

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 dynamics in structuring communities and ecosystems
- 4 Community composition, ecosystem processes have been shown to vary in response to the genetic variation of foundation species
- 5 Previous studies have examined aspects of networks but to date, no studies have examined the genetic basis of networks of interacting species
- 6 Here we examine the genetic basis of network structure on a community of sessile lignicolous

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

- 1 Lichen do not move among trees, although
2 asexual propagules could move to other
3 trees in the garden
- 4 Is not unapproachably complex
- 5 Is comprised of distinct individuals that
6 are small enough for an entire community
7 to occur on a single tree but not too small
8 to be quantified easily

Significance Statement

Evolution occurs in the context of ecosystems comprised of complex ecological networks. Research at the interface of ecology and evolution has primarily focused on pairwise interactions among species and have rarely included a genetic component to analyses. Here, we use a long-term common garden 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 genetically based and is correlated with heritable bark traits, including roughness and condensed tannins. These findings demonstrate the importance of genetic 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.

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

132 **Bark Lichen Observations.** On each tree, presence or absence of each lichen species was assessed in 50 total 1 cm² cells arrayed in a checkerboard pattern. Given the small size and sessile nature of lichens, we were able to rapidly assess lichen interactions by quantifying thalli in close contact. Sampling was restricted to the northern aspect of the trunk to maximize the abundance of lichen and control for the effect of trunk aspect. Two adjacent 10 cm² quadrats centered at 50 cm and 85 cm from ground level were sampled (Fig 1 A and B). The observed lichen community included (abbreviations are given for species present in study): Xg = *Xanthomendoza galericulata*, Xm = *X. montana*, Ch = *Caloplaca holocarpa*, Cs = *Candulariella subdeflexa*, Rg = *Rinodina glauca*, Lh = *Lecanora hagenii*, Pm = *Phyciella melanchra*, Pa = *Physcia adscendens*, Pu = *Physcia undulata*. Several other species were not observed in the present study but are known to occur in this region: *Phaeophyscia orbicularis*, *Phaeophyscia ciliata*, *Melanelia sublivacea*, *Meanelia elegantula*.

133 The cell size and checkerboard sampling pattern was chosen to isolate the individuals in each cell. In a previous survey of lichen thallus size in this common garden, we had observed a median thallus size of 0.12 ± 0.001 cm² (1 S.E.) (see Supporting Information). Based on the median thallus size, we expected thalli observed in each cell to generally be spatially independent of thalli present in other cells but exposed to similar micro-environmental conditions created by the bark and the location of the sampling area on an individual tree. Therefore, we were confident in treating the cell-wise observations in quadrats as independent with respect to lichen-lichen interactions.

134 We also measured several bark traits for each tree:
135 including, bark roughness and chemistry. **INSERT
136 FROM LAMIT.**

137 **Lichen Network Modeling and Analysis.** For each tree,
138 repeated observations of lichen were made in order to construct replicated interaction networks for each genotype.
139 We quantified the presence of lichen in the 1 cm² cells on
140 individual trees of *P. angustifolia*. Unipartite networks
141 were generated using the conditional probabilities of each
142 species pair, i.e. the probability of observing one species
143 given an observation of another species $P(S_i|S_j)$, based on
144 the method developed by (14). To calculate conditional
145 probabilities, we quantified the individual probabilities

146 of species occurrences $P(S_i)$ and the joint probability
147 of co-occurrences $P(S_i, S_j)$ using the frequencies of each
148 species and their co-occurrences. We were then able to
149 calculate the conditional probabilities of each species pair
150 as $P(S_i|S_j) = \frac{P(S_i, S_j)}{P(S_j)}$, based on the axioms of probability.
151 This yielded a matrix that could possibly be asymmetric, i.e.
152 $P(S_i|S_j)$ does not have to be equal to $P(S_j|S_i)$. Another
153 important property of this matrix is that the diagonal
154 (S_{ii}) was equal to one for all species present and zero for
155 species that were not observed in any cell.
156

157 We then applied an analytical procedure to remove
158 non-significant links between species. This procedure
159 determines if the joint probability of a species pair
160 (i.e. $P(S_i, S_j)$) is different from zero (Fig. 2). Here, a
161 confidence interval $CI_{95\%}$ is calculated as $CI_{95\%} = E[S_i S_j] * Z_{95\%} * \sqrt{V(S_i S_j)}$, where the expected frequency
162 of co-occurrences $E(S_i S_j)$ is the total number of cells surveyed (N)
163 times the independent probabilities of each species $P(S_i) * P(S_j)$, $Z_{95\%}$ is the Z-score for 95% from a Z-distribution and the expected variance
164 of $E(S_i S_j)$ is the total number of cells times the expected probability of $S_i S_j$ and its compliment (i.e.
165 $V(S_i S_j) = N * E[P(S_i, S_j)] * (1 - E[P(S_i, S_j)])$). If the
166 observed number of co-occurrence falls outside of the
167 confidence interval, the joint probability $P(S_i, S_j)$ is determined
168 to be equal to the product of the individual probabilities
169 (i.e. $P(S_i) * P(S_j)$), and the conditional probability reduces
170 to the individual probability of that species $P(S_i)$. Therefore,
171 unless the co-occurrence of a species pair falls outside the
172 confidence interval, the probability that the observation of one species given the other
173 is no different than simply observing that species alone.
174 This enables us to remove links from a given network by
175 re-scaling the resulting conditional probabilities by subtracting
176 the individual probabilities from the conditional probabilities
177 (i.e. how different the conditional probability is from the
178 independent probability), which makes any species with a non-significant conditional probability zero.
179 The resulting matrix ($\mathbf{D} = D_{ij}$) can be interpreted as
180 how one species impacts another with zero being no effect
181 and values less than or greater than zero interpreted as
182 negative and positive effects, respectively. Here, we will
183 refer to this matrix (\mathbf{D}) as an interaction matrix with
184 the properties that it can be asymmetric (i.e. P_{ij} does not
185 necessarily equal P_{ji}), and the diagonal (P_{ii}) is zero (i.e.
186 a species does not influence its own probability of being
187 observed).
188

189 **Statistical Analyses, Software and Data.** We used a combination of parametric and non-parametric, permutation
190 based frequentist statistical analyses to test for the effects
191 of genetic variation on lichen communities and their interaction
192 networks. To assess the effect of genotype on univariate
193 responses, we used additive, random effects models
194 with Restricted Maximum Likelihood (REML). We used
195 a combination of Least Squares Regression, Analysis of
196 Variance (ANOVA), and Generalized Linear Models (GLM).
197 We used the *lme4* package in R (R v3.6.1) to fit the
198 models. We used the *igraph* package in R (R v3.6.1) to
199 generate and analyze the interaction networks. We used
200 the *phyloseq* package in R (R v3.6.1) to process the
201 lichen data. We used the *ggplot2* package in R (R v3.6.1)
202 to generate the figures. We used the *gridExtra* package in R
203 (R v3.6.1) to combine the figures. We used the *knitr* package
204 in R (R v3.6.1) to generate the manuscript. We used the
205 *texreg* package in R (R v3.6.1) to generate the tables.
206



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 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. Naesbourg (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 cm^2 cells within a 10 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_iS_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. The project is also archived via Zenodo at zenodo.com/doiXXXXXX. All analyses were conducted using the programming language R version 3.6.1 (R Development Core Team 2019).

Results

1. Genotype influenced lichen network structure

- Tree genotype significantly predicted the similarity of lichen networks ($\text{Pseudo-}F_{9,27} = 3.58$, $H^2 = 0.41$, $p\text{-value} = 0.0537$).

- All network metrics examined responded significantly to tree genotype: including the number of links ($RLRT = ?$, $H^2 = 0.32$, $p\text{-value} = 0.0269$), AMI ($RLRT = ?$, $H^2 = 0.31$, $p\text{-value} = 0.0268$) and degree centralization ($RLRT = ?$, $H^2 = 0.33$, $p\text{-value} = 0.0196$).

- Fig 1. NMDS crosshair with vectors
- Supplementary Table. Vectors
- Supplementary Table. h2-net

2. Genotype impacts were on positive interactions mainly driven by Ch

- Tree genotype significantly predicted both in-degree ($RLRT = ?$, $H^2 = 0.35$, $p\text{-value} = 0.0196$).

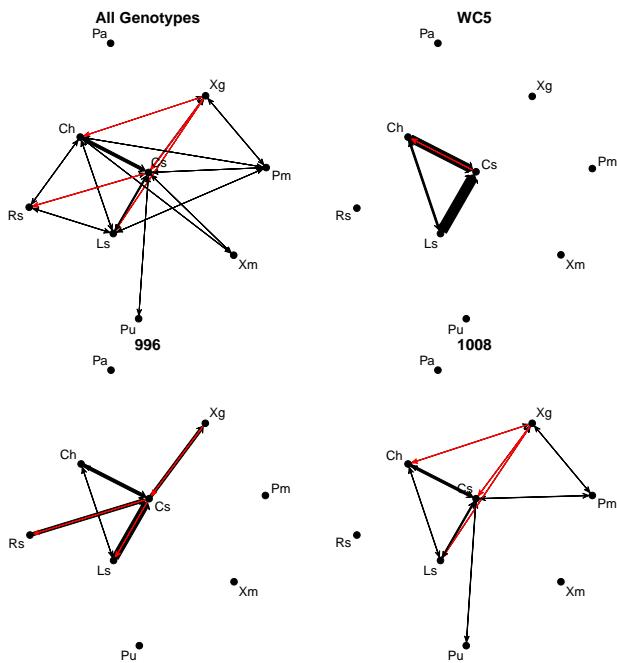


Fig. 3. Lichen networks varied in structure among tree genotypes. Network diagrams of the mean lichen interaction matrices averaged for all trees and for several individual genotypes showing a range of interaction network structure. Directionality (arrowheads) and sign (red = negative, black = positive) 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.

= 0.0157) and out-degree ($RLRT = ?, H^2 = 0.33, p\text{-value} = 0.0195$) centralization.

- *Caloplaca holocarpa* centrality was the only species to exhibit a significant response to tree genotype ($RLRT = ?, H^2 = ?, p\text{-value} = ?$).
- Fig 2. dot plot centralization in/out pos/neg
- REFER table: h2-net
- Supplementary Table: species centrality

3. Genotype indirectly influenced lichen network centralization via bark roughness

- BR Geno (REML), but not other traits ($RLRT = ?, H^2 = 0.32, p\text{-value} = 0.0128$)
- Net BR (PERMANOVA) ($F_{1,32} = 13.029, R^2 = 0.26, p\text{-value} = 0.0096$)
- Centrality was significantly correlated with bark roughness ($F_{1,32} = ?, R^2 = ?, p\text{-value} = ?$)

- However, tree genotype did not significantly predict the variation in the residuals from the regression of centrality and bark roughness ($RLRT = ?, H^2 = 0.011, p\text{-value} = 0.4219$)
- Fig. cross-hair plot Cen BR with trend line
- Table: h2-trait.tex
- Supplementary Table: cn-trait-perm.tex
- Supplementary Table: geno-trait-path.tex

4. Net(sim) Other lichen variation (LM) not genetically based (PERMANOVA)

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 2) 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 $r = 0.084, p\text{-value} = 0.556$).

response	statistic	H2	p-value
Lichen Network Similarity	3.5821	0.4130	0.0537
Average Mutual Information	3.5235	0.3101	0.0254
Degree Centralization	4.0444	0.3305	0.0184
In-degree Centralization	4.4812	0.3487	0.0142
In-Positive Centralization	3.9852	0.3309	0.0190
In-Negative Centralization	0.3304	0.1057	0.2508
Out-degree Centralization	3.8615	0.3193	0.0205
Out-Positive Centralization	3.5585	0.3119	0.0248
Out-Negative Centralization	0.0862	0.0513	0.3446
Number of Network Links	3.5175	0.3156	0.0255

Table 1. Genotypic effects on the associated lichen network structure.

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 6). Bark C:N ratio was also a significant predictor of network similarity, but, as shown previously (see Table 1), there is not sufficient evidence support a genetic basis for it. Bark pH was not a significant

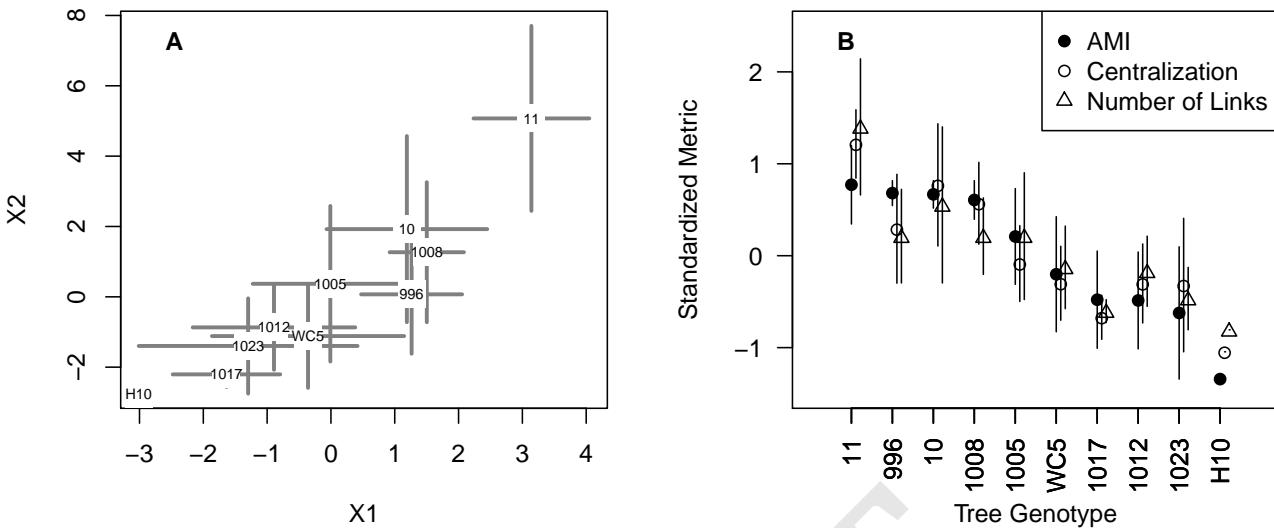


Fig. 4. Tree genotype affected lichen networks and several bark traits. A. The plot shows genotype centroids of NMDS ordinated ($R^2 = 0.999$, stress = 0.008) lichen networks (± 1 S.E.). Centroids that are closer are more similar in the structure of their lichen networks. B. Plot showing the standardized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

361 predictor of lichen network similarity (Table 6). The
 362 abundance, richness, evenness and diversity of the
 363 bark lichen community, although also not predicted
 364 by tree genotype, were all significantly correlated
 365 with lichen network structure (Table 6). Lichen com-
 366 munity composition was not correlated with lichen
 367 network similarity, either when species abundances
 368 were relativized (Mantel R = -0.09, p-value = 0.139)
 369 or not (Mantel R = -0.03, p-value = 0.573).

	df	SS	R2	F	p-value
geno	9.0000	44078.1327	0.5442	3.5821	0.0537
Residual	27.0000	36915.4605	0.4558		
Total	36.0000	80993.5932	1.0000		

**Table 2. PERMANOVA Pseudo-F Table of lichen net-
work similarity to genotype.**

370 Discussion

- 371 • We found:
 - 372 – Lichen networks genetically based
 - 373 – Bark roughness was the primary genetically
374 based trait driving network structure
 - 375 – Lichn networks also varied with cover, rich-
376 ness and diversity of the lichen commu-
377 nity, which were not correlated with rough-

378 ness and primarily driven by one dominant
379 species

- What mechanisms could be at play?
- Habitat filtering of communities (richness, com-
381 position) vs environmental influence on inter-
382 actions. Likely a combination of both of these
383 factors.
 - Lichen network structure correlated with
385 species richness, evenness and diversity
 - Lichen community composition not corre-
387 lated with network structure
 - None of these were genetically based
- An important consequence for diversity is that
390 genotypes could be supporting unique communi-
391 ties, even if the composition of the communities
392 is the same among individuals and genotypes.
- Genetic diversity could be influencing the stabil-
394 ity of communities through the effects on inter-
395 actions. Some network structures are likely to
396 be more stable, either in response to disturbance
397 or via self-organized dynamics. Although, none
398 of the metrics examined, such as the number of
399 links, modularity or centrality, showed a genetic
400 signature.

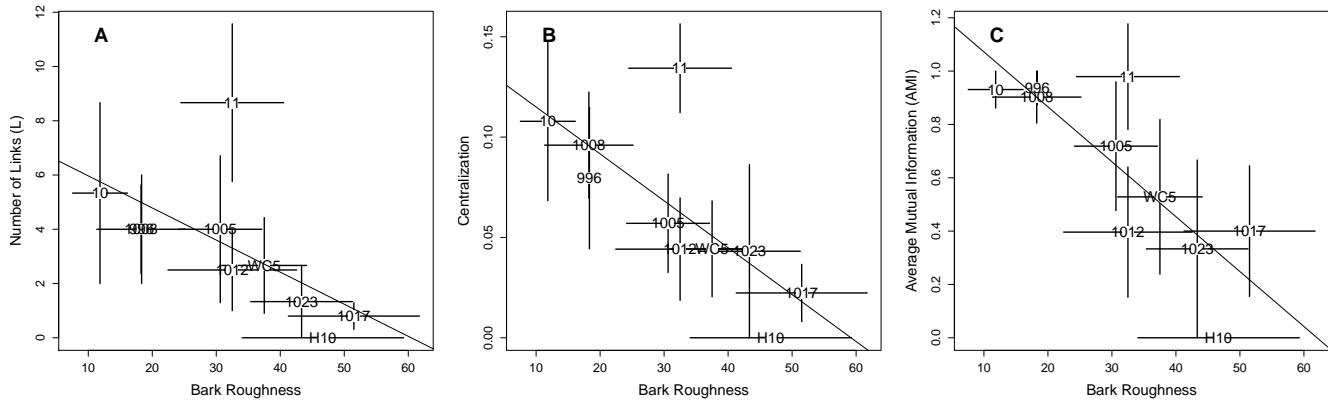


Fig. 5. Bivariate plots of the relationship between bark roughness and three network metrics: A) number of links (L), B) centralization and C) average mutual information (AMI). Each plot displays the genotype mean \pm 1 S.E. for both variables and a least-squares regression calculated using the genotype means.

- 402 • Important factors to consider in studies of other
403 ecological networks:
 - 404 – Relative body size
 - 405 – Mobility
 - 406 – Reproductive isolation
- 407 • Future work should consider the potential influence
408 on evolutionary dynamics of communities
 - 409 – Network structure influences network stability
 - 410 – Are the communities nested subsets?

412 **TGW: I think window is too vague and this**
413 **topic sentence needs to be much stronger for**
414 **a journal like PNAS. Might be stronger by**
415 **saying "Our findings argue there is a genetic**
416 **component to network structure, which im-**
417 **pplies that network structure could be subject**
418 **to selection and networks can evolve."**

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

- 424 • Genetic assembly rule = similar genetics will
425 have more similar communities
- 426 • What we don't know is whether or not these
427 interactions will also lead to similar interactions
428 among other species.

- 429 • Thus, it would be possible for genetics to not
430 only influence other species directly, but also
431 indirectly by influencing the interactions among
432 other species.

433 We observed significant lichen interaction struc-
434 ture that varied among genotypes of a foundation
435 tree species, narrowleaf cottonwood (*P. angustifo-*
436 *lia*). We found that a genetically based trait, bark
437 roughness, partially explained the variation in lichen
438 networks. Some of this variation in lichen
439 networks was related to both the overall abundance
440 and species richness of lichen; though, statistically
441 controlling for the effect of genotype on these vari-
442 ables indicates that a significant portion of the vari-
443 ance in lichen species richness is due to a factor
444 other than tree genotype. By using network metrics,
445 we were also able to probe for specific characteris-
446 tics of how these networks were responding to tree
447 genotype. We found that both number of links and
448 the centralization of the networks were highly corre-
449 lated with network similarity and that tree genotype
450 significantly predicted network centrality but only
451 marginally predicted the number of network links.
452 This latter result could be due to the relationship
453 between species richness and the number of links
454 in the network, which were significantly correlated
455 with each other. We also found that bark roughness
456 did not significantly predict either the number of
457 links or the centrality of lichen networks, suggesting
458 that bark roughness has some other effect on the
459 structure of the lichen networks. Taken together,
460 these findings support the hypothesis that genotypic
461 variation in a foundation species contributes to the

462 structure of a network of interacting species.
463 **LJL: I wonder if you need to have so much**
464 **on richness here. Overall, I think you want to**
465 **focus on the network responses and patterns**
466 **among genotype first, and then go into mech-**
467 **anism later. I think we don't quite have a**
468 **good mechanism yet so I don't think it needs**
469 **to come up in the first paragraph of the dis-**
470 **cussion.**

471 These findings point to the importance of under-
472 standing the community level effects of genetic varia-
473 tion in plant functional traits and highlights the
474 potential for indirect effects of genetic variation to
475 propagate through networks of interacting species
476 and trophic levels.

477 This work corroborates previous findings of the
478 importance of plant genetics in shaping community
479 structure and ecosystem processes. citepBangert2008

480 Altering the structure of interaction networks
481 presents a means for genetic effects to be magni-
482 fied within the system of interacting species. For
483 example, (8) showed that the genetics based interac-
484 tions of aphid resistant and aphid susceptible trees
485 resulted in different interaction networks of their
486 associated arthropod communities composed of 139
487 species. At the scale of ecosystems, trophic net-
488 works or food webs direct and control the rates of
489 energy and nutrient flux (16). Furthermore, in a
490 predator-prey-plant study, Smith (17), showed that
491 the interactions among species across trophic levels
492 depended on plant genotype.

493 Also, work by (18–20) observed consistent pat-
494 terns of centralized interactions of species modules
495 focused around hubs of plant-fungal interactions. In
496 other words, a small number of plant and fungal
497 symbionts tended to have disproportionate numbers
498 of interactions with other species and likely are the
499 drivers in determining community assembly, struc-
500 ture and dynamics.

501 More on the importance of ecological networks
502 (21, 22).

503 From Thompson2014

- 504
- 505 • Pairwise interactions are usually influenced by
other species
 - 506 • Selection favors the development of small webs
 - 507 • Evolution of new lifestyles leads to changes in
selection on large and small webs

508 Specific hypothesis from Thompson2014 509

510 **LJL: If I recall, the Elamo paper just looks**
511 **at genetic correlations between pairwise indi-**
512 **vidual abundances. I would suggest maybe it**
513 **doesn't deserve to be in this 1st paragraph.**
514 **Perhaps it actually should be in the 2nd or**
515 **3rd paragraph, just as a reference that points**
516 **to the potential for genotype to influence net-**
517 **works. Definately our 2015 JOE paper goes**
518 **much further, too, since it has whole com-**
519 **munities being correlationed. But, again, I**
520 **would put both of these as citation in the com-**
521 **munity genetics paragraphs (2 of 3) instead**
522 **of the first paragrpah, which focuses on the**
523 **general network lit.**

524 **LJL: It could be useful to point out that**
525 **our findings are not related to trophic inter-**
526 **actions, which is pretty cool. Also,we talk**
527 **about interaction networks but it is not clear**
528 **to me if the interactions tend to be positive**
529 **or negative. Can we get at that with the ap-**
530 **proach used?**

531 **TGW: Is there any adaptive component to**
532 **the tree in having certain lichen communi-**
533 **ties? e.g., can they feed back to affect tree**
534 **performance in some way or is this a pas-**
535 **sive outcome of a trait that affects bark for**
536 **other adaptive reasons and lichens are pas-**
537 **sive players that tag along for the ride? I**
538 **could envision that lichens covering the bark**
539 **of a tree act as a barrier between insects and**
540 **pathogens, much like ectomycorrhizae cover**
541 **fine roots as a first line of defense by invad-**
542 **ing microorganisms. Uptake of N that gets**
543 **passed to the tree??**

544 **LJL: I agree that there is a general overar-**
545 **ching theme that evolution occurs in a com-**
546 **munity network context, but I'm not sure**
547 **that we should state that as our main hypoth-**
548 **esis. It seems more that this is a fundamen-**
549 **tal foundation for our work. The hypoth-**
550 **esis is more what we are testing directly, but**
551 **we don't test this directly. I guess I don't**
552 **want to give the impression that our com-**
553 **munities are necessarily the result of each**
554 **species evolving into its place in the commu-**
555 **nity on these tree genotypes (although I do**
556 **understand this as Shuster et al 2006's funda-**
557 **mental explanation for why we see different**

558 communities on different genotypes; I don't
559 necessarily agree that this is the only rea-
560 son we would see different communities on
561 dif genotypes). Most of these are pretty gen-
562 eralist lichens, which could be found on other
563 deciduous trees in the surrounding city or nat-
564 ural areas. I would look at it more like an
565 assembling of lichen species into unique con-
566 figurations on genetically different substrates.
567 There may be some selection for different
568 genotype of lichen during the community as-
569 sembly process but we can't really tell that
570 just by differences in species abundances or
571 cocurneces. I guess to me the evolutionary
572 context that is more direclty related to this
573 work is that the tree genotype is a central
574 controller (indeed a sort of hub species in the
575 network) of network structure. By anchor-
576 ing the lichen network to tree genotype (and
577 variation among networks to variation among
578 tree genotypes), our study highlights the pos-
579 sibility that natural selection acting on the
580 trees may have an extended consequence for
581 the network structure of organisms living on
582 the trees...the extra thing we add to the field
583 is that we show interaction networks are sen-
584 sitive to genotype. I doubt the lichens have
585 a direct effect on tree fitness, but favorabil-
586 ity of some tree genotypes over others during
587 natural selection will then go on to favor and
588 disfavor certain lichen communities of differ-
589 ent network structures. By being sensitive
590 to tree genotype, the lichen community net-
591 works are passive riders on the waves of evolu-
592 tionary dynamics that occur within the tree
593 species they inhabit.

594 **MKL:** In response to Lamit's comment
595 above, I agree that it is not required that
596 there is co-evolution. Another, perhaps sim-
597 pler, explanation is that there is variation in
598 environmental filtering of lichen individuals
599 created in part by genetic variation in tree
600 individuals.

601 **TGW:** might be good to cite papers on
602 competition in lichens or other organizing fac-
603 tors to back up the least expected statement.
604 as epiphytes we might not expect them to
605 care.

606 **TGW:** I think we need to emphasize the

long-term nature of our common garden
607 study as very few common garden studies of
608 lichens likely exist. Any refs on this? If true
609 might want to mention this up front in intro.
610

611 **MKL:** Environmental filtering is evidenced
612 by species richness, but also possibly species
613 interaction varying based on environment as
614 networks varied in terms of sign and magni-
615 tude as well.

616 **MKL:** The effect of bark roughness on
617 network similarity was primarily genetically
618 based, and there are likely other factors at
619 play.

620 **Discussion of network implications for sta-**
621 **bility with genetics.**

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

625 Although our study was conducted with a commu-
626 nity of lichens, these results should be generalized
627 to other groups of diverse organisms around the
628 world that also exhibit significant genetic signals at
629 the community level (24, 25). In the face of the
630 high degree of complexity and potential context de-
631 pendence of ecological processes, the current study
632 points to the utility of considering the spatial and
633 temporal scales of interactions, as discussed to some
634 in previous studies (26–28). In the present study,
635 we found that community assembly processes, such
636 as environmental filtering and species interactions,
637 are genetically based. This is likely due, in part,
638 to the large difference in the differences in size and
639 longevity of the lichen and cottonwood individuals
640 with the trees determining the environment in which
641 the lichen occur. We suggest that future work would
642 be aided by determining these modules within the
643 biotic community that include species with similar
644 differences in body-size and time-scales. As heritable
645 variation is the raw material for natural selection
646 to act upon, a genetic basis for interaction network
647 structure indicates evolutionary dynamics should be
648 considered at the community level and that con-
649 serving genetic variation is important to consider in
650 efforts to restore or preserve complex species inter-
651 actions and their associated ecosystem functions (29).
652 With such findings, it appears that we are closer to
653 understanding the evolutionary drivers of Darwin's
654 entangled bank and the interconnectedness of species
655 in complex communities.

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Assessment and Results

- 723 • Network similarity not genetically based 724
- 724 • Genetically based number of links and centrality but 725
 725 not modularity 726
- 726 • Lichen cover, richness, evenness, diversity and com- 727
 727 position not genetically based 728
- 727 • Roughness genetically based but not bark condensed 729
 729 tannins, CN or pH 730
- 730 • Bark roughness correlation with number of links 731
 731 (yes) and centrality (yes)? <- TODO add figure A 732
 732 = mdc.plot(L, Cen), B = (ch.plot(L,Cen,geno), BR
 733 vector)) 734
- 734 • Centrality values for species <- censpp.pdf 735
- 735 • Redo haritability calculations 736
- 736 • Jamie double check genotype network permanova in 737
 737 PRIMER 738
- 738 • Jamie double check reml's in R 739

Tables.

740

response	statistic	H2	p-value
Lichen Network Similarity	3.5821	0.4130	0.0537
Average Mutual Information	3.5235	0.3101	0.0254
Degree Centralization	4.0444	0.3305	0.0184
In-degree Centralization	4.4812	0.3487	0.0142
Out-degree Centralization	3.8615	0.3193	0.0205
In-Positive Centralization	3.9852	0.3309	0.0190
In-Negative Centralization	0.3304	0.1057	0.2508
Out-Positive Centralization	3.5585	0.3119	0.0248
Out-Negative Centralization	0.0862	0.0513	0.3446
Number of Network Links	3.5175	0.3156	0.0255
Percent Lichen Cover	0.0000	0.0000	1.0000
Lichen Species Diversity	0.0000	0.0000	0.4543
Lichen Species Richness	0.0000	0.0000	0.4543
Lichen Species Evenness	0.0000	0.0000	1.0000
Percent Rough Bark	4.8526	0.3221	0.0113
pH	0.0000	0.0000	1.0000
Carbon-Nitrogen (CN) Ratio	0.0000	0.0000	1.0000
Condensed Tannins (CT)	0.0007	0.0041	0.4439
BR-L Residuals	0.0000	0.0000	1.0000
BR-Cen Residuals	0.0000	0.0000	1.0000
BR-AMI Residuals	0.0000	0.0000	1.0000

Table 1. Genotypic effects on tree traits and bark lichen.

response	statistic	H2	p-value
Lichen Network Similarity	3.5821	0.4130	0.0537
Average Mutual Information	3.5235	0.3101	0.0254
Degree Centralization	4.0444	0.3305	0.0184
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Out-Positive Centralization	3.5585	0.3119	0.0248
Out-Negative Centralization	0.0862	0.0513	0.3446
Number of Network Links	3.5175	0.3156	0.0255

Table 2. Genotypic effects on the associated lichen network structure.

	r	p-value
Bark Roughness	0.451	0.030
Number of Links	0.974	0.010
Centralization	0.961	0.010
AMI	0.903	0.010

Table 3. Correlation tests for vectors displayed in NMDS ordination of network similarity.

response	statistic	H2	p-value
Percent Rough Bark	4.8526	0.3221	0.0113
pH	0.0000	0.0000	1.0000
Carbon-Nitrogen (CN) Ratio	0.0000	0.0000	1.0000
Condensed Tannins (CT)	0.0007	0.0041	0.4439
BR-L Residuals	0.0000	0.0000	1.0000
BR-Cen Residuals	0.0000	0.0000	1.0000
BR-AMI Residuals	0.0000	0.0000	1.0000

Table 4. Genotypic effects on tree traits and residuals from trait regressions of lichen network structure.

Figures.

741

	r	R2	estimate	SE	t	p-value
br_L	-0.34	0.11	-0.07	0.03	-2.13	0.04
br_Cen	-0.39	0.15	-0.00	0.00	-2.52	0.02
br_AMI	-0.36	0.13	-0.01	0.00	-2.27	0.03
ct_L	0.34	0.11	0.57	0.27	2.13	0.04
ct_Cen	0.08	0.01	0.00	0.00	0.46	0.65
ct_AMI	0.02	0.00	0.00	0.03	0.12	0.91
ph_L	0.08	0.01	0.67	1.41	0.48	0.64
ph_Cen	0.13	0.02	0.02	0.02	0.78	0.44
ph_AMI	-0.04	0.00	-0.04	0.17	-0.21	0.83
cn_L	0.06	0.00	50.19	145.84	0.34	0.73
cn_Cen	0.16	0.03	2.14	2.18	0.98	0.33
cn_AMI	0.13	0.02	12.84	17.10	0.75	0.46

Table 5. Tests of the correlation between tree bark traits and lichen network structure

	df	SS	R2	F	p-value
geno	9.0000	44078.1327	0.5442	3.5821	0.0537
Residual	27.0000	36915.4605	0.4558		
Total	36.0000	80993.5932	1.0000		

Table 6. PERMANOVA Pseudo-F Table of lichen network similarity to genotype.

lichen species	mean	statistic	H2	p-value
Positive				
In-Degree				
X. galericulata	0.2703	0	0	1
C. subdeflexa	0.8919	2.1926	0.2158	0.0595
L. spp.	0.4324	0	0	1
C. holocarpa	0.5946	3.6146	0.3241	0.024
X. montana	0.0541	0	0	0.4543
P. melanachra	0.1351	0	0	1
P. adscendens	0			
P. undulata	0.027	0	0	0.4543
R. sp.	0.1351	2.049	0.2613	0.0656
Out-Degree				
X. galericulata	0.027	0	0	0.4543
C. subdeflexa	0.6757	0	0	1
L. spp.	0.5946	0.0061	0.0126	0.4246
C. holocarpa	0.7027	3.1318	0.2981	0.0327
X. montana	0.0811	2.9228	0.3163	0.0375
P. melanachra	0.1351	0	0	1
P. adscendens	0			
P. undulata	0.027	0	0	0.4543
R. sp.	0.2973	0.1505	0.0612	0.3119
Negative				
In-Degree				
X. galericulata	0			
C. subdeflexa	0.1892	0	0	0.4543
L. spp.	0.1892	0.0015	0.0057	0.4398
C. holocarpa	0.1351	0	0	1
X. montana	0.027	0.0377	0.0394	0.3807
P. melanachra	0			
P. adscendens	0			
P. undulata	0			
R. sp.	0.1622	0	0	1
Out-Degree				
X. galericulata	0.2432	0	0	1
C. subdeflexa	0.4054	0	0	0.4543
L. spp.	0.027	0	0	0.4543
C. holocarpa	0.027	0	0	0.4543
X. montana	0			
P. melanachra	0			
P. adscendens	0			
P. undulata	0			
R. sp.	0			

Table 8. REML tests of the effect of tree genotype on lichen species centrality.

	Df	SumOfSqs	R2	F	Pr(>F)
BR	1.0000	21021.8765	0.2595	13.0299	0.0096
CT	1.0000	2349.3142	0.0290	1.4562	0.2016
pH	1.0000	2098.8999	0.0259	1.3010	0.2899
CN	1.0000	3896.1757	0.0481	2.4150	0.1890
Residual	32.0000	51627.3270	0.6374		
Total	36.0000	80993.5932	1.0000		

Table 7. PERMANOVA Pseudo-F Table of lichen network similarity response to bark traits.

	BR	CT	pH	CN	PC	SR	SE	SD	L	Cen	AMI
BR									-0.34	-0.39	-0.36
CT						-0.34					
pH											
CN											
PC								0.49			-0.46
SR									0.76	0.47	
SE									0.85	0.45	
SD									0.59	0.33	
L									0.88	0.38	
Cen											0.57
AMI											

Table 9. Matrix of correlations among tree traits, lichen community metrics and network metrics

	Df	SumOfSqs	R2	F	Pr(>F)
geno	9.0000	1.5049	0.2001	0.7507	0.8878
Residual	27.0000	6.0143	0.7999		
Total	36.0000	7.5193	1.0000		

Table 10. Pseudo-F Table of lichen community similarity PERMANOVA.

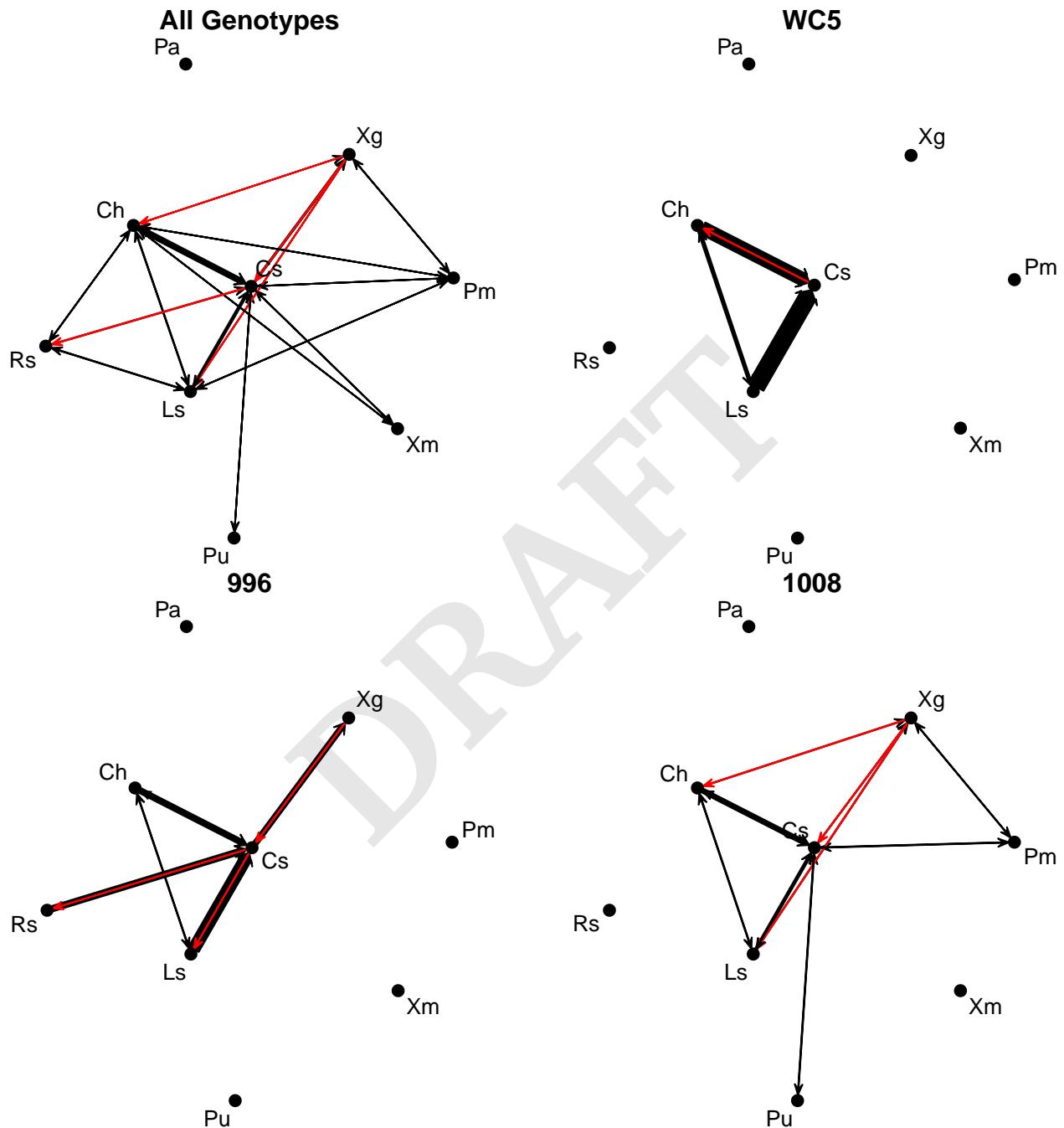


Fig. 1

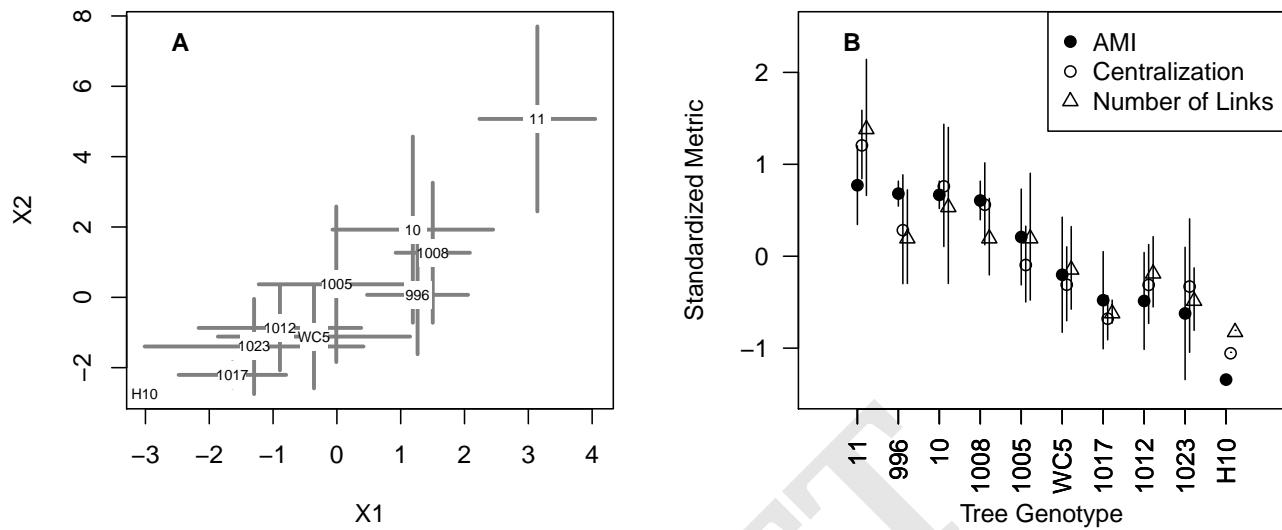


Fig. 2

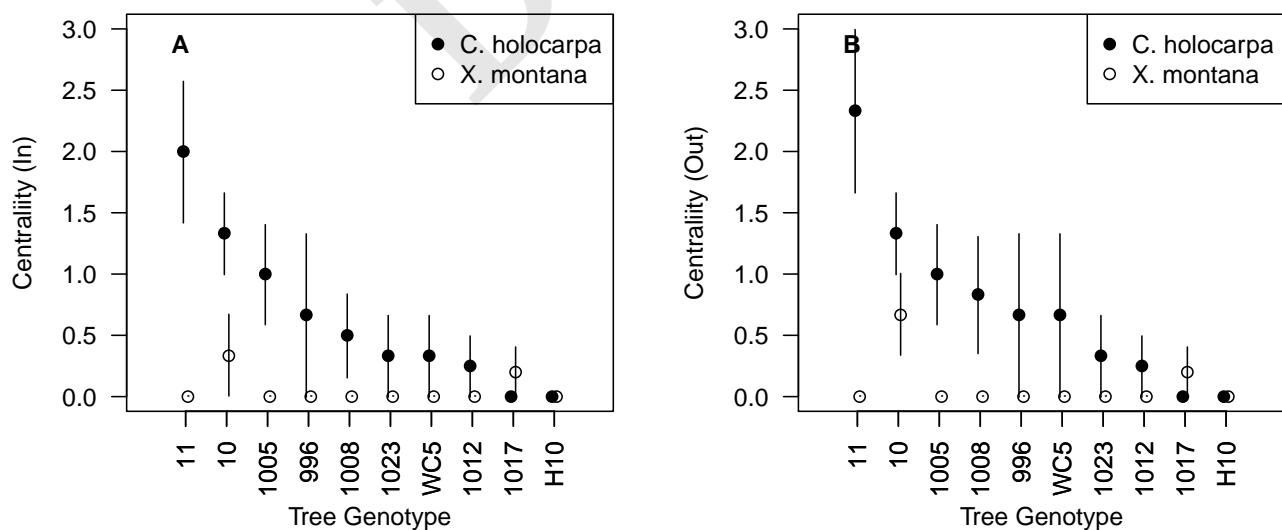


Fig. 3

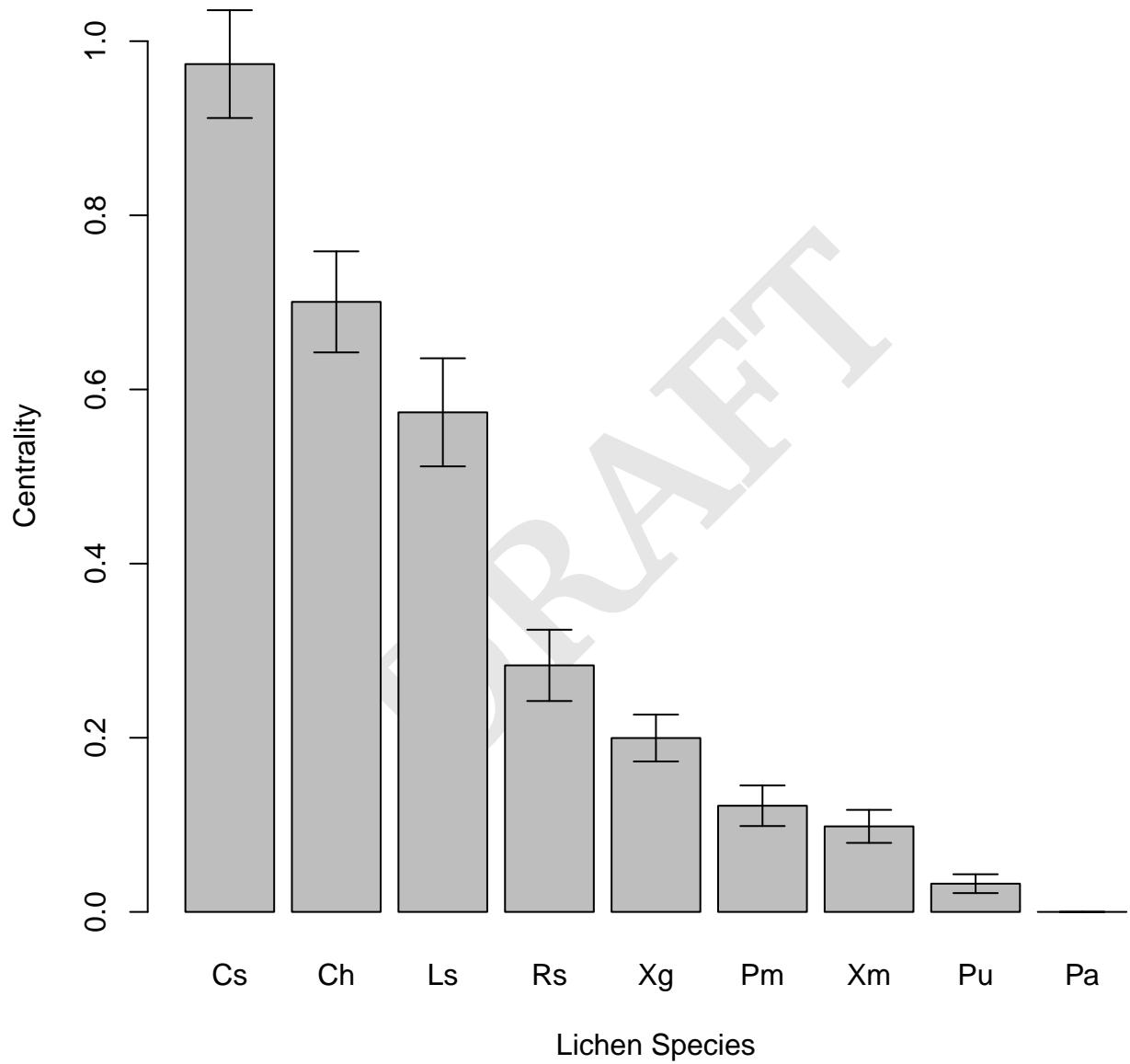


Fig. 4

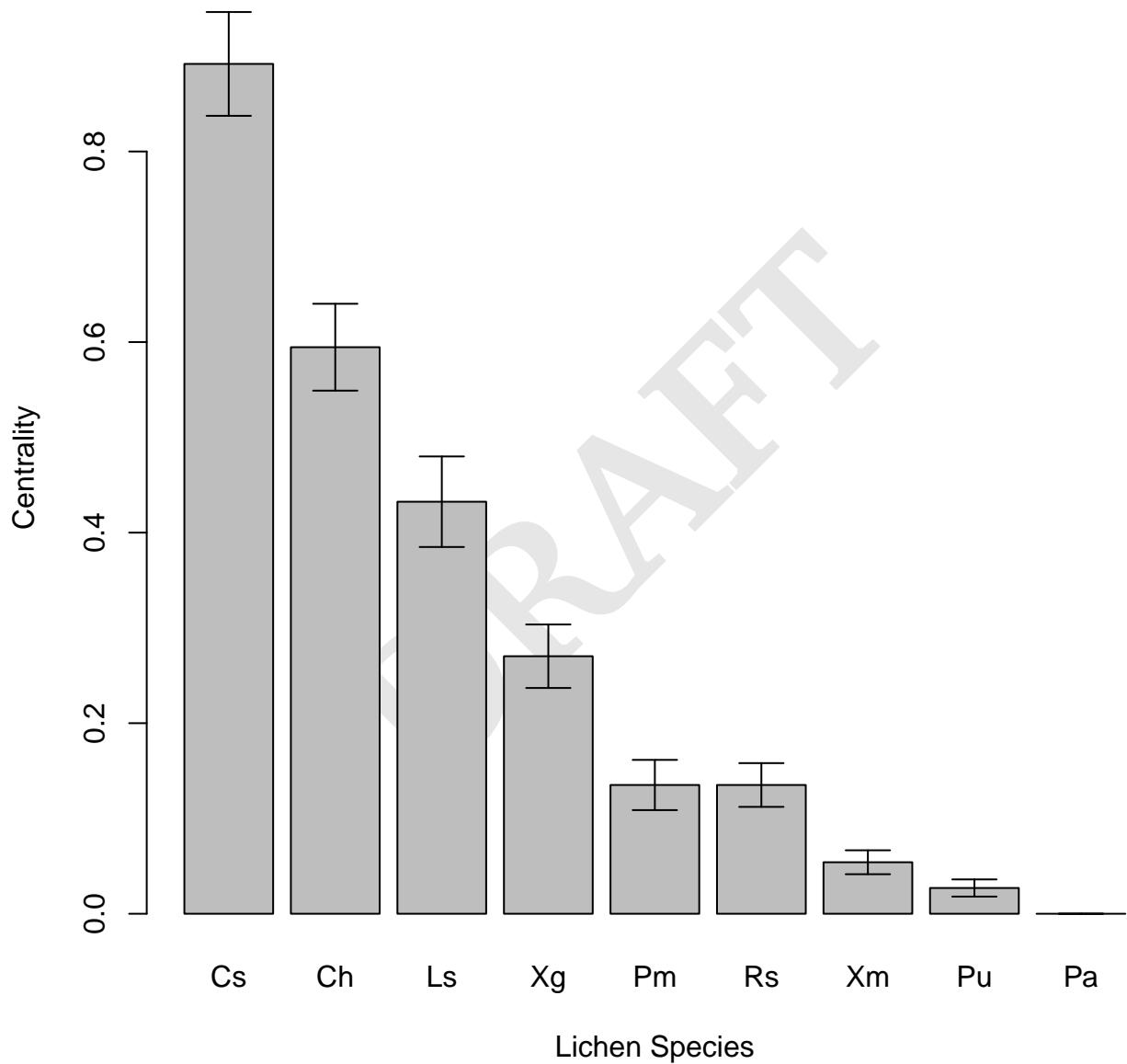


Fig. 5

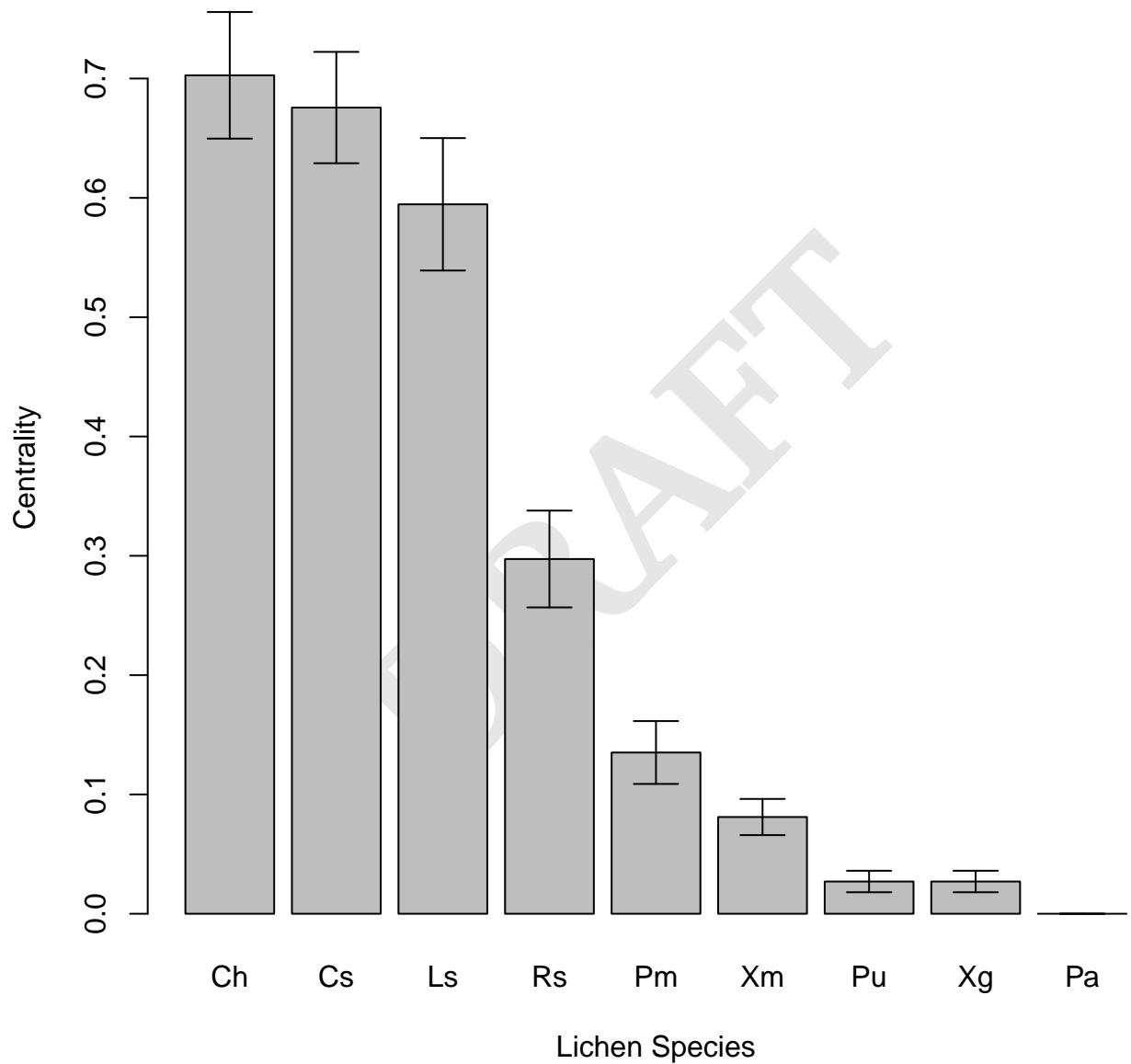


Fig. 6

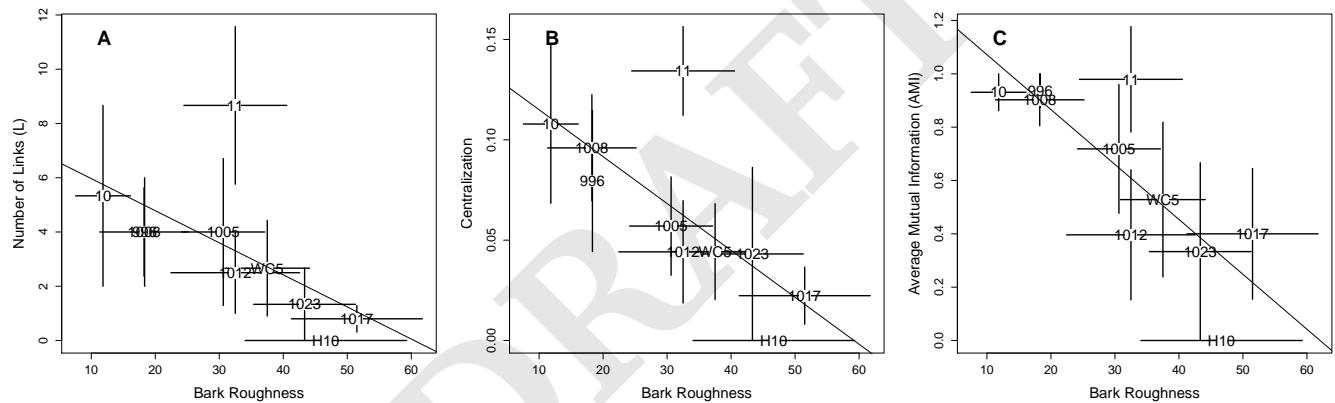


Fig. 7

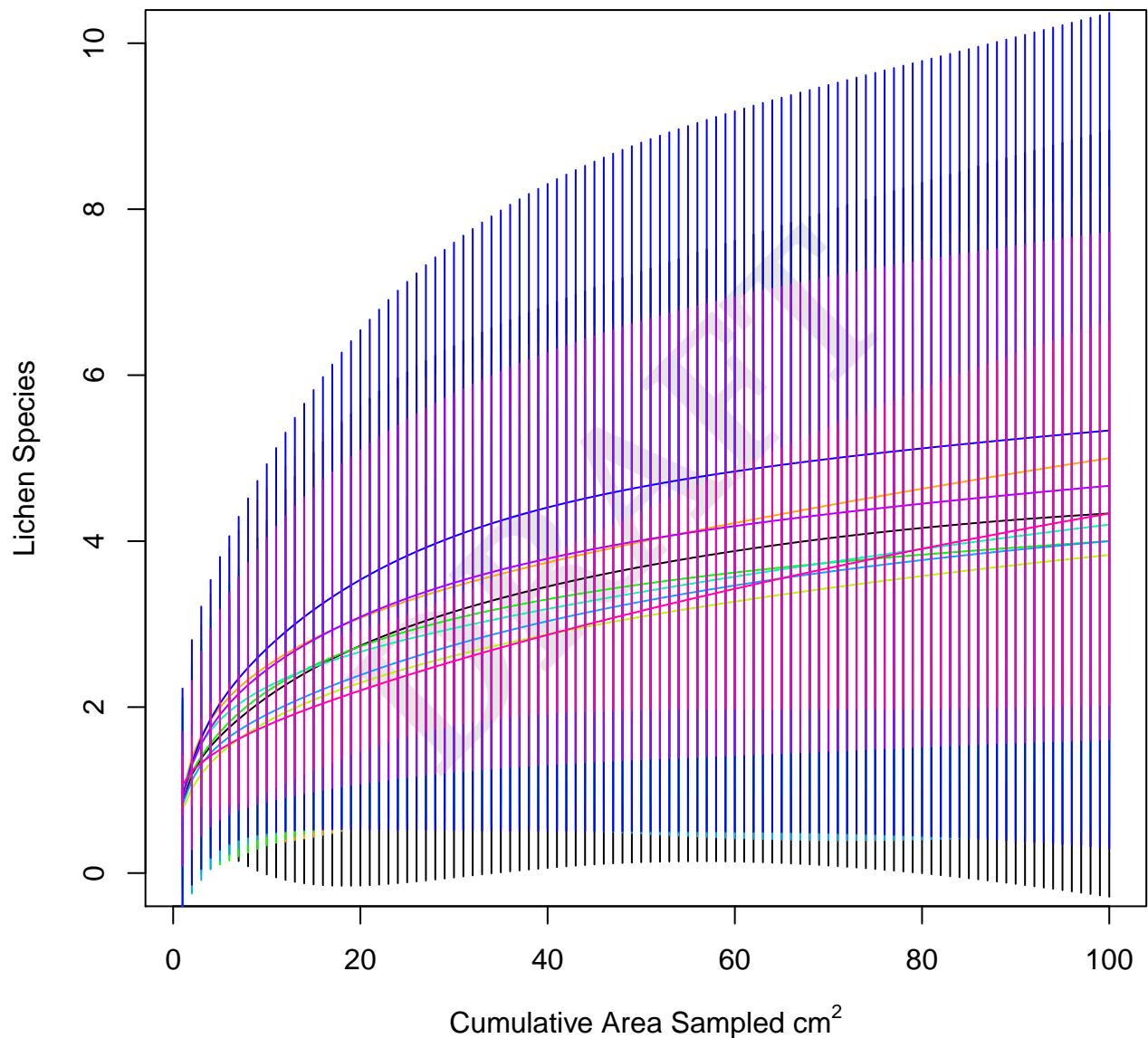


Fig. 8. Species-area curve by genotype.

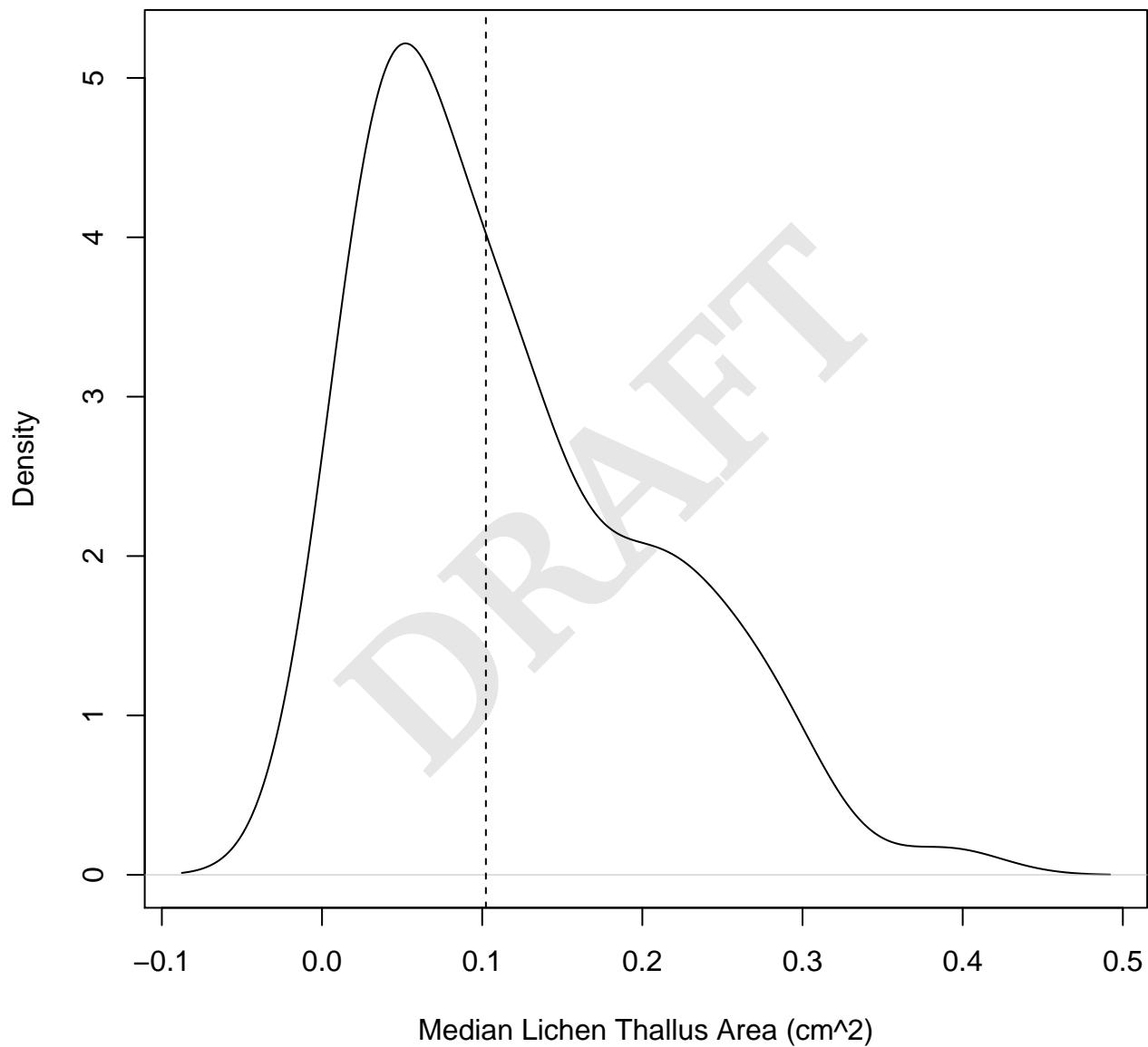


Fig. 9