

The geographic mosaic of coevolution in mutualistic networks

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Ecological interactions shape adaptations through coevolution not only between pairs of species but also through entire multispecies assemblages. Local coevolution can then be further altered through spatial processes that have been formally partitioned in the geographic mosaic theory of coevolution. A major current challenge is to understand the spatial patterns of coadaptation that emerge across ecosystems through the interplay between gene flow and selection in networks of interacting species. Here, we combine a coevolutionary model, network theory, and empirical information on species interactions to investigate how gene flow and geographical variation in selection affect trait patterns in mutualistic networks. We show that gene flow has the surprising effect of favoring trait matching, especially among generalist species in species-rich networks typical of pollination and seed dispersal interactions. Using an analytical approximation of our model, we demonstrate that gene flow promotes trait matching by making the adaptive landscapes of different species more similar to each other. We use this result to show that the progressive loss of gene flow associated with habitat fragmentation may undermine coadaptation in mutualisms. Our results therefore provide predictions of how spatial processes shape the evolution of species-rich interactions and how the widespread fragmentation of natural landscapes may modify the coevolutionary process.

coadaptation | ecological networks | gene flow | mutualism | trait matching

Ecological interactions are a fundamental component of biodiversity (1). Phenotypic traits of many species have evolved through selection imposed by ecological interactions, such as toxins in prey and resistance to toxins in their predators (2) or floral tubes of plants and mouthparts of their pollinators (3). These examples show how reciprocal selection shapes coadaptation in pairs or small groups of interacting species. However, small groups of species rarely interact in isolation. Species are usually embedded in networks containing dozens or even hundreds of interacting species (4, 5). Understanding how patterns of coadaptation arise and favor species persistence in large assemblages of interacting species is currently a major challenge requiring approaches at the interface of ecology, evolution, and network science (6–8).

For mutualisms, previous studies have explored how coevolution may affect network architecture—that is, the pattern of interactions among species—and, in turn, how such architecture may drive coevolution. The role of coevolution in shaping the organization of links of empirical networks is still uncertain (9–12). Nevertheless, it is known that network architecture varies with fundamental aspects of the natural history of interactions, potentially leading to distinct coevolutionary dynamics (7, 13). For example, multiple-partner mutualisms, in which an individual interacts with several individuals throughout its life, such as pollination or seed dispersal by animals, typically form species-rich and nested networks (14, 15). Theoretical evidence suggests that coevolution in multiple-partner mutualisms operates in part through indirect evolutionary effects—that is, evolutionary outcomes caused by species that are not

linked as interacting partners (7), favoring similarity in traits at the community level (i.e., trait convergence) (16, 17). In contrast, intimate mutualisms, in which an individual completes at least a life stage on a single host, such as protection of host plants by ants or protection of anemonefishes by host anemones, generate species-poor and modular networks (18, 19). Coevolution in intimate mutualisms is expected to exhibit frequent and reciprocal effects between species that interact directly (13), leading to the tight trait matching observed in many intimate interactions (20). Thus, studies of coevolution in mutualistic networks have shown how adaptive landscapes may be modified by the underlying network structure, molding trait patterns (Fig. 14).

Coevolution in multispecific interactions, however, is a geographic process, as the assembly of interaction networks and the ongoing coevolution in these networks may vary across space (1). In pairs or small groups of species, theoretical and empirical work on the geographic mosaic of coevolution have shown that patterns of adaptation vary widely across geographic regions depending on the distribution of local selection regimes (2, 21–23). In addition, the connection of different populations via gene flow as well as other genetic and genomic processes may remix trait distributions across the landscape, promoting or inhibiting the evolution of local coadaptation (24–27). Although gene

Significance

The reciprocal evolution of interacting species, or coevolution, generates impressive adaptations in pairs of species across geographic regions. However, we currently do not understand how coevolution shapes adaptations in large groups of species that interact not just locally but also across ecosystems. We use a mathematical model of coevolution and network tools to show that gene flow resulting from movement of individuals among populations may favor, rather than swamp, reciprocal adaptation in mutualisms, especially in large and heterogeneous networks typical of pollination and seed dispersal interactions. Our results suggest that the disruption of gene flow, fueled by human activities, may undermine long-term adaptation in mutualistic assemblages, with severe consequences for the functioning of ecological systems.

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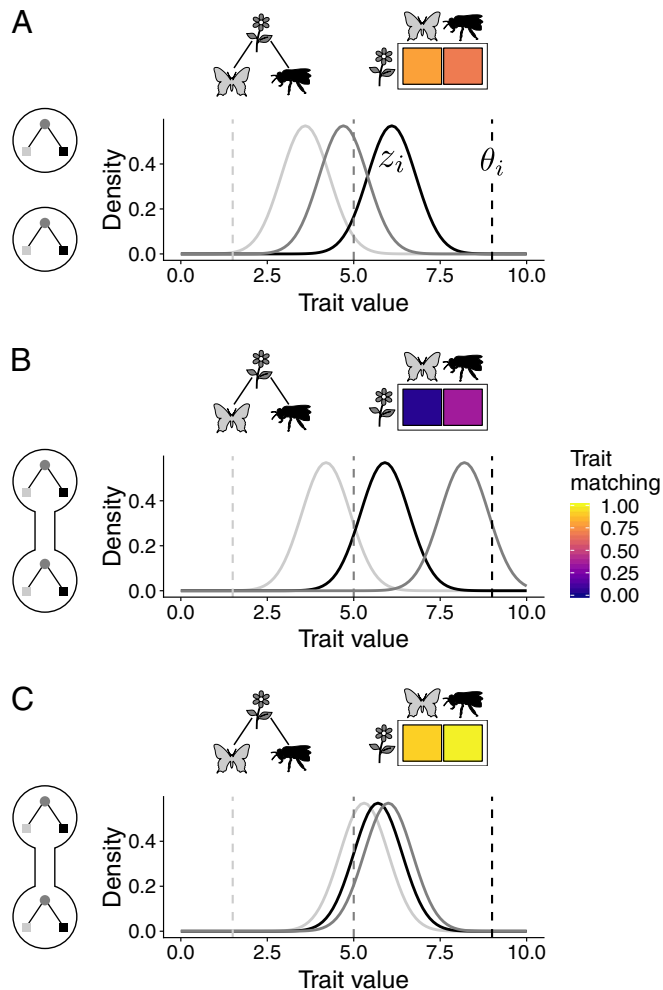
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Data deposition: All of the codes and empirical datasets required to reproduce our results are available at <https://github.com/wgar84/spatial.coevo-mutnet>.

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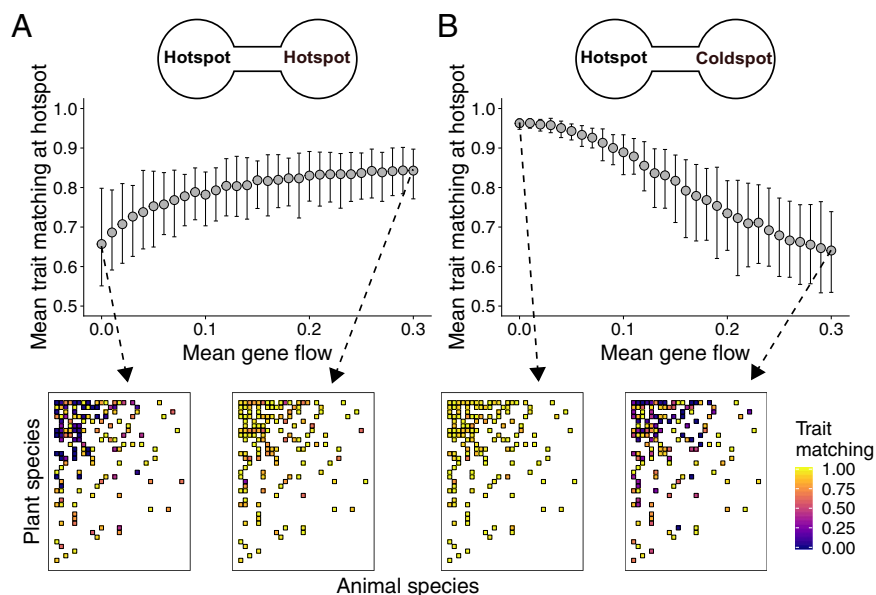


Fig. 2. Effects of gene flow on the evolution of trait matching in mutualistic networks. (A and B) Each point is the mean trait matching at equilibrium at the hotspot ($\bar{\tau}_A^*$) for 100 simulations parameterized with a seed dispersal network (network 64 in *SI Appendix*, Table S1), and bars show the 95% confidence interval. (A) When mutualistic selection is high at both sites ($\bar{m}_A = \bar{m}_B = 0.7$), gene flow favors trait matching at each hotspot. (B) When mutualistic selection is high at only one site ($\bar{m}_A = 0.9$, $\bar{m}_B = 0.1$), gene flow reduces trait matching at the hotspot. Changes in mean trait matching (A and B) are a consequence of changes in the matching among generalist species, as shown in the interaction matrices (colors depict equilibrium pairwise trait matching for one simulation with the indicated value of gene flow). Sample distributions and values for simulation parameters: $\varphi_{i,A}, \varphi_{i,B} \sim \mathcal{N}[\mu = 0.5, \sigma^2 = 10^{-4}]$, $\theta_{i,A} \sim \mathcal{U}[0, 10]$, $\theta_{i,B} \sim \mathcal{U}[10, 20]$, $m_{i,A} \sim \mathcal{N}[\bar{m}_A, 10^{-4}]$, $m_{i,B} \sim \mathcal{N}[\bar{m}_B, 10^{-4}]$, $g_i \sim \mathcal{N}[\bar{g}, 10^{-6}]$, and $\alpha = 0.2$.

a matrix (**T**) that contains direct and indirect coevolutionary effects: $\mathbf{z}^* = \mathbf{T}\boldsymbol{\theta}$ (7). Row i of **T** represents how other species directly or indirectly affect the adaptive landscape of species i . By measuring the correlation among rows of **T**, we showed that similar mutualistic adaptive landscapes among species favor trait matching and trait convergence (*SI Appendix*). Moreover, we found that increasing mutualistic selection leads to greater similarity of adaptive landscapes and higher trait matching, because indirect effects become stronger when mutualistic selection is higher (*SI Appendix*, Figs. S8 and S9). With two sites, the matrix **T** combines direct and indirect coevolutionary effects within and between sites. We found that increasing gene flow contributes to the similarity of adaptive landscapes, fueling trait matching in both mutualistic assemblages (*SI Appendix*, Figs. S10 and S11A). It does so by expanding the indirect effects of mutualistic selection across sites. In contrast, gene flow between a hotspot and a coldspot has an opposite effect and decreases trait matching (*SI Appendix*, Fig. S11B).

Network Structure and the Evolution of Trait Patterns. Our next step was to investigate how network structure influences coevolution and mediates the effects of gene flow. We characterized the structure of our 72 empirical networks using four metrics: species richness, connectance, nestedness, and modularity (*Materials and Methods*). We performed a Principal Component Analysis (PCA) of these metrics to obtain two variables ($PC1$ and $PC2$) that describe the range of variation in network structure in our empirical dataset (Fig. 3A and *SI Appendix*, Table S1).

In the absence of gene flow, species-poor, modular networks typical of intimate mutualisms favored the evolution of higher levels of trait matching than species-rich, nested networks typical of multiple-partner mutualisms (Fig. 3B, multiple linear regression: $\bar{\tau}^* \sim 0.73 - 0.01PC1 - 0.05PC2$, $\bar{m} = 0.7$, $\bar{g} = 0$). When gene flow is present, however, network structure has a weaker effect on the emergence of trait matching, allowing multiple-partner mutualisms to attain levels of trait

matching almost as high as the ones observed for intimate mutualisms (Fig. 3C, $\bar{\tau}_A^* \sim 0.86 - 0.005PC1 - 0.01PC2$, $\bar{m}_A = \bar{m}_B = 0.7$, $\bar{g} = 0.3$). This result occurs because networks of multiple-partner mutualisms contain a core of interacting generalists and the effect of gene flow on trait matching is stronger for pairs of generalist species than for other pairs of species (*SI Appendix*, Fig. S3). Our simulations using other combinations of mutualistic selection (\bar{m}_A , \bar{m}_B) support the interpretation that gene flow has a stronger effect on multiple-partner mutualisms (*SI Appendix*, Fig. S2).

Disruption of Gene Flow and Its Consequences for Coevolution.

Having shown that gene flow may favor the emergence of coadaptation in mutualistic networks, we next considered the consequences of the disruption of gene flow to trait evolution. To do so, we simulated a progressive loss of gene flow in two initially connected mutualistic assemblages and computed equilibrium trait values using our analytical approximation (*Materials and Methods*). We used empirical information on ecological dependencies between mutualistic partners (i.e., weights in adjacency matrices; *SI Appendix*, Table S1) of 29 networks in our dataset to parameterize the evolutionary effects (q_{ij}) of the matrix **T**. By removing gene flow from an increasing fraction of species, we altered the direct and indirect coevolutionary effects within and between networks present in **T**.

We found that the ongoing disruption of gene flow causes trait matching to decrease, but extreme loss of gene flow may recover some level of trait matching (Fig. 4 and *SI Appendix*, Fig. S12). Further analysis revealed that the lowest values of trait matching in these simulations occur when gene flow is highly variable across species in the network (*SI Appendix*, Fig. S13).

Discussion

The geographical and multispecific complexity of coevolution poses a challenge to our understanding of the evolution of

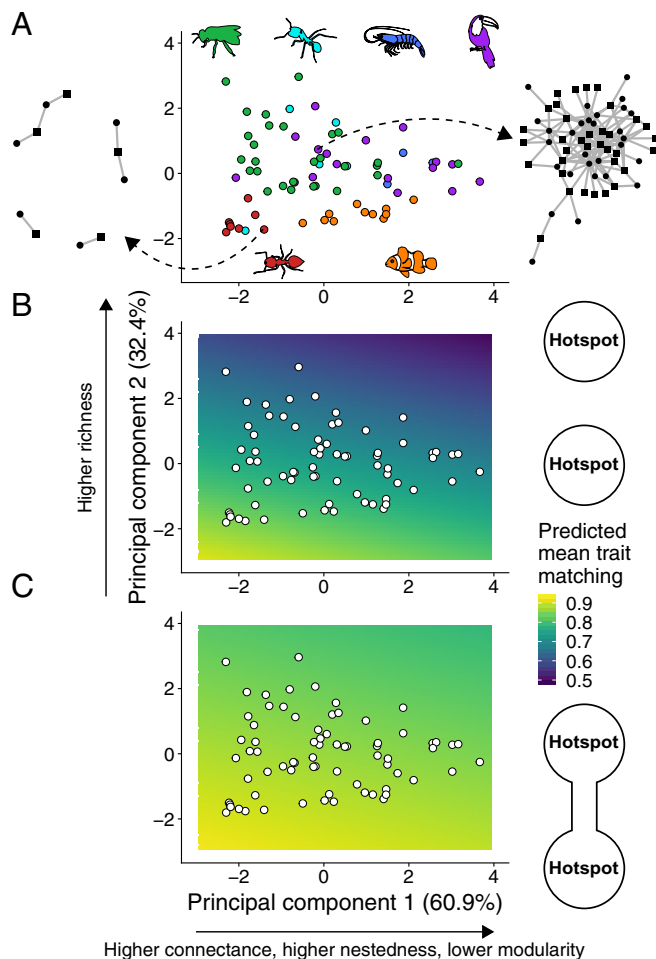


Fig. 3. Network structure, gene flow, and the emergence of trait matching in mutualistic networks. (A) PC1 and PC2 of a PCA using four network structure metrics measured for our 72 empirical networks. PC1 accounted for 60.9% of all variation and was strongly correlated with connectance (0.56), nestedness (0.58), and modularity (-0.56). PC2 accounted for 32.4% of all variation and was strongly correlated with species richness (0.81). Network structure was highly variable, as illustrated by an ants–myrmecophytes (Left, network 14 in *SI Appendix, Table S1*) and a seed dispersal (Right, network 64 in *SI Appendix, Table S1*) network. Types of mutualism: green, pollination; cyan, ants–nectary-bearing plants; dark blue, marine cleaning; purple, seed dispersal; red, ants–myrmecophytes; orange, anemones–anemonefishes. (B and C) Predicted mean trait matching at the hotspot ($\bar{\tau}_A^*$) for a linear model with PC1 and PC2 as explanatory variables and trait matching from simulations as the response variable (white points are the networks in A). (B) Species-poor, modular networks favored the emergence of trait matching in isolated hotspots ($\bar{m} = 0.7$, $\bar{g} = 0$, $n = 100$ simulations per network). (C) The effect of network structure is reduced when the two hotspots are connected by gene flow, and species-rich, nested networks may also favor high trait matching ($\bar{m}_A = \bar{m}_B = 0.7$, $\bar{g} = 0.3$, $n = 100$ simulations per network). Simulation parameters as in Fig. 2.

interacting species. In this study, we tackled this challenge by taking a first step in merging the geographic mosaic theory of coevolution with the recent approach of coevolutionary networks. Our framework combines a coevolutionary model and network theory to evaluate how gene flow, hotspots, and coldspots shape trait matching in multiple-partner and intimate mutualisms. Our findings reveal three main ways in which gene flow may be a fundamental process catalyzing the evolution of coadaptation in species-rich systems across simple landscapes.

First, gene flow may promote trait matching among mutualists within large networks. Previous results have shown that gene flow is capable of promoting adaptive evolution in natural populations by increasing local genetic variation (28) or when individuals disperse to specific habitats (32). Here, we reveal an additional mechanism for how gene flow may contribute to adaptation. When two mutualistic assemblages are connected by gene flow, the effects of environmental selection are canceled out, allowing mutualistic selection to drive trait evolution. As a consequence, gene flow makes the adaptive landscape of different species more similar to each other, erasing the conflicting selective pressures on highly interacting species and allowing trait matching and trait convergence to emerge. This result may provide a mechanism for one of the most challenging problems in coevolution, which is how local adaptation scales up to generate trait patterns in interacting species across broad geographical areas. We also found that gene flow may reduce trait matching for some specific scenarios, such as when a hotspot is linked to a coldspot. Therefore, specific combinations of gene flow and geographical variation in selection may generate trait mismatching in interacting species (2, 21). By analyzing pairs of interacting species, we showed that the observed changes in coadaptation patterns are mainly driven by species with a high number of interactions, such as generalist bees in pollination networks (33). This result, combined with our simulations incorporating simple spatial turnover in species composition, allows us to hypothesize that the observed effects of gene flow and geographical variation in selection should hold whenever generalist species are consistently present across local interaction networks. Our conclusions, however, may not hold for more complex landscapes, in which spatial heterogeneity may lead to unanticipated evolutionary dynamics.

Second, we show that network architecture mediates the effects of gene flow and geographical variation in selection on the evolution of trait patterns. The study of coadaptation in mutualistic

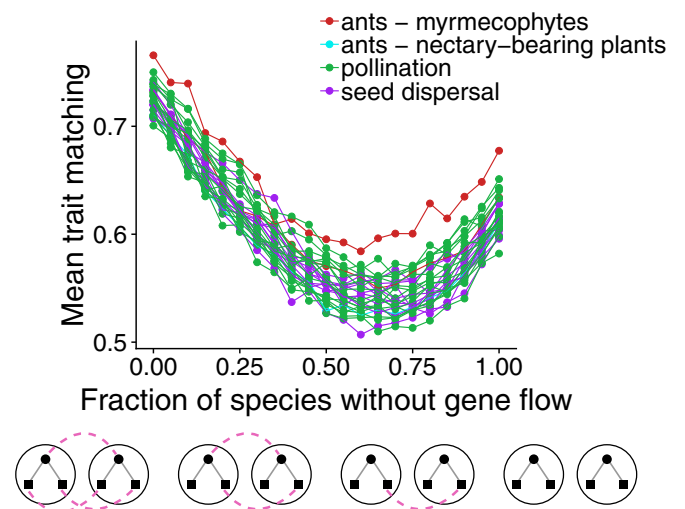


Fig. 4. Disruption of gene flow and its consequences for trait matching in mutualistic networks. Trait matching decreases as gene flow is progressively lost in mutualistic networks but increases slightly with an extreme loss of gene flow. Initially, all species in the network have a high value of gene flow ($g_i = 0.3 \forall i$), and species randomly lose gene flow until all species lack gene flow ($g_i = 0 \forall i$). Each point is the mean equilibrium trait matching at site A ($\bar{\tau}_A^*$) calculated with our analytical equilibrium expression using 10 different environmental optimum (θ) samples in each of 10 distinct simulations. Lines connect points from the same network, and different colors indicate different types of mutualism. Sample distributions and values for simulation parameters: $\varphi_{i,A} = \varphi_{i,B} = 1$, $\theta_{i,A} \sim \mathcal{U}[0, 10]$, $\theta_{i,B} \sim \mathcal{U}[10, 20]$, $m_{i,A} = m_{i,B} = 0.5$, and $\alpha = 0.2$.

Network Structure. We quantified four widely used metrics to characterize the arrangement of interactions in our networks: (i) species richness, (ii) connectance, (iii) nestedness, and (iv) modularity (*SI Appendix*). We used only information on the presence and absence of interactions (i.e., 1 and 0) to quantify these metrics. Species richness (N) is the total number of species in the network. Connectance (C) is the proportion of all possible interactions that are in fact realized (14). Nestedness measures how much the interactions of species with low degree values are proper subsets of the interactions of species with higher degree values (15). We quantified nestedness using the metric *NODF* (39). Finally, modularity measures how much the network is partitioned into groups of species with many interactions within groups and few interactions among different groups (33). We computed modularity using a simulated annealing algorithm to optimize the value of a bipartite version of the metric Q (40). Because network structure metrics are often highly correlated among each other, we used PCA to describe how the values of our four metrics covary across networks. We used the first and second principal components ($PC1$ and $PC2$) to describe the variation in network structure of our dataset and to explore how network structure affects the emergence of trait patterns.

Disruption of Gene Flow and Its Consequences for Coevolution. We used our analytical approximation of the coevolutionary model to simulate the

progressive loss of gene flow in two initially connected mutualistic assemblages (*SI Appendix*). We began each simulation by building a matrix T with $m_{i,A} = m_{i,B} = 0.5 \forall i$ and a high value of gene flow ($g_i = 0.3 \forall i$). We used the ecological dependencies between interacting species (i.e., weights in adjacency matrices; *SI Appendix, Table S1*) available for 29 networks in our dataset as proxies for the evolutionary effects (q_{ij}) in T . Then, we perturbed T by randomly removing gene flow from an increasing proportion of species (i.e., 0.05, 0.1, ..., 0.95, 1 of species without gene flow). The simulation ended when all species had lost gene flow ($g_i = 0 \forall i$). After each perturbation of matrix T , we sampled 10 different θ vectors using a statistical distribution and used our analytical equilibrium expression to calculate trait values (z^*) and trait matching (τ_{ij}^*). We performed simulations for many different combinations of $m_{i,A}$, $m_{i,B}$, and g_i (*SI Appendix*).

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