PREDICTING GENETIC PARAMETERS AND TOLERANCE TO PITCH CANKER IN SLASH PINE

Andrew D Sims[1], Gary F Peter [2], and Jeremy T Brawner [3]

[1] Program Manager, Cooperative Forest Genetics Research Program, University of Florida, Gainesville, FL, USA 32611 (adsims@ufl.edu);
[2] Professor, Forest Genetics and Genomics, University of Florida, Gainesville, FL, USA 32611
[3] Assistant Professor, Forest Pathology, University of Florida, Gainesville, FL, USA 32611

Pitch canker is an increasingly important threat to Southeastern forests, especially in slash pine (*Pinus elliottii* var. *elliottii* Engelm.). Its increasing prevalence in the region due to mechanical damage from increased storm activity has led to concern from private and public stakeholders about poor characterization of tolerance from available germplasm. Traditional testing methodologies established to characterize the genetic mechanisms controlling pitch canker tolerance were limited by poor characterization of *Fusarium* isolate virulence and experiment design limitations. Here we describe an alternative experiment design intended to greatly expand the numbers of families that may be screened and increase the power of differentiating among pine families and pathogen isolates evaluated at the USFS Resistance Screening Center. Using this alternative design, genetic parameter estimates for pitch canker tolerance are presented and their implications for the future development of a deployment-oriented slash pine population are discussed.