

**Intraspecific genetic variation increases network complexity:
empirical evidence from a plant-insect food web**

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Abstract

Theory predicts that intraspecific genetic variation can increase the complexity of an ecological network. To date though, we are lacking empirical knowledge of the extent to which genetic variation determines the assembly of ecological networks, as well as how the gain or loss of genetic variation will affect network structure. To address this knowledge gap, we used a common garden experiment to quantify the extent to which heritable trait variation in a host plant determines the assembly of its associated food web (network of trophic interactions), and drives overall food web complexity. We found that trait variation among host plant genotypes directly affected resistance to insect herbivores, which in turn, indirectly affected interactions between herbivores and their insect parasitoids. Direct and indirect genetic effects resulted in distinct compositions of trophic interactions associated with each host plant genotype. Moreover, we found that food web complexity increased by 50% over the range of genetic variation in the experimental population of host plants. Taken together, our results indicate that intraspecific genetic variation can play a key role in structuring ecological networks, which may in turn, affect network persistence.

Significance

We know that the gain or loss of species can have cascading effects on the complexity of a food web; however, it is less clear whether the gain or loss of genetic variation within species, an often over-looked component of biodiversity, will similarly affect food web structure. In this study, we document the mechanisms by which genetic variation within a host plant resulted in unique insect food webs associated with each host plant genotype.

Moreover, we found that higher levels of genetic variation lead to more complex food webs. Taken together, our results suggest that preserving genetic variation within key species may be critical for maintaining complex and robust food webs under future environmental change.

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Introduction

Network theory has provided both a conceptual and quantitative approach for mapping interactions between species and making predictions about how the gain or loss of species will affect the structure and dynamics of ecological networks (1–3). Representing a network at the species-level, however, makes the implicit assumption that each species consists of a homogenous population of individuals, all of which interact equally with individuals of different species. Yet, most populations are heterogeneous mixtures of individuals that vary in their phenotypes and there is growing evidence that this intraspecific variation is an important factor governing the assembly of ecological communities (4–6). Consequently, there is a clear need to account for the role of intraspecific variation in structuring ecological networks (7).

Genetic variation is a key driver of intraspecific variation and many studies have now demonstrated direct and indirect genetic effects on species interactions (8–10) and the composition of communities across multiple trophic levels (11–14). Nevertheless, there are two key components missing from previous work that is preventing us from scaling the effects of genetic variation on pairwise interactions to ecological networks. First,

69 prior studies have not quantified how genetic variation affects the composition of
70 pairwise interactions that determine network structure. Instead, studies have either
71 quantified the composition of species (11–14), thereby ignoring interactions, or
72 quantified a simple tri-trophic interaction (8–10), thereby ignoring the complex network
73 in which this interaction is embedded. As a result, the mechanisms by which genetic
74 variation shapes network structure remain unclear. Second, studies have not examined the
75 effect of genetic variation *per se* on network structure; rather, prior work has focused on
76 testing whether different genotypes interact with particular species (15). While
77 demonstrating the genetic specificity of interactions (i.e. differences among genotypes) is
78 a critical first step, we are currently ill posed for predicting how the gain or loss of
79 genetic variation will affect species interactions, and ultimately the structure of ecological
80 networks (6).

81
82 The structure of an ecological network can be affected by intraspecific genetic variation
83 through at least two different mechanisms. For a food web (network of trophic
84 interactions), genetic variation in the quality of a basal resource may alter the abundances
85 and/or phenotypes of consumer species (16). These direct genetic effects on consumers
86 may then have cascading effects on the strength of trophic interactions between
87 consumers and their predators (16), resulting in distinct compositions of trophic
88 interactions associated with different genotypes of the basal resource (Fig. 1). If such
89 genetic specificity in the composition of trophic interactions occurs, then theory predicts
90 that increasing genetic variation will result in more interactions per species (6, 17), and
91 therefore greater food web complexity (Fig. 2). Moreover, greater complexity may in turn

affect food web dynamics, as more complex food webs are predicted to be more robust to species extinctions (1, 18).

In this study, we quantify the genetic specificity of trophic interactions and test the hypothesis that increasing genetic variation results in greater network complexity using a common garden experiment of a host plant (Coastal willow, *Salix hookeriana*) and its associated food web of insect galls and parasitoids (Fig. 1). We focused on this plant-insect food web for three reasons. First, we have demonstrated in previous work that *S. hookeriana* (hereafter, willow) displays genetic variation in resistance to its community of galling herbivores (19). Second, the unique biology of galling insects makes them ideal for building quantitative food webs. In particular, galls provide a refuge for larva from attack by most generalist predators, thereby restricting their natural enemies to a relatively specialized community (20). In our system, all of the natural enemies are insect parasitoids that complete their development within the gall after parasitizing larva, making it easy to identify and quantify the source of larval mortality by dissecting galls or rearing out the insects. Third, the biology of galls is also ideal for identifying the mechanisms mediating trophic interactions. In particular, gall size is a key trait that affects the ability of parasitoids to successfully oviposit through the gall wall and into the larva within the gall (i.e. larger galls provide a refuge from parasitism) (21). Moreover, gall size is determined, in part, by the genotype of the plant (21), so we have a clear mechanism by which host plant genetic variation can affect the strength of trophic interactions. Taken together, our study seeks to test theoretical predictions for how intraspecific genetic variation influences the structure of ecological networks. In doing so,

our study takes a crucial step toward a more predictive understanding for how the gain or loss of genetic variation in a population will affect the dynamics of ecological networks.

Results and Discussion

Quantifying the genetic specificity of the willow-gall interaction network. In

concordance with previous work in this system (19), we observed clear differences in the abundance of 3 of the 4 galling insects among willow genotypes (multivariate GLM, $\chi^2_{25,119} = 202.40$, $P = 0.001$). Specifically, we found that the average abundance of leaf, bud, and apical-stem galls varied 10-, 8-, and 1.4-fold among willow genotypes, respectively (Fig. 2A-C), resulting in 69% dissimilarity in the average composition of gall communities ($F_{22,89} = 1.96$, $P = 0.001$). Moreover, we found that the average diameter of leaf galls varied 2-fold among willow genotypes (Fig. 2D). This observed genetic specificity in the abundance and phenotypes of insect herbivores corroborates decades of work in other plant-gall (8, 11, 21) and plant-herbivore systems (12, 15).

Importantly though, our extensive screening of willow phenotypes (*Materials and Methods*) enabled us to determine the traits mediating the genetic specificity of the willow-gall interaction network. In particular, we found that leaf C:N, certain leaf secondary metabolites (flavanones/flavanonols PC1), and plant size were associated with changes in the abundance of galling insects (multivariate GLM, $\chi^2_{3,104} = 28.44$, $P = 0.004$; Table S3), whereas leaf gall diameter was determined by variation in a different suite of leaf secondary metabolites (salicylates/tannins PC1 and flavones/flavonols PC1)(weighted linear model, $F_{2,59} = 8.27$, $P < 0.001$; Table S3). These results highlight

that accounting for intraspecific variation in multiple plant traits is important for predicting antagonistic interactions between plants and insect herbivores (19), and should therefore be incorporated into mechanistic models of food web structure.

Quantifying the genetic specificity of the gall-parasitoid interaction network. We found that the effects of willow genetic variation extended beyond pairwise interactions with herbivores (11, 12, 15) and simple food chains (8–10, 21) to determine the assembly of the gall-parasitoid interaction network (multivariate GLM, $\chi^2_{25,119} = 357.10$, $P = 0.001$; Table S1). In particular, we found that the frequency of parasitism from three parasitoids (*Platygaster* sp., *Mesopolobus* sp., and *Torymus* sp.) on leaf galls varied 270%, 30%, and 40% among willow genotypes, respectively (Fig. 3A-C), resulting in 78% dissimilarity in the average composition of gall-parasitoid interactions ($F_{12,45} = 1.57$, $P = 0.007$). In addition to the abundance of trophic interactions, the probability of a gall being parasitized also depended on willow genotype (Table S1), a pattern that was particularly strong for leaf galls (Fig. 3D).

The genetic specificity of the gall-parasitoid interaction network was determined by variation in both the abundance and size of galling insects. Specifically, we found that the abundance of 67% (8 of 12) of the gall-parasitoid interactions increased with the abundance of their associated galls, and that leaf gall size affected the abundance of trophic interactions with both leaf and bud galls (multivariate GLM, $\chi^2_{4,76} = 179.80$, $P = 0.001$; Table S3). In terms of interaction strength, we found that the odds of a leaf gall being parasitized decreased by 25% with every 1 mm increase in leaf gall diameter (GLM,

$\chi^2_{1,79} = 22.28, P < 0.001$). Nevertheless, the strength of trophic interactions with individual parasitoid species depended on both leaf gall size and abundance (Fig. 5A-B; Table S4), suggesting that natural selection has the potential to shape food web structure. For example, if there were selection on willows for increased resistance to leaf galls through smaller galls and lower gall abundances, then we would expect to see more parasitism overall and a shift in dominance from *Platygaster* to *Mesopolobus*, since *Mesopolobus* had its highest attack rates on small galls at low abundances (Fig. 5A). While our results are limited to examining the effects of standing genetic variation on a tri-trophic food web over a single season, there is ample evidence from other studies that eco-evolutionary dynamics can play an important role in determining pairwise, consumer-resource interactions (22, 23). Taken together, understanding how evolutionary processes affect the structure of ecological networks, and vice versa (24, 25), is likely a fruitful topic for future research.

Intraspecific genetic variation increases network complexity. To test this hypothesis, we used our empirical data to predict how the complexity of the plant-insect food web would change across different levels of genetic variation (no. of genotypes) in the plant population (*Materials and Methods*). We found that the genetic specificity of the willow-gall and gall-parasitoid interaction networks resulted in a 50% increase in average food web complexity over the range of willow genetic variation (Fig. 6A). In part, this positive relationship is due to random draws of genotypes with complex food webs (i.e. sampling effects, 26). However, the average complexity of food webs in polycultures with six or more genotypes was always greater than our expectation from sampling effects alone

(dashed line, Fig. 6A). Indeed, we found that willow genotypes differed by 73% in the average composition of their trophic interactions (Fig. 6B), suggesting that complementarity was an important contributor to the positive relationship between genetic variation and food web complexity. It is important to note though, that this analysis is limited to estimating the potential additive effects of genetic variation on food web structure. We do know that host plant genetic variation can have non-additive effects on the diversity of upper trophic levels (27, 28), but determining whether there are non-additive effects on the strength and composition of species interactions will require additional experimental work.

Our results clearly indicate that genetic variation in a host plant affects food web structure; however, there is a growing literature documenting the effects of genetic variation in herbivores and predators from a variety of taxa on community dynamics and ecosystem processes (14, 29–31). Network theory may be able to guide such empirical research by examining whether genetic variation at key nodes (e.g. keystone species) enhances the robustness of ecological networks compared to nodes of less structural importance. This direction will lend insight to a pressing question in community genetics research: what is the relative importance of genetic variation for predicting and maintaining community and ecosystem processes (32–34)?

Conclusions

Our results demonstrate that changes in genetic variation of a host plant species can fundamentally alter food web complexity and therefore the persistence of food webs.

There are two main conclusions from our work. First, intraspecific variation in multiple traits is an important driver of network structure; therefore, mechanistic models of food web structure should incorporate such variability within species (7), as this can enhance the accuracy of these models in predicting trophic interactions (35). Given that plants, insect herbivores, and their parasitoids comprise over half of all known species of metazoans (36, 37), accounting for intraspecific variation in a wide range of functional traits should be a priority for future food web models (38). Second, understanding the direct and indirect effects of genetic variation on trophic interactions is essential for predicting how evolutionary processes will affect the structure and persistence of food webs over time. Indeed, our analysis suggests that the loss of genetic variation will result in less complex food webs. Moreover, genetic variation provides the raw material for evolution by natural selection; therefore, losing genetic variation in key species may hinder the adaptive capacity of both the species and the food web under future environmental change (39, 40). Given that the current rate of population extinction is orders of magnitude higher than the rate of species extinction (41), our study highlights the pressing need for both theoretical and empirical work to further test how the loss of genetic variation within and among populations will affect food webs and the ecosystem services they provide (31, 42).

Materials & Methods

Common garden and plant trait sampling. To isolate the effects of coastal willow (*Salix hookeriana*) genetic variation on the plant-insect food web, we used a common garden experiment consisting of 26 different willow genotypes (13 males; 13 females),

located at Humboldt Bay National Wildlife Refuge (HBNWR) (40°40'53"N, 124°12'4"W) near Loleta, California, USA. Willow genotypes were collected from a single population of willows growing around Humboldt Bay. This common garden was planted in February 2009 with 25 clonal replicates (i.e. stem cuttings) of each willow genotype in a completely randomized design in two hectares of a former cattle pasture at HBNWR. Willows in our garden begin flowering in February and reach their peak growth in early August. During this study, willows had reached 2 - 4 m in height. Further details on the genotyping and planting of the common garden are available in (19) .

To identify the plant traits that determine resistance to galling insects, we measured 40 different traits associated with leaf quality (36 traits) and plant architecture (4 traits). Each of these 40 traits exhibited significant broad-sense heritable variation (i.e. proportion of variance due to willow genotype) (mean leaf quality $H^2 = 0.72$; mean architecture $H^2 = 0.27$; range of H^2 for all traits = 0.15 - 0.97). For further details on how these willow traits were sampled and quantified, see methods in (19). We then reduced these 40 traits into 13 composite traits that had a negligible degree of multicollinearity using either principle components analysis (PCA), sequential regression (residuals of one trait after accounting for correlation between two traits), or removing one trait from a pair of highly correlated traits (details on methods in 19). The final set of leaf quality traits included salicylates/tannins PC1, flavones/flavonols PC1-2, phenolic acids PC1-2, flavanones/flavanonols PC1 (Table S3 of 19), Carbon : Nitrogen (C:N), water content, specific leaf area (residuals from water content), and trichome density. The final set of plant architecture traits included plant size, plant height (residuals from plant size), and

foliage density (residuals from plant size).

Quantifying the genetic specificity of plant-insect food web structure. To quantify the plant-insect food webs associated with each willow genotype, we collected galls from about 5 randomly chosen replicates of each genotype in September 2012 (N = 145 willows, range = 4 - 9 replicates per genotype). For each replicate willow, we collected all galls occurring on one randomly selected basal branch. We restricted our gall collections to those induced by midges in the insect family Cecidomyiidae. These species included a leaf gall (*Iteomyia salicisverruca*), bud gall (*Rabdophaga salicisbrassicoides*), apical-stem gall (unknown midge species), and mid-stem gall (*Rabdophaga salicisbattatus*). To quantify the abundance of gall-parasitoid interactions, we placed collected galls into 30 mL plastic transport vials (loosely capped at the end), which we maintained at room temperature in the lab for four months. We then opened galls under a dissecting scope and determined whether the gall survived or was parasitized, and if parasitized, the identity of the parasitoid species. In total, we identified five species of hymenopteran parasitoids, including *Platygaster* sp. (Family: Platygastriidae), *Mesopolobus* sp. (Family: Pteromalidae), *Torymus* sp. (Family: Torymidae), *Tetrastichus* sp. (Family: Eulophidae), and an unknown species of Mymaridae (hereafter, Mymarid sp. A), as well as one predatory midge (*Lestodiplosis* sp., Family: Cecidomyiidae). This predatory midge is functionally similar to the other parasitoids so we collectively referred to this natural enemy community as parasitoids for brevity. We omitted from analyses those galls for which we could not reliably determine the cause of mortality. We quantified gall abundance by counting the number of surviving and parasitized larva for

each gall species collected from each branch. For gall size, we measured galls to the nearest 0.01 mm at their maximum diameter (perpendicular to the direction of plant tissue growth).

To quantify the genetic specificity of the willow-gall interaction network, we tested for differences in gall sizes, abundances, and community composition among willow genotypes. For gall size, we analyzed separate linear models with willow genotype as the predictor variable and average gall size as the response variable, but we weighted the analysis by the number of galls used to calculate average gall size. We weighted the linear model because we expected that averages based on more galls reflect a more accurate estimate of the average size of galls found on a willow individual. For gall abundances, we analyzed multivariate generalized linear models (multivariate GLMs, error distribution = negative binomial, link function = log) with willow genotype as the predictor variable and a matrix of gall abundances as the response variables. For gall community composition, we used permutational MANOVA (PERMANOVA) with willow genotype as the predictor variable and a matrix of Bray-Curtis dissimilarities in gall abundances as the response variable. To identify the plant traits mediating resistance to galling insects, we used the same, previous analyses for gall sizes (weighted linear models) and abundances (multivariate GLMs) except that our predictor variables was now a matrix of willow traits. To select a final model of willow traits, we sequentially removed traits based on Akaike information criteria (AIC) to identify a nested set of candidate statistical models. We then used likelihood ratio tests to identify the statistical model of willow traits that best predicted gall abundances or gall sizes.

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300 To quantify the genetic specificity of the gall-parasitoid interaction network, we tested for
301 differences in the abundance, composition, and strength of gall-parasitoid interactions
302 among willow genotypes. For gall-parasitoid interaction abundance and composition, we
303 used the same analytical approach as we did to test for differences in gall abundances (i.e.
304 multivariate GLMs: error distribution = negative binomial, link function = logit) and
305 composition (PERMANOVA, dissimilarity index = Bray-Curtis). For these analyses
306 though, we had a matrix of the abundance (multivariate GLMs) or dissimilarity
307 (PERMANOVA) of unique gall-parasitoid interactions as the response variables. To
308 identify the extent to which gall size and gall abundances determined the abundance of
309 gall-parasitoid interactions, we again used multivariate GLMs except that our predictor
310 variables was now a matrix of gall abundances and gall sizes. We then used the same
311 approach as we did to identify the willow traits that best predicted gall abundances (i.e.
312 AIC and likelihood ratio tests), to identify which gall sizes and abundances best predicted
313 the abundance of gall-parasitoid interactions. For the strength of gall-parasitoid
314 interactions, we used separate GLMs (error distribution = binomial, link function = logit)
315 with willow genotype as the predictor variable and the proportion of galls parasitized as
316 our response variable for each gall species. If we detected an effect on total parasitism
317 rates, then we analyzed separate GLMs for each parasitoid species to determine which
318 parasitoids were driving total parasitism rates. Finally, we again used AIC and likelihood
319 ratio tests to examine whether parasitism rates were due to gall abundances, gall size, or
320 their interaction.

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Intraspecific genetic variation increases network complexity. To test this hypothesis, we used our empirical data to predict the complexity of the plant-insect food web at different levels of willow genetic variation (range = 1 to 25 genotype polycultures). We omitted 1 of the 26 genotypes from this analysis (Genotype U) because we never collected any galls from the branches we sampled. To predict the structure of the average food web associated with each willow genotype (i.e. monocultures), we analyzed a multivariate GLM (error distribution = negative binomial, link function = log) with willow genotype as the predictor variable and an abundance matrix of willow-gall and gall-parasitoid interactions as the response variables. Next, we randomly sampled monoculture food webs from the pool of 25 genotypes (with replacement) for each level of genetic variation (2 to 25 genotype polycultures) and calculated the average abundance of each trophic interaction for each polyculture sample. Finally, we calculated quantitative weighted linkage density, LD_q , as an index of food web complexity (43, 44) for all monoculture and polyculture samples. LD_q is based on Shannon Entropy and is the average of the effective number of prey and predatory interactions for a given species, weighted by their energetic importance (details on how LD_q was calculated are available in the supplementary information). LD_q (hereafter, food web complexity) is less sensitive to variation in sample size compared to other measures of food web complexity (44), making it an appropriate measure of complexity for our quantitative food web. We repeated this sampling 1000 times, resulting in 2,221 unique monoculture and polyculture samples.

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Figure Legends

Fig. 1. Genetic specificity of trophic interactions in a plant-insect food web. This food web represents the trophic interactions aggregated from all plant individuals sampled in this common garden experiment, whereas each genotype subweb represents the trophic interactions aggregated from all plant individuals of the corresponding genotype. The species comprising this food web include a host plant (Coastal willow, *Salix hookeriana*), four herbivorous galling insects, and six insect parasitoids. The four species of galls include, from left to right, the apical-stem gall (*Cecidomyiid* sp. A), bud gall (*Rabdophaga salicisbrassicoides*), leaf gall (*Iteomyia salicisverruca*), and mid-stem gall (*Rabdophaga salicisbattatus*). The six species of parasitoids include, from left to right, *Torymus* sp., *Tetrastichus* sp., *Lestodiplosis* sp., *Mesopolobus* sp., *Platygaster* sp., and unknown species of Mymaridae (Mymarid sp. A). The width of each grey segment is proportional to the number of individuals associated with each trophic interaction. Note that we scaled the width of trophic interactions to be comparable among genotype subwebs, but not between subwebs and the aggregated food web, in order to emphasize the differences among genotype subwebs.

Fig. 2. Conceptual model of how increasing genetic variation (number of shades of green circles) results in greater food web complexity (number of interactions per species). If different genotypes of a basal resource are associated with distinct compositions of trophic interactions (i.e. genetic specificity of trophic interactions), then increasing genetic variation in the resource will result in a more complex food web because of the increase in the number of interactions per species at all three trophic levels. Colors

correspond to different trophic levels (green = basal resource, blue = primary consumer, orange = secondary consumer), while different shapes within each trophic level correspond to different species.

Fig. 3. Coastal willow (*Salix hookeriana*) exhibits genetic variation in resistance to galling herbivores. Among the 26 willow genotypes we surveyed in our common garden experiment, we found that: (A) average abundance of leaf galls varied 10-fold (GLM, $\chi^2_{25,119} = 74.60$, $P = 0.001$); (B) average abundance of bud galls varied 8-fold (GLM, $\chi^2_{25,119} = 55.02$, $P = 0.006$); (C) average abundance of apical-stem galls varied 1.4-fold (GLM, $\chi^2_{25,119} = 44.47$, $P = 0.042$); and (D) average diameter of leaf galls varied 2-fold (weighted linear model, $F_{23,57} = 2.17$, $P = 0.009$). Plots (A – C) display the median (bar within box), interquartile range (IQR = 25th to 75th percentiles, box edges), 1.5 * IQR (whiskers), and outliers (points) for gall abundances (no. per branch) found on each willow genotype. For plot (D), each circle corresponds to the average gall diameter associated with an individual willow and the size of the circle is scaled according to the number of galls used to calculate the weighted average for each willow genotype (diamond). Colors correspond to different gall species (orange = leaf gall, blue = bud gall, grey = apical-stem gall). For all plots, we ordered willow genotypes based on mean leaf gall abundance (low to high).

Fig. 4. Coastal willow (*Salix hookeriana*) exhibits genetic variation in the abundance and strength of gall-parasitoid interactions. Among the 26 willow genotypes we surveyed in our common garden experiment, we found that: (A) leaf gall parasitism by *Platygaster* sp.

varied 270% (GLM, $\chi^2_{25,119} = 79.51$, $P = 0.001$); (B) leaf gall parasitism by *Mesopolobus* sp. varied 30% (GLM, $\chi^2_{25,119} = 50.00$, $P = 0.009$); (C) leaf gall parasitism by *Torymus* sp. varied 40% (GLM, $\chi^2_{25,119} = 60.11$, $P = 0.001$); and (D) the proportion of leaf galls parasitized varied between 0.0 and 1.0 (GLM, $\chi^2_{23,58} = 75.79$, $P < 0.001$). Plots (A – C) display the median (bar within box), interquartile range (IQR = 25th to 75th percentiles, box edges), 1.5 * IQR (whiskers), and outliers (points) for the abundance of gall-parasitoid interactions (no. per branch) associated with each willow genotype. For plot (D), each circle corresponds to the proportion of galls parasitized on each replicate willow and the size of the circle is scaled according to the number of galls used to calculate the weighted average for each willow genotype (diamond). Colors correspond to different gall-parasitoid interactions. As with Fig. 3, we ordered willow genotypes based on mean leaf gall abundance (low to high).

Fig. 5. Variation in the size and abundance of leaf galls on willows determines the strength and composition of gall-parasitoid interactions. (A – B) In general, the proportion of leaf galls parasitized by both *Platygaster* (solid blue line) and *Mesopolobus* (short, dashed green line) decreases as gall size increases, while *Torymus* (dashed orange line) exhibits the opposite pattern. On willows with small leaf galls though (< 8 mm), *Mesopolobus* had the highest attack rate at low gall abundances (1 – 4 leaf galls per branch, N = 46 per parasitoid species), whereas *Platygaster* was the dominant parasitoid at high gall abundances (5 – 22 leaf galls per branch, N = 35 per parasitoid species). Lines correspond to slopes estimated from generalized linear models (GLMs), while each

line type and color corresponds to a different parasitoid species. Points were jittered slightly to avoid overlapping values.

Fig. 6. Increasing genetic variation in coastal willow (*Salix hookeriana*) results in a more complex plant-insect food web due to complementarity in trophic interactions. (A) The average complexity (LD_q , quantitative weighted linkage density) of the plant-insect food web increased by 50% over the range of genetic variation (no. of genotypes) in the experimental population of willows. (B) The average composition of trophic interactions (willow-gall and gall-parasitoid) differs by 73% among willow genotypes (PERMANOVA on Bray-Curtis dissimilarities, $F_{22,89} = 1.90$, $P = 0.001$). For plot (A), open, grey circles correspond to food web complexity of individual samples ($N = 100$ for polycultures of 4 - 20 genotypes; $N = 98$ for polycultures of 3, 21, and 22; $N = 89$ for polycultures of 2 and 23; $N = 1$ for the polyculture of 25; and $N = 25$ for monocultures), whereas solid, blue circles correspond to the average complexity of food webs at each level of genetic variation. The dashed line is the highest level of complexity observed on a single willow genotype and represents the expected magnitude of food web complexity under sampling effects alone. For ordination diagram (B), black letters and grey ovals correspond to the centroid and standard error of the centroid for each willow genotype, respectively, calculated from a constrained analysis of principal coordinates (CAP) on Bray-Curtis dissimilarities.