CORRELATIONS BETWEEN TRAITS IN LOBLOLLY PINE,INCLUDING INTERACTIONS WITH MYCORRHIZAL FUNGI

Bridget J. Piculell[1], C. Dana Nelson[2], James Roberds[1], and Jason D. Hoeksema[1]

Genetic correlations between traits may influence how species respond to both natural and artificial selection. Loblolly pine (*Pinus taeda*) is important both as an economic crop and as a wide-ranging dominant species throughout the southeastern United States. It is subject to natural selection from both biotic and abiotic sources, as well as artificial selection for favorable economic traits (such as disease resistance). Mycorrhizal fungi are common symbionts of most plants, including pines, deriving mineral nutrients from the soil and transferring them to the host, while the host provides carbohydrates to the fungi. Mycorrhizal fungi have also been shown to affect essential host traits such as drought and disease tolerance. Loblolly pine interacts with a diverse guild of ectomycorrhizal fungi, with host plants capable of simultaneous interaction with several fungal partners, each of which may play an important role in nutrient acquisition and soil health. We investigated the underlying genetic structure of multiple traits in loblolly pine. Specifically, we measured traits of 140 loblolly genotypes (each clonally triplicated) in a pedigree population to determine i) the narrow-sense heritability of traits, and ii) the degree to which these traits are genetically correlated with one another and with single-nucleotide polymorphisms (SNPs) in loblolly candidate genes.

In this field study, we found significant narrow-sense heritability for both above- and below-ground pine traits, including susceptibility to the disease-causing fusiform rust (*Cronartium fusiforme*), resistance to attack by tip moth (*Rhyacionia* sp.), compatibility in forming mycorrhizae with particular fungal species, and overall mycorrhizal fungal diversity. We also found significant additive genetic correlations between pairs of these traits, and associations between several of these traits and SNPs located in loblolly candidate genes. These results shed light on the underlying genetic structure of coevolving traits and how it may affect the evolution and adaptation of species. In addition, understanding the genomic architecture of how important adaptive traits are related to one another is an essential component of successful breeding and management strategies. Breeding practices that focus on one or a few traits, while neglecting other important traits may be inadvertently selecting for suboptimal genotypes, especially if variation in local planting site conditions are not considered.

---

[1] University of Mississippi, Oxford, MS

[2] Southern Research Station, Southern Institute of Forest Genetics, USDA Forest Service, Saucier, MS and Forest Health Research and Education Center, University of Kentucky, Lexington KY