

# Genotypic variation in a foundation tree drives ecological network structure

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## ABSTRACT

Biological evolution occurs in the context of complex networks of interacting species in which natural selection defines the structure of ecological networks. Fundamental to this evolutionary process is the discovery of a genetic basis to ecological network structure. Although previous work has demonstrated that tree genotype contributes to interaction network structure at the scale of forest stands, the contribution of tree genetics to localized interaction networks at the scale of individual trees has not yet been explored. To test the degree to which tree genetics can contribute to network structure across scales from trees to stands, we conducted quantitative modeling of interaction network for a community of epiphytic lichens in a long-term experimental common garden of genotyped trees of a foundation species (*Populus angustifolia*). We found three main results: 1) Tree genotype strongly contributed to network structure explaining over a third of the variation in lichen interaction networks, 2) Multiple aspects of interaction network structure varied in response to genotype, including network size, the number of interactions, linkage density and connectance, 3) At the stand scale, we also found significant modular structure of plant-lichen networks resulting in part from the combination of trees of the same genotype tending to have similar community compositions and supporting similar lichen interaction networks dominated by positive interactions. These results support the hypothesis that variation in ecological interaction networks can result from genetically based variation in foundation species. Although these results are for a community of sessile organisms in close proximity to the tree, this study opens the possibility for a genetic basis to both direct and indirect interactions among species in complex communities.

# 1 Introduction

## 2 Methods

### 3 Field observations in common garden and natural riparian forest stands

4 The study was conducted along the Weber River, UT (USA), which is a cottonwood (*Populus* spp.) dominated riparian  
5 ecosystem. Although two native species, *Populus angustifolia* (James) and *Populus fremontii* (S. Watson), occur here and are  
6 known to hybridize, only pure or advanced generation backcrosses of *P. angustifolia* were sampled in order to avoid the effect  
7 of the hybridization between these two species.

8 A common garden was used to isolate the effect of tree genotype from the effect of the localized microenvironment associated  
9 with each individual and spatial autocorrelation. Asexually propagated clones of genotyped *P. angustifolia* individuals were  
10 obtained from wild collections and planted randomly in a single field (0.025 km<sup>2</sup>) at the Ogden Nature Center, Ogden, UT in  
11 1992. A total of thirteen genotypes replicated between 3 and 8 times each, were chosen for sampling. Genotype names were  
12 previously published<sup>2</sup>. Observations were made in the common garden in October 2010 and May 2011.

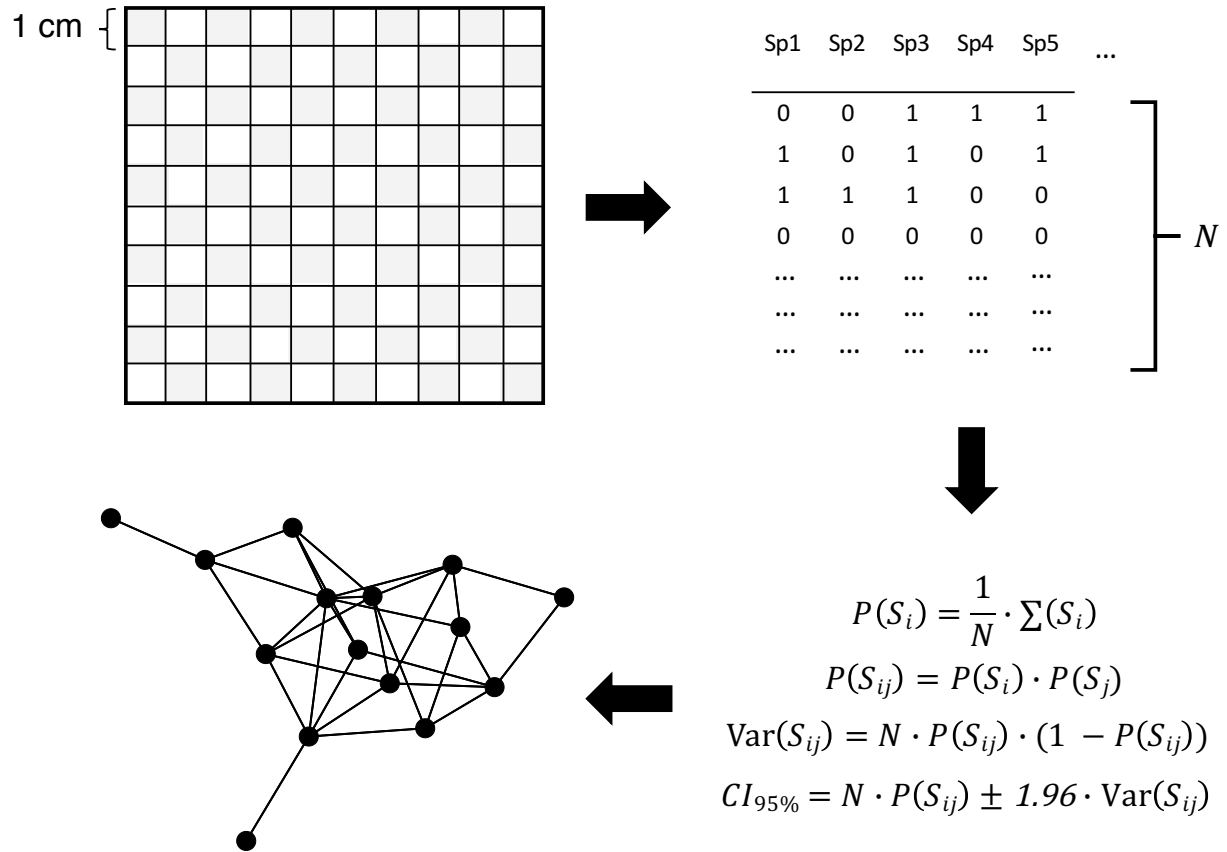
## 13 Results

Response	Predictor	p-value	H2
Percent Lichen Cover	Tree Genotype	0.0356	0.17
Lichen Species Richness	Tree Genotype	0.1443	0.1
Percent Rough Bark	Tree Genotype	8e-04	0.38
Lichen Network	Genotype	0.0431	0.17
Number of Network Links	Genotype	0.0796	0.15
Network Centrality	Genotype	0.1351	0.12

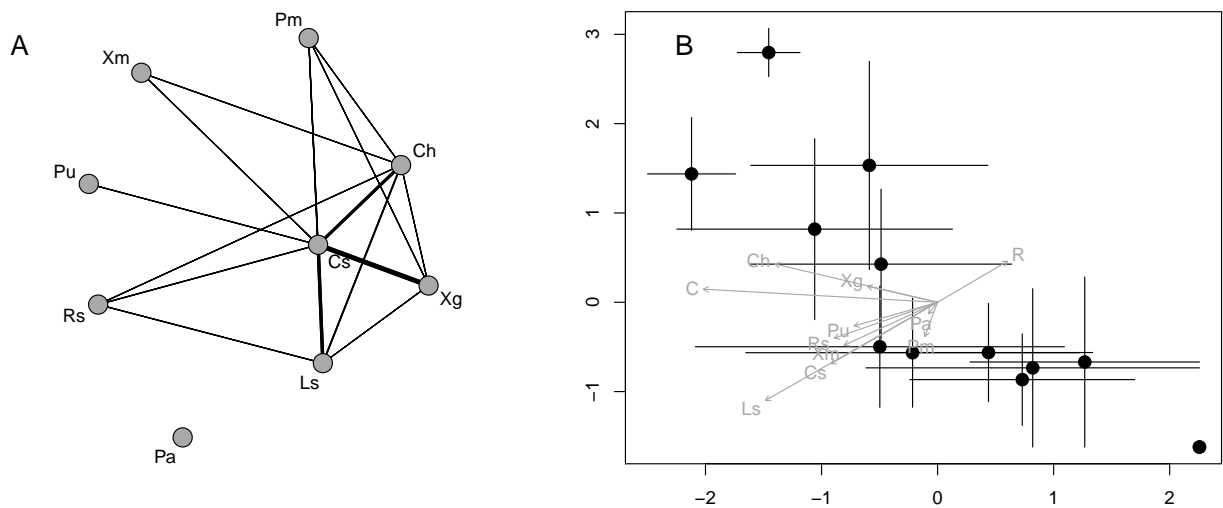
**Table 1.** Genotypic effects of cottonwood trees on the associated lichen community.

### 14 Network Response to Tree Variation

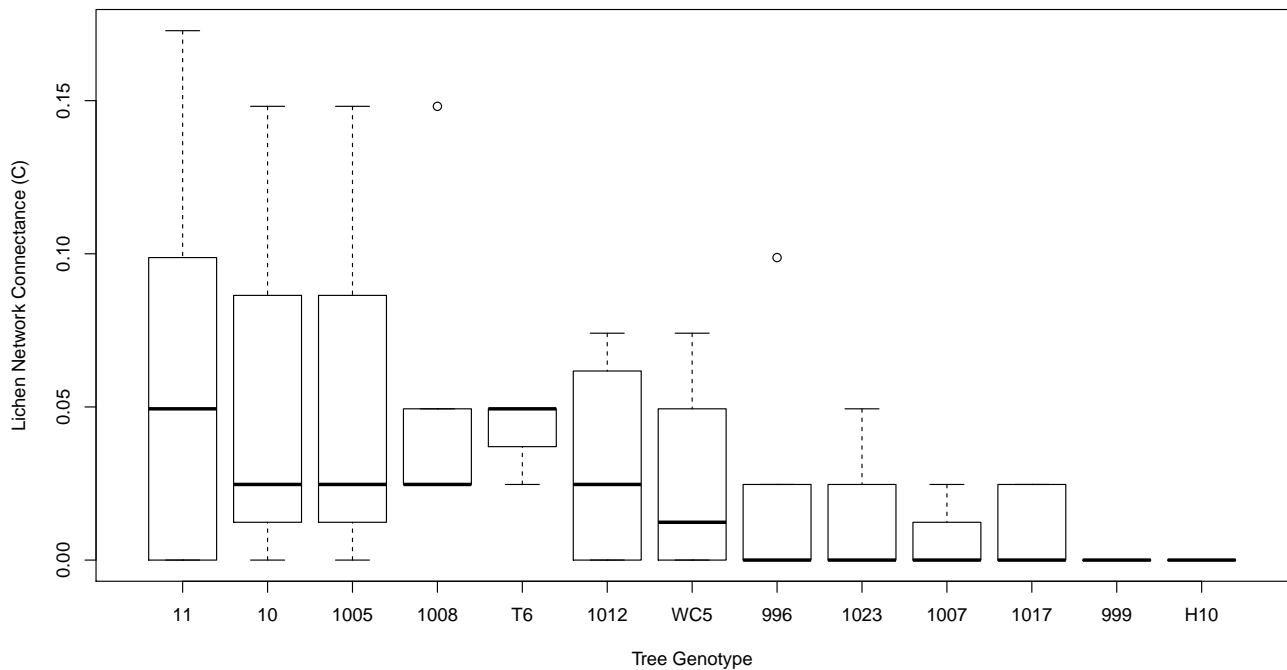
### 15 Genetic Structure Generates Forest Scale Network Structure



**Figure 1.** Lichen interaction networks were constructed by conducting field observations in 1 cm<sup>2</sup> cells within a 10 cm<sup>2</sup> grid on each tree using a checkerboard pattern (grey cells). Thus, a set of  $N$  total cell observations were recorded for each tree with the presence or absence of each species recorded for each cell. Applying a null-model based procedure<sup>1</sup>, we calculated and removed non-significant ( $\alpha = 0.05$ ) co-occurrences to produce the network associated with an individual tree.



**Figure 2.** Significant lichen interaction network structure resulting from tree genotypic variation was observed in the common garden. A) A network diagram showing significant interactions averaged over all trees shown as edges connecting lichen species shown as vertices. B) Genotype centroids (points) of NMDS ordinated lichen networks ( $\pm 1$  S.E.). Arrows show the magnitude and direction of correlation of the ordinated networks with tree bark roughness (R), network connectance and lichen species abundances (Xg = *Xanthomendoza galericulata*, Xm = *X. montana*, Ch = *Caloplaca holocarpa*, Cs = *Candelariella subdeflexa*, Rs = *Rinodina* (unknown species), Ls = *Lecanora* (unknown species), Pm = *Phyciella melanchra*, Pa = *Phycia adscendens*, Pu = *Phycia undulata*).



**Figure 3.** Connectance significantly varied among genotypes.



## 16 Discussion

## 17 References

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19 mate change. *Ecography (Cop.)*. **34**, 897–908 (2011). URL [http://dx.doi.org/10.1111/j.1600-0587.2011.](http://dx.doi.org/10.1111/j.1600-0587.2011.06919.x)  
20 [06919.x](http://dx.doi.org/10.1111/j.1600-0587.2011.06919.x) DOI 10.1111/j.1600-  
21 0587.2011.06919.x.

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## 26 Author contributions statement

27 M.L. and L.L. conceived the study, M.L. and L.L. conducted the field work, R.N. assisted in lichen identifications, M.L. wrote  
28 the first draft of the manuscript, S.B. and T.W. contributed substantively to the conceptual development, T.W. established the  
29 common garden. All authors contributed to revisions of the manuscript.

## 30 Additional information