

Bitrophic interactions shape biodiversity in space

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Ecologists and conservation biologists often study particular trophic groups in isolation, which precludes an explicit assessment of the impact of multitrophic interactions on community structure and dynamics. Network ecology helps to fill this gap by focusing on species interactions, but it often ignores spatial processes. Here, we are taking a step forward in the integration of metacommunity and network approaches by studying a model of bitrophic interactions in a spatial context. We quantify the effect of bitrophic interactions on the diversity of plants and their animal interactors, and we show their complex dependence on the structure of the interaction network, the strength of interactions, and the dispersal rate. We then develop a method to parameterize our model with real-world networks and apply it to 54 datasets describing three types of interactions: pollination, fungal association, and insect herbivory. In all three network types, bitrophic interactions generally lead to an increase of plant and animal spatial heterogeneity by decreasing local species richness while increasing β -diversity.

ecological networks | spatial ecology

Two major frameworks in biodiversity research are network and metacommunity theories. The metacommunity theory highlights the role of spatial processes in community dynamics (1), while the theory of ecological networks highlights the role of multitrophic interactions (2, 3). Metacommunity studies focus generally on one particular trophic group like plants (4–7), whereas network studies consider larger communities across several trophic groups but are generally local (7). From the metacommunity perspective, accumulating evidence suggests that ecological interactions impact community composition (8–10). From the network perspective, it is unclear whether the reported effects of network architecture on species richness (7) stand in spatially extended systems coupled through dispersal. In short, we need to add a spatial component to network studies or a network component to metacommunity studies (11–14).

In recent years, a number of studies have begun the integration of spatial processes and multispecies interactions by exploring community modules of two or three species (15, 16). These studies have shown that dispersal can stabilize pairwise trophic interactions (15), tritrophic food chains (11), and competitive interactions (17). Similarly, another source of multispecies stability is induced by the action of predators (18, 19).

Models at the module level have been very useful at providing a bridge between the complexity of entire communities and the simplicity of pairwise interactions (20). To go a step farther into closing the circle, a few theoretical papers have begun to study the role of spatial processes in models of entire ecological networks (13, 14, 21, 22). Here, we follow the same avenue, focusing on bitrophic ecological networks such as those networks describing pollination or herbivory between plants and insects. Our aim is to understand to what degree network structure affects the metacommunity dynamics of the two interacting groups.

We will use the neutral metacommunity model in the work by Hubbell (4) as our baseline reference. This minimal model encapsulates the combined role of dispersal limitation and stochasticity in metacommunity dynamics. Next, we will extend this framework by adding a deterministic component emerging from the nonrandom structure of bitrophic interaction networks.

Comparing the outputs of the extended model and the neutral one will allow us to assess the impact of bitrophic interactions on the composition and dynamics of the metacommunity.

When they act differentially among community members, bitrophic interactions induce fitness differences among individuals. For instance, if pollinators preferentially pollinate flowers with short corollas, flowers with long corollas will tend to produce fewer seeds and will be progressively filtered out of the plant community. Phrased in the terms of metacommunity theory, bitrophic interactions act as an environmental filter for some community members if these members suffer greater damages from antagonists or benefit less from mutualists than their competitors (23–25). Bitrophic interactions should, thus, decrease species richness.

However, bitrophic interactions can stabilize the coexistence of different species if different community members partition biotic resources (mutualists) or threats (antagonists) by having different specialized interactions. For instance, assume that plant species A is locally abundant and sustains a large population of herbivore species B. If such species B exclusively feeds on plants of species A, then individuals of a rare plant species C may have a competitive advantage against individuals of species A in suffering less from herbivory (18, 26, 27). Herbivory should now stabilize the coexistence of the two plant species. Inversely, the diversity of plants creates a diversity of food sources for the animals. This diversity can also increase the likelihood of coexistence of different animal species (28). More generally, bitrophic interactions are likely to affect the composition of a trophic group (e.g., plants) just like abiotic conditions (29). Their overall effect on community richness will depend on a balance between their filtering and stabilizing (niche partitioning) effects. This overall impact of bitrophic interactions on community richness is, thus, likely to depend on the architecture of the interaction network, just as the heterogeneity in the abiotic environment contributes to the assembly of each trophic group.

Here, we first perform extensive individual-based simulations to explore how interactions between two trophic groups can alter their composition and dynamics (Box 1). We consider two types of interactions independently: mutualistic (e.g., plants and their pollinators) and antagonistic (e.g., plants and their insect herbivores). Each trophic group experiences stochastic lottery-like dynamics (30) in a lattice of patches connected by dispersal. Interactions between the trophic groups are controlled by two trait-based rules used in isolation or combined: a threshold rule and a matching rule (31) (Box 1). Exploring a wide range of combinations of model parameters, we investigate under which circumstances bitrophic interactions have an overall positive or

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negative effect on community richness and other community characteristics.

After assessing the potential range of effects of bitrophic interactions, we confront our theoretical findings to real data of ecological networks. We, hence, develop a statistical method based on approximate Bayesian computation (ABC) (32, 33) (Box 2) to fit our model to 54 bipartite networks (23 plant–pollinator networks, 16 plant–fungi networks, and 15 plant–insect

herbivore networks) (SI Appendix). This procedure consists in simulating the model with a wide range of parameter values and retaining the parameter values that produce interaction networks that are closest to real ones. The combination of our theoretical exploration and empirical testing enables us to determine the likely impact of community-wide bitrophic interactions on community structure in nature and pinpoint knowledge gaps where efforts should be concentrated in the near future.

Box 1. Description of the Model

We model the dynamics of two trophic groups: plants and animals. The groups occupy a regular grid of $l \times l$ patches. Each patch contains N_p plants and N_a animals and follows stochastic dynamics with dispersal from the four neighboring patches at rates m_p and m_a and long distance dispersal from a pool of species at rates μ_p and μ_a (SI Appendix, Fig. S1). We consider that the patches are constantly saturated, and therefore at each generation, N_p and N_a descendants are drawn at random in a lottery manner (30) and replace their parents. For plants (similarly for animals replacing subindex p by a), the descendants of a patch P can come from either the present patch P , from one of the four neighboring patches, or from the regional pool. The respective probabilities of these three scenarios are $1/(1 + m_p + \mu_p)$, $m_p/(1 + m_p + \mu_p)$, and $\mu_p/(1 + m_p + \mu_p)$, respectively. We use regional pools of 300 species with equal species regional abundances. Immigrants from the regional pool, hence, belong to a randomly drawn species (of 300). Immigrants from the neighboring patches have the species identity of a randomly drawn individual in the neighboring patches. Descendants coming from the local patch have a species identity drawn at random with a probability proportional to the product of the local species abundance and its seed (egg) production. This seed (egg) production is affected, in part, by the local interaction with the other group as defined next.

Case 1: Mutualistic Interactions. For the group of plants (animals), the seed (egg) production f_i^p (f_i^a) of an individual of species i is equal to

$$f_i^p = (1 - c_p) + c_p \sum_{j=1}^{S_a} \frac{n_j^a I_{ij}}{\sum_{k=1}^{S_p} \left(\frac{n_k^p}{N_p} \sum_{l=1}^{S_a} n_l^a I_{kl} \right)} \quad [1]$$

and

$$f_i^a = (1 - c_a) + c_a \sum_{j=1}^{S_p} \frac{n_j^p I_{ji}}{\sum_{k=1}^{S_a} \left(\frac{n_k^a}{N_a} \sum_{l=1}^{S_p} n_l^p I_{lk} \right)} \quad [2]$$

where c_p (c_a) is the component of seed (egg) production that depends on the interaction with the other trophic group, n_i^p (n_i^a) is the number of individuals of species i in the group of plants (animals), and I_{ij} is the interaction strength between plant i and animal j .

For plants, the term $1 - c_p$ in Eq. 1 means that seed production is partially uncoupled from the interaction with animals (e.g., because of selfing). Eq. 1 also describes that plants compete to attract animals: a plant i interacts with animals at a total rate of $\sum_{j=1}^{S_a} n_j^a I_{ij}$. It will then receive a fraction of plant–animal interactions proportional to the term after c_p .

For animals, Eq. 2 is similarly constituted of two terms: the uncoupled egg production $1 - c_a$ and the coupled one,

where the term after c_a describes the competition among animals to obtain the reward offered by plants. An animal i will receive from a plant j a fraction of its reward proportional to $I_{ji}/[\sum_{k=1}^{S_a} (n_k^a/N_a) I_{jk}]$. This animal i will, thus, obtain a total reward from the plants given by the term after c_a (SI Appendix).

If c_p and c_a equal zero or if interactions between plants and animals are equivalent among species (i.e., I_{ij} is constant), the dynamics of plants and animals are purely neutral and uncoupled.

Case 2: Antagonistic Interactions. For antagonistic interactions, the seed production f_i^p is similarly modeled by

$$f_i^p = \sup \left\{ 0; 1 - c_p \frac{\sum_{j=1}^{S_a} n_j^a I_{ij}}{\sum_{k=1}^{S_p} \left(\frac{n_k^p}{N_p} \sum_{l=1}^{S_a} n_l^a I_{kl} \right)} \right\} \quad [3]$$

where $\sup\{0; x\}$ equals zero if $x < 0$ and x otherwise. f_i^a is given by Eq. 2.

Interaction Rules. Each species has a set of T independent trait values randomly drawn from the interval $[0, 1]$ according to a uniform probability density function. These trait values determine the interaction strength between plants and animals. For each of the T traits, one of two interaction rules is used.

The first interaction rule is a threshold rule: an animal j with trait value t_j^a can interact with a plant i with trait value t_i^p only if $t_j^a \geq t_i^p$. This rule increases the nestedness of the network: animals with low trait values are more specialist and interact with the subset of plants that have low trait values, whereas animals with large trait values are more generalist and interact with a larger subset of plants having both low and large trait values (45). Similarly, plants with large trait values are specialists and interact only with animals with large trait values, whereas plants with low trait values interact with a larger subset of animals.

The second interaction rule is a matching rule: an animal j with trait value t_j^a interacts with a plant i with trait value t_i^p with a probability proportional to $\exp[-(t_j^a - t_i^p)^2/2\sigma^2]$, where σ is a parameter measuring the specificity of the interaction. This rule increases the specificity of plant–animal interactions: plants and animals interact more if they have similar trait values. Consequently, plants (animals) with different trait values tend to interact with different subsets of animals (plants). In this rule, the smaller σ is, the more specific the interactions will be; with these two interaction rules and less than four independent traits, various topological properties of real ecological networks can be reproduced as shown by ref. 31.

Our model formulation presents several advantages (directly comparable with a neutral model, simulation speed, and control of community size) (SI Appendix), but it also makes a number of assumptions that need to be taken into account (Discussion).

Box 2. ABC Procedure

We compared our model to real data using an approximate Bayesian computation (ABC) (32, 33). The ABC procedure is represented in Fig. 1. It consists in replacing the computation of the model likelihood by simulations of this model (*SI Appendix*). This approximation is useful when likelihood formulas are unavailable as in the present case.

The ABC procedure consists in simulating the model multiple times. For each one of these replicates, we draw the parameter values in prior (here flat) distributions (Fig. 1A and *SI Appendix, Table S5*). At the end of each simulation, a network of interactions between plants and animals is simulated (Fig. 1D). To this end, we first choose at random a patch out of the $l \times l$ simulated patches. In this patch, N_n animals are drawn at random, and for each of them, the plant with which it interacts is also drawn at random with probability proportional to $n_i^p I_{ij}$, where n_i^p is the abundance of plant species i in the patch and I_{ij} is the interaction strength between plant species i and animal species j .

Four network properties are then computed: the number of both plant S_p^s and animal S_a^s species sampled by this procedure, the nestedness index of plants Ne_p (35), and an index of specialization ϕ defined as $\phi = 1 - H_i / \langle H_i \rangle$, where $H_i = -\sum n_{ij} \ln(n_{ij})$ and n_{ij} is the number of interactions between plant i and animal j divided by the total number of interactions ($\langle H_i \rangle$ is the average of H_i computed in 100 randomized networks). The null model used consists in

randomly drawing an interaction network with the same total number of plants, animals, and interactions and having each interaction independently placed between a plant i and an animal j with probability $I_{ij} = \sum_i n_{ij} \sum_j n_{ij}$. Note that $1 - \phi$ is close to the H'_2 value in the work by Blüthgen et al. (46), but the null model used here is different in that it does not constrain the number of interactions per plant and animal species. We use these last two indices to capture the effect of the different interaction rules on network structure: threshold rules tend to increase Ne_p , whereas matching rules tend to increase ϕ .

The properties of the simulated network are then compared with the ones of the real network, and therefore, the closest simulations according to these properties are retained (Fig. 1E).

These retained simulations are then used to quantify the impact of bi-trophic interactions on the composition and dynamics of the plant and animal groups. This quantified effect depends on badly fitted model parameters, mainly on m_p (m_a) and c_p (c_a), which are not well-fitted because of the limited information content of the data used (Figs. 1F and 3 and *SI Appendix, Figs. S7–S9*). Note that we used the ABC procedure to perform an approximate Bayesian model averaging. The goal here is neither to compare the different interaction rules (with threshold and/or matching rules) nor obtain precise model parameter estimates but constrain our simulations so that they fit observed network properties.

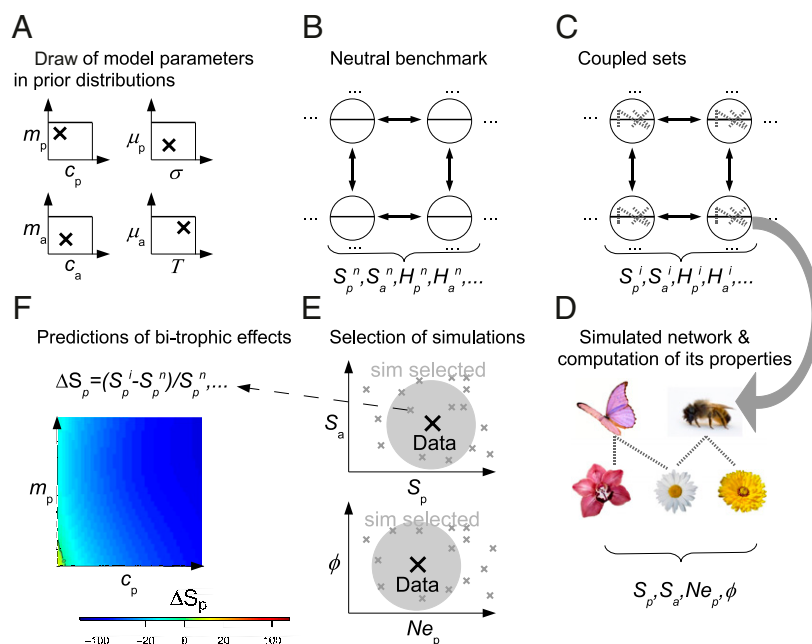


Fig. 1. Approximate Bayesian computation (ABC) procedure. (A) Model parameter values (symbolized by x) are randomly drawn in flat prior distributions (symbolized by rectangles). (B) A neutral metacommunity is simulated to form the benchmark. A grid of patches (circles) is connected by dispersal (arrows). Plants and animals (lower and upper semicircles, respectively) coexist in the patches, but they do not interact. Various community statistics are computed in this neutral benchmark ($S_p^i, S_a^i, H_p^i, H_a^i, \dots$). (C) The metacommunity dynamics are pursued including the bi-trophic interactions (dotted lines between the half circles) this time. Various community statistics are computed in this coupled metacommunity ($S_p^i, S_a^i, H_p^i, H_a^i, \dots$). (D) A network of bi-trophic interactions is simulated in a randomly chosen patch of the metacommunity, and its properties are computed (S_p, S_a, Ne_p, ϕ). (E) The properties of the simulated networks (small gray x) are compared with those properties of the real data (large black x), and the simulations with the best match are selected (gray circles). (F) Selected simulations are used to assess the effect of bi-trophic interactions. This assessment is done by comparing the final metacommunity structure in the simulation (C) with the one of the neutral benchmark (B). These bi-trophic effects are plotted against the two model parameters explaining the bulk of their variation: m_p and c_p for plants and m_a and c_a for animals.

Results

In this section, we will use the term animal to designate a plant's interactor, although it can be a fungus in the datasets studied.

Model Results. Our simulations show that mutualistic and antagonistic interactions can either increase or decrease local plant and animal species richness (Fig. 2 and *SI Appendix, Fig. S4*) depending on the balance between biotic filtering and niche partitioning. This balance, in turn, depends on the model parameters describing the structure of the interaction network, the dispersal rate across patches (m_p and m_a), and the strength of the interactions (i.e., the component of seed or egg production— c_p and c_a , respectively—accounted by the interaction with the other trophic group) (*SI Appendix, Tables S1 and S2*).

The stabilizing effect (34) of biotrophic interactions is induced, for plants, by the heterogeneity among animals in their plant preferences and for animals, by the diversity of plant resources. It can be detected by looking at the variance in trait values among community members. Communities tend to gain species with overdispersed traits during the coupled dynamics (*SI Appendix, Variance Test*).

The other effect of biotrophic interactions is to filter out community members by producing fitness differences among individuals. We detect this filtering effect by computing the average interaction strength between plant and animal individuals. When mutualistic interactions have a negative impact on plant (animal) species richness, the average interaction strength increases compared with the neutral case. The surviving plants (animals) are those plants that encounter more mutualists. For antagonistic interactions, the average interaction strength decreases (increases) for plants (animals) when biotrophic interactions have a negative impact on plant (animal) species richness. The surviving plants are

those plants that encounter fewer antagonists, whereas the surviving animals are those animals that have many interactions (*SI Appendix, Coupling Test*).

Bitrophic interactions, however, principally affect rare species: in 96% of the cases, the similarity in species composition between trophically coupled and uncoupled plant sets is larger when an abundance-weighted measure is used (*SI Appendix*).

Fig. 2 illustrates how the net effect of biotrophic interactions on local plant richness S_p depends on the plant dispersal rate m_p and the component of seed production dependent on biotrophic interactions c_p . In Fig. 2, various extremes of network structure are illustrated. These contrasting network architectures are produced with a threshold rule, a matching rule with high trait specificity, and a matching rule with low trait specificity, respectively. They result in nested, specialized, and generalized networks, respectively (Box 1 has details on these interaction rules and the resulting network structures).

Two points arising from Fig. 2 are worth mentioning. First, in the limits of low dispersal (low m_p) and weak interactions (low c_p), we recover the results shown in the work by Bastolla et al. (35)—namely, that nested networks tend to increase plant local richness (Fig. 2A, bottom left). Second, there is a strong interaction in the effect of the different model parameters on the outcome of biotrophic interactions. This finding means that, with such a relatively simple model, one can already produce very complex outcomes, and therefore, the effects of biotrophic interactions on metacommunity structure and dynamics are likely to be case-specific. A detailed interpretation of the patterns observed in Fig. 2 as well as the effect on biotrophic interactions on other community characteristics, including the animal group, can be found in *SI Appendix*.

Application to Real Networks. Because the theoretical exploration of our model revealed a rich variety of possible outcomes, we proceeded by assessing what specific patterns would emerge when the model was fitted to real data. We, therefore, developed a statistical technique to fit our biotrophic metacommunity model to local networks compiled in the literature. This fitting procedure is based on ABC (32, 33) (Box 2). The information available in the data was not sufficient to fully parameterize our metacommunity model and hence, precisely quantify the effect of biotrophic interactions on plant and animal richness in these datasets. It was, however, sufficient to greatly constrain our simulations, and therefore, the remaining variation in biotrophic effects on plant (animal) richness was highly dependent on two noninferred parameters: the plant (animal) dispersal rate between patches m_p (m_a) and the proportion of seed (egg) production c_p (c_a), which depends on trophic interactions (average $R^2 = 61\%$ and 23% , respectively) (Fig. 3).

We found that biotrophic interactions are likely to decrease local plant species richness in the three types of networks (Fig. 3A, C, and E), producing an increase in β -diversity (*SI Appendix, Fig. S2*). The sole exception is for very weak interactions and very low dispersal rates, where our model predicts an increase in local diversity. In plant–pollinator networks, we can estimate c_p with the index of pollen limitation, which compares the fruit set of freely pollinated flowers with the fruit set of encapsulated flowers. The average of reported indices of pollen limitation for angiosperms in the metaanalysis in the work by Larson and Barrett (36) is $c_p = 0.4$. This value is an order of magnitude higher than the value required for a positive effect of pollinators on local richness ($c_p < 0.02$). In plant–fungi and plant–herbivore networks, c_p is more difficult to relate to any direct empirical measure. However, even in these cases, we can use available information to set up some general limits to the potential range of variability in this parameter. In the case of herbivores, for example, defoliation, flower, and fruit consumption attributable to insects represent above 5% each of the corresponding biomass (37). It is then likely that c_p is generally well above 0.02 in real settings.

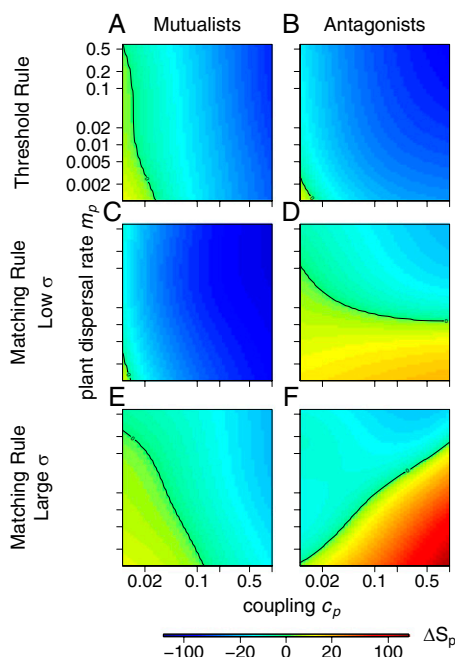


Fig. 2. Relative variation (in percentage) of plant α -diversity between trophically coupled and uncoupled communities. α -Diversity is measured as the local plant species richness S_p . A positive value means that trophically coupled communities are species-richer than uncoupled ones. Different panels show results for the threshold model with one trait (A and B), the matching model with one trait and $\sigma = 0.015$ (C and D), and the matching model with one trait and $\sigma = 1$ (E and F). A, C, and E correspond to mutualistic interactions, whereas B, D, and F correspond to antagonistic interactions. Parameter values are $\mu_p = \mu_a = 0.004$, $m_a = 0.625$, and $c_a = 0.16$.

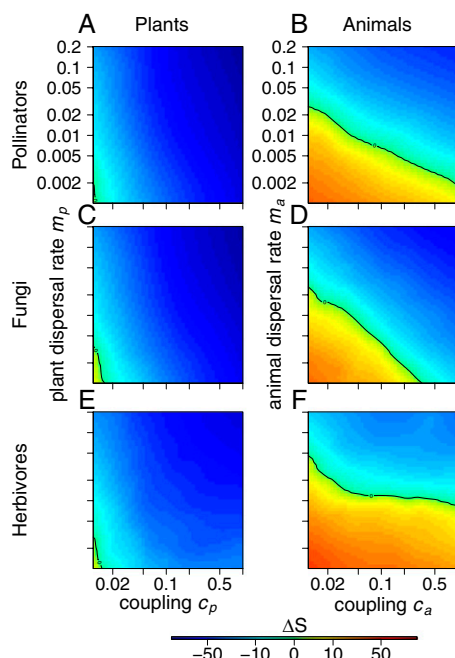


Fig. 3. Variation of plant and animal local species diversity between trophically coupled and uncoupled communities in simulations that best fit observed network structure in real datasets. (A, C, and E) Relative variation of plant α -diversity measured as local plant species richness S_p ; 70%, 64%, and 45%, respectively, of the variance is explained by the interpolation on average in each dataset. (B, D, and F) Relative variation of animal α -diversity measured as local animal species richness S_a ; 33%, 40%, and 30%, respectively, of the variance is explained by the interpolation on average in each dataset. (A and B) Plant–pollinator datasets ($n = 23$). (C and D) Plant–fungi datasets ($n = 16$). (E and F) Plant–insect herbivore datasets ($n = 15$).

From the animals' perspective, our model predictions are more dependent on the precise value of c_a and m_a (Fig. 3 B, D, and F). A combination of larger c_a and m_a is required for bitrophic interactions to lead to an increase in animal spatial structure. Because animal interactors feed on plants, c_a would likely be at least equal to 0.1 in real settings, whereas animal dispersal rates should be, in general, larger than those rates for plants. It is, consequently, likely that bitrophic interactions lead in general to an increase of animal spatial structure, although this result might be more context-dependent than for plants. Overall, our results suggest that, in the majority of real scenarios, bitrophic interactions will decrease local plant and animal species richness, while increasing plant and animal β -diversity. These predictions were qualitatively similar across the different empirical networks (*SI Appendix*, Figs. S11–S16) and when looking at local diversity using Shannon's index H (*SI Appendix*, Fig. S7).

Discussion

We have shown theoretically that bitrophic interactions can both decrease or increase local plant and animal species richness, whereas regional richness is far less affected or not affected at all (*SI Appendix*). This effect of bitrophic interactions was found to principally affect rare species. This finding implies that community ecologists may be safe while ignoring bitrophic interactions when looking at general trends in community composition. Nevertheless, if they want to truly understand the composition and dynamics of entire groups—not just of the most abundant species—it may be essential to take bitrophic interactions into account.

Our integrative framework confirms the importance of network structure for species richness, and it is in agreement with other recent approaches (35, 38) (*SI Appendix*). Similarly, our

study supports recent calls for looking at bitrophic interactions to understand plant community assembly and dynamics (10, 39). At the same time, however, our results show that knowing the structure of the interaction network is insufficient to fully predict the magnitude of this biotic filter: a large source of variation is explained by the properties of each trophic group and the proportion of fitness impacted by bitrophic interactions (Fig. 3).

For the same network structure, the decrease in local species richness is likely to be greater for less dispersal-limited systems (large m_p or m_a) and stronger coupling between plants and animals (large c_p or c_a). Our results suggest that dispersal rate and the strength of bitrophic coupling play similar roles in explaining variation in species richness.

By means of a computer-intensive statistical technique, we were able to relate this complex model to real world data. We have shown that, for realistic network structure, both mutualistic and antagonistic interactions are likely to reduce local plant and animal species richness and that the decrease in local species richness and associated increase in β -diversity can be substantial (Fig. 3 and *SI Appendix*, Fig. S10). Because our datasets encompass many different interaction types and geographical locations, our results are likely to be general and highlight the filtering role of bitrophic interactions at local scales. Neutral processes have already been shown to produce spatial community turnover (40). As shown here, this neutral spatial structuring can be amplified with realistic architectures of bitrophic interactions, with which different local assemblages will filter different local community members. These results are consistent with the recent analysis in the work by Pellissier et al. (41) showing that plant sets in the Swiss Alps present evidence of spatial structuring in traits related to pollination.

To be able to fit our model to available network data, we have made a number of simplifications that need to be acknowledged. First, we did not consider any spatial heterogeneity in the abiotic environment. Including this factor would add a new source of spatial structure in the plant and animal groups.

Second, another related simplification of our model was to ignore any kind of tradeoffs, such as those tradeoffs between the plant's resistance to herbivory and its growth rate and competitive ability (42). In the presence of such tradeoffs, trophic interactions would increase plant biodiversity by equalizing the fitness of otherwise unequal competitors (27, 34).

Third, we assumed that interactions had symmetrical effects on the plant and animal interactions. This assumption, which is not supported by real data on interaction networks, might be relaxed in future studies. To this goal, we need additional data on the fitness consequences of ecological interactions.

Fourth, our model ignored any variation in community size of plants and animals. In particular, year to year variation in animal community sizes could increase their impact on the plant set. Indeed, the competition among flowers to attract pollinators should be exacerbated in years of low pollinator abundance. Similarly, the impact of herbivores on the plant set should be maximal in years of high herbivore abundance. Again, a detailed analysis would be required to explore such possibilities.

Fifth, our lottery-like modeling framework is rather atypical in the literature on ecological networks (27, 43). The pros and cons of such a choice are detailed in *SI Appendix*. It would certainly be worth examining whether similar results were obtained with other modeling approaches, such as Lotka–Volterra-like equations, although this method would require solving additional challenges (*SI Appendix*). The fact that we recover the results from the work by Bastolla et al. (35) in the limit of low migration and coupling is reassuring and suggests that this finding might be the case.

We have pointed out a number of directions worth pursuing to better understand the combined effects of dispersal and trophic interactions on metacommunity dynamics in real world communities. Our study represents only a first step in this direction. Despite

the limitations of our approach, it illustrates how complex questions and models can be statistically compared with real world data through an ABC approach. It also points out that, to elaborate and test more complicated models of spatial network dynamics, new types of data should be concurrently gathered, informing us on the mechanisms of network assembly, the dispersal rates of organisms, and the impact of trophic interactions on organisms' fitness.

Materials and Methods

Model Outputs. The two trophic groups are initialized fixing c_p and c_a to zero. They are, thus, at a neutral dispersal-drift dynamic equilibrium that can be simulated quickly by coalescence (44). The coalescence procedure consists of tracing backward in time the genealogy of the individuals in the present. Because all individuals ultimately have a unique common ancestor, the number of individuals to simulate progressively decreases, making the computation quicker. Starting from this reference neutral point obtained by coalescence, the trophically coupled dynamics of the two groups are simulated forward in time during 100 generations (with c_p and c_a different from zero). Species richness in both a single patch (local) and all of the patches together (metacommunity) and species diversity (measured as Shannon's index) are recorded for both plants and animals and both before and after coupling the two trophic groups. The turnover in plant and animal composition from one generation to the next is also recorded (*SI Appendix, Temporal Turnover*). We measure the effect of the biotrophic interactions by the relative variation of plant and animal species richness between the coupled and uncoupled scenarios $\Delta S_p = (S_p^i - S_p^n)/S_p^n$ and $\Delta S_a = (S_a^i - S_a^n)/S_a^n$ (the superscripts i and n indicate with and without trophic interaction, respectively). We also monitor the relative variation of the other summary statistics in the same way.

Effect of the Interactions and Role of the Different Parameters. We performed simulations on a grid of parameter values: μ_p and μ_a in {0.0005, 0.004}, m_p and

m_a in {0.001, 0.005, 0.025, 0.125, 0.625}, and c_p and c_a in {0.01, 0.04, 0.16, 0.64, 1}. Eight different interaction rules were used based on a combination of zero, one, or two threshold rules and zero, one, or two matching rules, and each rule applies to independent and uncorrelated traits (hence, the number of traits T ranged between one and four depending on the interaction rule). Matching rules were used with σ in {0.015, 0.125, 1, 8}. For each interaction rule and set of parameter values, 10 independent communities were simulated, leading to a total of 1,300,000 simulations. We used $l = 5$, $N_p = 1,000$, and $N_a = 200$. The results were qualitatively similar with other choices of N_a and l (*SI Appendix*). Simulations were run with periodic boundary conditions. Results were similar in simulations with zero-flux boundary conditions and lost migrants at the boundary (*SI Appendix*). A detailed analysis of the effect of each model parameter as well as some community properties on the impact of biotrophic interactions are provided in *SI Appendix*.

To assess the robustness of our results to the specific choice of the component of seed (egg) production because of the trophic interaction, we studied an additional model where Eq. 2 is similar to Eq. 1, finding similar results (*SI Appendix*).

Compilation of Ecological Networks. Datasets were included based on two criteria: they had to be quantitative and built from a single study site (7). In the majority of cases, there is little information on the spatial dimension of these sampled networks, and here, we will be assuming that they correspond in our model to a single patch.

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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 expression: $c_p \frac{\sum_{j=1}^{S_a} n_j^a I_{ij}}{\sum_{k=1}^{S_p} \left(\frac{n_k^p}{N_p} \sum_{l=1}^{S_a} n_l^a I_{kl} \right)}$. 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

that animals compete for these resources, so that an animal of species j gathers from a 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 relative frequency of the plants, we recover Equation 2. We additionally studied another way to model animal fecundity, and obtained similar results (see *SI Section S2.11.2*). In the antagonistic case, the reasoning is the same, except that plants are negatively affected by the interaction.

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

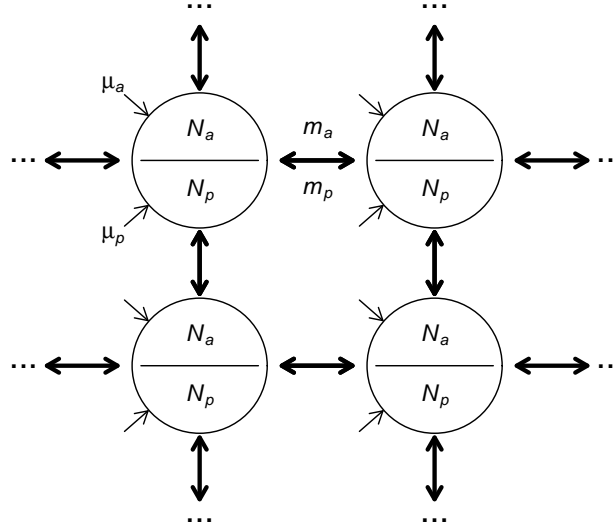


Fig. S1: Model representation. Circles stand for patches, horizontal and vertical arrows represent dispersal between neighboring patches, and oblique arrows indicate dispersal from the species pool. N_p (N_a) is the number of plant (animal) individuals in each patch. m_p (m_a) is the plant (animal) dispersal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

S2 Model results - impact on the plant set

S2.1 α diversity of plants

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

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

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

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

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

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

for specialized interactions. In contrast, we find the reverse relationship for antagonistic interactions: stronger coupling leads to an increased positive effect on plant richness, especially at low dispersal rates (Fig. 2F). Here the stabilizing effect of herbivores exceeds their filtering effect, so that the resulting effect of herbivores on plants is positive. Stronger coupling between plants and herbivores thus increase the magnitude of this positive effect, especially at low dispersal rates for which local interactions have the strongest impact on community dynamics.

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

S2.2 β diversity of plants

Up to here, we have described patterns of local species richness, namely, plant richness at each lattice site. Our framework also enabled us to study the effect of bi-trophic interactions 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.

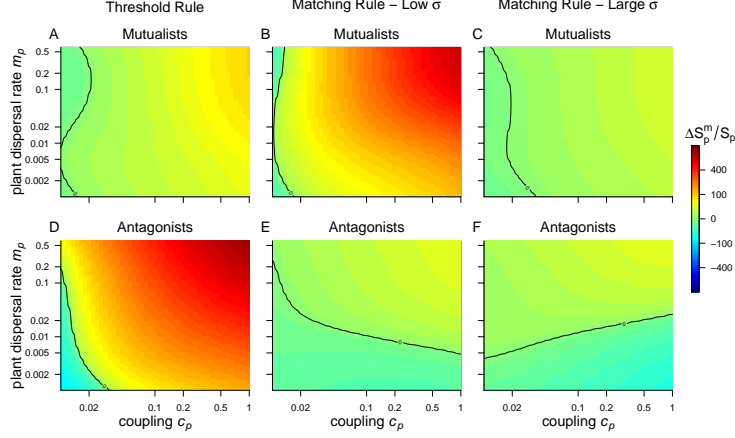


Fig. S2: Relative variation (in %) of plant β diversity between trophically coupled and uncoupled communities. β diversity is measured as the ratio of metacommunity over local plant richness S_p^m/S_p . Panels A and D display a threshold model of interaction with one trait; panels B and E show results 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 $\mu_p = \mu_a = 0.004$, $m_a = 0.625$, $c_a = 0.16$.

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

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

Less diverse, more dispersal-limited, and more strongly impacted plant sets are experiencing 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

5

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

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

5

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

S2.4 Coupling Test

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

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

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

where I_{ij} indicates the interaction strength between plant i and animal j . Before starting the dynamics with bi-trophic interactions, we compute the initial interaction strength IS^n between plants and animals. To do this, we use plant and animal abundances obtained with neutral assembly and I_{ij} values subsequently used in the dynamics with interactions. At the end of the dynamics with interactions (100 generations forward), we compute the final interaction strength IS^i between plants and animals, using final abundances of plants and animals. We record the variation of the interaction strength $\Delta IS = IS^i - IS^n$ due to the dynamics with bi-trophic interactions. When interactions are mutualistic and their impact on plants is dominated by the filtering effect, plants survive only if they encounter some well-adapted mutualists. Interactions should thus produce an increase of the statistics IS . For antagonistic interactions, on the contrary, plants survive only if they do not encounter well-adapted antagonists, and the statistics IS should then decrease. If our interpretation is correct, then ΔS_p should be negatively (positively) correlated with 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, $p < 0.001$).

S2.7 Effect of network richness on the impact of bi-trophic interactions

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

S2.8 Temporal turnover

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

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

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

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

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

Larger J and J_q values indicate a lower temporal turnover.

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

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

S2.9 Interactions mostly affect rare species

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

S2.10 Interactions produce a spatially heterogeneous filter

At the end of the coupled metacommunity dynamics, we test whether the filtering effect of the animal set on the plant one is homogeneous across space. To do this, we compute the relative fecundity of each plant species in each patch. The relative fecundity of plant 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 its relative fecundity is above 1, meaning that it obtains a local competitive advantage due to bi-trophic interactions. We find that 63% (56%) of the plant species are positively filtered in at least one patch due to mutualistic (antagonistic) interactions. To perform this analysis, we used a large grid of 20×20 patches, and a subset of parameter values: μ_p 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 considered interaction rules with one trait, using either a threshold rule or a matching rule with σ in $\{0.015; 1\}$. We performed 10 replicates per combination of parameters values.

S2.11 Robustness of the results

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

To perform this computer intensive study, we used a relatively small number of patches: a grid of $l \times l$ patches, with $l = 5$. We performed additional simulations with $l = 10$, and $l = 20$ for a subset of parameter values: $\mu_p = \mu_a = 0.005$, m_p in $\{0.001; 0.005; 0.025; 0.125; 0.625\}$, m_a in $\{0.005; 0.625\}$, c_p in $\{0.01; 0.04; 0.16; 0.64; 1\}$, and $c_a = 0.01$. For these simulations, we only considered interaction rules with one trait, using either a threshold rule, or a matching rule with σ in $\{0.015; 0.125; 1; 8\}$. We performed 10 replicates per combination of parameters values, and computed in each simulation the variation in plant metacommunity richness due to bi-trophic interactions ΔS_p^{met} , and the variation in local plant richness ΔS_p . As the number of patches in the metacommunity 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 ($|slope - 1| \leq 0.081$).

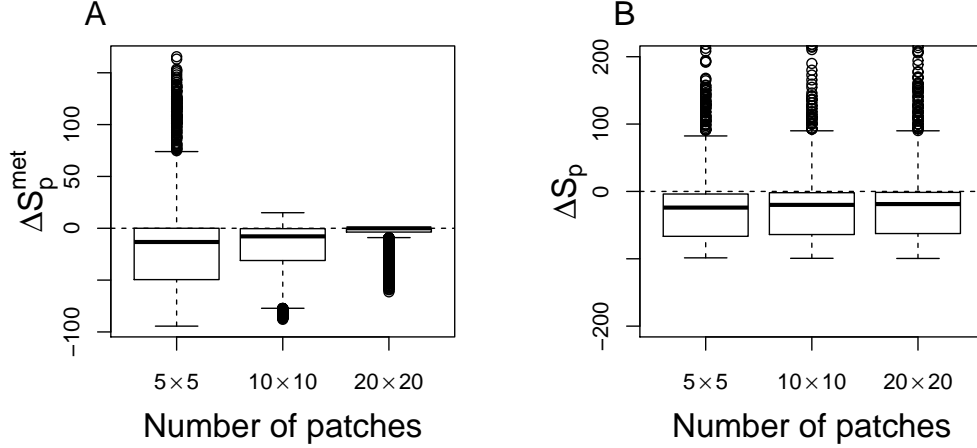


Fig. S3: Effect of system size on bi-trophic impact. Panel A: Distribution of ΔS_p^{met} as a function of the number $l * l$ of patches in the simulations. Panel B: Distribution of ΔS_p as a function of the number $l * l$ of patches in the simulations.

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 the 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 ($|slope - 1| \leq 0.046$).

S3 Model results - impact on the animal set

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

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

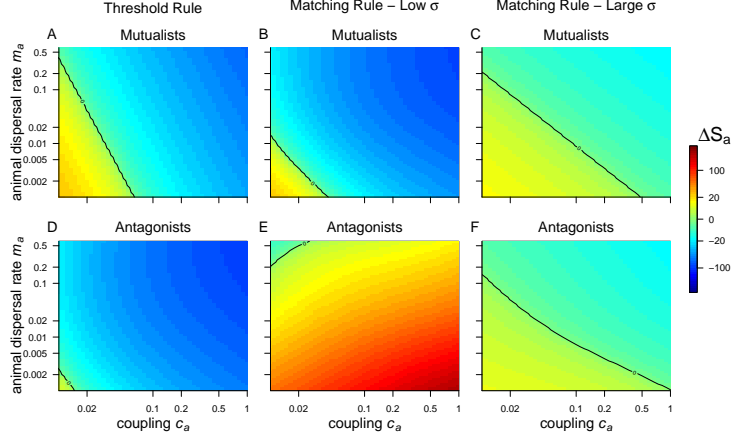


Fig. S4: Relative variation (in %) of animal α diversity between trophically coupled and uncoupled communities. α diversity is measured as the local animal species richness S_a . A positive value means that trophically coupled communities are species-richer than uncoupled ones. Different panels show 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 $\mu_p = \mu_a = 0.004$, $m_p = 0.625$, $c_p = 0.16$.

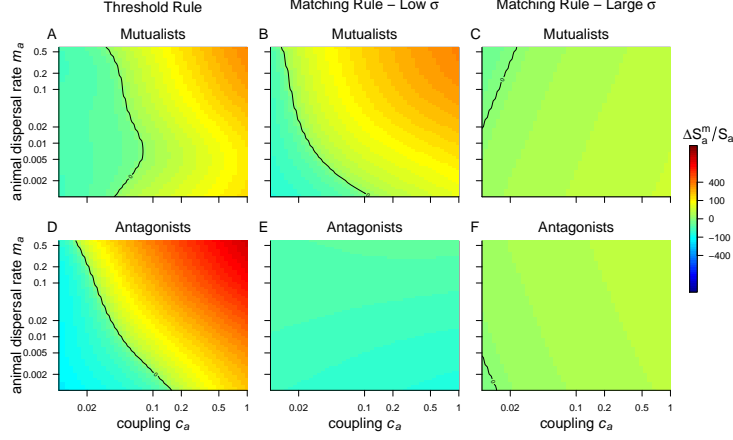


Fig. S5: Relative variation (in %) of animal β diversity between trophically coupled and uncoupled communities. β diversity is measured as the ratio of metacommunity over local animal richness S_a^m/S_a . Panels A and D display a threshold model of interaction with one trait; panels B and E show results 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 $\mu_p = \mu_a = 0.004$, $m_p = 0.625$, $c_p = 0.16$.

S4 Application to real datasets

S4.1 Approximate Bayesian Computation (ABC) procedure

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

First, we simulate a neutral uncoupled metacommunity of plants and animals to serve as a benchmark to quantify bi-trophic impact on the plant set, drawing at random all 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).

Table S5: Priors used for the Approximate Bayesian Computation.

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

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

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.

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

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

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).

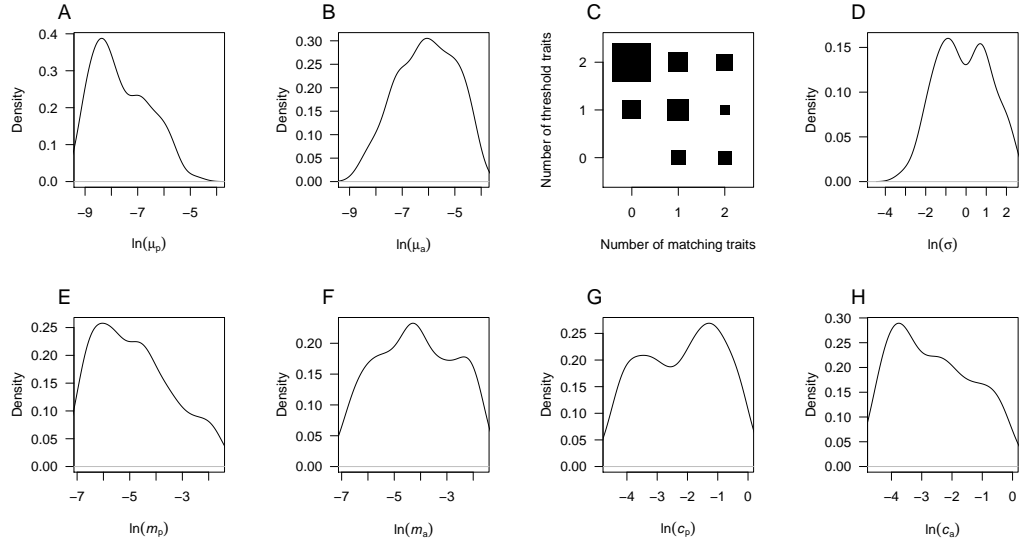


Fig. S6: Approximate posterior distribution of the model parameters. Panels A-B: approximate posterior distribution for parameters μ_p and μ_a . Panel C: posterior weight of the different interaction rules. The length of each square side is proportional to the number of retained simulations with the 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 .

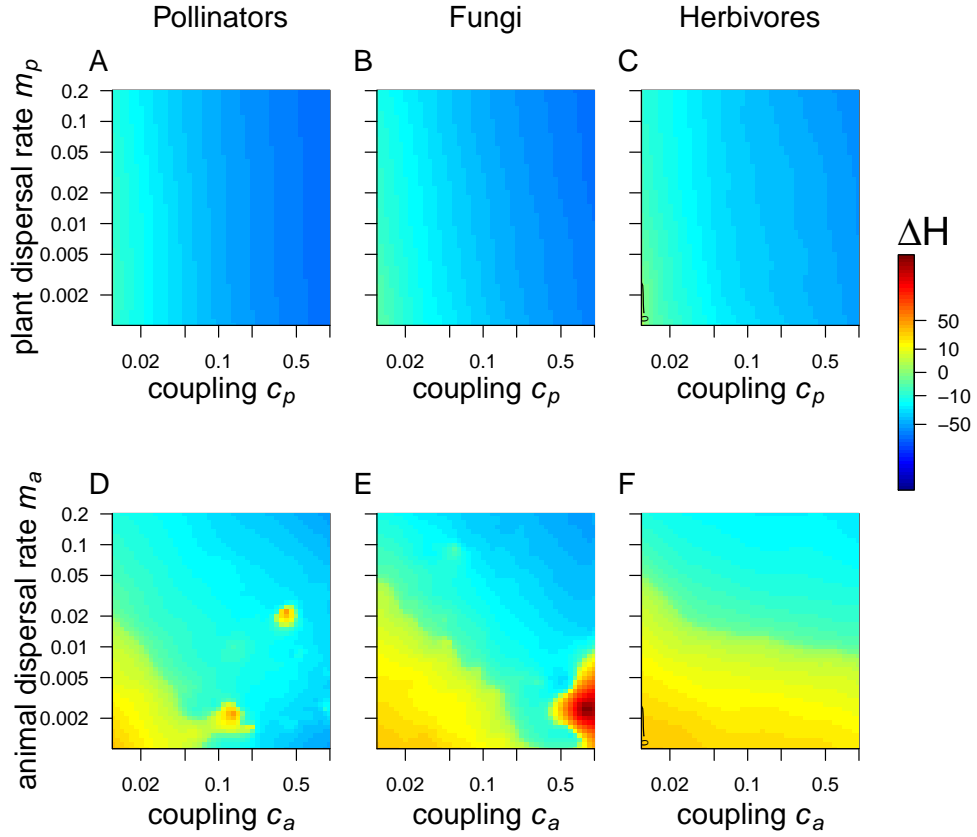


Fig. S7: Relative variation of plant and animal Shannon's index H between coupled and uncoupled communities in simulations which best fit observed network structure in real datasets. Panels A-C: results for plants. Panels D-F: results for animals. Panels A and D: Plant-pollinators datasets ($n=23$). 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.

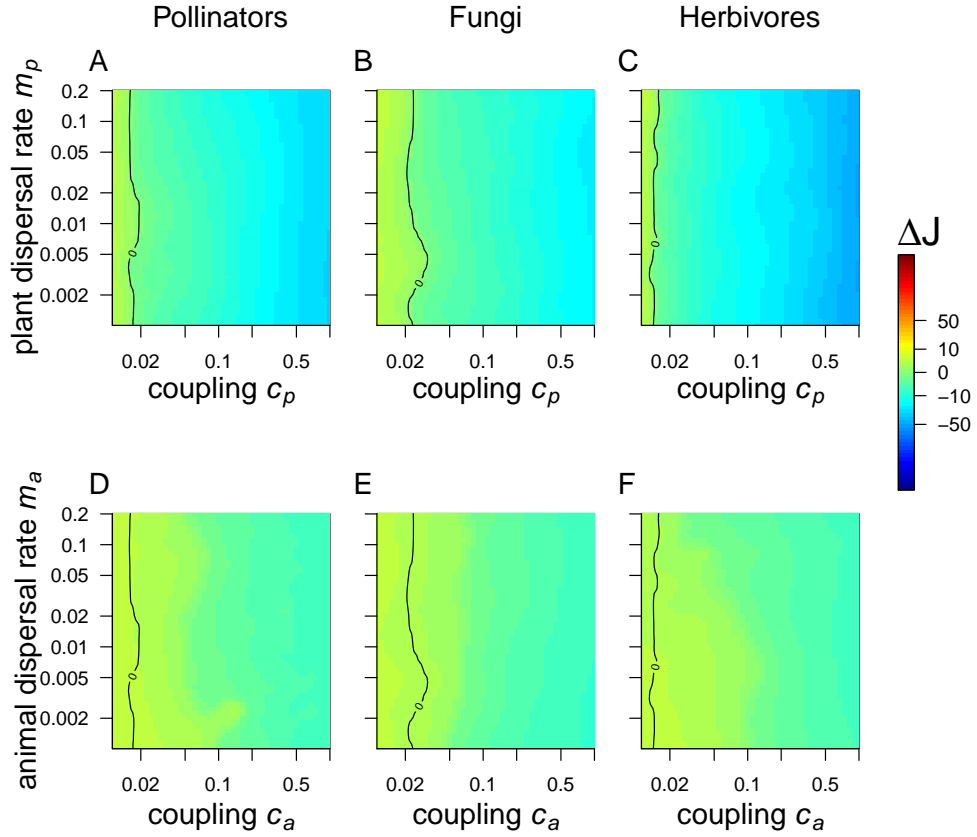


Fig. S8: Relative variation of plant and animal temporal similarity J between coupled and uncoupled communities in simulations which best fit observed network structure in real datasets. Panels A-C: results for plants. Panels D-F: results for animals. Panels A and D: Plant-pollinators datasets ($n=23$). 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.

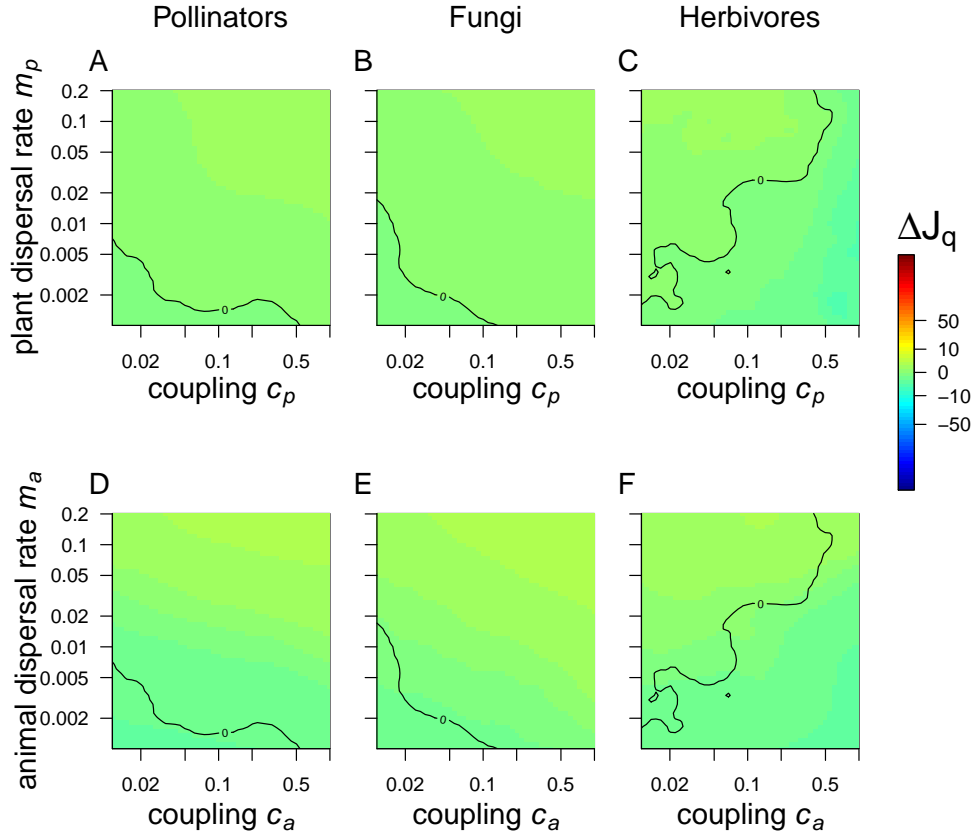


Fig. S9: Relative variation of plant and animal temporal similarity J_q between coupled and uncoupled communities in simulations which best fit observed network structure in real datasets. Panels A-C: results for plants. Panels D-F: results for animals. Panels A and D: Plant-pollinators datasets ($n=23$). 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.

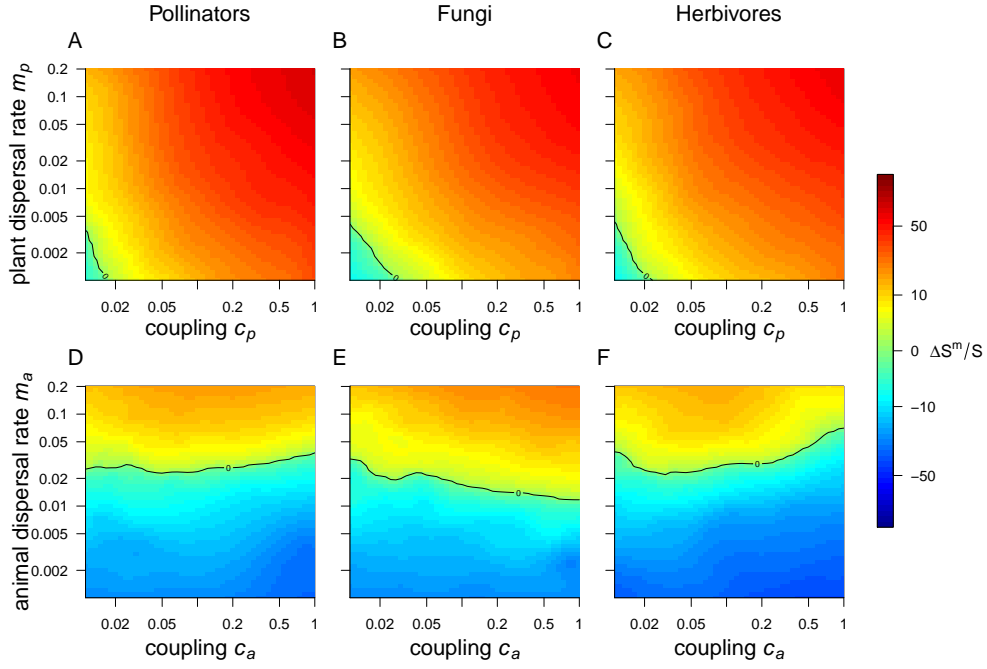


Fig. S10: Relative variation of plant and animal β diversity S^m/S between coupled and uncoupled communities in simulations which best fit observed network structure in real datasets. Panels A-C: results for plants. Panels D-F: results for animals. Panels A and D: Plant-pollinators datasets (n=23). Panels 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.

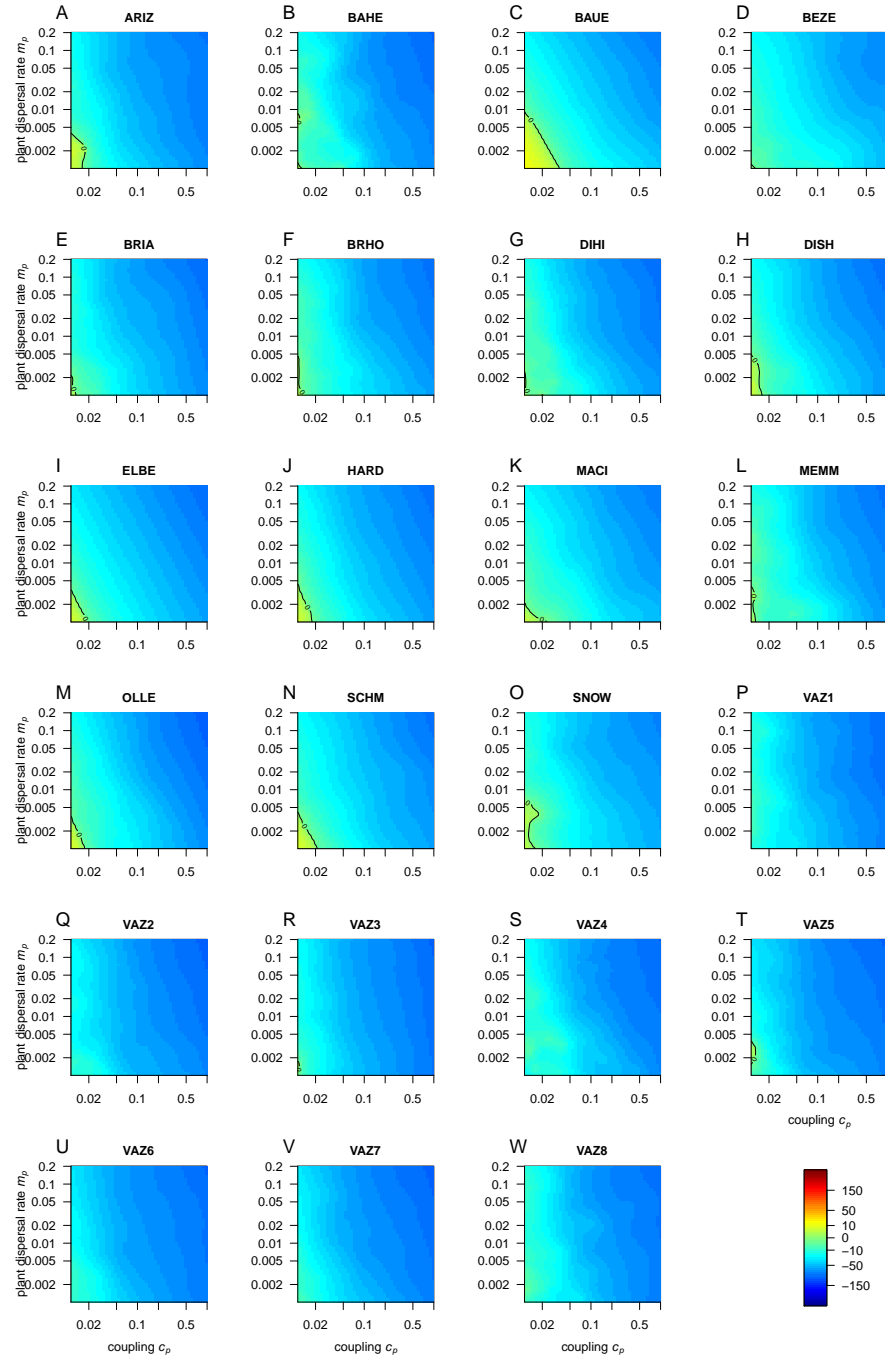


Fig. S11: Relative variation of plant species richness between coupled and uncoupled communities in simulations which best fit observed network structure in real plant-pollinator datasets.

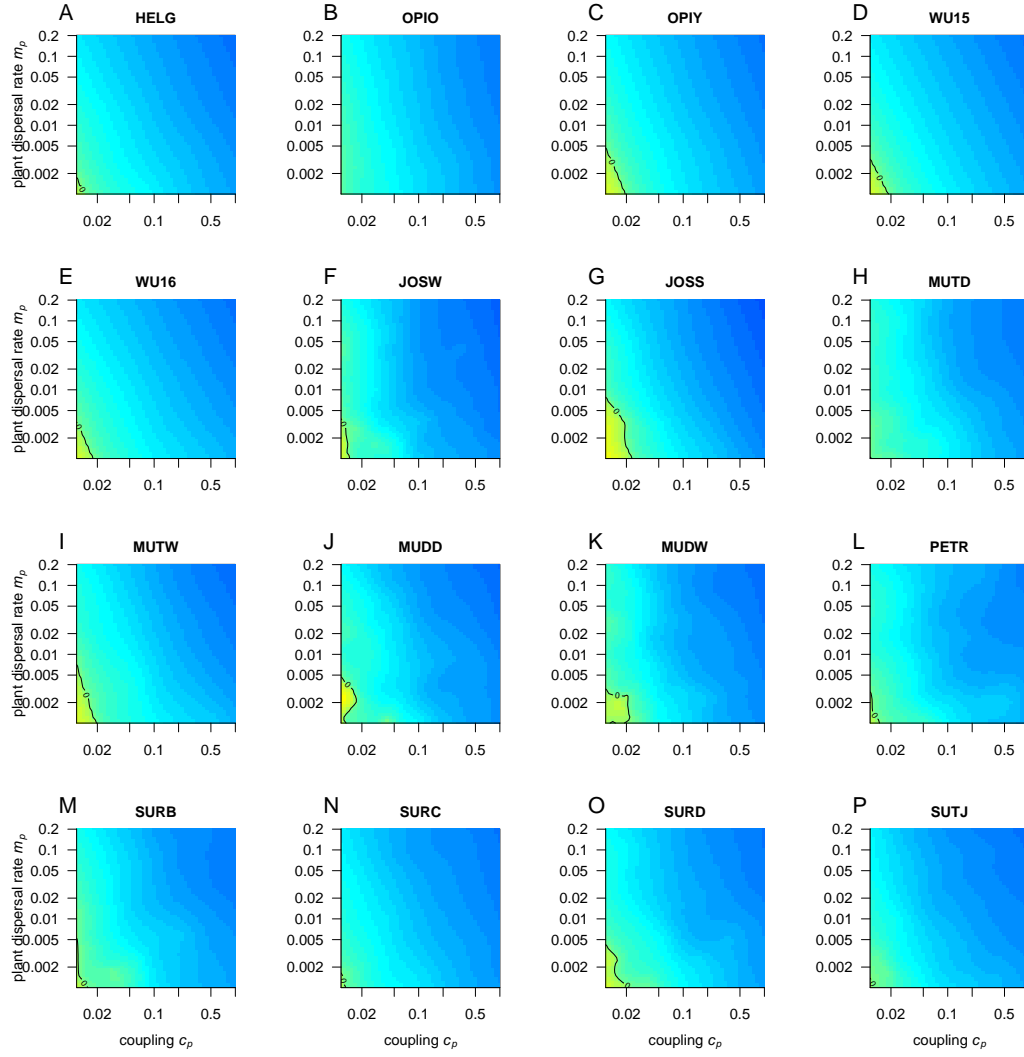


Fig. S12: Relative variation of plant species richness between coupled and uncoupled communities in simulations which best fit observed network structure in real plant-fungi datasets.

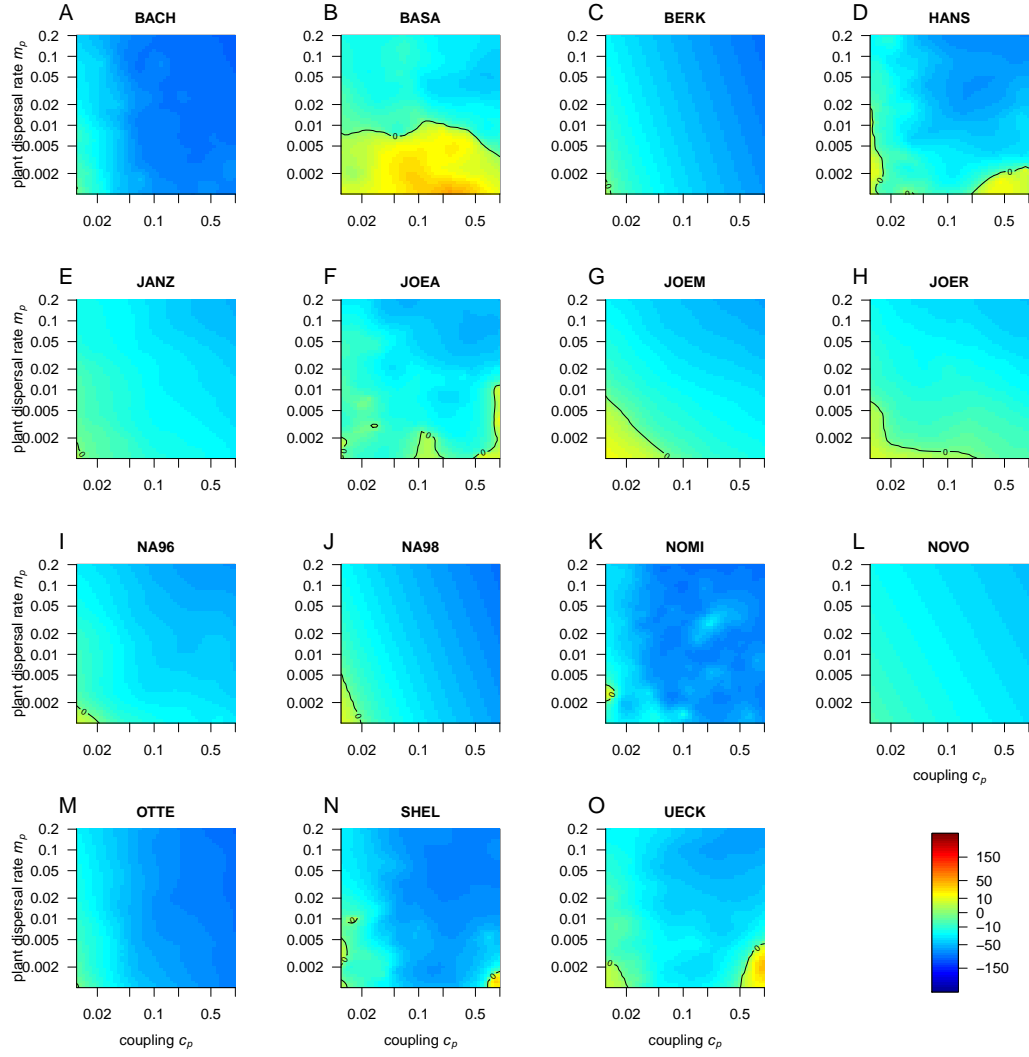


Fig. S13: Relative variation of plant species richness between coupled and uncoupled communities in simulations which best fit observed network structure in real plant-insect herbivores datasets.

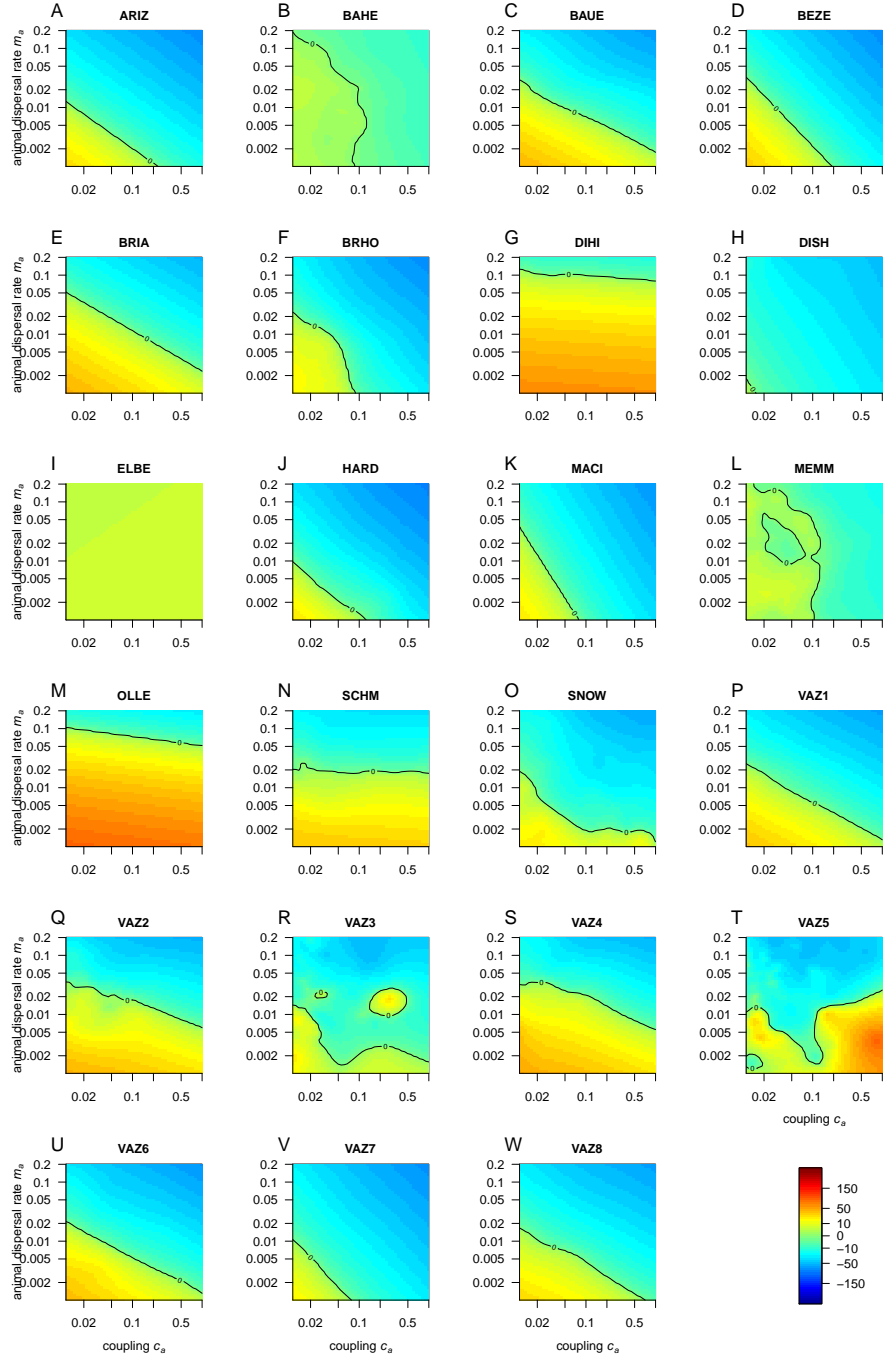


Fig. S14: Relative variation of animal species richness between coupled and uncoupled communities in simulations which best fit observed network structure in real plant-pollinator datasets.

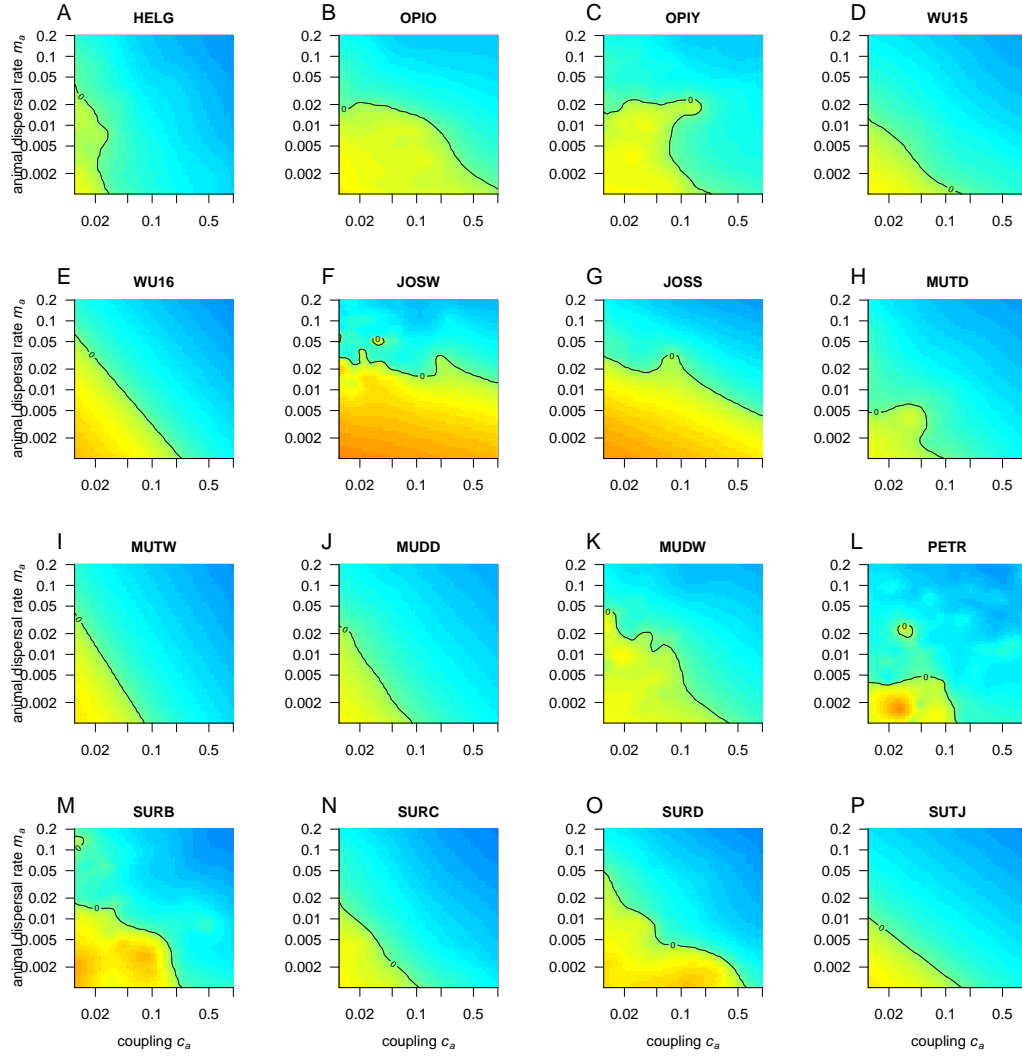


Fig. S15: Relative variation of animal species richness between coupled and uncoupled communities in simulations which best fit observed network structure in real plant-fungi datasets.

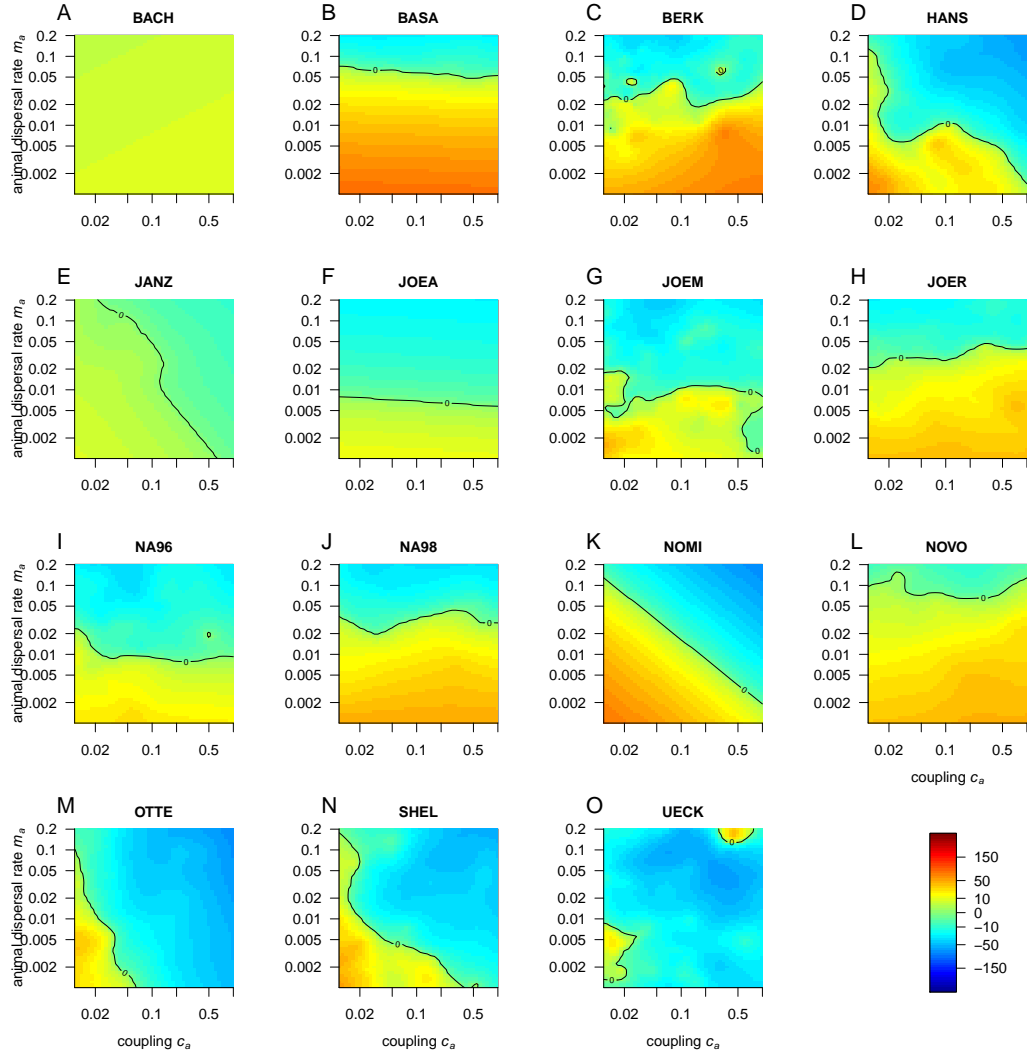


Fig. S16: Relative variation of animal species richness between coupled and uncoupled communities in simulations which best fit observed network structure in real plant-insect herbivores datasets.

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