

GENETIC BASIS OF FUSIFORM RUST DISEASE RESISTANCE IN LOBLOLLY PINE

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Abstract. Research using RAPD marker/disease phenotype associations to marker tag, map and thereby identify rust resistance genes in loblolly pine is in progress. In a study involving progeny from seven pine mother trees (families) inoculated with basidiospores from six single aeciospore rust isolates (SAIs), four different heterozygous resistance genes have been identified (one each) in four different mother trees. Apart from a single dominant resistance allele at a given locus in each of these four mother trees, other loci (in these four trees) with resistance potential, detectable with our isolates, appear homozygous recessive (lacking resistance). Five to 15 polymorphic RAPD markers now exist for the various resistance genes. A mother tree with dual resistance, two of the previously noted heterozygous resistance genes, has also been recognized in the study. Pine-rust interactions among the isolates and the five studied families clearly fit a gene for gene (complementary genetic system) model with four corresponding gene pairs. This model is expected to increase with regards to gene pairs. Marker and mapping data show that at least three of the four recognized genes reside in the same homologous linkage group in their respective mother trees and are therefore clustered. The position of the fourth gene is not yet determined. In the above noted dual resistance mother tree, the resistance alleles of the two different genes clearly reside on separate homologs in a single linkage group, reflecting their inheritance from two different parents. The observed clustering of resistance genes will impact resistance breeding. The search for additional resistance genes in loblolly and slash pine is continuing.

Keywords: *Pinus taeda*, *Cronartium quercuum* f. sp. *fusiforme*, RAPD markers