**Genotypic variation contributes to ecological network structure**

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**Abstract**

* Evolutionary and ecological processes are now recognized as operating on similar time scales, and species interactions have been shown to play an important role in driving these dynamics. Although studies of the effect of a focal species’ genetics on ecological communities have shown the importance of genetic variation in many ecosystems, they have not delved how these effects contribute to more complex patterns of species interactions, as is often analyzed using a network approach.
* In this study, we use a network perspective first to analyze an arthropod community dataset from a long-term common garden of plants with known genetic makeup and then to conduct a simulation experiment investigating how genetic variation in a foundation tree species contributes to interaction network structure and what consequences this might have for evolutionary dynamics.
* We found two main results:
  1. The empirical genotype-species network exhibited non-random co- network structure and co-occurrence patterns arising in part from genotypic variation even though the most conservative null model was used,
  2. Simulated genotype-species networks displayed increasing associated species co-occurrence patterns and network structure with increasing genotypic effect on the community.
* These findings demonstrate that the community level impact of genetic variation in a foundation species can alter the structure of species interaction networks, leads to more stable communities. This work points to a previously overlooked consequence of genetically based, intra-specific diversity and provides a mechanism for evolution to act on ecological network structure.

**Keywords:** foundation species, ecological networks, species interactions,co-occurrence, modularity, nestedness, centrality, genetics of networks, common gardens, long-term experiment

**Introduction**

The evolution of species interactions in complex communities is a central question at the interface of ecology and evolutionary biology. Species interactions play an integral role in ecosystems (Agrawal et al. 2007; Holland and Bronstein 2008; Winfree et al. 2011). How species interactions lead to evolutionary changes in participant species has been a topic of biology at least since Darwin’s study of orchid pollinators (Darwin 1862). Studies of co-evolution between pairs and small groups of species have expanded the theory and support for evolutionarily dynamic species interactions (Ehrlich and Raven 1964; Thompson 1982; Jones et al. 2009). Studies of plant-mutualist and plant-herbivore networks have more recently provided a broader perspective, addressing more complex relationships among many species in a community (Bascompte et al. 2003; Thebault et al. 2010). Studies of phylogenetic structure of these networks have demonstrated the contribution of evolutionary processes to the structure of ecological networks (Rezende et al. 2007; Rafferty and Ives 2013). The field of community genetics, which studies the genetic basis for interactions in complex communities, primarily focusing on foundation species (i.e., species that define much of the structure of a community by creating locally stabile conditions; Dayton 1972; Ellison et al. 2005) has demonstrated how genetic variation in a single species can determine the structure of whole communities (reviewed in Whitham et al. 2012; Rowntree et al. 2011; Gugerli et al. 2013); however, the ideas and approaches from community genetics and network ecology have not previously not yet been synthesized.

Studies of co-evolution and community genetics have expanded our view of the influence of genetic variation on communities associated with a focal species. Strauss et al. (2005) theoretically demonstrated that selection occurs in a community context whenever a species response to selection on a trait is altered by the presence of another interacting species. Empirical, studies of the response of arthropod communities to foundation tree species hybridization (Wimp et al. 2005), genotypic diversity (Crutsinger et al. 2006) and genetic similarity (Bangert et al. 2008) have demonstrated significant effects of genetic variability on community composition. Others have shown that variation at the finer genetic resolution of genotypes affects the composition of other associated communities, such as soil microbes (Schweitzer et al. 2008), arthropods (Keith et al. 2010), plants (Lamit et al. 2011), and fungal endophytes (Lamit et al. 2014). In addition, several community genetics studies have examined the impact of genetic variation beyond direct interactions with the focal species. Bailey et al. (2007) showed that genetically based resistance in *Populus angustifolia* (James) to an insect herbivore influenced a tri-trophic interaction. Mooney et al. (2012) demonstrated that ant-aphid interactions depended on milkweed (*Asclepias syriaca* L.) genotype. Busby et al. (2014) found that the plant genetics mediated the indirect interactions between leaf pathogens and cottonwood (*Populus* spp.) associated insect community. Together, these and other studies (see Rowntree et al. 2011) demonstrate the importance of genetic variation for both direct and indirect interactions among species, however, we are aware of no investigations combining both empirical data and simulation experiments to investigate the genetic basis for interaction network structure.

Given the known compositional effects of tree genotype, we examine the structure created by this genetic effect. First, we test for non-random network structure in the genotype-species network. Based on findings from plant-mutualistic and plant-herbivore networks, we hypothesize that genotype-species networks will exhibit structure distinct from that of a conservative null model. We then examine the effect that this structure has on the structure of interactions among species by testing for non-random co-occurrence patterns among associated species. We then conduct a simulation experiment to study the effect genotype has on network structure when controlling for covariates, such as species abundances.

In this study, we examine how genetic variation in a foundation species influences the structure of ecological networks in complex communities. We primarily use a bipartite network approach, which examines networks where interactions typically occur between two main groups (e.g., plant-mutualists or host-parasite). Using bipartite networks permits us to apply structural hypotheses developed by the extensive literature of plant-mutualist (Bascompte 2010), plant-herbivore (Thébault and Fontaine 2011) and other species-species networks to networks of foundation species genotypes interacting with associated species (i.e., genotype-species networks). We hypothesize that genotype-species networks will exhibit network structure that increases with the effect of genotype. In addition, we hypothesize that genotype-species bipartite network structure will influence the structure of interaction networks among the foundation species associated community members. We argue that, since species interactions tend to occur locally, shifting co-occurrences will produce shifts in interactions by altering the frequency with which species are physically located together. To test these hypotheses we first explore the structure of an empirical network of interactions between narrowleaf cottonwood (*P. angustifolia* James) and its associated canopy arthropod community using a conservative, null model based approach. We then conduct a simulation experiment where we vary the intensity of the community level effect of genotypic differences of a foundation species on its associated community and examine the structure of the resulting genotype-species interaction networks and co-occurrence patterns. As a genetic basis to traits is a key requirement for evolution by natural selection, and given that multiple studies have demonstrated rapid evolution of species in response to climate change (reviewed in Parmesan 2006), demonstrating a genetic basis for interaction network structure has important implications for ecological and evolutionary dynamics in many ecosystems.

**Methods**

*Empirical network analysis*

A network of interactions between canopy arthropod species and genotypes of *Populus angustifolia* James (narrowleaf cottonwood) consisted of data from Keith et al. 2014. In 1991 replicate clones of genotypes from the Weber River Watershed (Utah, U.S.A.) were randomly planted in a common environment (Ogden Utah, U.S.A., latitude = 41.248146, longitude = −111.999830, elevation = 1302 m) in order to both minimize and randomize the effect of local environmental variation with respect to genotype (Martinsen et al. 2001). Surveys of four replicate trees for each of 10 genotypes (n = 40 trees) were conducted in August of 2009 using timed sampling of similarly sized branches, and previous analyses have demonstrated community compositional effects of tree genotype (Keith et al. 2014). As plant-herbivore networks are typically highly asymmetric (Thébault and Fontaine), we interpret these connections as directed effects of the genotype on the associated community. Hereafter, we use network terminology to refer to the genotypes and species in the network collectively as “nodes” and their connections as “edges” (Wasserman and Faust 1994).

We then analyzed the structure of this empirical genotype-species network with three metrics (modularity, nestedness and centrality) and a measure of species co-occurrence. All three of the network metrics measure the global structure of the entire network. Modularity is a measurement of the degree to which the network is comprised of groups of nodes that are relatively more connected to each other, and for our analyses we used the method developed by Newman (2004). Nestedness was calculated for the observed network using the nestedness temperature metric developed by Atmar and Patterson (1993, see also Rodríguez-Gironés and Santamaria 2006), which measures the degree to which species tend to interact with subsets of the community across “parts” of the network. We used Freeman’s (1979) degree as our measure of centrality. We also measured the co-occurrence patterns among the associated community using Stone and Robert’s (199?), C-score, which is the number of “checkerboard units” averaged across all pairs of species. A checkerboard unit is measured as (*r*i-*S*ij)(*r*j-*S*ij), where *r* is the total number of occurrences for a given species and *S* is the total number of times a species pair occurs, and the C-score has been shown to have robust statistical properties (Gotelli 2001).

We tested for the significance of all network statistics and the C-score using a conservative null-model based randomization procedure. We chose this conservative null model because previous work has demonstrated the importance of controlling for the total abundances of species in plant-mutualistic bipartite networks (Blüthgen 2010). More specifically to our dataset, this null modeling method constrains the matrices to maintain the original genotype and species marginal totals, referred to as a fixed-fixed algorithm in the co-occurrence literature (Wright et al. 1998; Gotelli 2001). After an initial series of 100 “burn-in” permutations of the original matrix, a set of 5000 randomizations was generated and used to test the significance of the all metrics. For each metric we calculated a non-directional p-value as the proportion of null model metrics that were equal to or more extreme than the original (i.e., “observed”) metric. We also calculated a standardized score as *z* = (x - μ)/σ, where x is the observed metric and μ and σ are the mean and standard deviation for the null simulation metrics, respectively. Note that in the co-occurrence literature the standardized C-score is typically referred to as a standardized effect size (SES) value.

*Simulating genotypic effects on network structure and co-occurrence patterns*

As the structure of the empirical network could arise from factors other than phenotypic variation among foundation species genotypes, we conducted a simulation experiment testing the effect of genotype on genotype-species network structure. We used the community genetics simulation method previously developed in Shuster et al. (2006). Briefly, this method uses a combines both individual-based and mass-action modeling approaches, and starts by creating a population of individuals assigned a genotypic value (i.e., genotypes). Each genotype is comprised of multiple replicate individuals (i.e., clones), which are assigned phenotypic values as a single numeric value for each individual. This population represents the foundation species. Next, a set of species representing the associated community was assigned an average genotypic value that was then mapped to a numerical phenotypic value using an additive, bi-allelic genetic system. At each step of genotype-phenotype mapping, variance was introduced through random draws from a uniform distribution, simulating the introduction of phenotypic variance arising from non-genetically based “environmental” variation. It is important to note here that interactions among species, beyond the foundation species’ interaction with the community, is not explicitly accounted for in this process but introduced as a contribution to non-genetic, environmental variation. Last, mass-action methods were used to determine the equilibrium population value for each associated species given the phenotypic values for each foundation species individual and the carrying capacity of each associated community member (Ronce and Kirkpatrick 2001; Supplementary Materials Appendix 1).

We used this method to conduct simulations of communities with different levels of foundation species genotypic effect on the community. To do this, we adjusted the co-efficient determining the foundation species genotypic effect for each associated species, which modifies the fidelity of the mapping of genotype to phenotype to a species by varying the power of the co-efficient per the method of Shuster et al. (2006; Supplementary Materials Appendix 1). In addition, to explore the impact of variation in associated species abundances, we produced two sets of simulations, one (n = 80) with a carrying capacity (K) of 100 individuals, and a second set (n = 80) with carrying capacities for the dependent species selected from a Poisson distribution, ranging from K = 100 to K = 5. This distribution was chosen for its similarity to the highly skewed, “un-even” distribution of species total abundances commonly observed in ecological communities (Supplementary Materials Barplot). Simulated communities were generated using the same initial phenotypes for both the “foundation species” individuals (n = 100; 10 individuals for each of 10 genotypes) and the “associated species” (25 total). Similar to the results of Shuster et al. (2006) simulated communities differed in their individual phenotypic trait values (Fig. a) and produced significant variation in community composition in the simulated communities (Fig. 1b), which ranged in broadsense community heritability from 0 to an upper threshold of 0.60 (Fig. 1c) calculated using the multivariate community heritability method developed in Lamit et al. (2014). We used correlation analysis to test and compare the effect of genotype on the four metrics with Kendall’s τ, which is able to capture non-linear monotonic relationships.

*Simulation and analytical software*

All simulations and analyses were conducted in R version 3.0.2 (R Development Core Team 2014). Simulations were conducted using the *ComGenR* package (Lau 2014), and simulation scripts are publically available: <https://github.com/MKLau/cg_simulations>. Non-metric multidimensional scaling (NMDS) ordination and nestedness tests were conducted with *vegan* (Okasanen et al. 2013), and networks were plotted using *bipartite* (Dormann et al. 2008).

**Results**

The cottonwood canopy arthropod genotype-species network showed significant structure and co-occurrence patterns among associated species. For the genotype-species network of canopy arthropods on narrowleaf cottonwood (Fig. 2), modularity (observed = 0.22, *z* = 13.36, *P* < 0.001), nestedness (observed = 21.48, *z* = 8.60, *P* < 0.001), centrality (observed = 0.27, *z* = 5.99, *P* < 0.001) and C-score (observed = 12.76, *z* = 12.40, *P* = 0.0006) were all much greater than the null expectation.

Network structure and co-occurrence patterns increased with increasing genotypic effect but this effect depended on the distribution of the associated community. Even community network structure and co-occurrence patterns showed increasing structure with increasing genotypic effect with modularity (Fig. 4a; τ = 0.82, *P* < 0.001), nestedness (Fig. 4b; τ = 0.83, *P* < 0.001), centrality (Fig. 4c; τ = 0.89, *P* < 0.001) and C-score (Fig. 4d; τ = 0.70, *P* < 0.001) all showing significant, positive correlations with genotypic effect. The un-even network metrics also displayed significant relationships with genotypic effect: modularity (Fig. 4a; τ =0.69, *P* < 0.001), nestedness (Fig. 4b; τ = -0.28, *P* = 0.001) and centrality (Fig. 4c; τ = -0.87, *P* < 0.001). The C-score for the un-even community simulations across all levels of genotypic effect was not significant (Fig. 4d; τ = -0.01, *P* = 0.95); however, restricting to the simulations over a threshold where the genotypic effect corresponded to a broad-sense community heritability of 0.35 or greater, the correlation between the C-score and genotypic effect (Fig. 4d) increased to τ = 0.23 (*P* = 0.06).

**Discussion**

Our results support the hypothesis that genotypic variation in a foundation species can contribute to ecological network structure. We observed significant network structure for all metrics, including modularity, nestedness and centrality, as well as significant co-occurrence patterns, even though these metrics were tested against a highly conservative null model that controlled for both tree genotype and associated species marginal totals. In addition, our highly controlled simulation experiment, which manipulated both genotypic effect and community evenness, displayed significant effects of for all metrics with the exception of co-occurrence patterns when the distribution of species total abundances was un-even. Taken together, these two lines of evidence support the conclusion that genotypic differences among individuals of a foundation species contributes to the structure of interaction networks.

Empirical network patterns suggest... Previous studies have found… Centrality is related to species richness, but we use the network concept here to emphasize the structure of interactions.

Our simulation approach permits the control and manipulation of several variables that can influence network structure: 1) environmental and species interaction effects, 2) genotype and species abundances, and 3) genotypic effects. This is an obvious oversimplification; however, our goal here is not to predictively model but to demonstrate the possibility of an underlying genetic mechanism observed in an empirical dataset. Also, modeling the absolute effect is not essential to the initial demonstration of the effect of genetics on interactions network structure, as it is commonly assumed that intra-partite interactions (e.g., interactions among arthropods in plant-mutualist networks) are typically relatively small in comparison to the effect of the foundation species (Bascompte et al. 2003; Ellison et al. 2005). Also, the work presented here expands on previous empirical and simulation studies of community genetics, which have either examined indirect effects among species mediated by a third species (Bailey et al. 2007; Moya-Laraño 2011) or direct effects of a foundation species on a large community of species (Shuster et al. 2006; Keith et al. 2010, 2014; Lamit et al. 2011, 2013, 2014). No study that we are aware of has examined the bipartite network structure that results for community level genotypic effects.

Network structure has implications for the consequences of selection in a community context. Using a foundation species approach, we can focus on the effect that selection will have on the structure of genotype-species interaction networks. Directional, stabilizing and divergent selection will alter the structure of these interaction networks in ways that can affect the outcome of the selection. For example, if a selection event on the foundation species increases the abudandance of a “generalist” genotype (i.e., a genotype that interacts with a large number of the community members), which will reduce the modularity of the network (CITATION), increasing the frequency of co-occurrences among species and possibly increasing the rate of or generating novel species interactions. This will also increase the centralization of the network, making to the community more susceptible if a future selection event targets the same, generalist genotype.

We advocate that other community genetics datasets be analyzed using a bipartite network perspective to resolve the structure of the associated communities entangled in these datasets. Multivariate community analyses do not resolve the patterns of interactions elucidated by the network approach.

* Hypotheses supported
* Modules are microcosms of evolution
* Nestedness influences persistence and stability
* Co-occurrence patterns altered, could lead to altered interactions through encounter frequency, i.e. interactions depend on the genetic context
* **Centrality?**Centrality influences robustness and stability
* Evenness affects
* Scaling up to species-species networks
* Future work should introduce interactions among the associated species (Bastolla 2010, James 2012)

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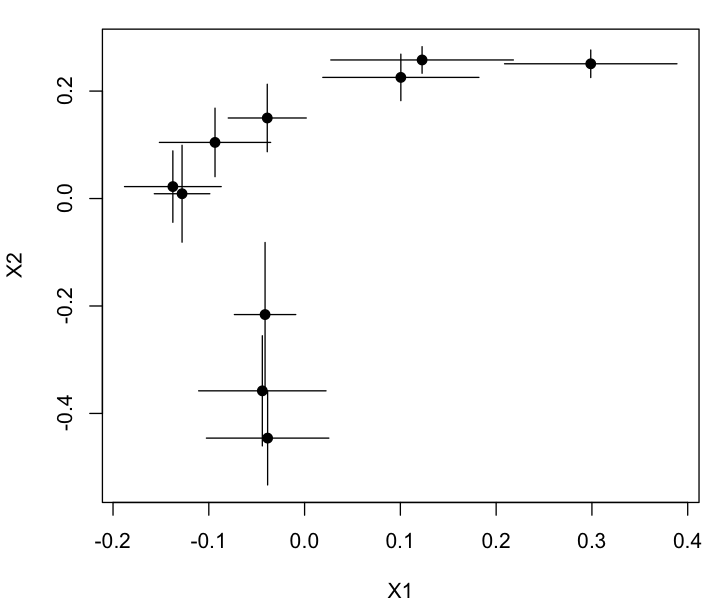
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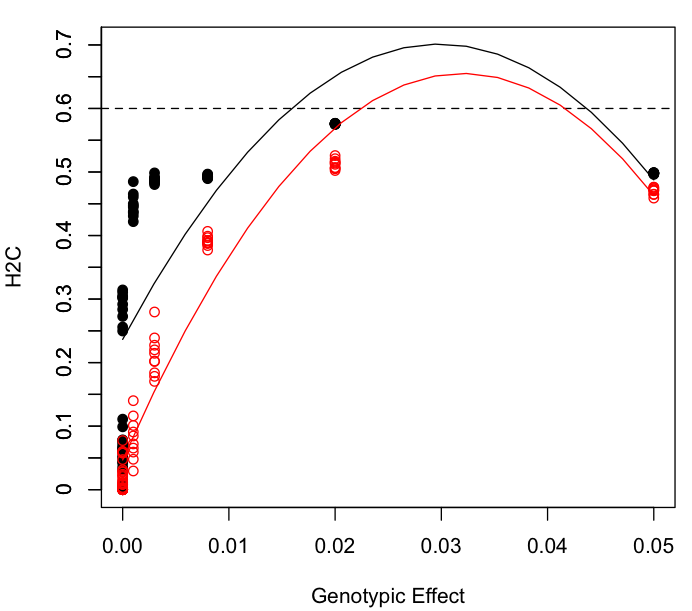
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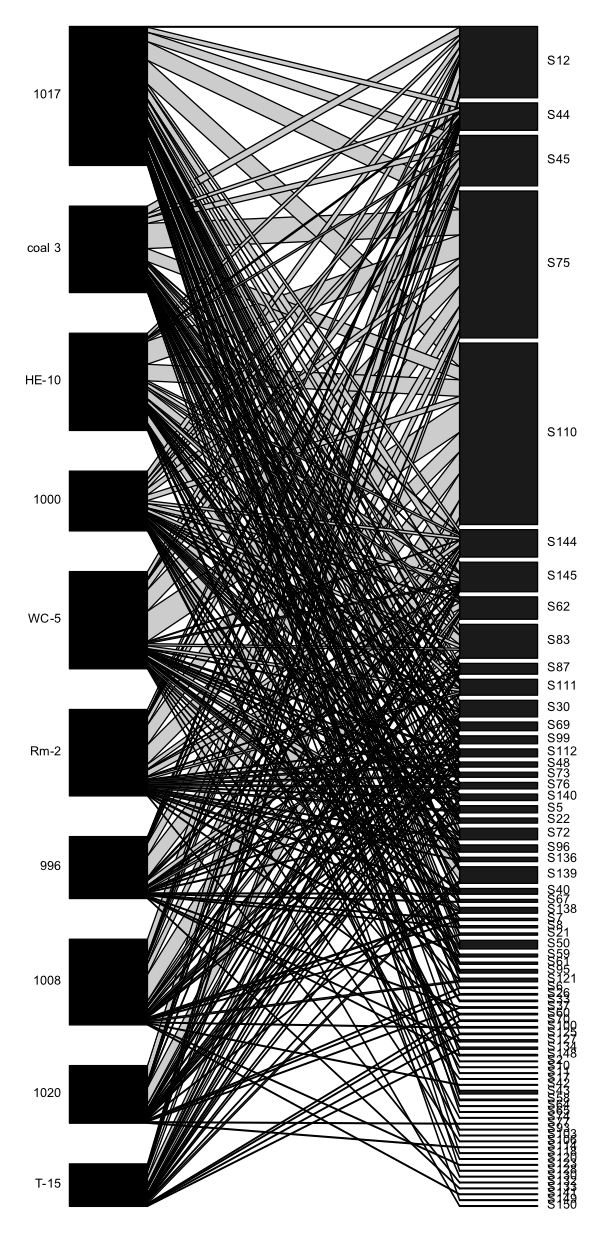
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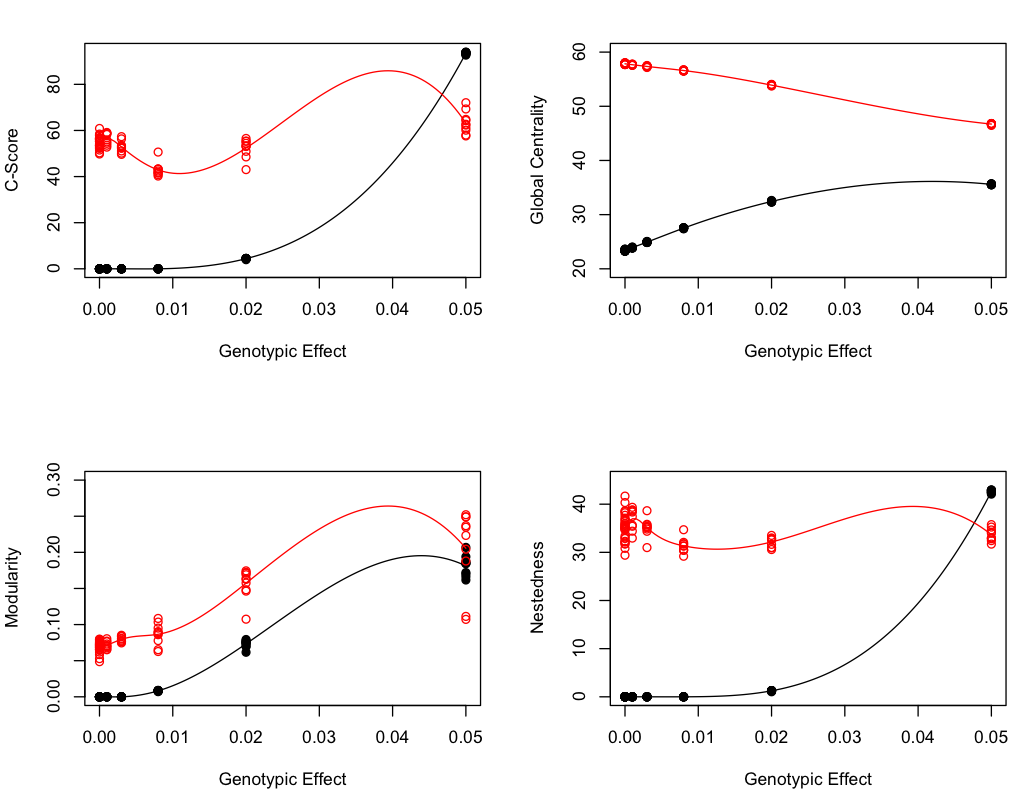
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Figures









Appendix

