**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 functional-trait diversity of willow genotypes –** The matrix of microsatellite markers for the 26 willow genotypes used in this study was published in Table S1 of (1); however, since the willow genotyping was only based on 2 markers, they were unable to infer the relatedness among 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/phenotypes. We can examine this phenotypic similarity by measuring the functional evenness and divergence of the 26 willow genotypes in multivariate trait space (2). 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 the phenotypes (in multivariate trait space) of each genotype are quite distinct from each other. 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.

Sampling interactions in gall-parasitoid network – The total number of potential gall-parasitoid interactions in this bipartite network is 24 (i.e. each of the 4 galls could interact with each of the 6 parasitoids, 6\*4 = 24). Interspecific differences among gall species (e.g. differences in gall morphology, phenology, plant part galled, etc.) and sampling effort likely constrain the number of potential interactions observed to considerably less than 24. While it was not the focus of our study to examine interspecific differences, it is important to demonstrate that we have sampled the majority of interactions in the gall-parasitoid network. To demonstrate this, we considered unique gall-parasitoid interactions as ‘species’ and used Chao 1 (5) to estimate the total number of interactions. While we documented 12 unique gall-parasitoid interactions, Chao 1 estimated the number of interactions to be 14.98 (std. error = 4.49), suggesting that we have sampled the majority of interactions in the gall-parasitoid network.

**Calculating quantitative-weighted linkage density (food-web complexity)** – Quantitative-weighted linkage density, , was calculated using the following equations (3). 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,

Asymptotic vs. non-asymptotic models – We fit both asymptotic and non-asymptotic phenomenological models (4) to extrapolate our estimates of food-web complexity. While more sophisticated and accurate models have been developed to extrapolate species richness (5), nothing has been developed for extrapolating food-web complexity. These phenomenological models have the advantage that they make no assumptions about the processes generating the data (5); therefore, they are likely a good starting point for extrapolating food-web complexity (4).

For our asymptotic model we used a scaled and shifted Michaelis-Menten function (4) of the form,

,

where *N* represents either the number of plants (sampling effort simulation) or the number of genotypes (genetic variation simulation). *LDq,N* is the predicted complexity at *N*,while *a* and *b* are phenomenological parameters that scale *LDq,N* and *N*, respectively. is a constant parameter, representing the average complexity for either 1-genotype 1-plant (sampling effort simulation) or 1-genotype 4-plants (genetic variation simulation). Adding the constant, , and subtracting the constant, 1, shift the function so that when *N* = 1, . We used non-linear least squares to estimate parameters *a* and *b*. For the non-asymptotic models, we fit log-log () and log-linear (). The asymptotic and non-asymptotic models we chose have been widely used for extrapolating species richness (4), which is why we used them for food-web complexity.

Results for simulations of sampling effort and genetic variation – We fit the asymptotic and non-asymptotic models to our sampling effort simulations of 1-genotype mixtures of 1 to 4 plants (1,000 estimates per level of sampling effort, details in *Materials and Methods*). We found that all of the models gave a similar fit to the data; however, they gave very different predictions for the complexity of 1-genotype 100-plant mixtures (Table S4). Therefore, to evaluate which of these models was more realistic, we re-fit these models to our genetic variation simulations of 1 to 25 genotypes (grey circles in Fig. 6 of main text).

We found that the asymptotic model provided a much better fit (*R2* = 0.96) and more accurate predictions than either of the non-asymptotic models (Table S5). In particular, the asymptotic model’s predicted complexity of 25-genotype 100-plant mixtures deviated less than a tenth of 1% from the observed average (*LDq* = 2.208), whereas the non-asymptotic models overestimated complexity between 2 and 4%.

Table S4: Comparing asymptotic and non-asymptotic models for predicting the complexity of 1-genotype 100-plant mixtures. Note that for these data (sampling effort simulation), *N* represents the number of plants.

|  |  |  |  |
| --- | --- | --- | --- |
| Model type | Equation | *R2* | Predicted *LDq* 1-genotype  100-plant mixture |
| Asymptotic  (Michaelis-Menten) |  | 0.89 | 1.84 |
| Non-asymptotic  (log-log) |  | 0.88 | 2.45 |
| Non-asymptotic  (log-linear) |  | 0.88 | 2.17 |

Table S5: Comparing asymptotic and non-asymptotic models for predicting the complexity of 25-genotype 100-plant mixtures. The observed complexity of the 25-genotype 100-plant mixture was 2.208. Note that for these data (genetic variation simulation), *N* represents the number of genotypes.

|  |  |  |  |
| --- | --- | --- | --- |
| Model type | Equation | *R2* | Predicted *LDq* 25-genotype  100-plant mixture |
| Asymptotic (Michaelis-Menten) |  | 0.96 | 2.209 |
| Non-asymptotic (log-log) |  | 0.87 | 2.260 |
| Non-asymptotic (log-linear) |  | 0.89 | 2.280 |

Assessing the accuracy of the asymptotic model – After we identified the asymptotic model as the most appropriate for our data, we wanted to evaluate whether the model was likely to over- or under-estimate the complexity of 1-genotype 100-plant mixtures. To do this, we took advantage of the complete data set we had for the genetic variation simulation. Specifically, we refit the asymptotic model with smaller fractions of data to examine how accurately it extrapolated to predict the complexity of 25-genotype 100-plant mixtures. When we did this, we found that the model began to increasingly overestimate food-web complexity. For example, using only the first 40% of the data (i.e. 1 to 10 genotypes), the model overestimated food-web complexity by less than 1%; however, using only the first 12% of the data (e.g. 1 to 3 genotypes), the model overestimated food-web complexity by about 3%. While these predictions are still quite accurate, our asymptotic model for the sampling effort simulation is extrapolating based on 4% of the potential data (4 of 100 plants). Therefore, the predicted complexity of 1-genotype 100-plant mixtures is likely an overestimate, suggesting that the reported effect of 20% is a conservative estimate of the additive effects of genetic variation.

**Structural equation model of food-web complexity** – Fig. S1 shows the data used to evaluate the structural equation model in Fig. S2. We found that this model provided a good fit to the data with no evidence of missing pathways (Fisher *C* = 0.88, k = 6, *P* = 0.99). In particular, we found that genetic variation increased food-web complexity primarily by: (i) an increase in gall richness that directly increased complexity (0.49\*0.78 = 0.38); and (ii) an increase in gall abundance that indirectly increased complexity by increasing gall vulnerability (0.69\*0.62\*0.65 = 0.28). Interestingly, gall evenness had a small overall negative effect on complexity ((-0.19\*0.58) + (-0.19\*-0.32\*0.65) + (-0.19\*0.28\*0.26) = -0.09).

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Figure S1. One of 40 replicate simulations, showing the positive relationship between willow genetic variation and food-web complexity. Grey circles represent estimates of food-web complexity for specific samples, whereas blue circles represent the average complexity at each level of genetic variation. These data were used in the structural equation model (Fig. S2).

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Figure S2. Structural equation model of the paths by which genetic variation increases food-web complexity. Blue and red arrows indicate positive and negative relationships, respectively. One-way arrows indicate modelled paths, whereas double-headed arrows indicate correlated relationships. Numerical values in the middle of each path represent the standardized path coefficients and can be used to determine the magnitude of direct and indirect effects.

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