

1 **Table S1:** Statistical models testing the genetic specificity of the plant-insect food web.  
2

Response	df	<i>F</i> or $\chi^2$	<i>P</i>
Gall size <sup>1</sup>			
Leaf gall	23,57	2.17	<b>0.009</b>
Bud gall	21,44	0.98	0.504
Apical-stem gall	16,12	0.29	0.988
Gall abundance <sup>2</sup>	25,119	202.40	<b>0.001</b>
Leaf gall		74.60	<b>0.001</b>
Bud gall		55.02	<b>0.006</b>
Apical-stem gall		44.47	<b>0.042</b>
Mid-stem gall		28.27	0.295
Composition of gall community <sup>3</sup>	22,89	1.96	<b>0.001</b>
Abundance of gall-parasitoid interactions <sup>2</sup>	25,119	357.10	<b>0.001</b>
Leaf gall			
<i>Platygaster</i> sp.		79.51	<b>0.001</b>
<i>Mesopolobus</i> sp.		50.00	<b>0.009</b>
<i>Torymus</i> sp.		60.11	<b>0.001</b>
<i>Tetrastichus</i> sp.		32.96	0.105
Mymarid sp. A		6.37	0.448
Bud gall			
<i>Platygaster</i> sp.		18.04	0.276
<i>Mesopolobus</i> sp.		6.37	0.497
<i>Torymus</i> sp.		39.81	0.079
<i>Tetrastichus</i> sp.		18.09	0.492
<i>Lestodiplosis</i> sp.		16.05	0.552
Apical-stem gall			
<i>Torymus</i> sp.		23.13	<b>0.048</b>
Mid-stem gall			
<i>Platygaster</i> sp.		6.64	0.452
Composition of gall-parasitoid interactions <sup>3</sup>	12,45	1.57	<b>0.007</b>
Proportion of galls parasitized <sup>4</sup>			
Leaf gall	23,58	75.79	<b>&lt;0.001</b>
<i>Platygaster</i> sp.		93.47	<b>&lt;0.001</b>
<i>Mesopolobus</i> sp.		42.56	<b>0.008</b>
<i>Torymus</i> sp.		42.92	<b>0.007</b>
<i>Tetrastichus</i> 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 web <sup>3</sup>	22,89	1.90	<b>0.001</b>

Notes: <sup>1</sup>GLM (error distribution = Gaussian, link function = identity), log-transformed;  
<sup>2</sup>multivariate GLM (error distribution = negative binomial, link function = log);  
<sup>3</sup>PERMANOVA on Bray-Curtis dissimilarities (999 permutations);  
<sup>4</sup>GLM (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 size <sup>1</sup>	Salicylates/ Tannins PC1	Flavones/ Flavonols PC1		
Leaf gall	<b>-0.20</b>	<b>-0.26</b>		
Gall abundance <sup>2</sup>	C:N	Flavanones/ Flavanonols PC1	Plant size	
Leaf gall	<i>0.04</i>	-0.03	-0.36	
Bud gall	<i>0.08</i>	-0.07	<b>-1.01</b>	
Apical-stem gall	0.01	<b>0.46</b>	0.26	
Mid-stem gall	0.02	-1.81	<i>-4.77</i>	
Abundance of gall-parasitoid interactions <sup>2</sup>	Leaf gall size	Leaf gall abundance	Bud gall abundance	Apical-stem gall abundance
Leaf gall				
<i>Platygaster</i> sp.	<b>-0.22</b>	<b>1.22</b>	0.20	-0.15
<i>Mesopolobus</i> sp.	<b>-0.27</b>	<b>0.90</b>	-0.26	0.44
<i>Torymus</i> sp.	<i>0.19</i>	<b>0.76</b>	-0.30	0.72
<i>Tetrastichus</i> sp.	-0.24	0.71	0.45	-1.09
Mymarid sp. A	-1.67	<b>20.83</b>	-2.07	3.35
Bud gall				
<i>Platygaster</i> sp.	0.43	0.23	<b>5.81</b>	-14.25
<i>Mesopolobus</i> sp.	0.16	0.30	0.77	1.95
<i>Torymus</i> sp.	<b>-0.17</b>	0.31	<b>1.39</b>	-0.43
<i>Tetrastichus</i> sp.	0.15	0.51	<b>1.83</b>	0.08
<i>Lestodiplosis</i> sp.	0.04	-0.61	<i>1.46</i>	1.75
Apical-stem gall				
<i>Torymus</i> sp.	-0.12	0.05	-0.64	<b>4.09</b>
Mid-stem gall				
<i>Platygaster</i> sp.	1.54	<i>-15.03</i>	0.53	-9.23

Notes: <sup>1</sup>GLM (error distribution = Gaussian, link function = identity), log-transformed;  
<sup>2</sup>multivariate 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	$\chi^2$	P
Total parasitism	Gall size	1,79	22.28	<0.001
<i>Platygaster</i> 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
<i>Mesopolobus</i> 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
<i>Torymus</i> 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 multivariate phenotypes of each genotypes 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.

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

**Quantitative**-weighted linkage density,  $LD_q$ , was calculated using the following equations (3). Given an  $s$ -by- $s$  food web matrix  $\mathbf{b} = [b_{ij}]$ , with  $b_{ij}$  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,  $b_{i.}$  is the sum of row  $i$ ,  $b_{.j}$  is the sum of column  $j$ , and  $b_{..}$  is the total sum. The Shannon indices for the prey and predatory interactions were calculated as,

$$H_j = - \sum_{i=1}^s \frac{b_{ij}}{b_{.j}} \ln \frac{b_{ij}}{b_{.j}}$$

$$H_i = - \sum_{j=1}^s \frac{b_{ij}}{b_{i\cdot}} \ln \frac{b_{ij}}{b_{i\cdot}}$$

The effective number of prey and predatory interactions were calculated as  $N_j^* = \exp(H_j)$  and  $N_i^* = \exp(H_i)$ , respectively. Finally, quantitative-weighted link density was calculated as,

$$LD_q = \frac{1}{2b_{\cdot\cdot}} \left( \sum_{i=1}^s b_{i\cdot} N_i^* + \sum_{j=1}^s b_{\cdot j} N_j^* \right)$$

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

$$LD_{q,N_m} = \frac{a(N_m-1)}{(b+(N_m-1))} + \overline{LD}_{q,1},$$

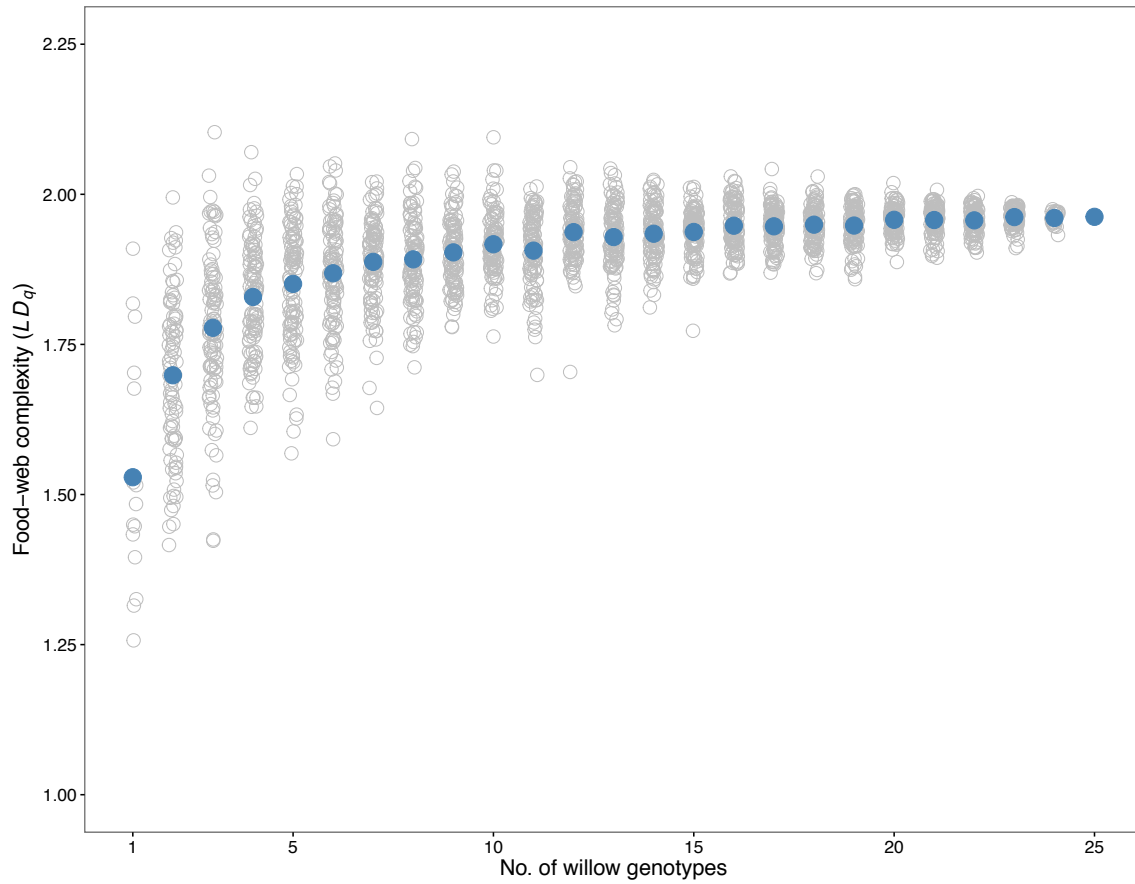
where  $N_m$  is the number of plants in monoculture,  $LD_{q,N_m}$  is the complexity at  $N_m$ ,  $a$  and  $b$  are phenomenological parameters that scale  $LD_{q,N_m}$  and  $N_m$ , respectively, and  $\overline{LD}_{q,1}$  is a constant parameter, representing the average complexity for 1-plant monocultures. Adding the constant,  $\overline{LD}_{q,1}$ , and subtracting the constant, 1, shift the function so that when  $N_m = 1$ ,  $LD_{q,N_m} = \overline{LD}_{q,1}$ . We used non-linear least squares to estimate parameters  $a$  and  $b$ . Our asymptotic model appeared to provide a good fit to the data ( $R^2 = 0.88$ ,  $LD_{q,N_m} = \frac{0.62(N_m-1)}{(3.62+(N_m-1))} + 1.25$ ) and predicted a value of 1.84 for the complexity of 100 plant monocultures ( $LD_{q,100} = 1.84$ ).

To examine whether this asymptotic model was appropriate for our data, we applied it to the results of our primary simulation (data presented in Fig. 6 of main text). Specifically, we replaced  $N_m$  with  $N_G$ , the number of genotypes sampled, and  $\overline{LD}_{q,1}$  is the average complexity for genotype monocultures, and re-estimated the scaling parameters  $a$  and  $b$ . We found that this model provided an excellent fit to our data ( $R^2 = 0.96$ ,  $LD_{q,N_G} = \frac{0.76(N_G-1)}{(2.23+(N_G-1))} + 1.52$ ). Indeed, the predicted complexity of 25-genotype polycultures was 2.209, which only deviated less than a tenth of 1% from the average calculated from our resampling procedure ( $LD_{q,25} = 2.208$ ). We also tried fitting non-asymptotic models (5) to our data; however, we found that both a log-linear ( $R^2 = 0.89$ ,  $LD_{q,N_G} = 0.19 * \log(N_G) + 1.65$ ) and log-log ( $R^2 = 0.87$ ,  $\log(LD_{q,N_G}) = 0.10 * \log(N_G) + 0.50$ ) model had relatively low  $R^2$ , highly biased residuals, and overestimated food-web complexity by 2 and 3%, respectively, compared to the asymptotic model (predicted  $LD_{q,25}$ : log-linear = 2.26; log-log = 2.28).

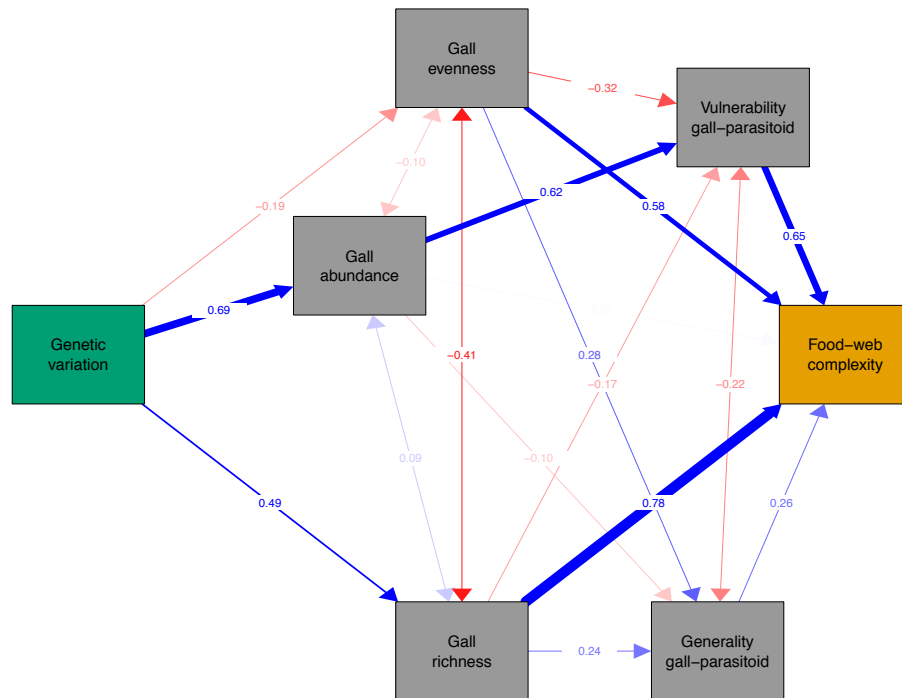
While the above analysis suggests that our asymptotic model provides a good fit to our data, it does not give much insight into how accurate the model's predictions will be when we extrapolate beyond the original data. One way we can examine this

is by refitting our model with smaller fractions of our data and seeing how accurately it extrapolates to predict the complexity of 25-genotype polycultures. When we did this, we found that the model began to increasingly overestimate food-web complexity. For example, with the first 40% of the data (i.e. 1 to 10 genotypes), the model overestimated food-web complexity by less than 1%; however, with 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 monocultures is extrapolating based on 4% of the potential data (4 of 100 plants). Therefore, it seems reasonable to suggest that the predicted complexity of 100-plant monocultures may be overestimated by ~5%. So while this asymptotic model likely gives a more accurate baseline for estimating the additive effects of complementarity, it also suggests that the reported effect of 20% is a slightly conservative estimate.

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 ( $0.49 \times 0.78 = 0.38$ ); and (ii) an increase in gall abundance that indirectly increased complexity by increasing gall vulnerability ( $0.69 \times 0.62 \times 0.65 = 0.28$ ). Interestingly, gall evenness had a small overall negative effect on complexity ( $(-0.19 \times 0.58) + (-0.19 \times -0.32 \times 0.65) + (-0.19 \times 0.28 \times 0.26) = -0.09$ ).



**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).**



**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.**

## References

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