

Bulked Fusiform Rust Inocula and Fr Gene Interactions in Loblolly Pine

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Abstract

Fusiform rust disease in loblolly (*Pinus taeda* L.) and slash (*Pinus elliottii* Engelm. var *elliottii*) pine plantations in the southern United States causes multi-million dollar annual losses. The disease is endemic to the region. The fusiform rust fungus (*Cronartium quercuum* sp. *fusiforme*) infects young pine trees and develops galls on stems and branches. Single pathogen gene and single host (pine) gene interactions can predict phenotype (disease expression) with high accuracy (Wilcox et al. 1996). There are nine known pathotype-specific Fr genes in seven loblolly pine families. The R alleles condition resistance to specific genotypes of the fungal pathogen while r alleles do not condition for resistance.

We investigated interactions of R genotypes (seedlings bearing R allele) and r genotypes (seedling bearing r allele) of seven families with 10 bulked inocula. Our specific objectives were to (i) understand the response of pine R and r genotypes to different bulked inocula and (ii) assess the level of virulence in the fungus population that are able to overcome resistance in pine families. Such results would have significant effect on the breeding and disease management in pine plantations. Half-sib progeny of seven loblolly pine families were challenged with 10 different bulked inocula of the fusiform rust fungus and assessed for disease incidence in greenhouse. Progeny of these families were genotyped to identify carriers of known alleles, “R” for resistance or “r” for lack of resistance/susceptibility.

Significant differences were detected among bulked inocula with regards to their ability to incite disease at the family level (F test $Pr < 0.001$). Bulked inocula were also significantly different in virulence against R ($Pr = 0.002$) and r genotypes ($Pr = 0.007$). Across the inocula, disease levels differed significantly among half-sib families ($Pr < 0.001$). Seedlings that carried only r alleles typically exhibited higher disease rates than did carriers of R alleles within each family. Interaction of bulked inocula with R genotypes from seven families was highly significant (< 0.001), but it was not significant with r genotypes because regardless of inocula, r genotypes developed high levels of disease. However, the response of R genotypes varied across inocula. The magnitude of difference (odds ratio) between the R vs. r genotypes for disease incidence within each family varied from 1.0 times to 32 times. The results demonstrate that greenhouse assessments of pathogen virulence against known fusiform rust resistance alleles can detect virulence variation among inocula. Such virulence assessments should be effective guides for the field deployment of plants carrying specific R alleles to regions where inocula samples are observed to show low or no corresponding virulence.

Literature Cited

Wilcox, P.L.; Amerson, H.V.; Kuhlman, E.G.; Liu, B.H.; O’Malley, D.M.; Sederoff, R.R. 1996. Detection of a major gene for resistance to fusiform rust disease in loblolly pine by genomic mapping. Proceedings of the National Academy of Science USA. 93: 3859–3864.

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