**Genetically based variation in response to an insect herbivore alters interaction network structure**

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Abstract

* Although evolutionary forces, such as selection, have been proposed as a mechanism that creates these network structures and genetic variation within foundation species has been shown to contribute to community composition and shifts in species interactions, the effect of genetic variation on the structure of ecological interaction networks has not been examined.
* Here we examine the impact that genetic variation in a tree’s response to an insect herbivore has on interaction network structure.
* We found three main results:
  + Early senescence of leaves was driven by genetically based susceptibility to *Pemphigus betae*
    - Percent leaves with *P. betae* decreased 31% from live to senesced leaves
    - *P. betae* on live leaves was heritable (=0.39, 2=6.75, *P*=0.009), but not senesced leaves (2=3.32, *P*=0.07)
    - Genotype affected composition (relativized by species max) of living leaves (*F*=1.85, *P*=0.004, *R2*=0.28)
  + Both living and senesced leaves showed significant co-occurrence patterns with high amounts of community aggregation
    - SESlive = -7.865, P << 0.001
    - SESsenesced = -4.447, P << 0.001
    - Co-occurrence network structure differed between live and senescent (QAP: *z*=7.454, *P*<<0.001)
    - Genotype did not influence co-occurrence patterns within trees (2=0.00, *P*=1.00)
  + Living but not senesced genotype-herbivore bipartite network structure was significantly nested
    - Live: *z*=-2.2931, *P*=0.023
    - Senesced = *z*=-1.786, *P*=0.086
* These results demonstrate how genetic variance in a foundation species can affect the structure of an ecological interaction networks. This has important implications for both the effect of genetic diversity on communities and how natural selection may act in the context of complex ecological communities.

Introduction

Methods

Results

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Discussion

Acknowledgements

References

Tables

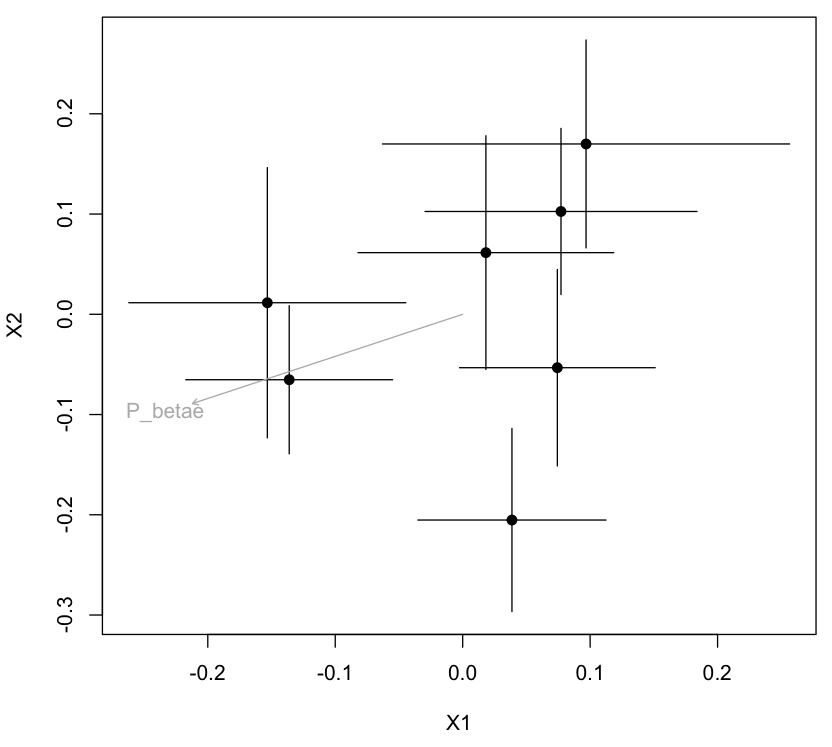
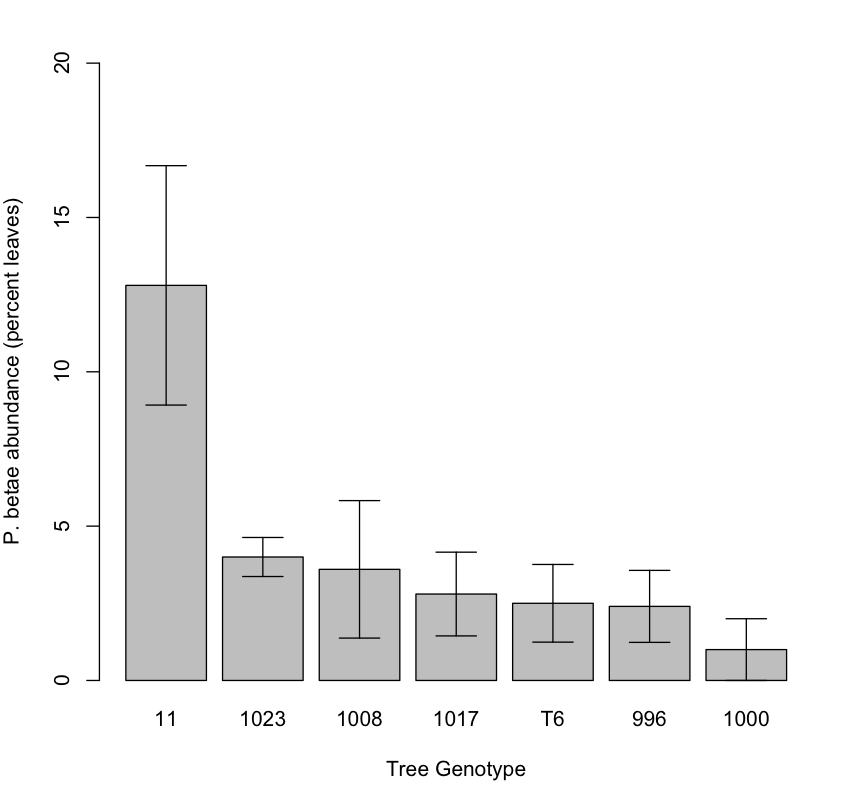
**Figure Legends**

Figure 1. Plots showing the genetic basis of the gall forming herbivore (*Pemphigus betae*) susceptibility and leaf modifier community composition. (A) Barplot showing the variation in *P. betae* abundance among genotypes. (B) NMDS ordination of the leaf modifier with a vector showing the correlation with *P. betae* abundance.

Figure 2. Plot of the leaf modifier uni-partite network. Species (see Supplementary Materials, Table 1) are shown as nodes (i.e. points) scaled by the log of their total abundance and the difference in significant co-occurrence patterns between the living and senescent leaves are shown as edges (i.e. lines) connecting points.

Figure 3. (A) Live and (B) senesced genotype-insect networks.

Figure 1



**A**

**B**

Figure 2.

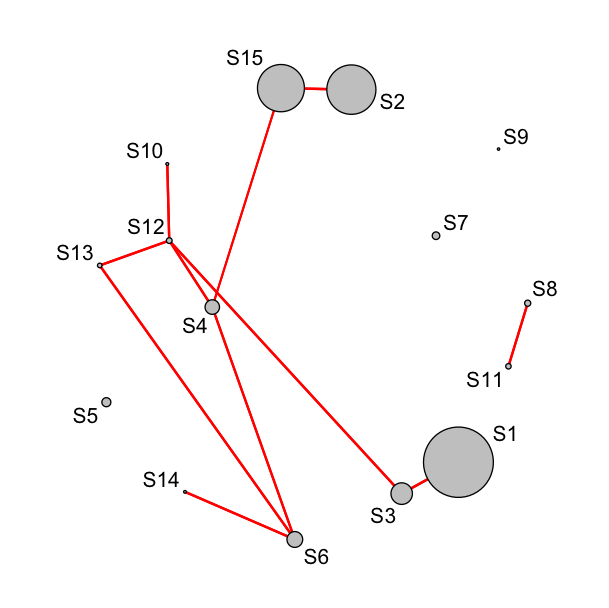
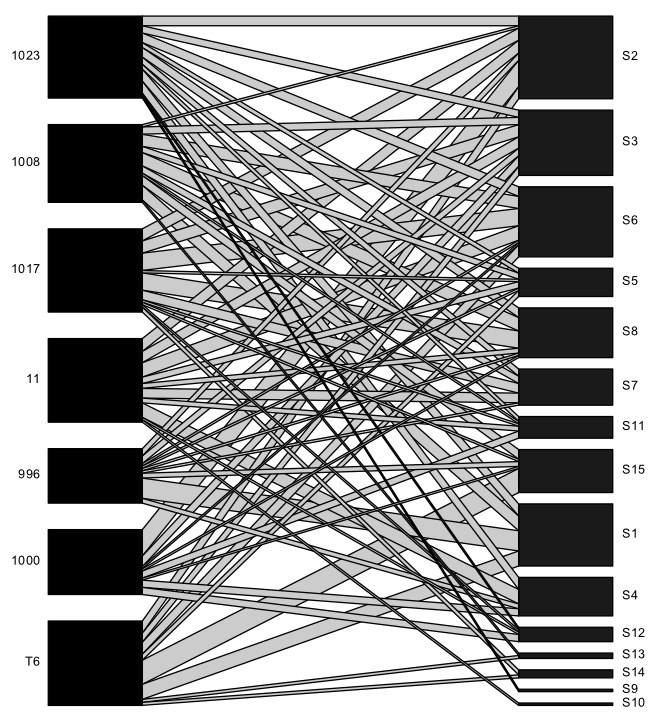
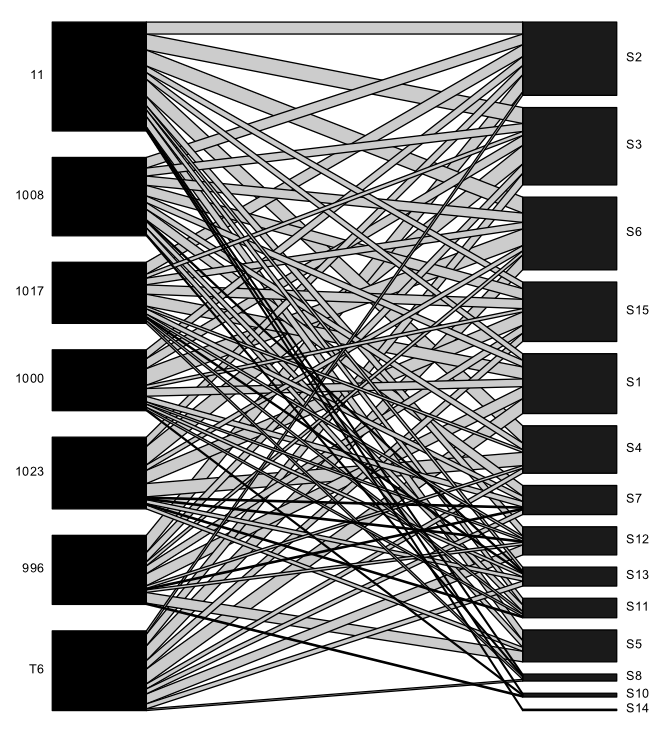


Figure 3

**B**

**A**



Supplementary Materials

Table 1. Leaf modifiers associated with labels used in figures.

|  |  |
| --- | --- |
| Label | Leaf Modifier |
| S1 | chew.edge |
| S2 | scrape |
| S3 | chomp |
| S4 | pb.pred |
| S5 | pb.abort |
| S6 | chew.holes |
| S7 | thrips |
| S8 | tier |
| S9 | fish.eye |
| S10 | tip.miner |
| S11 | edge.miner |
| S12 | mid.miner |
| S13 | pinch |
| S14 | edge.fold |
| S15 | pb |