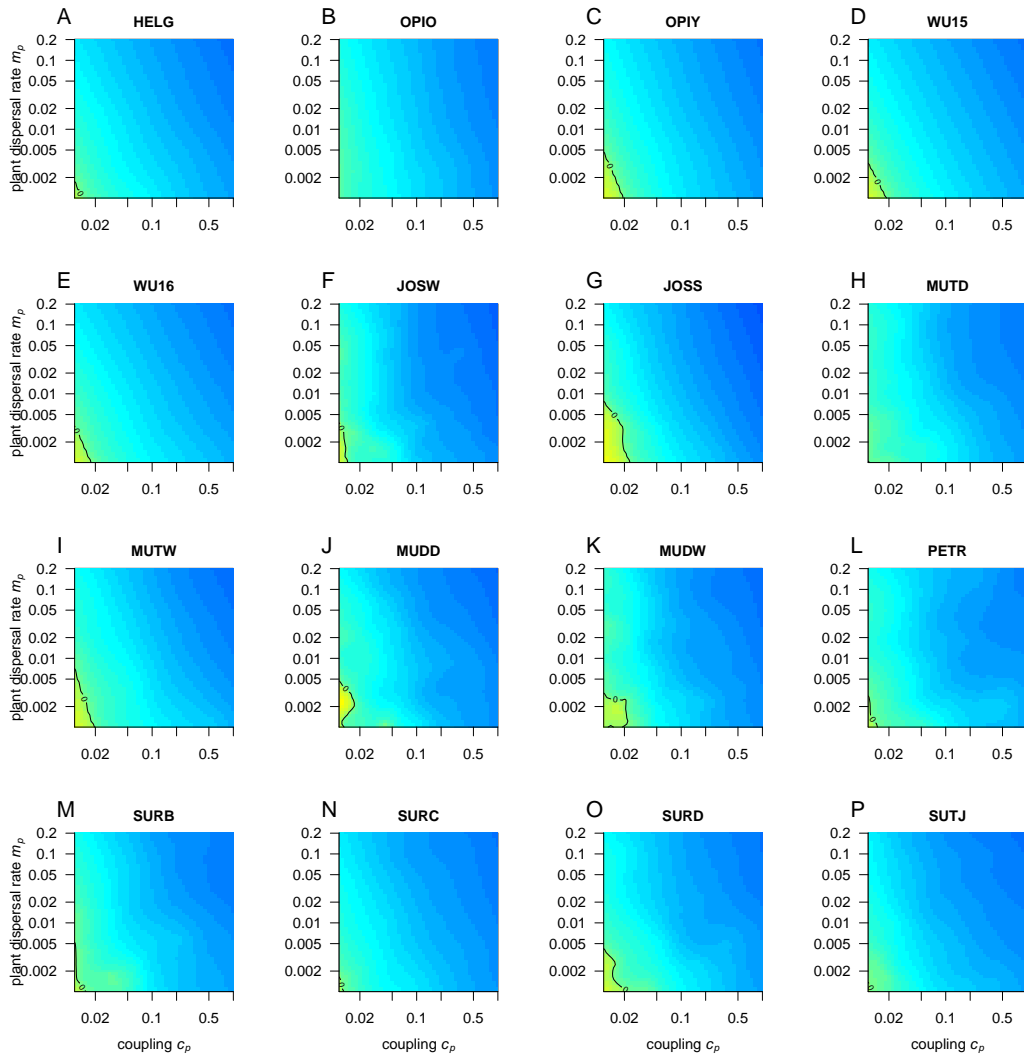


Fig. S12: Relative variation of plant species richness between coupled and uncoupled communities in simulations which best fit observed network structure in real plant-fungi datasets.

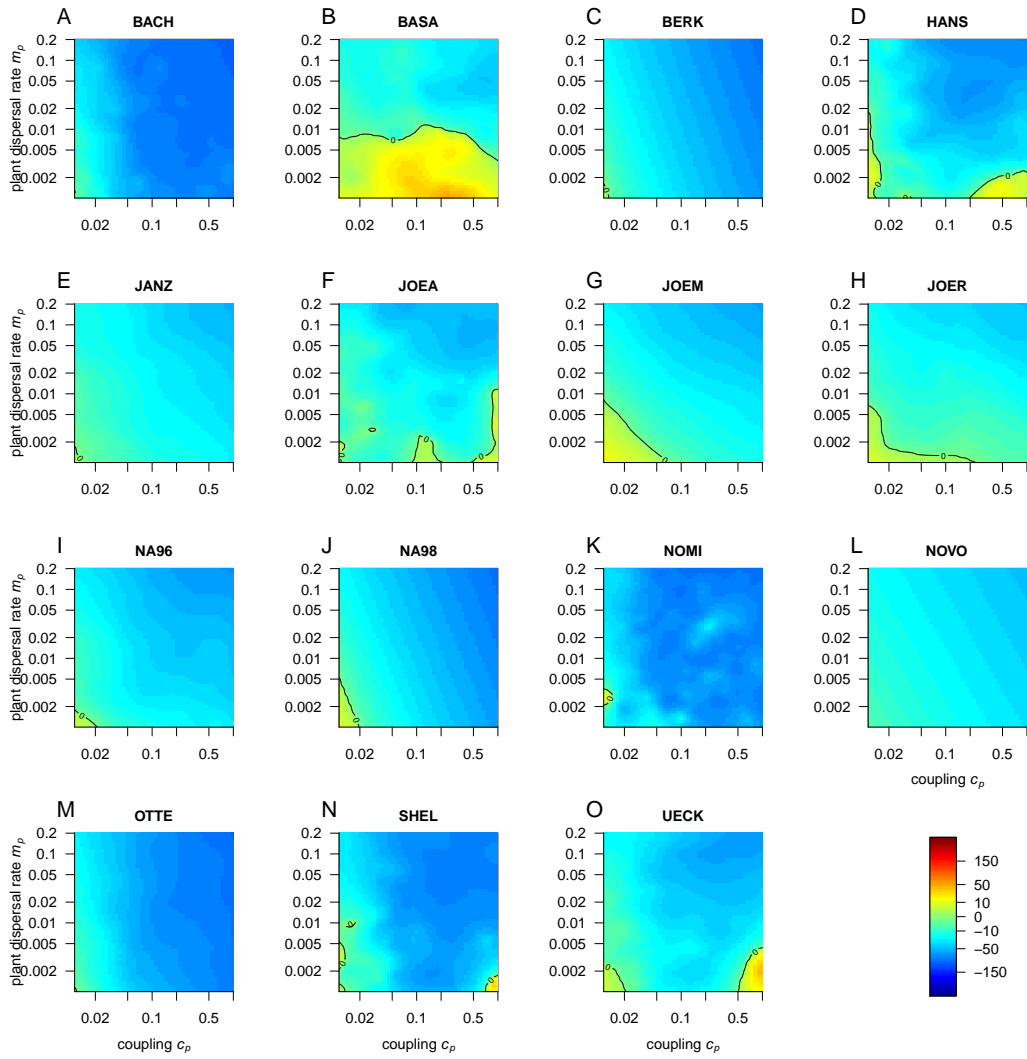


Fig. S13: Relative variation of plant species richness between coupled and uncoupled communities in simulations which best fit observed network structure in real plant-insect herbivores datasets.

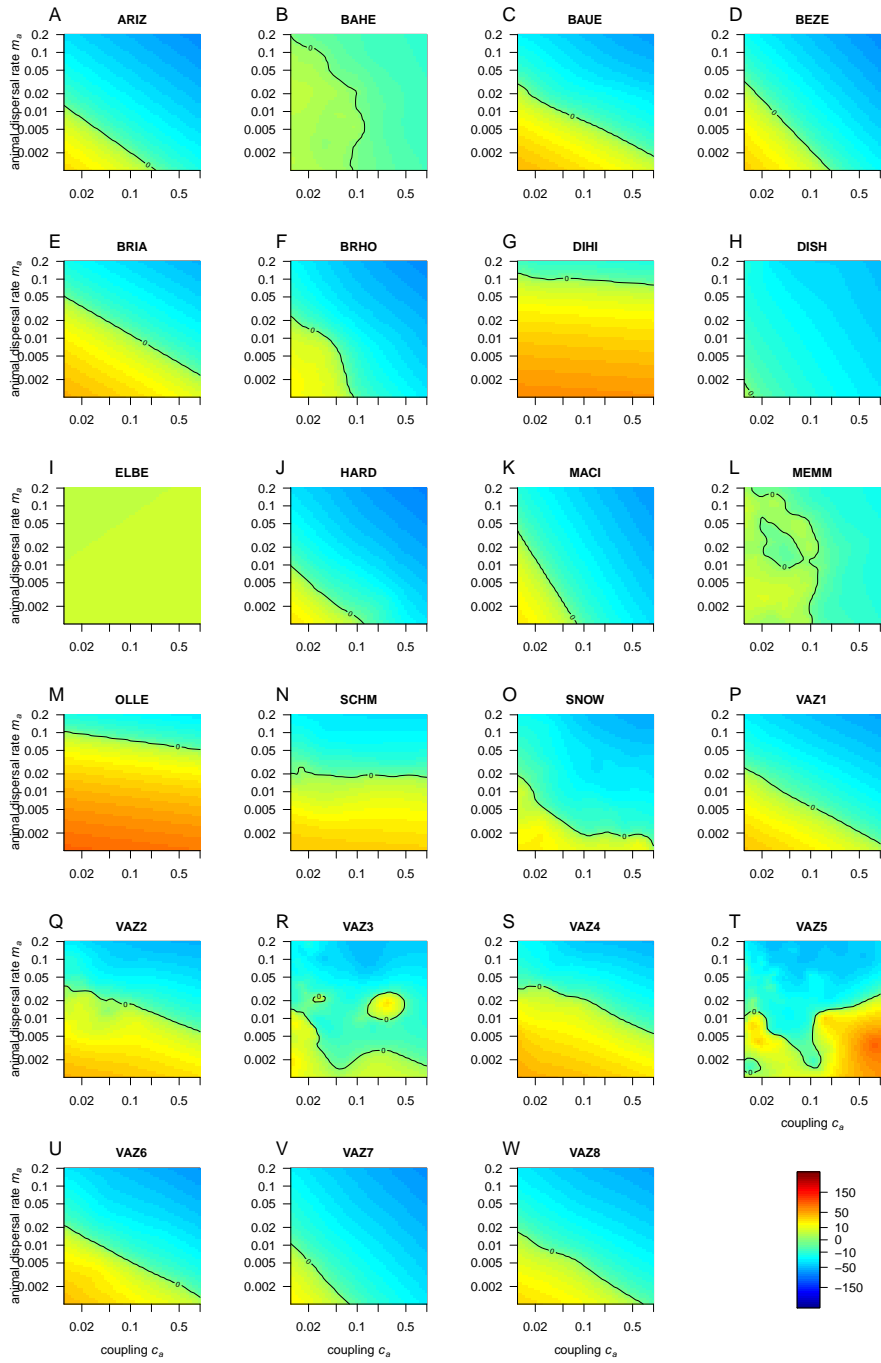


Fig. S14: Relative variation of animal species richness between coupled and uncoupled communities in simulations which best fit observed network structure in real plant-pollinator datasets.

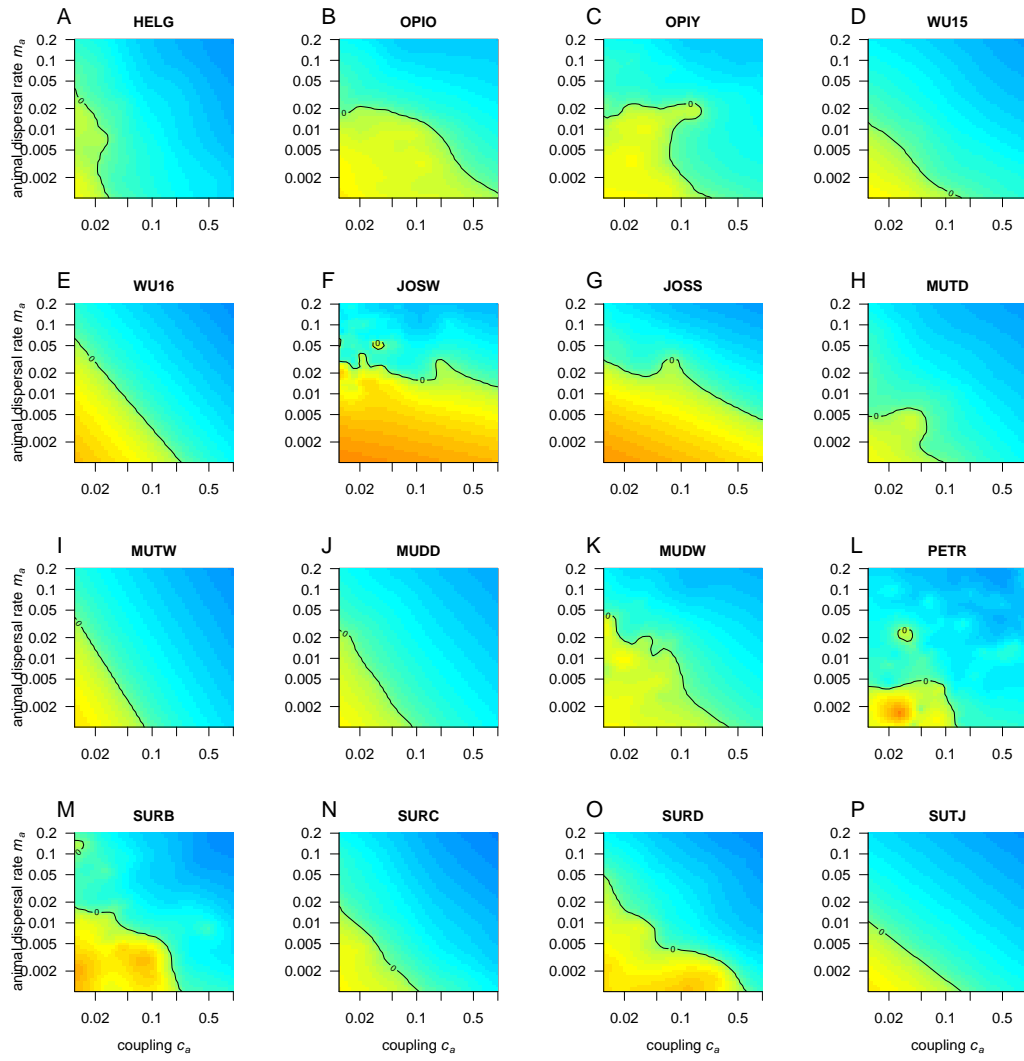


Fig. S15: Relative variation of animal species richness between coupled and uncoupled communities in simulations which best fit observed network structure in real plant-fungi datasets.

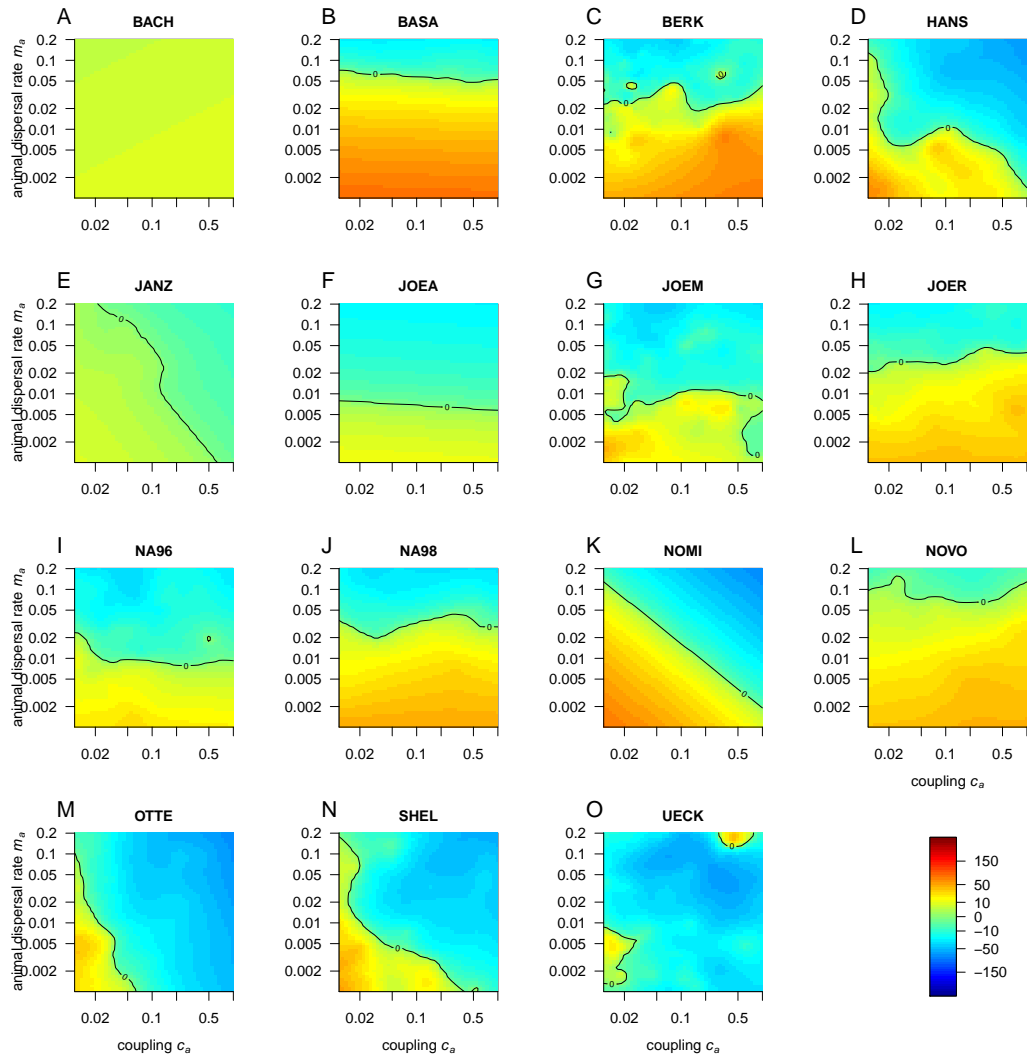


Fig. S16: Relative variation of animal species richness between coupled and uncoupled communities in simulations which best fit observed network structure in real plant-insect herbivores datasets.

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