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

M.K. Lau

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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 created co-occurrence patterns among simulated species even in the absence of explicit interactions among these species
  2. Nestedness increased as broad-sense community heritability increased
  3. The impact of selection on co-evolved traits was lower in more highly nested communities
* 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 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,

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.

In an appendix, develop the use of permanova R2, inlcuding: 1) Calculation using Anderson's method, 2) Comparison to NMDS method in Shuster 2006

*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 diversity creates nestedness within bipartite networks

When genetic effects is high, selection on tree species is more destabilizing for communities

Discussion

Acknowledgements

References

Tables

Figures

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 at different levels of foundation species genetic variance (increasing from red-yellow) and (B) co-occurrence patterns.

Figure X. Bipartite network of a simulated genotype-species network.

Figure X. Scatterplot showing the relationship between selection intensity and nestedness.

Figure X. 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.

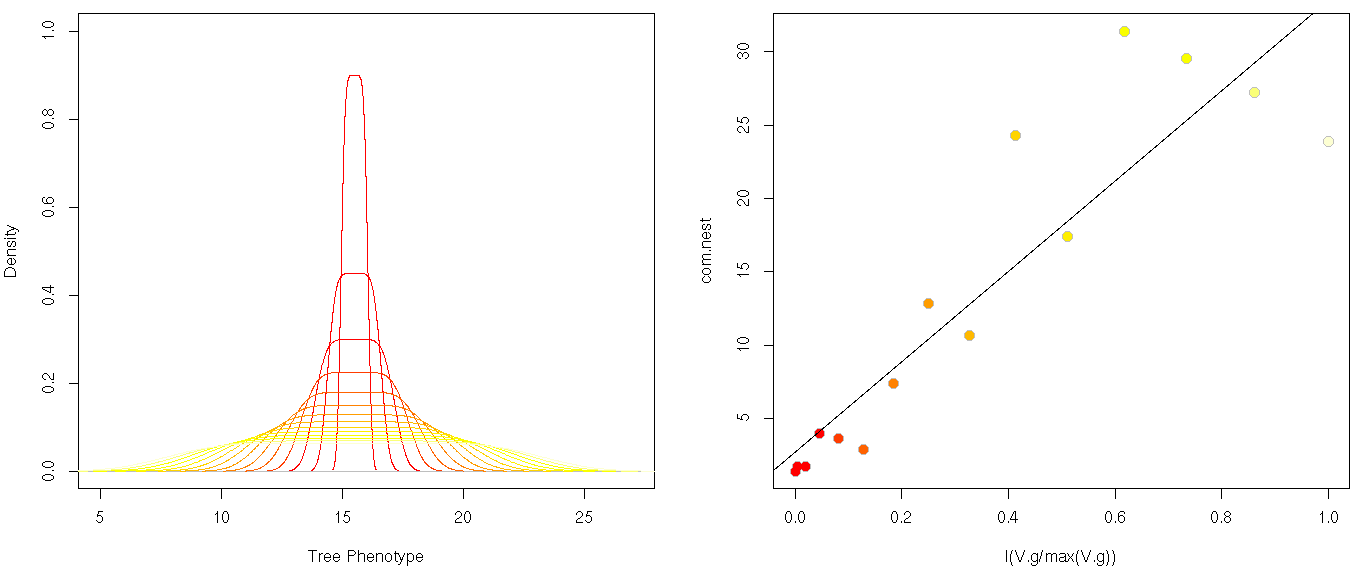
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Figure 3.

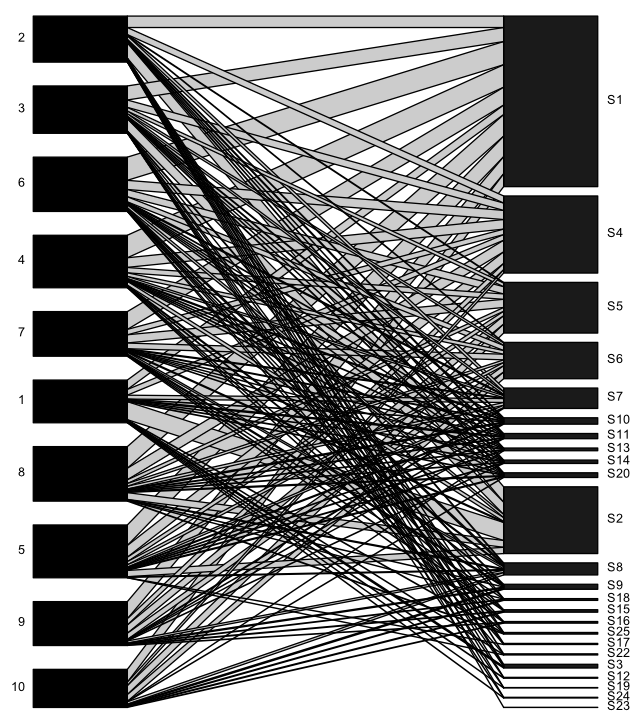


Figure 4.

Figure 5.

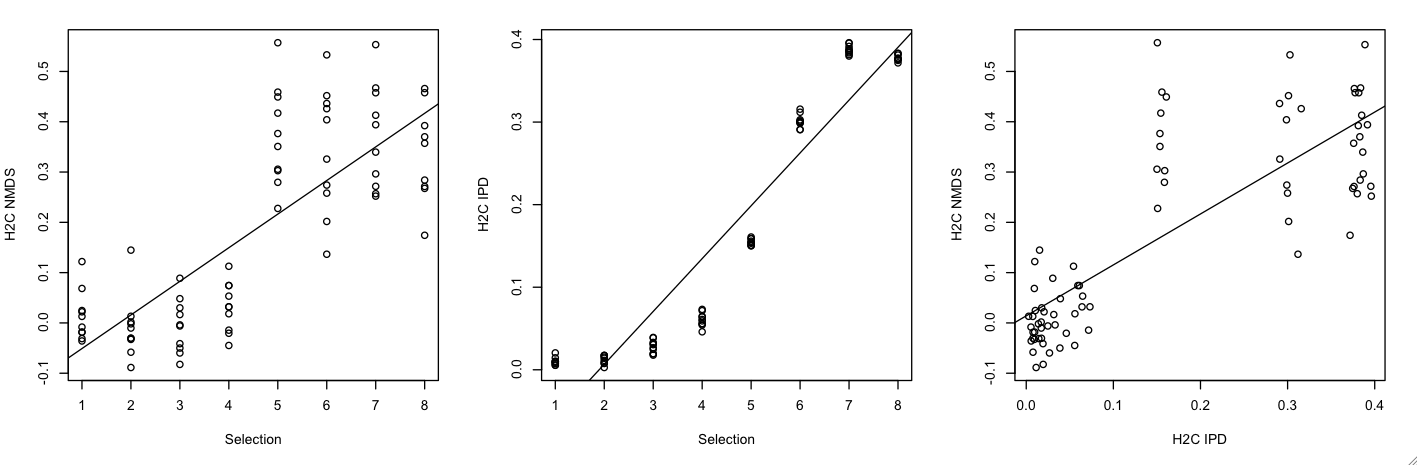
Appendix 1.

**Using inter-point distance based *R*2 to measure multivariate heritability.**

Measuring the community level effects of genetic variance presents two main challenges. The first is that communities are inherently multi-dimensional. Thus, species can be responding in complex ways to the effect of genetic variation, similar to correlated traits in complex phenotypes. The second is that species’ abundances tend to not be normally distributed, making standard parametric statistical methods invalid due to violations of important data distribution assumptions. In the community genetics literature, methods have primarily followed the methods of Shuster et al. 2006, which employs ordination to produce a low dimensional representation (usually a vector) of the variation in the community using an NMDS (Non-metric Multi-Dimensional Scaling) approach using Bray-Curtis dissimilarity to handle the data distribution assumptions.

In the main body of the manuscript we use the inter-point distance method of Anderson 2001 to calculate the multivariate *R*2 for the effect of tree genotype on community composition. This methods addresses both the issue of multi-dimensionality and the non-normal distribution of species abundances. Like the Shuster et al. 2006 method, it uses Bray-Curtis dissimilarity; however, it has the advantage of not reducing the variation in the community through dimensionality reduction. Thus, the inter-point distance (IPD) *R*2 should be a more robust measure of the community level effect of genetic variance, as it takes into account the full variation present in the community, and should perform better as a measure of community heritability (HC2).

Indeed, comparing the NMDS and IPD methods for measuring HC2 we find that the IPD method is much more consistent than NMDS when calculated for the simulated communities (Fig. 1). We therefore use this metric throughout the study when measure HC2.



**Figure 1.** Three panel figure showing the relationship between selection and the two community heritability metrics (H2C NMDS and H2C IPD) and the relationship between the two metrics themselves.