**Genetic variance contributes to nestedness in ecological networks**

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Abstract

* Genetic variance has been shown to have important community and ecosystem level impacts. Studies of ecological networks have demonstrated the importance of indirect effects of interactions in communities to contribute to community dynamics but have not incorporated genetics.
* Here, we conduct a series of community genetics simulations to develop a framework for a genetic basis of interaction network structure and test its possible effect on community level responses to selection on co-evolved traits.
* We found three major results:
  1. Genetic variance altered community composition and co-occurrence patterns among simulated species even in the absence of explicit interactions among associated species
  2. Nestedness of genotype-species networks increased as the effect of genetic variation increased
  3. The impact of selection on co-evolved traits was higher in communities where evenness was low
* These findings demonstrate that the community level impact of genetic variance can have a major impact on the structure of species interaction networks, which leads to more stable communities. This work points to a previously overlooked impact that genetically based, intra-specific diversity can have on ecological dynamics.

Introduction

Genetic variation within foundation species is known to have profound effects at the community and ecosystem scales,

It is really important to note that stability or other community properties may arise from the structure of the network, which has not been suggested to be a function of genetic diversity in prior research.

Beyond purely ecological consequences of genetic variation, genetic correlation among individuals of different species has important implications for evolutionary dynamics. Kin selection, group selection and co-evolutionary theory all provide examples of how genetic correlations can be both manifested and selected on at levels higher than the individual and beyond the population.

Networks are important.

The field of ecological networks has demonstrated some ecological mechanisms for how indirect effects can influence community dynamics; however, none of these studies have included genetic variation, and thus, are limited in establishing how evolutionary mechanisms that are playing a role in structuring ecological networks.

Although the consequences of this variation are known to impact biological diversity across multiple spatial scales, the effect this variation has on the structure of ecological interaction networks has not been explored (Fig. 1).

In this study, first, we use an established mass-action community simulation method to develop to simulate genotype-species interaction networks, and, second, we test this framework using several empirical community datasets. We hypothesize that the community compositional effects of foundation species genotype will contribute to interaction network structure. A genetic basis to ecological networks has important implications for understanding how evolutionary forces act to structure interactions among species in ecosystems.

Methods

*Simulations*

We used the community genetics simulation method previously developed in Shuster et al. 2006. Briefly, this method starts by creating a population of individuals assigned a genotypic value (i.e. genotypes). Each genotype is comprised of multiple individuals (i.e. clones), which are mapped to numerical phenotypic values. This population represents the foundation species. Next, a set of species representing the rest of the community is assigned an average genotypic value that is then also mapped to a numerical phenotypic value using an additive, bi-allelic genetic system. At each step of genotype-phenotype mapping variance is introduced through random draws from a uniform distribution, which simulates the introduction of phenotypic variance arising from non-genetically based “environmental” variation, including interactions among species in the community. It is important to note here that interactions among species beyond the foundation species’ effect on the community is not explicitly accounted for in this process but introduced as a contribution to non-genetic variation. Finally, the foundation species phenotypic values for each individual is used to determine the stable population value for each species in the community.

*Nestedness*

Measure nestedness and examine correlation between genetic variance and nestedness

*Selection Experiments*

Conduct Removal experiments (random vs targeted removal): 1) Random removal, 2) Genotype removal based on phenotpic similarity and 3) Centralized species removal

Results

*Genetic variation altered species co-occurrence patterns to produce nestedness*

Composition and co-occurrence patterns of the simulated communities were affected by tree genetics (Fig. 2).

The nestedness of simulated networks increased with the intensity of selection (Fig. 3).

*Genetically based nestedness increases network robustness*

Communities with carrying capacities drawn from a Poisson distribution were on average 19% less even (Pielou’s Evenness) than communities with a fixed carrying capacity for all species (*t* = 154.55, *P* <<< 0.001).

Networks with low evenness were more susceptible to removals overall, but this susceptibility was driven by the species abundances and not the effect of genotype. When species abundances were even, the effect of selection on a genetically based phenotype had a strong impact on the robustness of the community to fluctuations in the foundation species (Fig. 4).

Discussion

Acknowledgements

References

**Figure Legends**

Figure 1. Although interspecific variation in interaction traits is known to lead to nested ecological networks (e.g. mutualistic networks), the contribution of intra-specific variation to network structure has not been explored. This figure shows a bipartite graph of a mutualistic network of plant species (left; green circles) and associated species (right; red circles) connected by light grey lines representing their interactions. The center set of green nodes shows a hypothetical scenario in which the top-most plant species is comprised of two genotypes that have distinct phenotypes that affect their interactions between species (dark grey lines).

Figure 2. Plots of the (A) densities of tree phenotypic values and (B) the NMDS ordination of the simulated communities for each tree genotype.

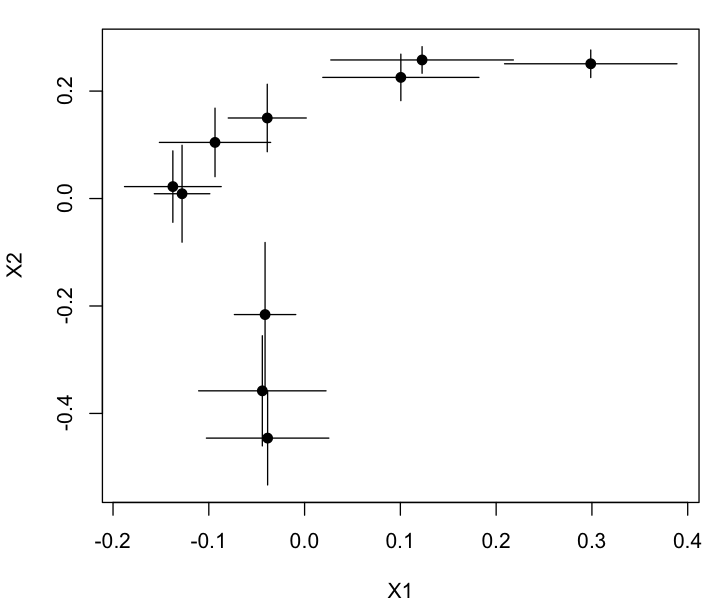
Figure 3. The scatterplot on the left shows the effect of selection intensity on nestedness temperature. The effect of selection on nestedness increases non-linearly because levels of selection intensity were scaled exponentially. An example simulated bipartite genotype-species network is shown on the right with tree genotype (left) and associated species (right) where connections are scaled by the average species abundance across genotype replicates and nodes are scaled by the number of connections. This network displays a high degree of nestedness with genotypes and species of lower connectedness being subsets of the community.

Figure 4. Scatterplots showing the relationship between selection intensity and the removal first to first extinction metric (see text) for (A) high and (B) low evenness communities.

Figure 1.

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Figure 2.



**B**

**A**

Figure 3.

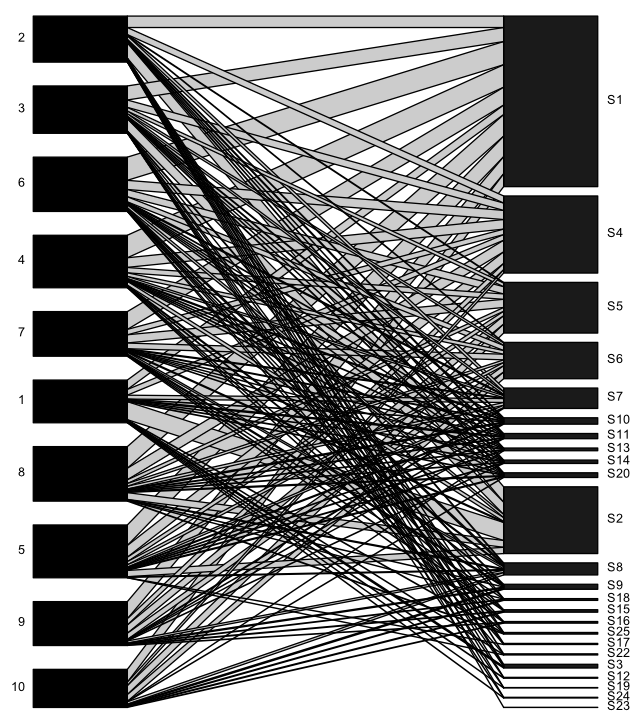
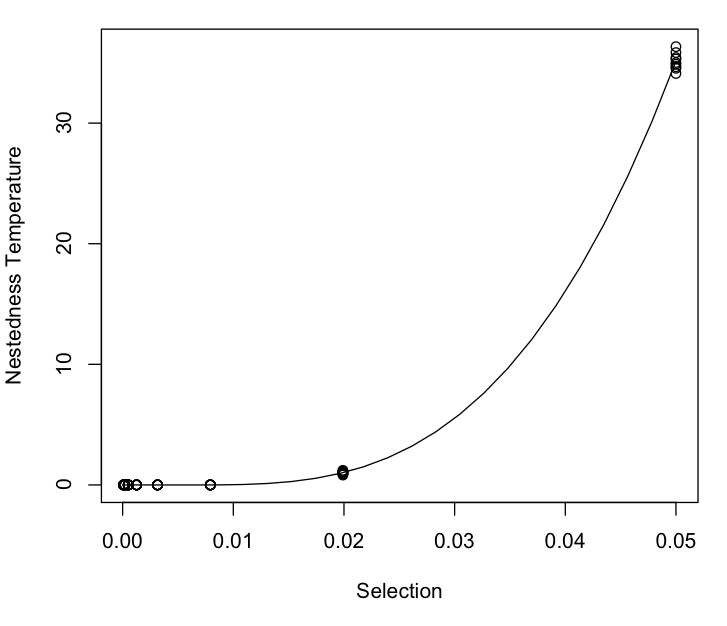
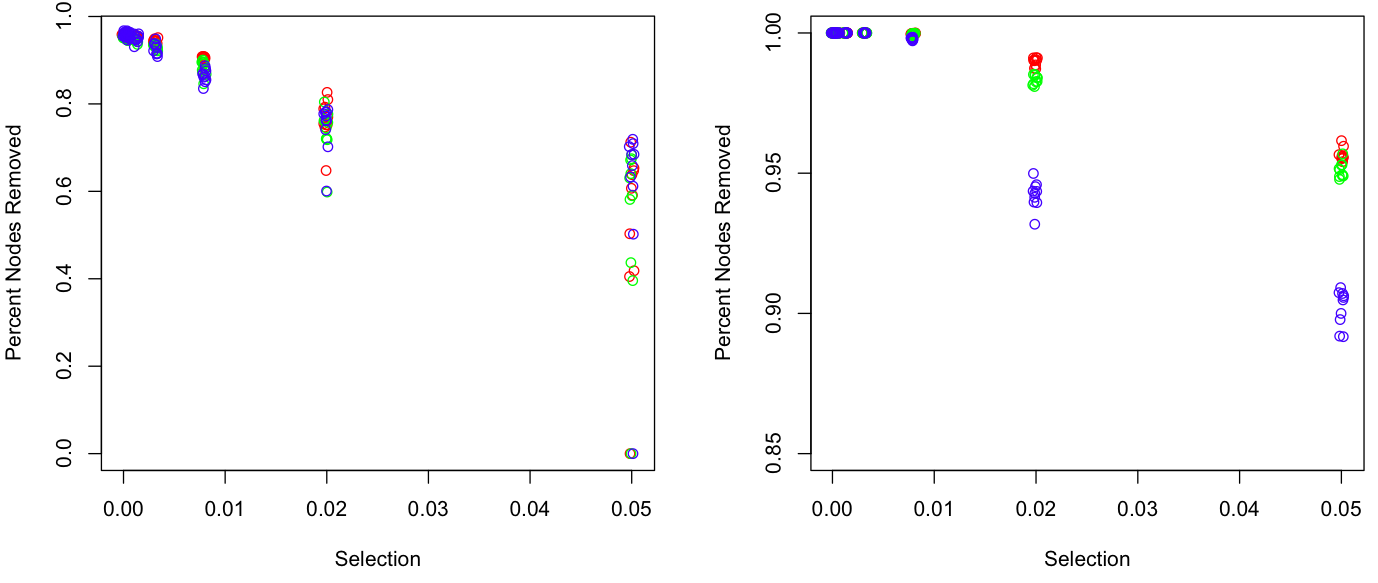


Figure 4.



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