BROAD-BASED TESTING COMPARED TO LOCAL TESTING OF FAMILIES OF LOBLOLLY PINE FOR RESISTANCE TO FUSIFORM

Jesse Spitzer[1], Steve Mckeand, Ross Whetten, Fikret Isik

[1]North Carolina State University Tree Improvement Program, Raleigh, NC

Breeding Loblolly pine *Pinus taeda* L. trees with resistance to fusiform rust is a central focus of Southeast tree improvement programs. Annual losses from this disease are estimated in the range of $24 to $135 million, making it the most economically important disease of loblolly pine. Identification and deployment of pine families with enhanced resistance to fusiform rust across a broad range of sites are critical for the full benefit of breeding programs to be realized. Interactions of families' susceptability/ resistance and specific pathogen avirulence/virulence among sites has been reported both in field trials and in controlled inoculations at the USDA Forest Service Resistance Screening Center in Asheville, NC, but the consistency and utility of these interactions have been limited. We will compare rust breeding values from the a series of trials planted across many sites (the Cooperative's Plantations Selection Seed Source Study - PSSSS) to breeding values from trials established in more narrow geographic regions The PSSSS used 80+ families that were also tested locally in Plantation Selection Diallel trials. By comparing the two breeding values for each family to see how much genotype by environment (e.g. family by virulence) interaction is occurring, we can elucidate any evidence for virulence variation in the locally tested breeding values. It is predicted that locally tested families of loblolly pine are reliable across a wide geographic range and little interaction is occurring.