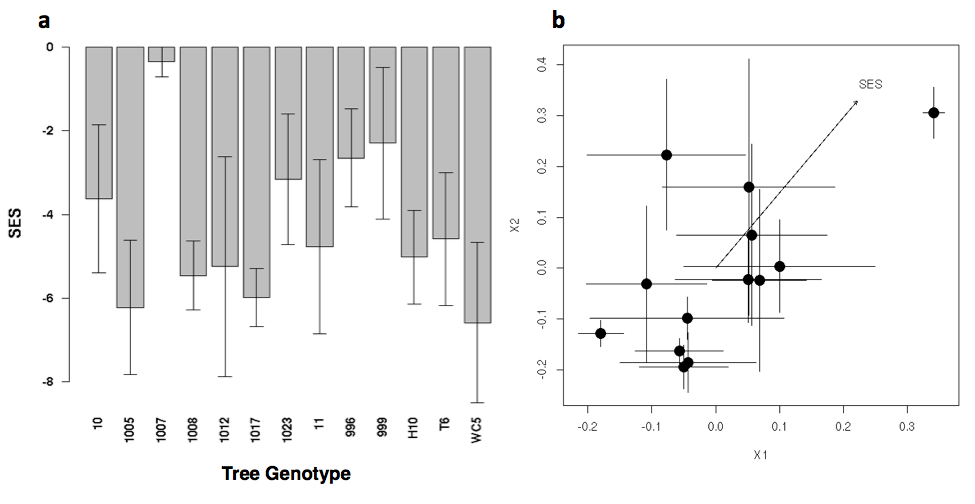
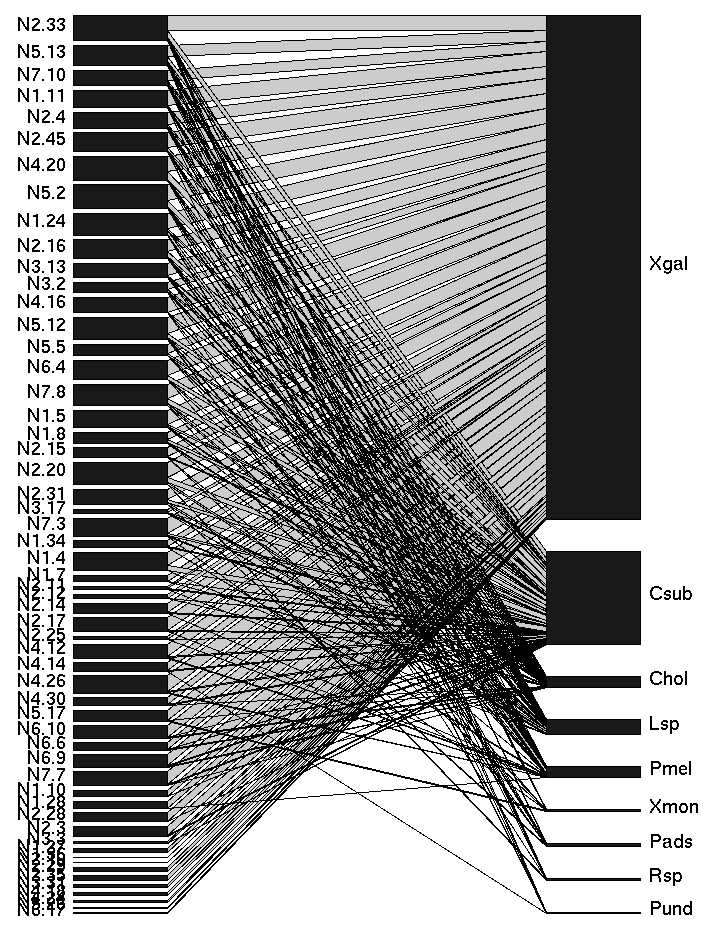
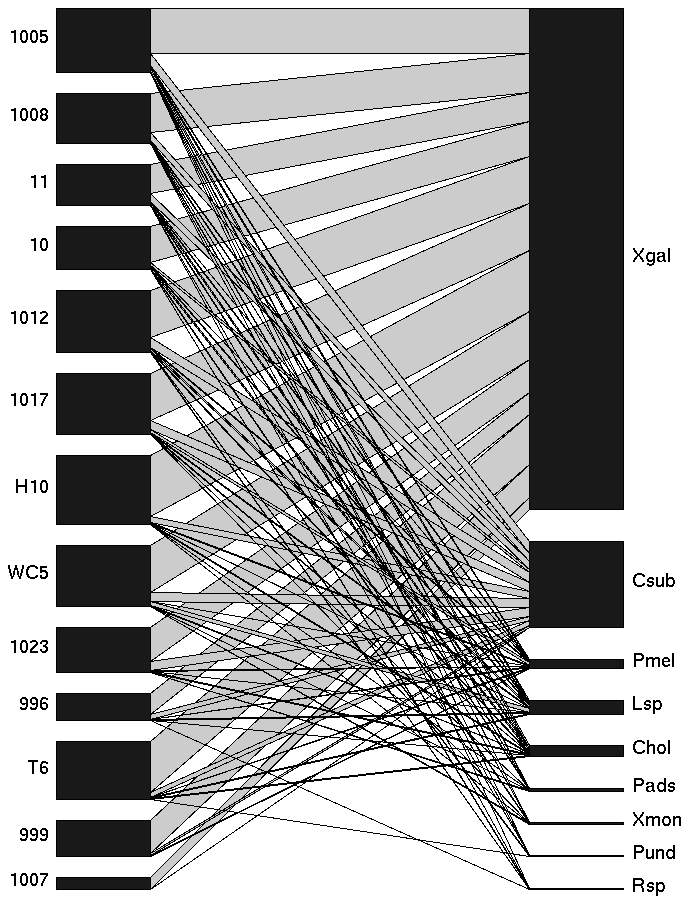
**Genetic variation in a foundation tree species creates ecological network structure in an associated community**

M.K. Lau, L.J. Lamit, R.R. Naesbourg, T.G. Whitham

* The structure of networks of interactions among species contribute to the dynamics and function of ecosystems,
* Although evolutionary mechanisms, such as selection, have been suggested to reinforce interaction network structure and that genetic variation within foundation species contributes to community composition and shifts in species interactions, the effect of genetic variation on the structure of ecological interaction networks has not been tested,
* In this study, we use data from both a natural and common garden stand of a foundation tree species (*Populus angustifolia*, James), where the genetic composition is known, to test how genetic variation contributes to network structure of a model community of epiphytic lichen,
* Our study yielded three primary results:
  1. Tree genetics contributed to significant co-occurrence patterns of epiphytic lichen,
  2. As with species-species bipartite networks in other studies, the individual-species and genotype-species networks showed significant nestedness,
  3. Variation in bark roughness, a genetically based tree trait, produced similar patterns of co-occurrence and network nestedness in the natural stand,
* Based on these results, we conclude that genetic variation in foundation species contributes to the structure of ecological interaction networks for species with a high degree of dependence. This finding provides the first evidence that variation in ecological network structure can be subject to the evolutionary force of natural selection.



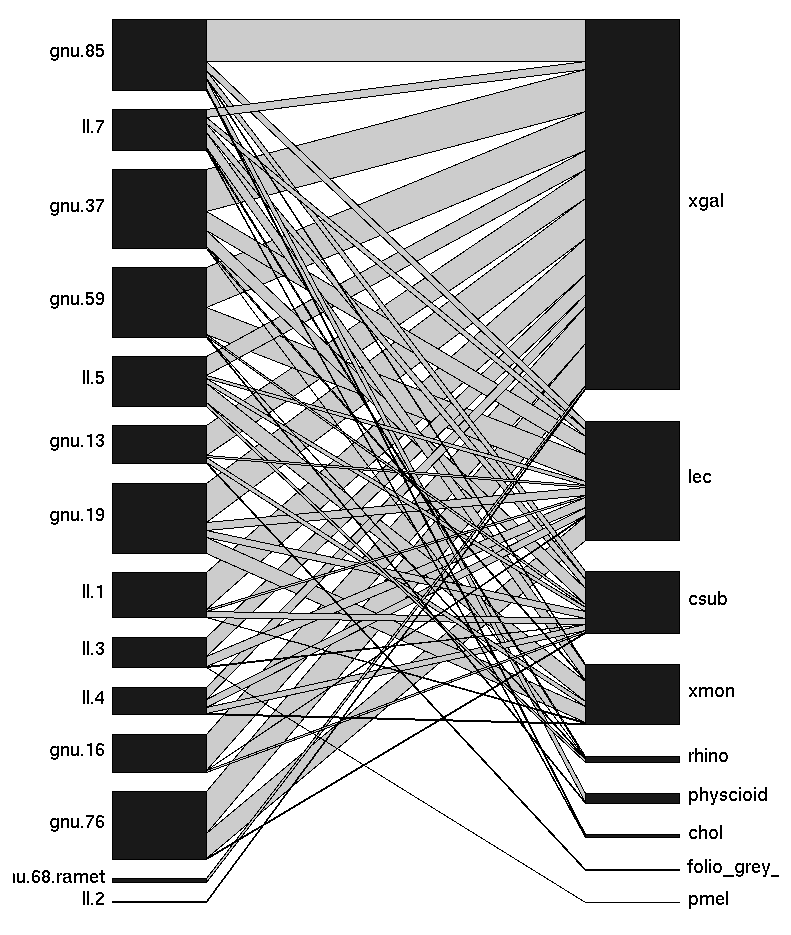
**Figure 1**. The barplot (**a**) shows the mean (±1 S.E.), tree-level standardized effect sizes (SES) on each genotype and the NMDS ordination plot (**b**) shows the ordinated lichen community composition (genotype centroids with bars showing ±1 S.E.) and the multivariate correlation between the ordinated scores and the SES values (arrow scaled by the magnitude of the correlation and oriented in the direction of the correlation).

**B**

**A**

**Figure 2.** Plots showing the structure of the bipartite networks for (A) tree-species and (B) genotype-species for the *Populus angustifolia* epiphytic lichen community in the common garden, Ogden, UT, USA. Nodes in each part of the network (i.e. tree, genotype or species) are arranged in order of increasing number of connections from bottom to top.

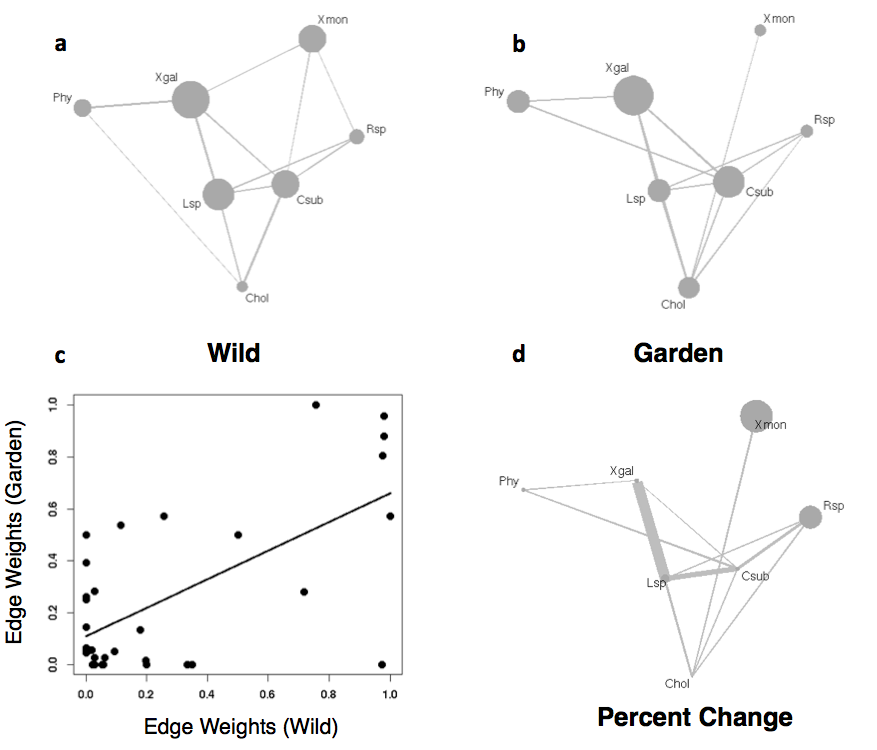
 

**B**

**A**

**Figure 3.** (A) Scatterplot showing the correlation between the epiphytic lichen community co-occurrence patterns (Standardized Effect Size = SES) and bark roughness. (B) The tree-species bipartite network for the natural stand showing significant nestedness.

**Appendix 1.**



**Figure 1**. Plots showing the significant network patterns for the epiphytic lichen at the scale of the entire stand (**a** and **b**). Species and significant co-occurrence patterns are shown as nodes scaled by log of the relative, total abundance of taxon and lines connecting edges scaled by the dependency value, which is the probability the one species occurs with another species relative to occurring at all. The correlation between the structure of the two stand-level networks (**c**). The network diagram (**d**) shows the percent change between the wild and garden of both the total relative abundances and the edge weights.