

Foundation species genetics impacts lichen community networks

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1 Summary

- Interactions among species are important determinants of biodiversity through both ecological and evolutionary processes.
- Bark lichen communities offer a unique study system for exploring the genetic underpinnings of inter-specific interactions due to the spatial and temporal scales at which they operate.
- Here we examine the potential for interactions among lichen species to be influenced by the genetics of a foundation species (*Populus angustifolia*).
- Three main findings emerged:
 1. Co-occurrence analysis indicate that species relationships were primarily aggregative, indicative of facilitative relationships
 2. Community network structure differed between sampling heights (45-55cm and 80-90cm) with the higher sampling height having fewer connections among species
 3. Community network structure varied significantly among genotypes; however this depended on the location that the communities were sampled on the tree
- These results suggest that community assembly and/or interactions among lichen species can be influenced by the genetics of a foundation species; however these effects are dependent upon variation within individuals.

2 Methods and Results

2.1 Sampling

- Data were collected from a common garden of replicated *P. angustifolia* clones at the Ogden Nature Center (Ogden, UT) in May 2010 and 2011.
- The presence of lichen species was assessed within 50 1cm² cells in a 10cm² grid arrayed in a checkerboard pattern, chosen in accordance with the average thallus size of the largest lichen (data?) to avoid overlapping lichen thalli between cells.
- The γ diversity of the study was 9 species. These lichen species were crustose and foliose with the dominant lichen species being the foliose (*Xanthomendoza galericulata*).
- Quadrats were surveyed on the north side of each replicate tree at two heights: 45-55cm and 80-90cm.
- Modeling and analyses were conducted in R.

2.2 Co-Occurrence Analysis

- Co-occurrence analysis was conducted to test for significant patterns of either segregative (e.g., competitive) or aggregative (e.g., facilitative) relationships among species.
- Each quadrat on a tree (45-55cm and 80-90cm) was analyzed separately for co-occurrence patterns.
- Stone and Roberts (1990) c-score was used because of its performance in null-model based co-occurrence analysis and interpretability of community-wide patterns of co-occurrence.
- To test for significance we used a sequential swap randomization algorithm that maintained species totals but allowed observation totals to vary.
- A total of 10,000 randomizations with a 500 iteration burn-in were used to calculate a standardized effect size (i.e., $(c\text{-score}_{\text{observed}} - \mu_{\text{simulated}}) \div sd_{\text{simulated}}$) and a P-value for each quadrat.
- SES did not vary significantly among genotypes, but there was an overall trend of negative SES values indicating aggregation (i.e., species tended to occur together more often than expected under the null-model) (Fig. 1).

2.3 Community Network Modeling

- Community networks were modeled for each quadrat by testing for significant, non-linear correlations among species using Kendall's Tau.
- Network structure, measured by the number of connections in the network (size) and the distribution of connections among species (centralization; 0 = all species have equal numbers of connections to 1 = one species is connected to all other species), was analyzed by testing for the effect of genotype and quadrat position (i.e., 45-55cm and 80-90cm) nested within tree individuals (see Table 1).
- The lower (45-55cm) quadrat had more connections on average than the upper quadrat (80-90cm) (Fig. 2).
- Both the size and centralization of the community networks varied significantly among among genotype; however this depended on the position of the quadrat on the tree (Fig 3; also see code for analyses).

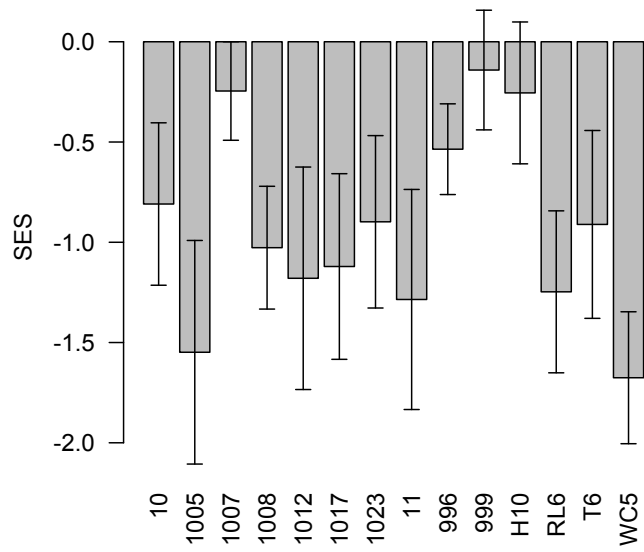
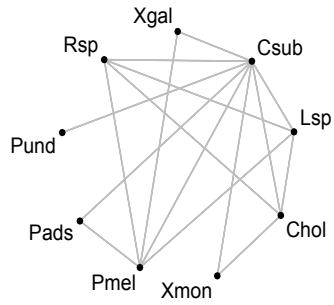
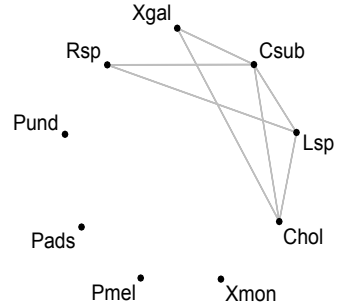


Figure 1: The mean standardized effect size (SES) \pm 1 S.E. for each genotype.



45-55cm



80-90cm

Figure 2: Network graphs for the lower (45-55cm) and upper (80-90cm) quadrats. Connections in the graphs are the average across all network models for quadrats at their respective heights.

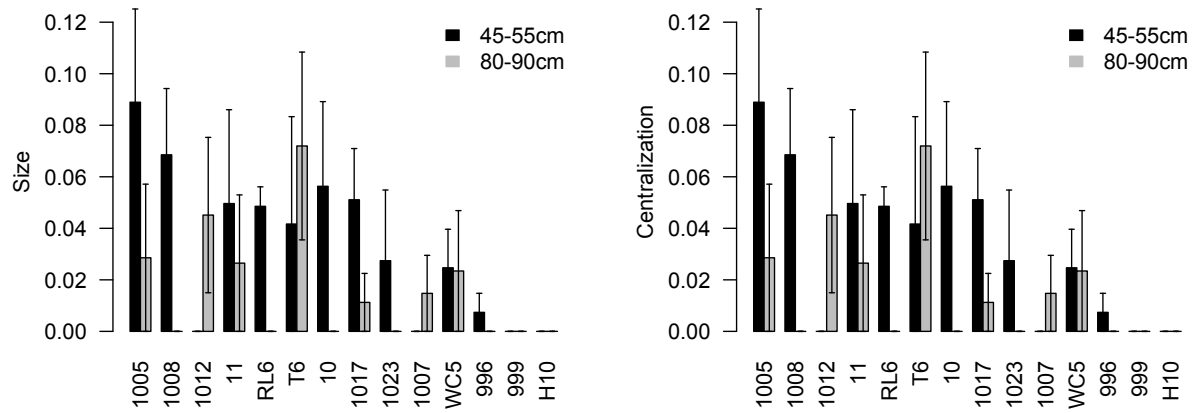


Figure 3: The mean size and centralization scores ± 1 S.E. for each genotype by quadrat position.

Screen Only Analyses

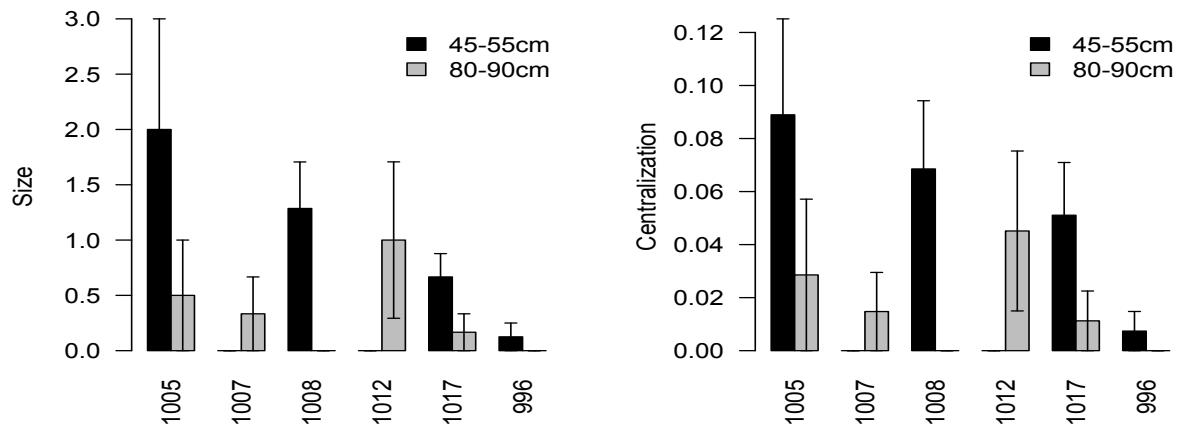


Figure 4: The mean size and centralization scores ± 1 S.E. for each genotype by quadrat position for the genotypes from the Screen site only.

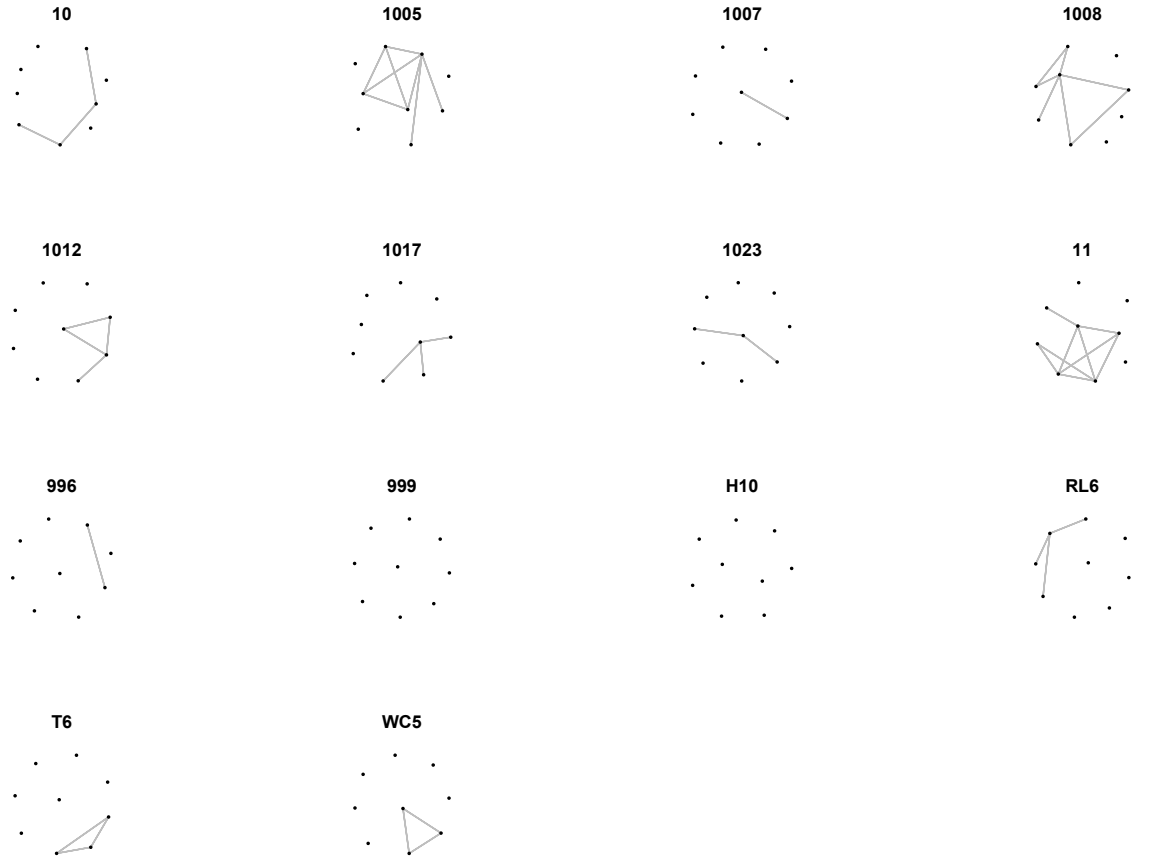


Figure 5: Network graphs for each genotype where the connections are averages of replicate networks for each genotype.


```
> summary(aov(sqrt.netc~geno.net*quad.net+Error(tree.net/(quad.net))))
```

```
Error: tree.net
```

	Df	Sum Sq	Mean Sq	F value	Pr(>F)
geno.net	13	0.33475	0.025750	2.0624	0.03559 *
Residuals	47	0.58681	0.012485		

```
---
```

```
Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

```
Error: tree.net:quad.net
```

	Df	Sum Sq	Mean Sq	F value	Pr(>F)
quad.net	1	0.15557	0.155567	9.4199	0.003559 **
geno.net:quad.net	13	0.36137	0.027797	1.6832	0.096450 .
Residuals	47	0.77619	0.016515		

```
---
```

```
Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

```
> summary(aov(sqrt.netd~geno.net*quad.net+Error(tree.net/(quad.net))))
```

```
Error: tree.net
```

	Df	Sum Sq	Mean Sq	F value	Pr(>F)
geno.net	13	6.4509	0.49622	1.7952	0.07218 .
Residuals	47	12.9918	0.27642		

```
---
```

```
Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

```
Error: tree.net:quad.net
```

	Df	Sum Sq	Mean Sq	F value	Pr(>F)
quad.net	1	2.6064	2.60638	8.5173	0.005383 **
geno.net:quad.net	13	7.6168	0.58591	1.9147	0.052721 .
Residuals	47	14.3825	0.30601		

```
---
```

```
Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

```
> exactRLRT(lmer(sqrt.netd~(1|geno.net)+(quad.net.:tree.net)))
```

```
simulated finite sample distribution of RLRT. (p-value based on 10000
simulated values)
```

```
data:
```

```
RLRT = 3.1349, p-value = 0.0332
```

```
> exactRLRT(lmer(sqrt.netc~(1|geno.net)+(quad.net.:tree.net)))
```

```
simulated finite sample distribution of RLRT. (p-value based on 10000
simulated values)
```

```
data:
```

```
RLRT = 2.2151, p-value = 0.0550
```

```

> summary(aov(s.scr~g.scr*q.scr+Error(t.scr/(q.scr))))

Error: t.scr
      Df Sum Sq Mean Sq F value Pr(>F)
g.scr   5  8.5357  1.70714   2.0739 0.1012
Residuals 26 21.4018  0.82315

Error: t.scr:q.scr
      Df Sum Sq Mean Sq F value Pr(>F)
q.scr   1  3.0625  3.06250   7.4172 0.01139 *
g.scr:q.scr  5 10.2024  2.04048   4.9419 0.00260 **
Residuals  26 10.7351  0.41289
---
Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
> summary(aov(c.scr~g.scr*q.scr+Error(t.scr/(q.scr))))

Error: t.scr
      Df Sum Sq Mean Sq F value Pr(>F)
g.scr   5 0.019944 0.0039889   2.0574 0.1035
Residuals 26 0.050409 0.0019388

Error: t.scr:q.scr
      Df Sum Sq Mean Sq F value Pr(>F)
q.scr   1 0.009862 0.0098624   7.5842 0.01060 *
g.scr:q.scr  5 0.023243 0.0046486   3.5748 0.01360 *
Residuals  26 0.033810 0.0013004
---
Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

```

Table 2: Analysis and output for the network statistics for the genotypes from the Screen site only.