**Introduction**

Plant genes determine individual phenotypes, which can have cascading effects on associated species and entire communities of organisms (Fritz & Price 1988; Maddox & Root 1990; Antonovics 1992; Lamit *et al.* 2015) . While the importance of plant genes for associated communities is well established in common gardens where environmental variation is minimized, the relative importance of plant genotype vs. the environment still remains an open question (Hersch-Green *et al.* 2011; Tack *et al.* 2012; Crutsinger 2015) . Addressing this question is critical for understanding the dynamic interplay between ecological and evolutionary processes in shaping communities (Johnson & Stinchcombe 2007; Hughes *et al.* 2008; Hersch-Green *et al.* 2011) .

In genotype-by-environment studies, “environment” is often a catch-all term that encompasses a diversity of abiotic and biotic factors. For example, many studies manipulate the environment by planting common gardens in distant locations that likely differ in both abiotic (e.g. soil properties) and biotic (e.g. species pool) factors. This work has provided invaluable insight to the importance of spatial scale (Johnson & Agrawal 2005; Tack *et al.* 2010; Silfver *et al.* 2015); however, it is difficult to tease apart the effects of the many abiotic and biotic factors that could affect community assembly. Studies conducted at smaller spatial scales are advantageous in that they can focus on a single abiotic or biotic factor (Johnson 2008; Abdala‐Roberts *et al.* 2012; Abdala‐Roberts & Mooney 2013); still though, we have a limited understanding of the relative importance of local abiotic and biotic factors in shaping communities associated with host-plants.

While there have been several studies examining the joint contribution of the environment and host-plant genotype to associated communities, the processes generating community responses often remain unclear (Hersch-Green *et al.* 2011; Crutsinger 2015). This is because many studies do not measure the plant phenotypes mediating the interactions between plant genotype and the associated community. Identifying these key phenotypes is also crucial for teasing apart the direct and indirect (via plant traits) effects of the environment on community assembly. Indeed, we should be able to predict which phenotypes are more likely to be influenced by the environment based on prior estimates of heritability. Heritability measures the proportion of variance in a phenotype explained by genotype (Lynch & Walsh 1998); therefore, we expect that traits with low heritability are more likely to be altered by the environment compared to traits that are highly heritable. This can have important consequences for predicting community assembly depending on whether species are cueing in on traits that are weakly or strongly heritable.

Host-plants are usually colonized by a diverse group of organisms, including arthropods, fungi, and bacteria; however, most studies examine the associations between host-plant genotype and a particular taxonomic group (reviewed in Whitham *et al.* 2012; but see Crutsinger 2014; Lamit *et al.* 2015). In particular, the majority of studies have been conducted on aboveground arthropods, with comparatively little attention given to belowground mycorrhizal and bacteria communities. As a consequence, it is unclear whether these diverse communities exhibit similar or different responses to genetic and environmental variation. A recent meta-analysis of the well-studied introgression between *Populus fremontii* and *Populus angustifolia* suggests that aboveground arthropods are more tightly coupled to host-plant genotype than belowground microbes/fungi (Bailey *et al.* 2009). However, there has been little work that has simultaneously examined above- and belowground community responses within genotype-by-environment studies.

Here, we use common garden experiments to examine how host-plant genetics as well as the abiotic and biotic environment structure communities associated with the willow *Salix hookeriana* in a coastal dune ecosystem. Prior work in this system has shown that willow genotypes host distinct arthropod communities and that multiple plant phenotypes are important in determining community assembly (Barbour *et al.* 2015, 2016). Importantly, these phenotypes varied substantially in the degree of heritability (plant growth, mean *H*2 = 0.26; leaf quality, mean *H*2 = 0.72), suggesting that the environment may differentially influence them. We sought to address the following questions: (1) what is the relative importance of willow genotype vs. the abiotic and biotic environment in determining willow phenotypes and associated communities? (2) What are the mechanisms by which willow genetic and environmental variation affects community responses? (3) Do host-associated arthropods, fungi, and bacteria exhibit similar or contrasting responses to willow genetic and environmental variation?