

# Genotypic variation in a foundation tree alters ecological network structure of an associated community

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1 Biological evolution occurs in the context of complex networks of  
2 interacting species in which natural selection defines the structure  
3 of ecological networks. Fundamental to this evolutionary process  
4 is the discovery of a genetic basis to ecological network structure.  
5 Although previous work has demonstrated that tree genotype con-  
6 tributes to interaction network structure at the scale of forest stands,  
7 the contribution of tree genetics to localized interaction networks  
8 at the scale of individual trees has not yet been explored. To test  
9 the degree to which tree genetics can contribute to network struc-  
10 ture we conducted quantitative modeling of interaction networks. We  
11 constructed networks of epiphytic lichen associated with individual  
12 trees that were a part of a long-term experimental common garden  
13 of genotypes of (*Populus angustifolia*), a foundation species. We  
14 found three main results. First, tree genotype significantly predicted  
15 lichen network similarity, i.e. trees of the same genotype had more  
16 similar lichen networks. Second, bark roughness and condensed  
17 tannin concentration were both predicted by tree genotype and cor-  
18 related with lichen network similarity. Third, the network metrics, the  
19 number of links and centrality, were both correlated with several tree  
20 traits, including bark roughness and condensed tannin concentra-  
21 tion. We conclude that tree genotype influences lichen interaction  
22 network structure with two potential pathways through bark rough-  
23 ness and condensed tannin concentration. These results provide  
24 evidence that variation in ecological networks can result from genet-  
25 ically based variation in foundation species.

networks | heritability | community | genetics | lichen | cottonwood |  
Populus | common garden

- 1 • Evolution occurs in complex ecosystems
- 2 • Community genetics studies have demonstrated  
3 the importance of genetics and evolutionary dy-  
4 namics in structuring communities and ecosys-  
5 tems
- 6 • Community composition, ecosystem processes  
7 have been shown to vary in response to the  
8 genetic variation of foundation species
- 9 • Previous studies have examined aspects of net-  
10 works but to date, no studies have examined the  
11 genetic basis of networks of interacting species
- 12 • Here we examine the genetic basis of network  
13 structure on a community of sessile lignicolous

(i.e. bark) lichen on cottonwood trees. This  
14 system is ideal for examining for this kind of  
15 study because it:

- 16 1. Lichen do not move among trees, although  
17 asexual propagules could move to other  
18 trees in the garden
- 19 2. Is not unapproachably complex
- 20 3. Is comprised of distinct individuals that  
21 are small enough for an entire community  
22 to occur on a single tree but not too small  
23 to be quantified easily

## Significance Statement

Evolution occurs in the context of ecosystems com-  
prised of complex ecological networks. Research  
at the interface of ecology and evolution has primar-  
ily focused on pairwise interactions among species  
and have rarely included a genetic component to  
analyses. Here, we use a long-term common gar-  
den experiment to reveal the effect that genotypic  
variation can have on networks of lichens that occur  
on the bark of a foundation tree species. We found  
that lichen interaction network structure is genet-  
ically based and is correlated with heritable bark  
traits, including roughness and condensed tannins.  
These findings demonstrate the importance of ge-  
netic variation and evolutionary dynamics in shaping  
ecological networks as evolved traits.

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 the first draft of the manuscript, S.B. and T.W. contributed substantively to the conceptual development, T.W. established the common garden. All authors contributed to revisions of the manuscript.

The authors have no conflicts of interest.

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- 25 • We hypothesize that trees will vary in some  
 26 phenotypic traits, such that trees of the same  
 27 genotype will tend to have similar traits produc-  
 28 ing similarities in lichen network structure. To  
 29 test this hypothesis, we use a common garden  
 30 of cottonwood trees with lichen communities.

31 **E**volution occurs in the context of complex eco-  
 32 logical networks. Initially, evolution in a com-  
 33 munity context was focused on examples of highly  
 34 co-evolved pairs of species (e.g. Darwin's famous  
 35 prediction of the Sphinx Moth and Christmas  
 36 Orchid) citeWade2007. However, studies of dif-  
 37 fuse co-evolution (*sensu* citeJanzen1980) citeStinch-  
 38 combe2002, Strauss2007, Dicke2010, geographic mo-  
 39 saics of co-evolution citeThompson2005 and com-  
 40 munity genetics citeWhitham2006 have provided an  
 41 in-road for ecological network approaches citeFor-  
 42 tuna2009, Keith2017, Lau2016 to illuminate a more  
 43 complex perspective of the interface between eco-  
 44 logical and evolutionary dynamics. There is now  
 45 evidence to support that selection tends to occur  
 46 among groups of species citeWade2007, Pieterse2007,  
 47 Dicke2010 favoring the development of small webs  
 48 citeNuismer2006, Guimaraes2007, Gomez2009 and  
 49 that genetic variation and phylogenetic relatedness  
 50 contributes to variation in community assembly (1)  
 51 and species interactions citeWhitham2006a, Bai-  
 52 ley2009, Moya-Larano2011, which shapes the eco-  
 53 logical interaction networks (2).

54 Community genetics studies (3) have shown that  
 55 genetic variation in foundation species (4) plays a  
 56 significant role in defining distinct communities of in-  
 57 teracting organisms: such as, endophytes, pathogens,  
 58 lichens, arthropods, and soil microbes. Multiple stud-  
 59 ies have now demonstrated that genetic variation  
 60 influences numerous functional traits (e.g., phyto-  
 61 chemical, phenological, morphological) produces a  
 62 multivariate phenotype (5) that contributes to varia-  
 63 tion in associated communities (6). The importance  
 64 of genetic variation in structuring ecological systems  
 65 was recently reviewed by Des Roches et al. (2018).

66 Additional work has provided support for the hy-  
 67 pothesis that not only does composition vary among  
 68 genetically distinct genotypes of foundation species,  
 69 it also impacts the structure of the network of species  
 70 interactions in these communities. Two studies have  
 71 demonstrated conceptually (7) and empirically (8).  
 72 However, studies in the network ecology literature  
 73 generally do not include a genetic component (see

74 review by Borrett et al. 2014) and community genet-  
 75 ics papers do not have data on network structure of  
 76 associated communities. Currently, we are aware of  
 77 only one paper that empirically examines the genetic  
 78 basis of network structure of a community citeBar-  
 79 bour2019.

80 Here, we investigate how genetic variation in a  
 81 foundation tree species determines the structure of a  
 82 network of interactions among a community of tree  
 83 associated lichen species. Using a long-term (20+  
 84 years), common garden experiment with replicated  
 85 individuals of known genetic identity and a naturally  
 86 established stand of *Populus angustifolia*. We focused  
 87 on a model community of 9 epiphytic lichen species,  
 88 as previous research has demonstrated significant  
 89 compositional responses of epiphytes to genotypic  
 90 variation (9, 10). In addition, the life-history char-  
 91 acteristics of lichens, having highly localized, direct  
 92 contact interactions and slow population turnover  
 93 rates, allowed us to assess interactions among lichen  
 94 species on individual trees. We hypothesize that in  
 95 natural systems evolution occurs in a community  
 96 context involving interactions of complex networks  
 97 of interacting species (7, 8, 11, 12). If correct, we  
 98 expect to find that network structure is genetically  
 99 based in which different plant genotypes support  
 100 different interaction networks and that these interac-  
 101 tions networks can function as indicators of ecologi-  
 102 cal dynamics important for conserving biodiveristy.  
 103 Applying a probability-theory based network mod-  
 104 eling approach, we constructed a set of interaction  
 105 network models for the lichens associated with indi-  
 106 vidual trees. Using these models, we then examined  
 107 the genetic basis of the structure of these ecological  
 108 networks.

## Materials and Methods

109 The study was conducted along the Weber River, UT  
 110 (USA), which is a cottonwood (*Populus* spp.) dominated  
 111 riparian ecosystem. Although two native species, *Populus*  
 112 *angustifolia* (James) and *Populus fremontii* (S. Watson),  
 113 occur here and are known to hybridize, only pure or  
 114 advanced generation backcrosses of *P. angustifolia* were  
 115 sampled. Bark lichens have been extensively studied  
 116 in this system and provide an ideal system in which to  
 117 observe and model lichen interaction networks, as their  
 118 sessile nature permits accurate identification of individuals  
 119 (13).

120 A long-term, common garden experiment was used  
 121

123 to isolate the effect of tree genotype from the effect of  
124 the localized microenvironment associated with each individual  
125 and spatial autocorrelation. Established in 1992,  
126 asexually propagated clones of genotyped *P. angustifolia*  
127 individuals were obtained from wild collections and  
128 planted in fully randomized design at the Ogden Nature  
129 Center, Ogden, UT. From the population of established  
130 individuals in the common garden, we chose a total of  
131 thirteen genotypes, replicated between 3 and 8 times each,  
132 for sampling.

133 **Bark Lichen Observations.** On each tree, presence or absence  
134 of each lichen species was assessed in 50 total 1 cm<sup>2</sup>  
135 cells arrayed in a checkerboard pattern. Given the small  
136 size and sessile nature of lichens, we were able to rapidly  
137 assess lichen interactions by quantifying thalli in close  
138 contact. Sampling was restricted to the northern aspect  
139 of the trunk to maximize the abundance of lichen and  
140 control for the effect of trunk aspect. Two adjacent 10  
141 cm<sup>2</sup> quadrats centered at 50 cm and 85 cm from ground  
142 level were sampled (Fig 1 A and B). The observed lichen  
143 community included (abbreviations are given for species  
144 present in study): Xg = *Xanthomendoza galericulata*, Xm  
145 = *X. montana*, Ch = *Caloplaca holocarpa*, Cs = *Candeliella subdeflexa*, Rg = *Rinodina glauca*, Lh = *Lecanora hagenii*, Pm = *Phyciella melanchra*, Pa = *Physcia adscendens*, Pu = *Physcia undulata*. Several other species were  
149 not observed in the present study but are known to occur  
150 in this region: *Phaeophyscia orbicularis*, *Phaeophyscia ciliata*, *Melanelia sublivacea*, *Meanelia elegantula*.

152 The cell size and checkerboard sampling pattern was  
153 chosen to isolate the individuals in each cell. In a previous  
154 survey of lichen thallus size in this common garden, we  
155 had observed a median thallus size of 0.12 ± 0.001 cm<sup>2</sup> (1  
156 S.E.) (see Supporting Information). Based on the median  
157 thallus size, we expected thalli observed in each cell to  
158 generally be spatially independent of thalli present in  
159 other cells but exposed to similar micro-environmental  
160 conditions created by the bark and the location of the  
161 sampling area on an individual tree. Therefore, we were  
162 confident in treating the cell-wise observations in quadrats  
163 as independent with respect to lichen-lichen interactions.

164 We also measured several bark traits for each tree:  
165 including, bark roughness and chemistry. **INSERT  
166 FROM LAMIT.**

167 **Lichen Network Modeling and Analysis.** For each tree,  
168 repeated observations of lichen were made in order to construct  
169 replicated interaction networks for each genotype.  
170 We quantified the presence of lichen in the 1 cm<sup>2</sup> cells on  
171 individual trees of *P. angustifolia*. Unipartite networks  
172 were generated using the conditional probabilities of each  
173 species pair, i.e. the probability of observing one species  
174 given an observation of another species  $P(S_i|S_j)$ , based on  
175 the method developed by (14). To calculate conditional  
176 probabilities, we quantified the individual probabilities

177 of species occurrences  $P(S_i)$  and the joint probability  
178 of co-occurrences  $P(S_i, S_j)$  using the frequencies of each  
179 species and their co-occurrences. We were then able to  
180 calculate the conditional probabilities of each species pair  
181 as  $P(S_i|S_j) = \frac{P(S_i, S_j)}{P(S_j)}$ , based on the axioms of probability.  
182 This yielded a matrix that could possibly be asymmetric, i.e.  
183  $P(S_i|S_j)$  does not have to be equal to  $P(S_j|S_i)$ . Another  
184 important property of this matrix is that the diagonal  
185 ( $S_{ii}$ ) was equal to one for all species present and zero for  
186 species that were not observed in any cell.

187 We then applied an analytical procedure to remove  
188 non-significant links between species. This procedure  
189 determines if the joint probability of a species pair  
190 (i.e.  $P(S_i, S_j)$ ) is different from zero (Fig. 2). Here, a  
191 confidence interval  $CI_{95\%}$  is calculated as  $CI_{95\%} =$   
192  $E[S_i S_j] * Z_{95\%} * \sqrt{V(S_i S_j)}$ , where the expected  
193 frequency of co-occurrences  $E(S_i S_j)$  is the total number  
194 of cells surveyed ( $N$ ) times the independent probabilities  
195 of each species  $P(S_i) * P(S_j)$ ,  $Z_{95\%}$  is the Z-score  
196 for 95% from a Z-distribution and the expected variance  
197 of  $E(S_i S_j)$  is the total number of cells times the  
198 expected probability of  $S_i S_j$  and its compliment (i.e.  
199  $V(S_i S_j) = N * E[P(S_i, S_j)] * (1 - E[P(S_i, S_j)])$ ). If the  
200 observed number of co-occurrence falls outside of the  
201 confidence interval, the joint probability  $P(S_i, S_j)$  is de-  
202 termined to be equal to the product of the individual  
203 probabilities (i.e.  $P(S_i) * P(S_j)$ ), and the conditional prob-  
204 ability reduces to the individual probability of that species  
205  $P(S_i)$ . Therefore, unless the co-occurrence of a species  
206 pair falls outside the confidence interval, the probabil-  
207 ity that the observation of one species given the other  
208 is no different than simply observing that species alone.  
209 This enables us to remove links from a given network by  
210 re-scaling the resulting conditional probabilities by sub-  
211 tracting the individual probabilities from the conditional  
212 probabilities (i.e. how different the conditional probability  
213 is from the independent probability), which makes any  
214 species with a non-significant conditional probability zero.  
215 The resulting matrix ( $\mathbf{D} = D_{ij}$ ) can be interpreted as  
216 how one species impacts another with zero being no effect  
217 and values less than or greater than zero interpreted as  
218 negative and positive effects, respectively. Here, we will  
219 refer to this matrix ( $\mathbf{D}$ ) as an interaction matrix with  
220 the properties that it can be asymmetric (i.e.  $P_{ij}$  does not  
221 necessarily equal  $P_{ji}$ ), and the diagonal ( $P_{ii}$ ) is zero (i.e.  
222 a species does not influence its own probability of being  
223 observed).

224 **Statistical Analyses, Software and Data.** We used a com-  
225 bination of parametric and non-parametric, permutation  
226 based frequentist statistical analyses to test for the effects  
227 of genetic variation on lichen communities and their inter-  
228 action networks. To assess the effect of genotype on uni-  
229 partite responses, we used additive, random effects models  
230 with Restricted Maximum Likelihood (REML). We used  
231 a combination of Least Squares Regression, Analysis of



**Fig. 1.** The communities of bark lichens were observed in a common garden of replicated genotypes of narrowleaf cottonwood trees (*P. angustifolia*) at the Ogden Nature Center (Ogden, UT). Lichens were sampled within a fixed area ( $10 \text{ cm}^2$ ) on individual trees at two heights, 40cm and 80cm from the ground (A and B, respectively). (C) a photo of a typical community of bark lichen species interacting on the trunk of a cottonwood tree, including one of the more abundant species, *Xanthomendoza galericulata*, in the center. (D-K) shows the other lichen species observed, respectively: *X. montana*, *Candelariella subdeflexa*, *Rinodina* sp., *Caloplaca holocarpa*, *Physcia adscendens*, *Phyciella melanchra*, *Physcia undulata* and *Lecanora hagenii*. Photo Credits: L.J. Lamit (A-C) and R.R. Naesbour (D-K).

232 Variance (ANOVA) and correlation tests to quantify and  
 233 test for the relationship among other variables. Bark  
 234 roughness, lichen cover and species richness were square-  
 235 root transformed to meet the assumptions of homogeneity  
 236 of variance and normality for these tests.

237 For multivariate response variables, such as lichen com-  
 238 munity composition and network structure, we used dis-  
 239 tance based multivariate statistical approaches, including  
 240 Permutational Analysis of Variance (PERMANOVA) and  
 241 Mantel tests. For some analyses, community composition  
 242 was relativized by species maxima to reduce the effect  
 243 of the highly abundant *X. galericulata*. For community  
 244 composition we used Bray-Curtis dissimilarity, which has  
 245 optimal performance with count data citepMinchen1998.  
 246 To quantify the similarity of lichen networks among indi-  
 247 vidual trees, we calculated the pairwise Euclidean distance  
 248 of the **D** interaction matrices among all pairs of trees.

249 For visualization of multivariate patterns, we used Non-  
 250 metric Multi-Dimensional Scaling (NMDS) citeecodist  
 251 to produce dimensionally reduced ordinations of these  
 252 multi-variate responses and fitted vectors for continuous  
 253 predictor variables to the ordinated values citevegan. Us-  
 254 ing random initial configurations with a maximum of 500

iterations and a change in stress threshold of less than  
 $10^{-12}$ . Final configurations has the lowest stress with at  
 most a stress level of 0.10.

255 For each network, we also calculated metrics that mea-  
 256 sure different structural aspects. Although there are many  
 257 other metrics, for the sake of simplicity we focus on a sub-  
 258 set that represent several interesting features of network  
 259 structure (see (15)). We calculated the number of interac-  
 260 tions or “links” in each network, which provides a measure  
 261 of the size of the network citepLau2015, Borrett2014. We  
 262 also calculated the centralization of each network, which  
 263 measures the evenness of the distribution of interactions  
 264 among the species in the network citeButts2005. In a net-  
 265 work with a low level of centralization species have similar  
 266 amount of interaction in the network, while a network  
 267 with a high level of centralization tends to have one or  
 268 small number of species that interact with other species.  
 269 We used a related function to calculate the centrality of  
 270 each species (i.e. node level centrality) in each network  
 271 as well. The modularity of each network was also quanti-  
 272 fied using a weighted algorithm citeBeckett2016, which  
 273 measures the degree to which a given network is divided  
 274 into groups of species more connected to each other than  
 275



**Fig. 2.** Lichen interaction networks were constructed by conducting field observations in  $1 \text{ cm}^2$  cells within a  $10 \text{ cm}^2$  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 the probability-based network modeling method adapted from (14), we calculated the conditional probabilities,  $P(S_i|S_j)$ , for all species pairs and removed (i.e. set equal to zero) species pairs whose joint probabilities,  $P(S_i, S_j)$ , were not significant using a confidence interval based comparison of their observed co-occurrence frequency,  $S_i S_j$ , to that expected due to chance alone,  $E[P(S_i, S_j)] = P(S_i)P(S_j)$ , and  $P(S_i|S_j)$  reduces to  $P(S_i)$ , the observed individual probability of species  $S_i$ .

other species. As with the other response variables, the number of links was log-transformed and both modularity and centralization scores were fourth-root transformed to meet variance and normality assumptions.

All code and data for the project are openly available online. Code and data are available at [github.com/ecgen/comgen](https://github.com/ecgen/comgen). The project is also archived via Zenodo at [zenodo.com/doi/XXXXXX](https://zenodo.com/doi/XXXXXX). All analyses were conducted using the programming language R version 3.6.1 (R Development Core Team 2019).

## Results

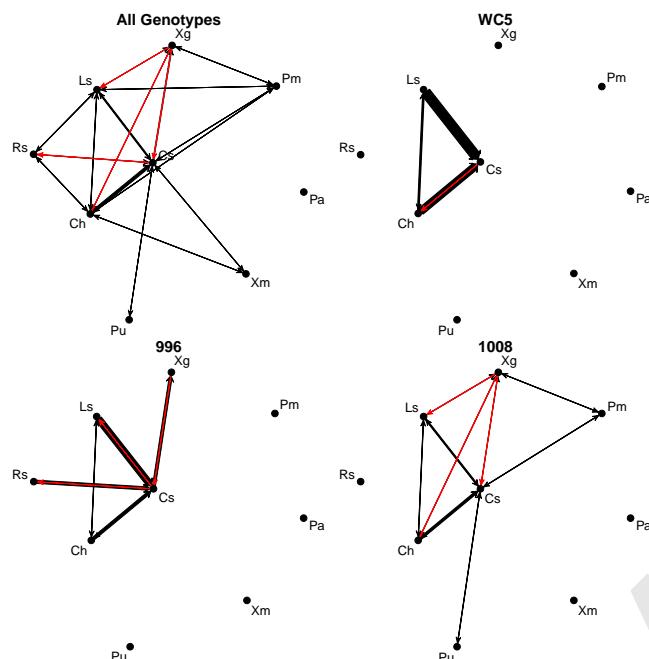
Network similarity and several tree traits were genetically based. Tree genotype was a significant predictor of network similarity ( $H^2 = 0.16$ ,  $p\text{-value} \leq 0.001$ ). Bark roughness ( $H^2 = 0.38$ ,  $p\text{-value} \leq 0.001$ ) and condensed tannin concentration ( $H^2 = 0.28$ ,  $p\text{-value}$

$= 0.014$ ) also showed a signature of tree genotype (Fig. 4); however, this was not the case for other tree traits, bark pH and carbon to nitrogen ratio. Also, none of the lichen network metrics were significantly predicted by tree genotype, either at the scale of the entire network (Table 1) or for individual species (see Supporting Information). Although both showed a response to tree genotype, bark roughness and condensed tannins were not correlated (Pearson's  $r = 0.084$ ,  $p\text{-value} = 0.556$ ).

Tree traits and lichen community metrics were correlated with lichen networks. The genetically based traits, bark roughness and condensed tannins were both significant predictors of network similarity (Table 2). Bark C:N ratio was also a significant predictor of network similarity, but, as shown previously (see

|          | df      | SS       | R2     | F      | p-value |
|----------|---------|----------|--------|--------|---------|
| geno     | 9.0000  | 257.2922 | 0.3710 | 1.7697 | 0.0957  |
| Residual | 27.0000 | 436.1515 | 0.6290 |        |         |
| Total    | 36.0000 | 693.4437 | 1.0000 |        |         |

**Table 2. PERMANOVA Pseudo-F Table of lichen network similarity.**



**Fig. 3.** Lichen networks varied in structure among tree genotypes. Network diagrams of the mean lichen interaction matrices averaged for all trees and for several individual genotypes showing a range of interaction network structure. Directionality (arrowheads) and sign (red = negative, black = positive) of interactions are shown as edges between species (abbreviated by the first letter of the genus and specific epithet), which are scaled by their magnitude. The sign of the interaction is indicative of greater (positive) or lesser (negative) paired occurrences than expected relative to the overall frequency of occurrence of each species. Ecologically, the links in the network are likely the product of multiple types of interactions (e.g. mutualism, parasitism, competition, facilitation) that could vary over both space and time.

310 Table 1), there is not sufficient evidence support a  
311 genetic basis for it. Bark pH was not a significant  
312 predictor of lichen network similarity (Table 2). The  
313 abundance, richness, evenness and diversity of the  
314 bark lichen community, although also not predicted  
315 by tree genotype, were all significantly correlated  
316 with lichen network structure (Table 2). Lichen com-  
317 munity composition was not correlated with lichen  
318 network similarity, either when species abundances  
319 were relativized (Mantel R = -0.09, p-value = 0.139)  
320 or not (Mantel R = -0.03, p-value = 0.573).

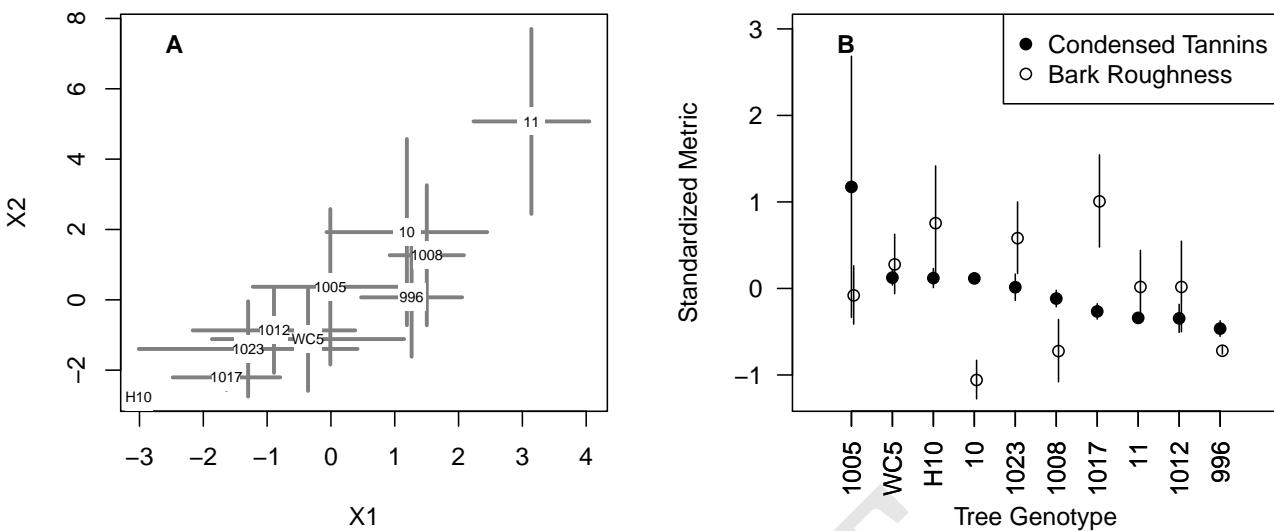
## 321 Discussion

- 322 • We found:
  - 323 – Lichen networks genetically based

| Response                   | H2      | p-value |
|----------------------------|---------|---------|
| Lichen Network Similarity  | 0.1734  | 0.0957  |
| Number of Network Links    | 0.3156  | 0.0267  |
| Network Centrality         | 0.3305  | 0.0196  |
| Network Modularity         | 0.0012  | 0.4507  |
| Percent Lichen Cover       | 0       | 1       |
| Lichen Species Richness    | 0       | 0.458   |
| Lichen Species Evenness    | 0       | 0.4574  |
| Lichen Species Diversity   | 0       | 0.4558  |
| Community Composition      | -0.0789 | 0.8469  |
| Percent Rough Bark         | 0.3221  | 0.0128  |
| Condensed Tannins (CT)     | 0.0041  | 0.4513  |
| Carbon-Nitrogen (CN) Ratio | 0       | 1       |
| pH                         | 0       | 1       |

**Table 1. Genotypic effects on the associated lichen community.**

- Several genetically based traits also explained variation in lichen network structure 324  
325  
326
- Although correlated with lichen network structure, the network metrics explored 327  
328  
329 were not genetically based
- Genetic response of lichen networks is not a function of the abundance, richness, diversity 330  
331 or composition of lichen communities and is not 332  
333 reducible to simple network metrics. This is 334  
335 likely the result of having similar interactions 336  
337 among similar species in networks on trees of the 338 same genotype. This is difficult to disentangle 339  
339 with the current set of analyses. Future work  
should apply a structural statistical approach,  
such as SEM or path analysis.
- Habitat filtering of communities (richness, composition) vs environmental influence on interactions. Likely a combination of both of these factors. 340  
341  
342  
343
  - Lichen network structure correlated with species richness, evenness and diversity 344  
345
  - Lichen community composition not correlated with network structure 346  
347
  - None of these were genetically based 348



**Fig. 4.** Tree genotype affected lichen networks and several bark traits. A. The plot shows genotype centroids of NMDS ordinated ( $R^2 = 0.999$ , stress = 0.008) lichen networks ( $\pm 1$  S.E.). Centroids that are closer are more similar in the structure of their lichen networks. B. Plot showing the standardized ( $\frac{x - \bar{x}}{\sigma}$ ) means ( $\pm 1$  S.E.) for the two genetically based tree traits: tree bark roughness and condensed tannin concentration.

- An important consequence for diversity is that genotypes could be supporting unique communities, even if the composition of the communities is the same among individuals and genotypes.
- Genetic diversity could be influencing the stability of communities through the effects on interactions. Some network structures are likely to be more stable, either in response to disturbance or via self-organized dynamics. Although, none of the metrics examined, such as the number of links, modularity or centrality, showed a genetic signature.
- Important factors to consider in studies of other ecological networks:
  - Relative body size
  - Mobility
  - Reproductive isolation
- Future work should consider the potential influence on evolutionary dynamics of communities
  - Network structure influences network stability
  - Are the communities nested subsets?

TGW: I think window is too vague and this topic sentence needs to be much stronger for a journal like PNAS. Might be stronger by saying "Our findings argue there is a genetic component to network structure, which implies that network structure could be subject to selection and networks can evolve."

TGW: Could we also make the comparison that genetically more similar trees also have more similar communities? We've done this in the past and it has worked, e.g., Randy's genetic similarity rule.

- Genetic assembly rule = similar genetics will have more similar communities
- What we don't know is whether or not these interactions will also lead to similar interactions among other species.
- Thus, it would be possible for genetics to not only influence other species directly, but also indirectly by influencing the interactions among other species.

We observed significant lichen interaction structure that varied among genotypes of a foundation

394 tree species, narrowleaf cottonwood (*P. angustifolia*). We found that a genetically based trait, bark  
395 roughness, partially explained the variation in lichen  
396 interaction networks. Some of this variation in lichen  
397 networks was related to both the overall abundance  
398 and species richness of lichen; though, statistically  
399 controlling for the effect of genotype on these vari-  
400 ables indicates that a significant portion of the vari-  
401 ance in lichen species richness is due to a factor  
402 other than tree genotype. By using network metrics,  
403 we were also able to probe for specific characteris-  
404 tics of how these networks were responding to tree  
405 genotype. We found that both number of links and  
406 the centralization of the networks were highly corre-  
407 lated with network similarity and that tree genotype  
408 significantly predicted network centrality but only  
409 marginally predicted the number of network links.  
410 This latter result could be due to the relationship  
411 between species richness and the number of links  
412 in the network, which were significantly correlated  
413 with each other. We also found that bark roughness  
414 did not significantly predict either the number of  
415 links or the centrality of lichen networks, suggesting  
416 that bark roughness has some other effect on the  
417 structure of the lichen networks. Taken together,  
418 these findings support the hypothesis that genotypic  
419 variation in a foundation species contributes to the  
420 structure of a network of interacting species.  
421

422 **LJL: I wonder if you need to have so much**  
423 **on richness here. Overall, I think you want to**  
424 **focus on the network responses and patterns**  
425 **among genotype first, and then go into mech-**  
426 **anism later. I think we don't quite have a**  
427 **good mechanism yet so I don't think it needs**  
428 **to come up in the first paragrpah of the dis-**  
429 **cussion.**

430 These findings point to the importance of under-  
431 standing the community level effects of genetic vari-  
432 ation in plant functional traits and highlights the  
433 potential for indirect effects of genetic variation to  
434 propagate through networks of interacting species  
435 and trophic levels.

436 This work corroborates previous findings of the  
437 importance of plant genetics in shaping community  
438 structure and ecosystem processes. citepBangert2008

439 Altering the structure of interaction networks  
440 presents a means for genetic effects to be magni-  
441 fied within the system of interacting species. For  
442 example, (8) showed that the genetics based interac-

443 tions of aphid resistant and aphid susceptible trees  
444 resulted in different interaction networks of their  
445 associated arthropod communities composed of 139  
446 species. At the scale of ecosystems, trophic net-  
447 works or food webs direct and control the rates of  
448 energy and nutrient flux (16). Furthermore, in a  
449 predator-prey-plant study, Smith (17), showed that  
450 the interactions among species across trophic levels  
451 depended on plant genotype.  
452

453 Also, work by (18–20) observed consistent pat-  
454 terns of centralized interactions of species modules  
455 focused around hubs of plant-fungal interactions. In  
456 other words, a small number of plant and fungal  
457 symbionts tended to have disproportionate numbers  
458 of interactions with other species and likely are the  
459 drivers in determining community assembly, struc-  
460 ture and dynamics.  
461

462 More on the importance of ecological networks  
(21, 22).

463 From Thompson2014

- 464 • Pairwise interactions are usually influenced by  
other species
- 465 • Selection favors the development of small webs
- 466 • Evolution of new lifestyles leads to changes in  
selection on large and small webs

467 Specific hypothesis from Thompson2014

468 **LJL: If I recall, the Elamo paper just looks**  
469 **at genetic correlations between pairwise indi-**  
470 **vidual abundances. I would suggest maybe it**  
471 **doesn't deserve to be in this 1st paragraph.**  
472 **Perhaps it actually should be in the 2nd or**  
473 **3rd paragraph, just as a reference that points**  
474 **to the potential for genotype to influence net-**  
475 **works. Definately our 2015 JOE paper goes**  
476 **much further, too, since it has whole com-**  
477 **munities being correalated. But, again, I**  
478 **woudl put both of these as citation in the com-**  
479 **munity genetics paragraphs (2 of 3) instead**  
480 **of the first paragrpah, which focuses on the**  
481 **general network lit.**

482 **LJL: It could be useful to point out that**  
483 **our findings are not related to trophic inter-**  
484 **actions, which is pretty cool. Also,we talk**  
485 **about interaction networks but it is not clear**  
486 **to me if the interactions tend to be positive**  
487 **or negative. Can we get at that with the ap-**  
488 **proach used?**

490 TGW: Is there any adaptive component to  
491 the tree in having certain lichen communi-  
492 ties? e.g., can they feed back to affect tree  
493 performance in some way or is this a pas-  
494 sive outcome of a trait that affects bark for  
495 other adaptive reasons and lichens are pas-  
496 sive players that tag along for the ride? I  
497 could envision that lichens covering the bark  
498 of a tree act as a barrier between insects and  
499 pathogens, much like ectomycorrhizae cover  
500 fine roots as a first line of defense by invad-  
501 ing microorganisms. Uptake of N that gets  
502 passed to the tree??

503 LJL: I agree that there is a general over-  
504 arching theme that evolution occurs in a com-  
505 munity network context, but I'm not sure  
506 that we should state that as our main hypothe-  
507 sis. It seems more that this is a fundamen-  
508 tal foundation for our work. The hypothe-  
509 sis is more what we are testing directly, but  
510 we don't test this directly. I guess I don't  
511 want to give the impression that our com-  
512 munities are necessarily the result of each  
513 species evolving into its place in the commu-  
514 nity on these tree genotypes (although I do  
515 understand this as Shuster et al 2006's funda-  
516 mental explanation for why we see different  
517 communities on different genotypes; I don't  
518 necessarily agree that this is the only rea-  
519 son we would see different communities on  
520 dif genotypes). Most of these are pretty gen-  
521 eralist lichens, which could be found on other  
522 deciduous trees in the surrounding city or nat-  
523 ual areas. I would look at it more like an  
524 assembling of lichen species into unique con-  
525 figurations on genetically different substrates.  
526 There may be some selection for different  
527 genotype of lichen during the community as-  
528 sembly process but we can't really tell that  
529 just by differences in species abundances or  
530 coocurrence. I guess to me the evolutionary  
531 context that is more directly related to this  
532 work is that the tree genotype is a central  
533 controller (indeed a sort of hub species in the  
534 network) of network structure. By anchor-  
535 ing the lichen network to tree genotype (and  
536 variation among networks to variation among  
537 tree genotypes), our study highlights the pos-  
538 sibility that natural selection acting on the

539 trees may have an extended consequence for  
540 the network structure of organisms living on  
541 the trees... the extra thing we add to the field  
542 is that we show interaction networks are sen-  
543 sitive to genotype. I doubt the lichens have  
544 a direct effect on tree fitness, but favorabil-  
545 ity of some tree genotypes over others during  
546 natural selection will then go on to favor and  
547 disfavor certain lichen communities of differ-  
548 ent network structures. By being sensitive  
549 to tree genotype, the lichen community net-  
550 works are passive riders on the waves of evolu-  
551 tionary dynamics that occur within the tree  
552 species they inhabit.

553 MKL: In response to Lamit's comment  
554 above, I agree that it is not required that  
555 there is co-evolution. Another, perhaps sim-  
556 pler, explanation is that there is variation in  
557 environmental filtering of lichen individuals  
558 created in part by genetic variation in tree  
559 individuals.

560 TGW: might be good to cite papers on  
561 competition in lichens or other organizing fac-  
562 tors to back up the least expected statement.  
563 as epiphytes we might not expect them to  
564 care.

565 TGW: I think we need to emphasize the  
566 long-term nature of our common garden  
567 study as very few common garden studies of  
568 lichens likely exist. Any refs on this? If true  
569 might want to mention this up front in intro.

570 MKL: Environmental filtering is evidenced  
571 by species richness, but also possibly species  
572 interaction varying based on environment as  
573 networks varied in terms of sign and magni-  
574 tude as well.

575 MKL: The effect of bark roughness on  
576 network similarity was primarily genetically  
577 based, and there are likely other factors at  
578 play.

579 Discussion of network implications for sta-  
580 bility with genetics.

581 Bark roughness had previously been shown to be  
582 an important tree trait influencing bark lichens (13)  
583 that is under strong genetic control (23).

584 Although our study was conducted with a commu-  
585 nity of lichens, these results should be generalized  
586 to other groups of diverse organisms around the  
587 world that also exhibit significant genetic signals at

the community level (24, 25). In the face of the high degree of complexity and potential context dependency of ecological processes, the current study points to the utility of considering the spatial and temporal scales of interactions, as discussed to some in previous studies (26–28). In the present study, we found that community assembly processes, such as environmental filtering and species interactions, are genetically based. This is likely due, in part, to the large difference in the differences in size and longevity of the lichen and cottonwood individuals with the trees determining the environment in which the lichen occur. We suggest that future work would be aided by determining these modules within the biotic community that include species with similar differences in body-size and time-scales. As heritable variation is the raw material for natural selection to act upon, a genetic basis for interaction network structure indicates evolutionary dynamics should be considered at the community level and that conserving genetic variation is important to consider in efforts to restore or preserve complex species interactions and their associated ecosystem functions (29). With such findings, it appears that we are closer to understanding the evolutionary drivers of Darwin's entangled bank and the interconnectedness of species in complex communities.

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