This manuscript was compiled on November 6, 2020

Genotypic variation in a foundation tree results in heritable ecological network structure of an associated community

Matthew K. Lau[1,2], **Louis J. Lamit**[2], **Rikke R. Naesbourg**[3], **Stuart R. Borrett**[4], **Matthew A. Bowker**[5], **and Thomas G. Whitham**[6]

[1]**Department of Biological Sciences and Merriam-Powell Center for Environmental Research, Northern Arizona University, Flagstaff, AZ 86011, USA**
[2]**Harvard Forest, Harvard University, 324 N Main St, Petersham, MA 01366, USA**
[3]**Department of Biology, Syracuse University, 107 College Place Syracuse, NY 13244, USA**
[4]**University of California Berkeley, Berkeley, CA, USA**
[5]**Department of Biology and Marine Biology, University of North Carolina Wilmington, 601 South College Road, Wilmington, NC, 28403, USA**
[6]**School of Forestry, Northern Arizona University, Flagstaff, AZ 86011, USA**

ABSTRACT

Biological evolution occurs in ecosystems whereby natural selection defines the structure of ecological networks. Therefore, elucidating the genetic basis to ecological network structure is fundamental to understanding evolution. Although previous work has demonstrated that genetic variation can influence food webs and trophic chains, we are unaware of a study that quantified the contribution of phenotypic variation to heritable variation in network structure. To examine this, in a 20+ year common garden we observed nine epiphytic lichen species associated with narrowleaf cottonwood (*Populus angustifolia*), a riparian ecosystem foundation species. We constructed and conducted genetic analyses of signed, weighted, directed lichen interaction networks. We found three primary results. First, genotype identity significantly predicted lichen network similarity; i.e., replicates of the same genotype supported more similar lichen networks than different genotypes. Second, broad sense heritability estimates showed that plant genotype explained network similarity (H^2 = 0.41), degree (H^2 = 0.32) and centralization (H^2 = 0.33). Third, of several tree phenotypic traits examined, bark roughness was both heritable (H^2 = 0.32) and significantly correlated with lichen network similarity (R^2 = 0.26). These results support a mechanistic, genetic pathway from variation in a heritable tree trait to ecological network structure and demonstrate that evolution can act at the community level to influence not only abundances of organisms but also interactions at the scale of entire networks. Given that network structure has determines system-wide stability and resilience, our findings have important implications for how evolution acts in ecosystems.

INTRODUCTION

Thanks for using Overleaf to write your article. Your introduction goes here! Some examples of commonly used commands and features are listed below, to help you get started.

METHODS AND MATERIALS

Guidelines can be included for standard research article sections, such as this one.

SOME LaTeX EXAMPLES

Use section and subsection commands to organize your document. LaTeX handles all the formatting and numbering automatically. Use ref and label commands for cross-references.

Figures and Tables

Use the table and tabular commands for basic tables — see Table 1, for example. You can upload a figure (JPEG, PNG or PDF) using the project menu. To include it in your document, use the includegraphics command as in the code for Figure 1 below.

Figure 1. An example image of a frog.

Item	Quantity
Candles	4
Fork handles	?

Table 1. An example table.

Citations

LaTeX formats citations and references automatically using the bibliography records in your .bib file, which you can edit via the project menu. Use the cite command for an inline citation, like **?**, and the citep command for a citation in parentheses (**?**).

Mathematics

LaTeX is great at typesetting mathematics. Let $X_1, X_2, \ldots, X_n$ be a sequence of independent and identically distributed random variables with $\mathrm{E}[X_i] = \mu$ and $\mathrm{Var}[X_i] = \sigma^2 < \infty$, and let

$$S_n = \frac{X_1 + X_2 + \cdots + X_n}{n} = \frac{1}{n}\sum_{i}^{n} X_i$$

denote their mean. Then as n approaches infinity, the random variables $\sqrt{n}(S_n - \mu)$ converge in distribution to a normal $\mathcal{N}(0, \sigma^2)$.

Lists

You can make lists with automatic numbering ...

1. Like this,
2. and like this.

... or bullet points ...

- Like this,
- and like this.

... or with words and descriptions ...

Word Definition

Concept Explanation

Idea Text

ACKNOWLEDGMENTS

Additional information can be given in the template, such as to not include funder information in the acknowledgments section.