**Host-plant genotype predicts individual and community phenotypes across diverse environments**

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**Abstract**

**Introduction**

P1. Need for GxE studies.

- Plant genetic effects can have strong effects on plant phenotypes which can have cascading affects on associated communities of organisms, ranging from foliar arthropods to root mychorrizal (Whitham et al. 2012).

- However, the relative importance of plant genotype vs. environmental factors still remains an open question (Hersch-Green et al. 2012, Tack et al. 2012).

- This is important to know because it’ll determine if/when a genes-to-ecosystems approach is warranted (Whitham et al. 2006)

P2. Identifying key gaps in past GxE studies

- Thus far, there have been several studies that examine the relative importance of plant genotype vs. other environmental factors.

- These studies fall into the following categories: common gardens at large spatial scales (think Ayco Tack and a bit of Marc Johnson with scale-dependent hypothesis); manipulating presence of herbivores and seeing how that affects the preference and performance of other herbivores; manipulating access of predators (mainly ants) to see how that affects multi-trophic interactions.

- Few studies actively measure plant traits or other characteristics of the environment to try and understand how the direct and indirect effects of plant genotype and the environment on associated communities.

- Also, the vast majority of this work has examined associated arthropod communities with little attention paid to the diversity of other organisms that inhabit genotypes.

P3. Predictive framework lacking for the importance of Genotype across diverse environments.

- Recent meta-analysis showing the predictive power of plant genotype tends to decrease at higher levels of biological organization (phenotype > community > ecosystem, Bailey et al. 2012). This makes sense intuitively; however, this pattern doesn’t always hold true suggesting the responses may be system specific (Bailey et al. 2012). As a corollary, we would exhibit that genetic correlations in phenotypes would depend on the heritability of a phenotype. In other words, we would expect that phenotypes with a high degree of heritability would be more predictable, even across diverse environments.

P4. Summarize what we did and the questions we examined.

- Here, we use multiple common garden experiments to quantify the relative importance of host-plant genotype vs. the environment in shaping individual- and community-level phenotypes of the willow *Salix hookeriana* in a coastal dune ecosystem.

- Prior work in this system has shown that willow genotypes host distinct herbivore communities and that multiple plant traits are important in determining community assembly (Barbour et al. 2015).

- We addressed the following questions: (1) Does the type of environmental stressor influence the effect of plant genotype on individual and community phenotypes? (2) Does the relative importance of plant genotype decrease at higher level of biological organization (i.e. from individual to community phenotypes)?

Methods

*Study Site*

We conducted this research at Lanphere Dunes (40**°** 53’29.85”N, 124**°** 8’49.06”W), a pristine coastal dune ecosystem managed by US Fish and Wildlife service in Humboldt County, California. Coastal willow (*Salix hookeriana* ex Barratt ex Hooker) naturally occurs in nearshore dune swales – seasonal freshwater wetlands that form in depressions between dune ridges (Pickart 2009). Aside from coastal willow (hereafter willow), the dominant vegetation in these swales consists of beach pine (*Pinus contorta* ssp. *Contorta*) and slough sedge (*Carex obnupta*).

During preliminary surveys, we qualitatively identified two important sources of environmental variation for willows in the dune swale habitat – wind exposure and aphid herbivory. Willows growing in wind-exposed habitats often exhibit reduced growth, especially at the their leading edge, appearing to be “swept back” by the wind (Fig. 1a). In prior work, we showed that abundance of several herbivore species and guilds was positively associated with willow size (Barbour et al. 2015). Therefore, we hypothesized that willows growing in wind-exposed areas would exhibit reduced growth, which in turn would result in lower arthropod richness and abundance.

For willows in this coastal dune ecosystem, the aphid *Aphis farinosa* was an abundant herbivore in 2012. *Aphis farinosa* is usually found at the tips of new shoot growth where they feed on willow phloem. Phloem is high in sugars, but low in proteins, so aphids have to ingest large volumes of phloem to get a balanced diet (cite). As a result, aphids excrete carbohydrate-rich honeydew, which attracts ants that tend the aphids and feed on the honeydew (citation). This ant-aphid interaction is often mutualistic, because the ants will defend aphids from predatory arthropods (citation). The ant species we observed most frequently tending *A. farinosa* was the western thatching ant, *Formica obscuripes* (Fig. 1b). *F. obscuripes* colonies create distinct dome-shaped mounds from nearby plant-material. Since ants will defend aphids from predatory arthropods, we predicted that both *A. farinosa* and *F. obscuripes* would reach higher abundances on willows growing near mounds of *F. obscuripes*. The abundance of *A. farinosa* and *F. obscuripes* could affect the associated arthropod community in several ways. In the absence of *F. obscuripes*, aphids could either inhibit or facilitate the colonization of other herbivore species through a variety of mechanisms, but we would always expect aphids to attract predatory arthropods. However, since *F. obscuripes* is a large generalist predator, we would expect its presence to reduce the abundance of herbivores and other predators.

*Experimental Design*

Prior to bud burst in February 2012, we took shoot cuttings (40 cm length & ~0.5 cm diameter) from one to two replicates of 10 different willow genotypes from a pool of 26 locally collected willow genotypes planted in a large common garden experiment. Details about the establishment of this common garden are given in Barbour et al. (2015). These 10 genotypes displayed substantial variation in both plant-growth and leaf traits (Barbour et al. 2015). Shoot cuttings were soaked in water overnight and then planted in a mixture of 80% perlite, 20% peat moss (dolomite lime added to balance pH) inside ‘cone-tainers’. We grew cuttings under ambient weather conditions outside the greenhouse at Humboldt State University.

Wind experiment – In late May 2012, we planted 200 willow cuttings in a split-plot experimental design at Lanphere Dunes. At 10 different willow patches (blocks), we established an ‘exposed’ and ‘unexposed’ common garden. Each garden consisted of one replicate cutting of each of 10 genotypes randomly planted in 2 m by 0.5 m grid with 0.5 m spacing between plants. The center of exposed and unexposed gardens within each block were the same distance (2 m) from the edge of the willow patch to control for insect accessibility; however, exposed gardens faced prevailing winds during the growing season. To estimate the maximum amount of wind speed (km/h) experienced by exposed vs. unexposed plants, we went out on a windy afternoon in September 2012 (weather station estimated wind speeds of 22 km/h during this period) and use a hand-held anemometer (Kestrel 1000) to measure wind speed at a height of 37 cm aboveground (approximate height of tallest plants in the garden in 2012) in each plot of our experiment. Maximum wind speed measurements were taken over a 30 s period and haphazardly collected on either an exposed or unexposed site first.

Ant-aphid experiment – We established common gardens around 5 different ant mounds (blocks) in late May of 2012. Within each block, we randomly planted 20 cuttings (aphid and control treatment of each of 10 genotypes) with 0.5 m spacing at each distance of 1, 6, and 12 meters from the edge of the ant mound, for a total of 60 cuttings per ant mound (300 cuttings for entire experiment). We removed all arthropods on the willows at the time of planting. On May 22, we collected aphids (*Aphis farinosa*) and placed 5 adult apterate aphids on willow cuttings in the aphid treatment. We bagged aphids onto the apical shoots of cuttings using organza bags to promote aphid establishment in spite of oncoming inclement weather (wind and rain). We also placed organza bags on all control plants as well. On May 27, we checked aphid treatments to ensure there were 5 adult aphids and removed bags from all cuttings. If necessary, we added aphids to these treatments until there were 5 adults and we removed any aphid nymphs that were produced since initial establishment. We checked plants for aphids on June 6, June 13, June 24, July 4, July 14, and July 20, 2012. On May 27, we double-checked willows to ensure that all arthropods (spiders and leaf rollers; except for a couple of stem galls) were removed. Up until May 27, we supplemented planted cuttings with water to promote the survival of cuttings. The ant-aphid experiment was restricted to the summer of 2012, because in the summer of 2013 there was high willow mortality (\_% of plants died by DATE) and *Aphis farinosa* was not in high enough abundance on naturally occurring willows to repeat the aphid treatment.

*Measuring willow phenotypes*

Plant-growth traits – To quantify plant-growth traits, we measured plant height, the number of shoots produced, and average shoot length in late July of each year (end of growing season). We quantified plant height as the distance (mm) from the ground to the tip of the tallest shoot. We quantified average shoot length by measuring every shoot on each plant to the nearest millimeter and calculating the average shoot length for each plant.

Leaf traits – We measured several traits that could shape leaf quality for herbivores, including leaf area, specific leaf area (SLA), water content, trichome density, percentage carbon (C) and nitrogen (N), and C:N. To measure these traits, we excised fully expanded and undamaged leaves from plants in late July of each year, stored leaf samples with a moist paper towel in separate plastic bags within a cooler and immediately brought them back to the laboratory. We then weighed leaves to obtain fresh mass (g), digitally scanned them to measure leaf area (mm2) using ImageJ (Abrámoff, Magalhães, and Ram 2004), and oven-dried them at 60 °C for 72 h to obtain dry weight (g) (Cornelissen et al. 2003). We calculated SLA as (Cornelissen et al. 2003). We calculated leaf water content as the (Munns & PrometheusWiki Contributors 2010). To measure trichome density, we counted the number of trichomes along an 11 mm by 1 mm transect in the center of the leaf, halfway between the leaf edge and the mid-vein, under a dissecting scope. To measure percentage C and N, we ground oven-dried leaves to a fine powder using a ball mill (Mixer/Mill 8000D, SPEX SamplePrep; Metuchen, NJ, USA). Subsamples of each material were then analyzed for percentage C and N on an elemental analyzer (ECS 4010; Costech Analytical Technologies, Valencia, California, USA) using atropine (4.84% N and 70.56% C) as a reference standard.

*Surveying Associated Communities*

Arthropod community – We visually surveyed plants for arthropods to determine the abundances of different (morpho)species. For the wind experiment, we surveyed arthropods once at the end of July 2012 and then once a month in May, June, and July of 2013. For the ant-aphid experiment, we surveyed arthropods on 5 different occasions between early June and late July 2012. So that individuals were not counted twice between sampling dates, we took the maximum abundance for each arthropod (morpho)species from each plant across all sampling dates within each year. This approach provides a conservative estimate of the total number of individuals of each (morpho)species that occurred on individual plants through the summer. Given the relatively low abundances of individual morphospecies, we grouped arthropods at the Family-level for insects and at the Order-level for other arthropods.

Mycorrhizal and Bacterial communities – In late July of 2013, we dug up the willows from the wind experiment in order to sample the mychorrizal and bacterial communities associated with the willow roots. We did not sample the belowground communities of plants in the ant-aphid experiment due to the high mortality of plants in 2013. To sample these belowground communities, we carefully removed dirt until we found all of the living root tissue. We then stored the root tissue of each plant in separate plastic bags within a cooler which were immediately transported back to the lab and kept in a freezer at \_°C until further processing. *(need further details on quantifying the belowground communities from Sonya).*

*Soil characteristics*

Soil nutrients, total organic matter, and moisture may all influence plant phenotypes and the assembly of mychorizzal and bacterial communities on plant roots (cite). Moreover, we expected that wind exposure to affect these soil characteristics (cite); therefore, we measured soil nutrients, percent organic matter, and moisture within each plot of the wind experiment (one exposed and one unexposed plot per block).

To estimate soil nutrient uptake by willows, we installed Plant Root Simulator (PRS) Probes (Western Ag Innovations, Saskatchewan, Canada) at three randomly selected locations within each plot for 11 days in September 2012. PRS Probes estimate nutrient supply rates to roots by continuously adsorbing charged ionic elements over the burial period. For our study, we estimated potential root uptake of NO3+, NH4-, Ca, Mg, K, P, Fe, Mn, Cu, Zn, B, S, Pb, Al, and Cd. From this nutrient data, we calculated total N as NO3+ + NH4-, and then used principal components analysis to condense these nutrients into a single axis (nutrients PC1) that explained 34% of the variation. Nutrients PC1 described the negative correlation between nitrogen compounds (NO3+, NH4-) and the rest of the ionic elements, with positive values indicating high supply rates of all ionic elements except for the nitrogen compounds. To measure percent organic matter content (%OM), we used a trowel to collect soil (depth = 0 – 15 cm) adjacent to the randomly positioned PRS probes in September 2012. Soils were transported back to the lab in plastic bags, sieved into fragments less than 2 mm, randomly subsampled using a soil splitter, and dried at 105 **°**C for 72 hours. We then weighed a subsample of the oven dried soil into an oven dried crucible and placed the crucible and soil into a furnace to be combusted at 375 **°**C for 16 hours. We then weighed the combusted samples, placed them in a desiccator for 20 minutes, and weighed them again. We calculated percent organic matter as . To measure soil moisture (volumetric water content, m3/m3), we used a 5TE soil sensor coupled to an EM50 Digital/Analog Data Logger (Decagon Devices, Pullman, Washington, USA). In September 2012, while PRS probes were in the ground, we measured soil moisture at a depth of 5 cm in three random locations within each plot on three different days between 1100 – 1500 hours. We repeated this same sampling scheme in early July 2013. Plot levels measurements of soil moisture were highly correlated between years (Pearson’s *r* = 0.93, *t*18 = 10.91, P < 0.001), so we averaged these soil moisture estimates to determine a single soil moisture value per plot.

*Predicting individual and community phenotypes*

From these experiments, we only had data on a subset of plant traits and community responses measured from our prior common garden experiment (Barbour et al. 2015). The plant traits included plant height, leaf water content, specific leaf area (SLA), leaf C:N, and leaf trichome density. These traits varied substantially in their broad-sense heritability, from 0.15 for SLA to 0.62 for leaf trichome density. Only two guilds of herbivores, leaf mining moths (Family: Gracilliaridae) and galling midges (Family: Cecidomyiidae), were abundant enough in our prior common garden experiment and our current experiments to compare the broad-sense heritability estimates. We also had data on aggregate herbivore abundance of both experiments, which we also used in our analyses.

*Statistical Analyses*

We used generalized linear mixed-effect models to examine how willow genotype and environmental factors influenced willow phenotypes and univariate community responses (e.g. total abundance, total richness, guild abundance). For the wind experiment, we specified block (willow patch) and plots nested within block (2 wind exposure treatments) as random effects. We specified willow genotype, wind treatment, sampling year, and their 3-way interaction as fixed effects in the model. For some willow phenotypes and guild abundances we did not have data for both years so we removed sampling year from those models. For the ant-aphid experiment, we specified block (ant mound) and plots nested within block (3 different distances from ant mound) as random effects. We specified willow genotype, aphid treatment, distance from ant mound, and their 3-way interaction as fixed effects in the model. For both experiments, we used ‘sum contrasts’ and Type III sum-of-squares in order to reliably test the significance of both main effects and interactions between fixed effects in the full model. For continuous responses (plant height, average shoot length, leaf water content, leaf area, SLA, and leaf C:N) we specified Gaussian error distributions in our models and tested the significance of fixed effects using F-tests with Kenward-Roger approximated degrees of freedom (cite). For count responses (shoot count, trichome density, arthropod richness, and abundance) we specified Poisson error distributions in our models and tested the significance of fixed effects using Wald Chi-square tests. If necessary, we modeled overdispersion in these Poisson models by specifying an individual-level random effect (cite).

For the mycorrhizal and bacterial community data, we used separate redundancy analyses (RDA) to examine how willow genotype, wind exposure, and their interaction influenced the proportional abundance of species (i.e. community composition). To do this, we applied a Hellinger transformation to the community data prior to analysis, as this has been shown to reliably characterize the dissimilarity of diverse communities (Legendre and Gallagher 2001). To test the significance of each term, we compared the observed community dissimilarities to the dissimilarities we would expect by random chance with a permutation test that controls for the blocked design of our experiment.

To examine the effect of wind exposure on maximum wind speed and soil characteristics (total N, nutrients PC1, %OM, and soil moisture), we used separate mixed effect models with wind treatment as a fixed effect and block (willow patch) as a random effect. Since all soil characteristics were continuous responses, we specified Gaussian error distributions in our models and tested the significance of fixed effects using F-tests with Kenward-Roger approximated degrees of freedom (cite).

Calculating Effect Sizes — We used a recently developed method for calculating *R*2 in mixed-effect models (Nakagawa and Schielzeth 2013) to estimate the effect sizes of willow genotype and environmental factors on willow phenotypes and community responses. Prior to calculating *R*2, we fit reduced models with only the significant fixed effects included. If willow genotype and/or its higher-order interactions with the environment were significant, we refit them as random effects. We re-specified genotype as a random effect because preliminary analyses found that treating it as a fixed effect overestimated the variance explained. This is likely because *R*2is estimated without degrees-of-freedom (*df*) correction (Nakagawa and Schielzeth 2013). For example, when willow genotype is specified as a fixed effect it has *df* = 9 whereas each of our environmental factors has *df* = 1, which inherently bias genotype towards a higher amount of variance explained even if it is not significant as a fixed effect. An alternative approach that has been advocated for calculating effect sizes in genotype-by-environment experiments is to treat both genotype and environment factors as random effects (Hersch-Green et al. 2012). However, experimental manipulations of the environment often have a smaller number of levels (e.g. ‘exposed’ and ‘unexposed’ wind treatments) and it is known that mixed-effect models underestimate the variance explained by random effects with a small number of levels (i.e. < 5). Therefore, we feel this hybrid-approach (environment as a fixed effect and genotype as a random effect) is a robust approach for comparing the relative importance of genotype vs. the environment in our study and likely others.

Predicting the effects of willow genotype —To analyze these data, conducted linear regressions to determine whether estimates of broad-sense heritability from the common garden experiment were positively correlated with broad-sense heritability estimates from both of the other experiments. As another way to test these predictions, we calculated the mean values of individual and community phenotypes from the common garden experiment to see whether they predicted the rank order of values from our current experiments. We included experiment type as a covariate in all of these analyses.

All analyses were conducted in R version \_\_ (R Core Team YEAR). All code and data to replicate these analyses has been deposited in Zenodo (DOI: \_\_\_).

**Results**

*Wind experiment*

Willows growing in wind-exposed plots experienced up to 3.7-fold higher wind speeds compared to unexposed plots (F1,9 = 187.32, P < 0.001). Despite these large differences in wind exposure, we observed only modest effects of wind exposure on soil properties. Specifically, soil in wind-exposed plots tended to be drier (F1,9 = 3.52, P = 0.093) with higher amounts of total Nitrogen (F1,9 = 5.08, P = 0.051). There was no difference in percent organic matter (F1,8.4 = 0.68, P = 0.434) or nutrient composition (PC1: F1,9 = 1.31, P = 0.282) between soils in wind-exposed and unexposed plots. Although most of these soil properties were highly correlated (supplementary table), only soil moisture had a detectable effect on plant traits. Soil moisture was positively correlated with plant height (r = 0.58, t18 = 3.03, P = 0.007) and shoot count (r = 0.46, t18 = 2.18, P = 0.043), but negatively correlated with leaf water content (r = -0.58, t18 = -2.99, P = 0.008).

Individual phenotypes:We found that plant-growth traits were influenced by wind exposure, sampling year, and willow genotype (Table 1). Wind exposure negatively affected all plant-growth traits, resulting in willows that were 23% shorter in height (*R2* = 0.07), produced 22% fewer shoots (*R2* = 0.05), and grew 28% shorter shoots (*R2* = 0.04) compared to willows in plots protected from the wind. The negative effects of wind on plant growth traits were primarily due to direct effects of wind pruning (height std. = -0.28; shoot count std. = -0.21) rather than an indirect effect mediated by reduced soil moisture (height std. = -0.08; shoot count std. = -0.05)*.* For both plant height and the number of shoots, the negative effects of wind exposure were magnified in 2013 compared to 2012 (plant height, EWINDEYEAR *R2* = 0.02; shoot count, EWINDEYEAR *R2* = 0.02). Sampling year had a large effect on plant-growth traits; by the second year of the experiment, willows were 39% shorter in height (*R2* = 0.24) and grew 43% shorter shoots (*R2* = 0.13). Willow genotype also had a pronounced effect on all plant-growth traits, resulting in willows that varied 2-fold in height (*H2* = 0.12), 2.3-fold in number of shoots (*H2* = 0.11), and 2.2-fold in shoot length (*H2* = 0.07) among the most disparate genotypes. Although willow genotype explained more of the variance in plant-growth traits than wind exposure, the aggregate effects of the environment (Ewind + Eyear + EwindEyear) were often more important (plant height: environment *R2* = 0.35; shoot count: environment *R2* = 0.10; shoot length: environment *R2* = 0.17).

In contrast to plant-growth traits, willow genotype was the primary factor in determining leaf traits across both years of the experiment (Table 1). The leaves of willow genotypes varied 46-fold in trichome density (*H2* = 0.65), 1.5-fold in SLA (*H2* = 0.25), and 1.6-fold in C:N (*H2* = 0.25). We had data available on leaf water content for 2012 and 2013, and we found that the broad-sense heritability of leaf water content depended on the sampling year (2012, *H2* = 0.11; 2013, *H2* = 0.16).

Community phenotypes: The responses of the arthropod community mirrored those of plant-growth traits, depending on wind exposure, sampling year, and willow genotype (Table 1). The composition of the arthropod community differed between wind-exposed and unexposed willows, with wind-exposed willows having higher relative abundances of aphids and leaf-tiering moths. This was because aphids and leaf-tiering moths were insensitive to wind exposure, while other key arthropod taxa (gall midges, leaf mining moths, and spiders) were much less abundant on wind-exposed willows (Table 1). The negative response of these key arthropods to wind exposure resulted in 51% fewer species (*R2* = 0.10) and 47% fewer individuals (*R2* = 0.03) on willows in wind-exposed plots. The negative effect of wind exposure on arthropod richness was not solely due to lower arthropod abundance, as rarefied richness was also 60% less on wind-exposed willows (*R2* = 0.20). Overall, these negative effects of wind exposure were primarily mediated by an indirect effect on plant height (abundance, std. = ; richness, std. = ) rather than a direct effect of being exposed to a more windy environment (abundance, std. = ; richness, std. = ).

Willow genotype also had a strong effect on the arthropod community, with the majority of the key taxa varying in abundance among willow genotypes (Table 1), but with little coherence in their responses (i.e. no genetic correlation, Table \_). Still, willow genotype influenced arthropod richness and abundance, with arthropods varying 3.1-fold in richness (*R2* = 0.04) and 4.7-fold in abundance (*R2* = 0.06) among the most disparate willow genotypes (Table 1). Unlike wind exposure, the effect of willow genotype on arthropod richness appeared to be solely due to abundance, as rarefied richness did not differ among willow genotypes (Table 1).

In contrast to the arthropod community, the richness and abundance of root-associated fungi and bacteria did not appear to be influenced by wind exposure or willow genotype (Table 1). However, the composition of both mycorrhizal and bacterial communities were distinct between wind-exposed and unexposed plots (Table 1). In addition, we observed distinct differences in the mycorrhizal, but not bacterial, communities of willow genotypes (Table 1).

*Ant-aphid experiment*

Individual phenotypes:In contrast to the wind experiment, we found that both plant-growth and leaf traits were influenced solely by willow genotype in the ant-aphid experiment (Table 2). For example, willow genotypes varied 2-fold in plant height (*H2* = 0.27) and 30-fold in leaf trichome density (*H2* = 0.76). We also observed strong effects of willow genotype on the number of shoots produced (*H2* = 0.16) and shoot length (*H2* = 0.15), but there was little apparent effect of willow genotype on leaf water content in this experiment (Table 2).

Community phenotypes: In contrast to the plant traits, the responses of the arthropod community were contingent on the presence of aphids, distance from mounds of *F. obscuripes*, and willow genotype (Table 2). In the presence of *A. farinosa*, the abundance of other arthropods increased 1.8-fold on willows that were further from mounds of *F. obscuripes*, an effect that was primarily driven by leaf-mining herbivores (Family: Gracilliaridae). The presence of *A. arinose* also modified the effect of willow genotype on arthropod abundance, an effect that was primarily due to the response of other aphids. In spite of these biotic interactions, willow genotype still had a strong effect on the richness and abundance of arthropods, which varied 2.6- and 4-fold, respectively, among the most disparate willow genotypes. The effect of willow genotype on arthropod richness appeared to be due to correlated responses in arthropod abundance, as willow genotype had no effect on the rarefied richness of arthropods.

**Discussion**

Key Findings:

- Biotic interactions had little effect on willow phenotypes, but directly affected the willow’s associated arthropod community. Still, genotype was the primary determinant of variation in its phenotype and its associated community.

- Abiotic interactions had strong effect on willow growth traits, which had strong indirect effects on the richness, abundance, and composition of the arthropod community. However, genotype was still comparable in its effects on willow growth traits and its associated arthropod community. However, the traits we measured were insufficient to explain the effect of willow genotype on the arthropod community. This result has repeated itself in previous work in this system (Barbour et al. 2015). To date, the functional trait approach (quantifying easy to measure traits) is failing in its ability to predict arthropod community responses. How do we improve this? I think it will involve careful consideration of which plant traits arthropods are responding too. We also, don’t really have a good sense for how much of the variation we should expect traits to explain. Is it all of it? Perhaps we need to start incorporating stochasticity into arthropod community ecology. This may give us a more realistic benchmark for how much variation we expect to be explained by plant traits.

**Acknowledgements**

**References**

**Figures**

**Figure Legends**

**Tables**

**Table 1**:

|  |  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- | --- |
| Response | Genotype (G) | Ewind | GEwind | Eyear | GEyear | EwindEyear | GEwindEyear |
| **Plant-growth traits** |  |  |  |  |  |  |  |
| Plant height | **7.46** | **26.87** | 0.79 | **183.73** | 1.05 | **9.70** | 1.62 |
| Shoot count | **54.02** | **11.74** | 11.58 | 2.39 | 15.12 | **9.91** | 5.78 |
| Shoot length | **4.70** | **9.86** | 0.80 | **75.07** | 1.43 | 0.11 | 0.70 |
| **Leaf traits** |  |  |  |  |  |  |  |
| Trichome density2012 | **81.35** | 0.11 | 10.77 | - | - | - | - |
| C:N2013 | **4.98** | 0.74 | 1.30 |  |  |  |  |
| Water content | **4.89** | 0.93 | 0.44 | 2.51 | **2.73** | 1.80 | 1.56 |
| SLA2013 | **5.89** | 0.44 | 0.86 | - | - | - | - |
| **Root traits** |  |  |  |  |  |  |  |
| C:N2013 | 0.91 | 0.23 | 0.30 | - | - | - | - |
| **Arthropods** |  |  |  |  |  |  |  |
| Total abundance | **28.63** | **10.96** | 8.08 | 2.25 | 9.88 | **3.90** | 11.54 |
| Total richness | **26.39** | **21.60** | **3.39** | 4.31 | 8.28 | 0.63 | 7.02 |
| Total PIE | 1.65 | **8.74** | 1.61 | 0.04 | - | 1.17 | - |
| Leaf-mining moths (Gracilliaridae) | **17.15** | **9.42** | - | **4.26** | - | 0.09 | - |
| Gall midges (Cecidomyiidae) | **19.26** | **17.59** | - | **38.07** | - | - | - |
| Leaf-tiering moths (Tortricidae) | **24.78** | 1.34 | 11.50 | **117.19** | - | 2.65 | - |
| Aphididae2012 | 4.31 | 0.32 | - | - | - | - | - |
| Spiders | 8.27 | **6.04** | - | **6.54** | - | 0.20 | - |
| **Mychorrizae2013** |  |  |  |  |  |  |  |
| Total abundance | 1.01 | 0.95 | 1.03 | - | - | - | - |
| Total richness | 1.65 | 1.85 | 1.23 | - | - | - | - |
| Community composition | **1.00** | **2.07** | 0.87 | - | - | - | - |
| **Bacteria2013** |  |  |  |  |  |  |  |
| Total abundance | 1.25 | 2.18 | 0.64 | - | - | - | - |
| Total richness | 1.30 | *4.17* | 0.87 | - | - | - | - |
| Community composition | 0.93 | **1.99** | 0.87 | - | - | - | - |

|  |  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- | --- |
| **Response** | **Genotype (G)** | **Eaphid** | **Eant** | **GEaphid** | **GEant** | **EaphidEant** | **GEaphidEant** |
| **Plant-growth traits** |  |  |  |  |  |  |  |
| Plant height | **15.39** | 0.19 | 0.38 | 0.93 | 0.95 | 0.16 | 1.62 |
| Shoot count | **60.40** | 0.60 | 0.38 | 10.67 | 8.29 | 2.76 | 9.17 |
| Shoot length | **6.55** | 1.67 | 0.30 | 1.07 | 0.68 | 0.88 | 0.56 |
| **Leaf traits** |  |  |  |  |  |  |  |
| Trichome density | **46.99** | 0.22 | 0.34 | - | 8.79 | 0.43 | - |
| Water content | 1.56 | 0.01 | 0.17 | - | 0.87 | 0.44 | - |
| **Arthropods** |  |  |  |  |  |  |  |
| Total abundance | **43.44** | *3.08* | 0.79 | **18.15** | 10.13 | **7.96** | 0.36 |
| Total richness | **46.74** | 2.49 | 0.68 | 7.67 | 8.91 | 0.86 | 6.60 |
| Total PIE | 1.09 | 1.49 | 2.04 | 1.54 | 0.88 | 0.03 | 0.67 |
| *Aphis farinosa* | **18.17** | - | 1.21 | - | 9.33 | - | - |
| *Formica obscuripes* | R | **7.45** | *3.10* | - | - | - | - |
| Gracilliaridae (leaf mines) | **35.43** | 1.56 | **5.21** | 11.41 | *15.06* | **4.19** | - |
| Tortricidae (leaf tiers) | **24.55** | 0.03 | **11.87** | - | - | *3.65* | - |
| Aphididae (non-*Aphis*) | **30.89** | 0.07 | 0.52 | **19.00** | 5.87 | *3.82* | 6.88 |
| Spiders (predators) | *14.61* | 0.24 | 0.93 | 12.28 | 8.85 | 0.01 | - |
| Formicidae (non-*F. obscuripes*) | **20.65** | **14.71** | 1.29 | 4.89 | 6.76 | 0.73 | - |
| Cicadellidae (sap feeder) | **18.88** | 0.85 | 2.13 | 6.65 | 10.15 | 1.68 | - |