

Complementary Pairs Interaction of Resistance Genes and Avirulent Genes in Loblolly Pine: Fusiform Rust Pathosystem Using Diallel Data

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Abstract

Loblolly pine (*Pinus taeda* L.) seedlings from 12 full-sib families were obtained from a 6-parent half diallel mating design. These seedlings were challenged using two inocula of the fusiform rust fungus (*Cronartium quercuum* f.sp. *fusiforme*) at extremely high spore density (250,000sp/ml ~ 300,000sp/ml) with replications in the greenhouse (concentrated basidiospore spray method). Each basidiospore inoculum originated from a mixed gall collection of aeciospores obtained from field-infected trees. Presence or absence of rust galls was recorded at four and half months & nine months after inoculation and infection percentages were calculated. The rust infection rates were high for every full-sib family and were above 90% for most of full-sib families for both inocula. However, the infection in family of 28-321 by 28-301progeny was relatively lower. The analysis showed that the rust infection of 28-321 by 28-301progeny was not significant different from 75% for both inocula. Two pairs of complementary genes could explain the observed percent infection levels in this diallel based on a gene-for-gene hypothesis. The 75% infection in the full-sib family of 28-321 by 28-301 may be explained by epistasis between two resistance genes. The putative genotypes of host parents and virulence compositions of mixed inocula were postulated. A bulk-segregant analysis based on phenotype (gall vs no gall) was used to search for dominant molecular markers associated with the potential resistance genes in the host parents. Few candidate marker polymorphisms were observed between the gall vs no gall bulks and none of the candidates co-segregated with phenotype when tested across the progeny set.

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