**Table S1:** Statistical models testing the genetic specificity of the plant-insect food web.

|  |  |  |  |
| --- | --- | --- | --- |
| **Response** | **df** | ***F*** or **χ2** | ***P*** |
| Gall size1 |  |  |  |
| Leaf gall | 23,57 | 2.17 | **0.009** |
| Bud gall | 21,44 | 0.98 | 0.504 |
| Apical-stem gall | 16,12 | 0.29 | 0.988 |
| Gall abundance2 | 25,119 | 202.40 | **0.001** |
| Leaf gall |  | 74.60 | **0.001** |
| Bud gall |  | 55.02 | **0.006** |
| Apical-stem gall |  | 44.47 | **0.042** |
| Mid-stem gall |  | 28.27 | 0.295 |
| Composition of gall community3 | 22,89 | 1.96 | **0.001** |
| Abundance of gall-parasitoid interactions2 | 25,119 | 357.10 | **0.001** |
| Leaf gall |  |  |  |
| *Platygaster* sp. |  | 79.51 | **0.001** |
| *Mesopolobus* sp. |  | 50.00 | **0.009** |
| *Torymus* sp. |  | 60.11 | **0.001** |
| *Tetrastichus* sp. |  | 32.96 | 0.105 |
| Mymarid sp. A |  | 6.37 | 0.448 |
| Bud gall |  |  |  |
| *Platygaster* sp. |  | 18.04 | 0.276 |
| *Mesopolobus* sp. |  | 6.37 | 0.497 |
| *Torymus* sp. |  | 39.81 | *0.079* |
| *Tetrastichus* sp. |  | 18.09 | 0.492 |
| *Lestodiplosis* sp. |  | 16.05 | 0.552 |
| Apical-stem gall |  |  |  |
| *Torymus* sp. |  | 23.13 | **0.048** |
| Mid-stem gall |  |  |  |
| *Platygaster* sp. |  | 6.64 | 0.452 |
| Composition of gall-parasitoid interactions3 | 12,45 | 1.57 | **0.007** |
| Proportion of galls parasitized4 |  |  |  |
| Leaf gall | 23,58 | 75.79 | **<0.001** |
| *Platygaster* sp. |  | 93.47 | **<0.001** |
| *Mesopolobus* sp. |  | 42.56 | **0.008** |
| *Torymus* sp. |  | 42.92 | **0.007** |
| *Tetrastichus* sp. |  | 29.55 | 0.163 |
| Mymarid sp. A |  | 3.97 | 0.999 |
| Bud gall | 21,46 | 49.84 | *0.072* |
| Apical-stem gall | 18,12 | 15.69 | 0.614 |
| Composition of trophic interactions in the plant-insect food web3 | 22,89 | 1.90 | **0.001** |

Notes: 1GLM (error distribution = Gaussian, link function = identity), log-transformed; 2multivariate GLM (error distribution = negative binomial, link function = log); 3PERMANOVA on Bray-Curtis dissimilarities (999 permutations);

4GLM (error distribution = binomial, link function = logit). *P*-values in bold (*P* < 0.05), italics (*P* < 0.10), and normal font (*P* > 0.10) denote degree of statistical significance.

**Table S2:** Statistical models explaining insect food web responses to genetic variation in coastal willow (*Salix hookeriana*). We report the coefficients of all predictor variables that were included in the final statistical models, which were determined using AIC and likelihood-ratio tests.

|  |  |  |  |  |
| --- | --- | --- | --- | --- |
| **Response** | **Predictors** | | | |
| **Gall size1** | **Salicylates/**  **Tannins PC1** | **Flavones/**  **Flavonols PC1** |  |  |
| Leaf gall | **-0.20** | **-0.26** |  |  |
| **Gall abundance2** | **C:N** | **Flavanones/**  **Flavanonols PC1** | **Plant size** |  |
| Leaf gall | *0.04* | -0.03 | -0.36 |  |
| Bud gall | *0.08* | -0.07 | **-1.01** |  |
| Apical-stem gall | 0.01 | **0.46** | 0.26 |  |
| Mid-stem gall | 0.02 | -1.81 | -*4.77* |  |
| **Abundance of gall-parasitoid interactions2** | **Leaf gall**  **size** | **Leaf gall abundance** | **Bud gall abundance** | **Apical-stem gall abundance** |
| Leaf gall |  |  |  |  |
| *Platygaster* sp. | **-0.22** | **1.22** | 0.20 | -0.15 |
| *Mesopolobus* sp. | **-0.27** | **0.90** | -0.26 | 0.44 |
| *Torymus* sp. | *0.19* | **0.76** | -0.30 | 0.72 |
| *Tetrastichus* sp. | -*0.24* | 0.71 | 0.45 | -1.09 |
| Mymarid sp. A | -1.67 | **20.83** | -2.07 | 3.35 |
| Bud gall |  |  |  |  |
| *Platygaster* sp. | 0.43 | 0.23 | **5.81** | -14.25 |
| *Mesopolobus* sp. | 0.16 | 0.30 | 0.77 | 1.95 |
| *Torymus* sp. | **-0.17** | 0.31 | **1.39** | -0.43 |
| *Tetrastichus* sp. | 0.15 | 0.51 | **1.83** | 0.08 |
| *Lestodiplosis* sp. | 0.04 | -0.61 | *1.46* | 1.75 |
| Apical-stem gall |  |  |  |  |
| *Torymus* sp. | -0.12 | 0.05 | -0.64 | **4.09** |
| Mid-stem gall |  |  |  |  |
| *Platygaster* sp. | 1.54 | -*15.03* | 0.53 | -9.23 |

Notes: 1GLM (error distribution = Gaussian, link function = identity), log-transformed; 2multivariate GLM (error distribution = negative binomial, link function = log). *P*-values in bold (*P* < 0.05), italics (*P* < 0.10), and normal font (*P* > 0.10) denote degree of statistical significance.

**Table S3:** Generalized linear models (error distribution = binomial, link function = logit) explaining the proportion of leaf galls parasitized. Final models were determined using AIC and likelihood-ratio tests.

|  |  |  |  |  |
| --- | --- | --- | --- | --- |
| **Response** | **Predictor** | **df** | **χ2** | ***P*** |
| Total parasitism | Gall size | 1,79 | 22.28 | **<0.001** |
| *Platygaster* sp. | Gall size | 1,77 | 17.58 | **<0.001** |
|  | Gall abundance | 1,77 | 0.73 | 0.394 |
|  | Gall size x abundance | 1,77 | 8.71 | **0.003** |
| *Mesopolobus* sp. | Gall size | 1,77 | 7.28 | **0.007** |
|  | Gall abundance | 1,77 | 0.29 | 0.588 |
|  | Gall size x abundance | 1,77 | 4.21 | **0.040** |
| *Torymus* sp. | Gall size | 1,78 | 3.83 | *0.050* |
|  | Gall abundance | 1,78 | 5.24 | **0.022** |

**Relatedness and phenotypic redundancy of willow genotypes –** The matrix of microsatellite markers for the 26 willow genotypes used in this study was published in Table S1 of Barbour et al. (2015); however, since the willow genotyping was only based on 2 markers, they were unable to infer the relatedness of these genotypes. If certain genotypes are more closely related to each other, and consequently have very similar phenotypes, this could introduce spurious confidence in our associations between willow traits and gall abundances. We can examine the degree of phenotypic redundancy among the 26 genotypes by measuring their functional evenness and divergence in multivariate trait space (Villéger et al. 2008). To do this, we calculated the average trait value for each of the 40 traits we measured for each willow genotype. We then calculated functional evenness and functional divergence using the ‘*FD*’ package in R. For both indices, values close to zero correspond to functional redundancy, while values close to one indicate functional distinctiveness. We found that functional evenness and divergence were equal to 0.94 and 0.87, respectively, suggesting that there is little phenotypic redundancy among these willow genotypes. Therefore, we argue that not knowing the relatedness among the 26 genotypes probably introduces little bias in our trait associations with the abundances and sizes of galls.

**Calculating quantitative-weighted linkage density (food-web complexity).**

Quantitative-weighted linkage density, , was calculated using the following equations. Given an *s*-by-*s* food web matrix **b** = , with corresponding to the number of individuals of species *j* (galls or parasitoids) emerging from species *i* (willow or galls) per willow branch over a single growing season, is the sum of row *i*, is the sum of column *j*, and is the total sum. The Shannon indices for the prey and predatory interactions were calculated as,

The effective number of prey and predatory interactions were calculated as and respectively. Finally, quantitative-weighted link density was calculated as,

Assumptions underlying our simulation

**(A) We are assuming that our simulation estimates the additive effects of increasing genetic variation on food-web complexity.** For composite indices, such as food-web complexity, additive effects of genetic variation may result from two different types of ‘selection’ effects (sensu Loreau and Hector 2001, *Nature* 412:72-76): (1) selecting genotypes with high food-web complexity; and/or (2) selecting genotypes that host distinct trophic interactions. Our results suggest that selecting genotypes that host distinct trophic interactions was an important contributor to additive effects of genetic variation in increasing food-web complexity. For example, we found that gall species were associated with different willow traits, and that the three dominant parasitoid species (*Platygaster*, *Mesopolobus*, and *Torymus*) responded differently to the size and density of the dominant gall species (leaf galler, *Iteomyia salicisverruca*). These results suggest that if there is less variation in willow traits as well as leaf gall density and size, as would be expected in a genotype monoculture, then we would expect to observe less complex food webs.

Our common garden experiment was designed to control for non-additive effects resulting from particular combinations of genotypes (e.g. neighbouring plants altering each others phenotypes through competition or facilitation, associational resistance and susceptibility, source-sink dynamics) by spacing willows 3 m apart from each other in a completely randomized design (Barbour et al. 2015, *Functional Ecology* VOL:PAGES). However, since our common garden is a polyculture of 26 genotypes, we were unable to control for non-additive effects such as insects perceiving polycultures different than monocultures (cite study, maybe Root 1973, *Ecol. Mono.* 43:95-120; Rodriguez-Saona and Thaler 2005, *Ecol. Entomol.* 30:156-163). We address how these potential non-additive effects would alter our qualitative conclusion in (C) below.

**(B) Our simulation assumes that we sampled a sufficient number of willows to reliably estimate average food-web complexity for a genotype monoculture.** To examine this, we estimated average complexity of food webs for genotype monocultures when we randomly sampled (without replacement) 1 to 4 replicate plants for each genotype. Figure S1 suggests that our estimate of average food-web complexity for genotype monocultures is beginning to plateau at 3 to 4 replicate plants, suggesting that we sampled a sufficient number of willows to reliably estimate average food-web complexity for a genotype monoculture.

**(C) We are assuming that our qualitative conclusion (i.e. genetic variation increases food-web complexity) would be the same even if we had conducted an experiment that manipulated genetic variation.** For our plant-insect food web, we argue that our qualitative conclusion would hold unless an experiment demonstrates that there are negative, non-additive effects that are greater than or equal in magnitude to the positive, additive effects we observed in our common garden. We might expect negative, non-additive effects on food-web complexity to be important if species at the same trophic level responded similarly to trait variation at lower trophic levels, because we might expect one species to dominate and competitively exclude the other in polycultures. In our system though, it appears that different gall species respond to different willow traits, and similarly, parasitoid species respond different to variation in gall density and size, suggesting that this type of negative, non-additive effect would likely not be strong enough to dominate the strong additive effects we observed.

will only be false if negative, non-additive effects on food-web complexity are present *and* greater than or equal in magnitude to the additive effects. While other studies have documented negative, non-additive effects on arthropod diversity (McArt et al. 2012, *Oecologia* 168:1013-1021)

evidence of spread of dominant that suppresses richness? For negative, non-additive effect…

Interestingly, if there are positive, non-additive effects, then our simulation actually *underestimates* the positive relationship between genetic variation and food-web complexity. Therefore, while our results do not experimentally examine the consequences of genetic variation for food-web complexity, our results suggest that the positive relationship between genetic diversity and food-web complexity we observed is likely to be real for our system.

**Structural equation model of food-web complexity** – To examine whether the relationship between willow genetic variation and food-web complexity was solely due to an increase in the total abundance of galls and frequency of gall-parasitoid interactions, we generated a piecewise structural equation model using the ‘*piecewiseSEM*’ package in R. We first fit a full-mediation model, where the effect of genetic variation on food-web complexity was solely mediated through total gall abundance and the frequency of gall-parasitoid interactions. This model provided a poor-fit to the data and subsequent tests for ‘missing paths’ suggested we add a path between total gall abundance and food-web complexity as well as a direct path between genetic variation and food-web complexity. This updated model provided a substantially better fit to the data. When we examined the standardized path coefficients of this model, we found that the effect of genetic variation on food-web complexity was virtually independent of any effect of genetic variation mediated by total gall abundance and frequency of gall-parasitoid interactions. These results provide further support for our argument that the effects of genetic variation on food-web complexity

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