GENETIC PARAMETER ESTIMATES FOR FUSIFORM RUST DISEASE FROM A MULTI-ENVIRONMENT TRIAL OF LOBLOLLY PINE (*PINUS TAEDA* L.)

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Fusiform rust, caused by the fungus *Cronartium quercuum* f. sp. *fusiforme*, is an important disease of loblolly pine (*Pinus taeda*) plantations in the Southern United States, causing multimillion dollar losses to landowners. In controlled seedling inoculation trials, fusiform rust resistance segregates within families like a traditional Mendelian gene. However, at the population level in the field, rust resistance appears more quantitative in nature. This is due to the presence of multiple R genes segregating among different families, conferring resistance to different races of the pathogen. In this study, a dataset of 11,987 trees from 68 half-sib families of loblolly pine tested across 10 environments was analyzed to understand the inheritance and patterns of GxE interactions for fusiform rust resistance. Heritability of family means was 0.91, indicating that a substantial amount of phenotypic variation in the field can be explained by genetic differences between families. The type B genetic correlation was 0.77, indicating a small amount of GxE. When the rust resistance breeding values for each family within each environment were ranked, the most resistant and most susceptible genotypes tended to have the same rank across environments and families with moderate levels of resistance showed frequent changes in rank. The results of this study indicate that substantial gain can be made through traditional family selection by exploiting the additive genetic variance component.

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