STABILITY OF FUSIFORM RUST RESISTANCE IN LOBLOLLY PINE

Steve McKeand and Bailian Li'

Abstract:--In a series of 28 progeny trials across a range of rust infection levels (17% to 74%) in the Gulf and Atlantic Coastal Plains, rust infection was assessed at age 8 years for 43 open-pollinated families. Family means for rust resistance from each test were regressed on the site means to develop prediction equations for rust resistance. The slope of each regression (b) is a measure of stability for each family.

Slopes of the mean family rust level - mean site rust level regressions for 28 of the 43 families did not differ significantly from b=1.0 indicating average stability for 8-year rust resistance for the majority of the families. The highly significant GxE interaction sum of squares from the analysis of variance was contributed by relatively few interacting families. Large variation in R-50 values, ranging from a low of 22% to a high of 75%, indicated substantial variation in fusiform rust resistance in loblolly pine.

Keywords: *Cronartium quercuum*, genetic correlation, genetic variation, heritability, *Pinus taeda*

Introduction

Identification of families of loblolly pine that are resistant to fusiform rust across a broad range of sites is critical to realizing the benefits of breeding programs where rust resistance is important. Most breeding and testing programs assess rust resistance in a relatively small number of tests, and no opportunities exist to assess genetic variation and patterns of resistance across a wide range of rust hazard sites. If important genotype x environment (GxE) interactions exist for rust resistance, either due to differential infection levels or due to differences in rust virulence, testing in relatively few locations under a narrow range of infection levels may not be adequate.

Data from the Good General Combiner (GGC) trials established in the mid-1970's by the members of the N.C. State University-Industry Cooperative Tree Improvement Program were used to study GxE for rust resistance across a wide geographic range in the Gulf Coast and Atlantic Coastal Plains.

Cooperative Tree Improvement Program, Department of Forestry, North Carolina State University, Raleigh, NC 27695-8002.

Material and Methods

Details of the experimental design and measurements are in Li and McKeand (1989). Briefly, each test was a randomized complete block with six replications of 10-tree row plots of 30-50 seedlots. Rust infection was assessed at age 8 years for 43 open-pollinated families established in 28 test in the coastal plain from southeast Louisiana to eastern North Carolina. Each of the 43 families analyzed was in at least 6 tests.

Analyses of variance were conducted on plot means to determine the significance of family and site by family interactions. Heritabilities and genetic correlations were calculated using variance and covariance component estimates from the VARCOMP procedure (REML estimates) in SAS (SAS Institute Inc. 1989).

Rust infection across the tests averaged 39%, ranging from as low as 17% to as high as 74%. Mean rust infection for each family and check seedlot was computed for each test site. The test site mean was computed by averaging all the seedlot means at each site (average of 42 seedlots per site), not just those families that were used for the stability analyses.

To determine the genetic stability of rust resistance, family means from each test were regressed on the site means. The slope of each regression (b) is a measure of stability for each family. Families with a slope not significantly different from b=1.0 have an average stability since their rust infection level directly reflects the average rust infection level of a site. Families with slopes > 1.0 are unstable and are more susceptible than average to increased rust. Families with slopes < 1.0 have high stability and are not as sensitive to increases in rust infection levels.

The predicted rust infection that each family in the GGC trial would have if it had been planted on a rust hazard site of 50% (R-50 value) was estimated through the use of regression equations developed in the stability analysis.

Results and Discussion

Highly significant family effects for rust infection across the 28 tests were found (Table 1). Predicted R-50 values ranged from a low of 22.4% to a high of 75.3%. The wide range of family differences is also demonstrated by the high family-mean heritability of 1.0. The heritability is inflated above what we normally see for rust because of the diverse origin of the families. Provenance differences are confounded with the family differences in this trial.

The family x test interaction was highly significant in the analysis of variance (Table 1) suggesting that GxE for rust resistance could be important. Further analysis of the GxE interaction indicated that GxE for rust resistance is of relatively minor importance. The family x test component of variance was only 3.7% of total variation in the study, while the family variance was 3.6 times larger and contributed 13.5% of the total variance.

Slopes of the mean family rust level regressed on the mean site rust level for 28 of the 43 families did not differ significantly from b=1.0 indicating average stability for 8-year rust resistance for 2/3 of the families. The relatively high coefficients of determination (r^2) and examination of residuals indicated that the linear models fit the data well. The highly significant GxE interaction sum of squares from the analysis of variance was contributed by about 1/3 interacting families. As previously reported (Li and McKeand 1989), most of the GxE was of minor importance since it was due to heterogeneous regressions and not family rank change at the different sites.

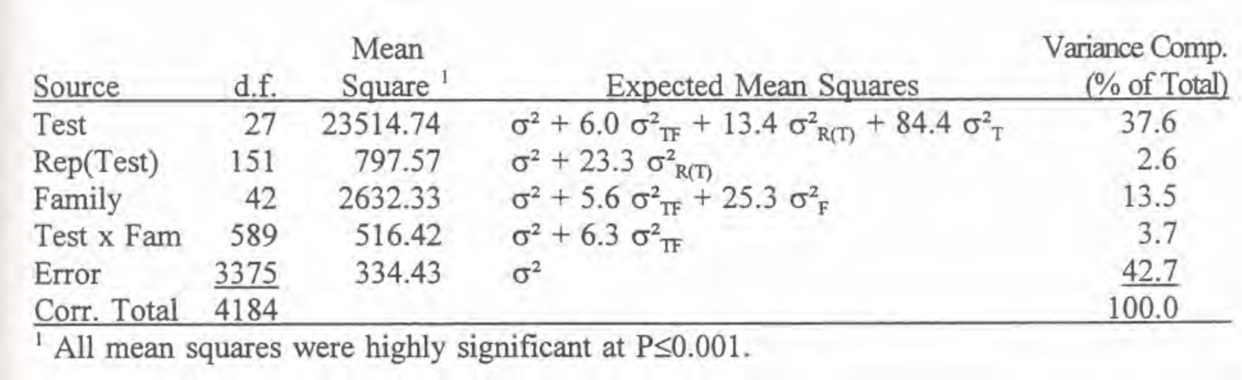
While rust resistance for most families is fairly predictable (average $r^2 = 0.78$), the regression equations for predicting rust resistance are substantially lower than for predicting stem volume in the same tests where average $r^2 = 0.94$ (McKeand et al. 1997). The deviations from regression (e.g. relatively low r^2 values) for the rust regressions suggest more important genotype by environment interactions for rust than for volume. For a family like 11010 (Figure 1) where the $r^2 = .59$, the points that deviate the most from the regression line could be due to 11010's susceptibility or resistance to rust spores of different virulence. No geographic patterns of susceptibility or resistance was evident. For example, 11010 appeared to be very susceptible to rust in the McIntosh, GA test, but in tests in Effingham, GA and Camden, GA the only other tests in that region, the observed rust level was very near the predicted rust level.

The lack of a geographic pattern for differential expression does not preclude the possibility that different virulence strains of fusiform rust exist. Rust virulence variation may not follow any predictable geographic pattern, since we were not able to detect any patterns for resistance or susceptibility.

Deployment Examples

Most families were of average stability and performance (b = 1.0 and intercept = 0), but there were some noted exceptions. About 1/4 of the families were unstable (b > 1.0) for rust resistance. The best example of this type of family is 08061 which would be a poor family to deploy on high rust hazard sites (Figure 1). It's performance is good on low hazard sites (intercept = -10.9) where resistance is not important, but it is very unstable (b = 1.33) and would be susceptible on the high hazard sites.

Table 1. Analysis of variance for % rust infection in the 28 GGC trials at age 8 years.



Source	d.f.	Mean Square [1]	Expected Mean Squares	Variance Comp. (% of Total)
Test	27	23514.74	$\sigma^2 + 6.0\,\sigma^2_{TF} + 13.4\,\sigma^2_{R(T)} + 84.4\,\sigma^2_{T}$	37.6
Rep(Test)	151	797.57	$\sigma^2 + 23.3\,\sigma^2_{R(T)}$	2.6
Family	42	2632.33	$\sigma^2 + 5.6\,\sigma^2_{TF} + 25.3\,\sigma^2_{F}$	13.5
Test x Fam	589	516.42	$\sigma^2 + 6.3\,\sigma^2_{TF}$	3.7
Error	3375	334.43	σ^2	42.7
Corr. Total	4184			100.0

[1] All mean squares were highly significant at $P \leq 0.001$.

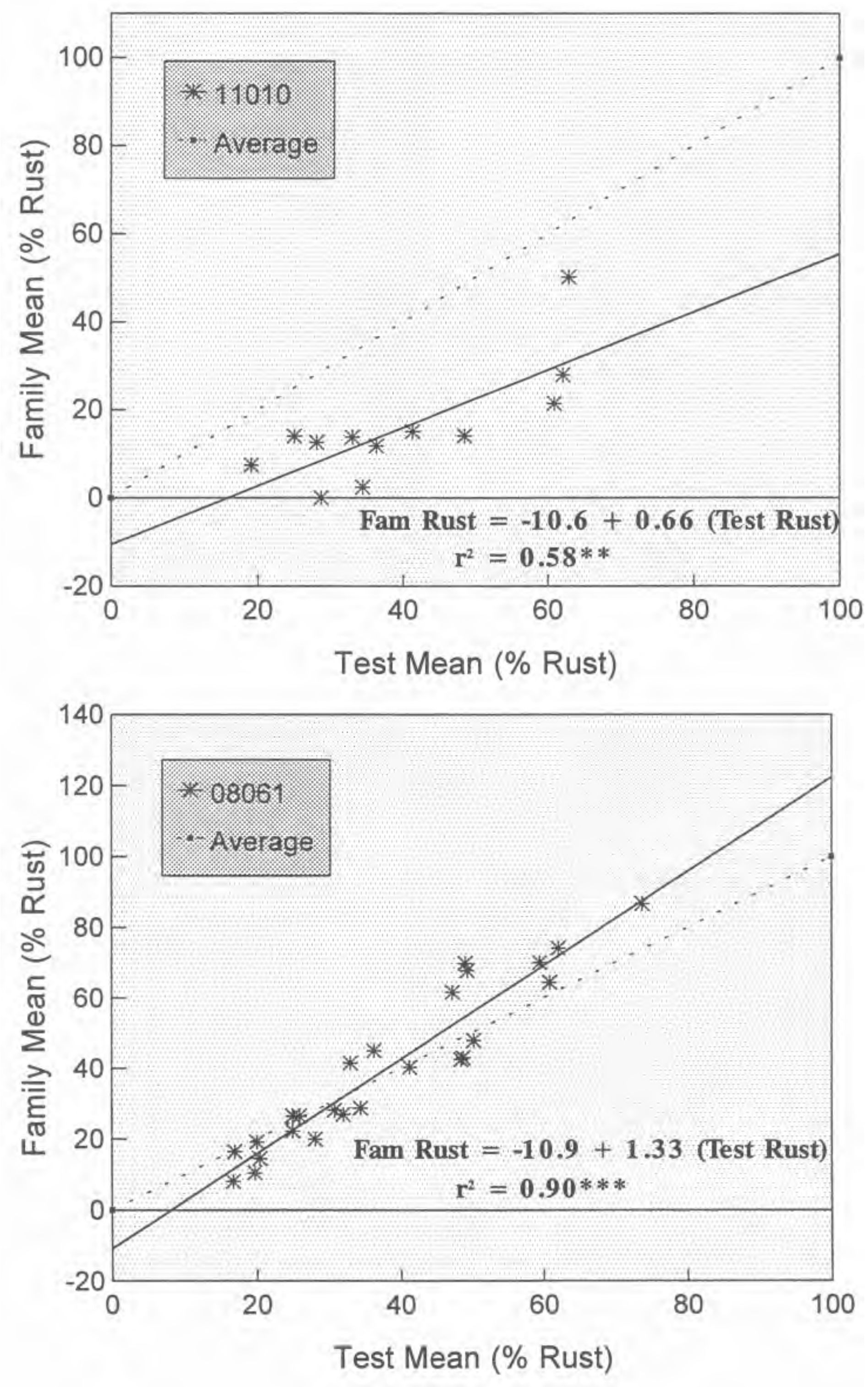


Figure 1. Rust infection for family 11010 (top) and family 08061 (bottom) in the 28 trials used in the stability analyses. (Dashed lines indicate performance of average families).

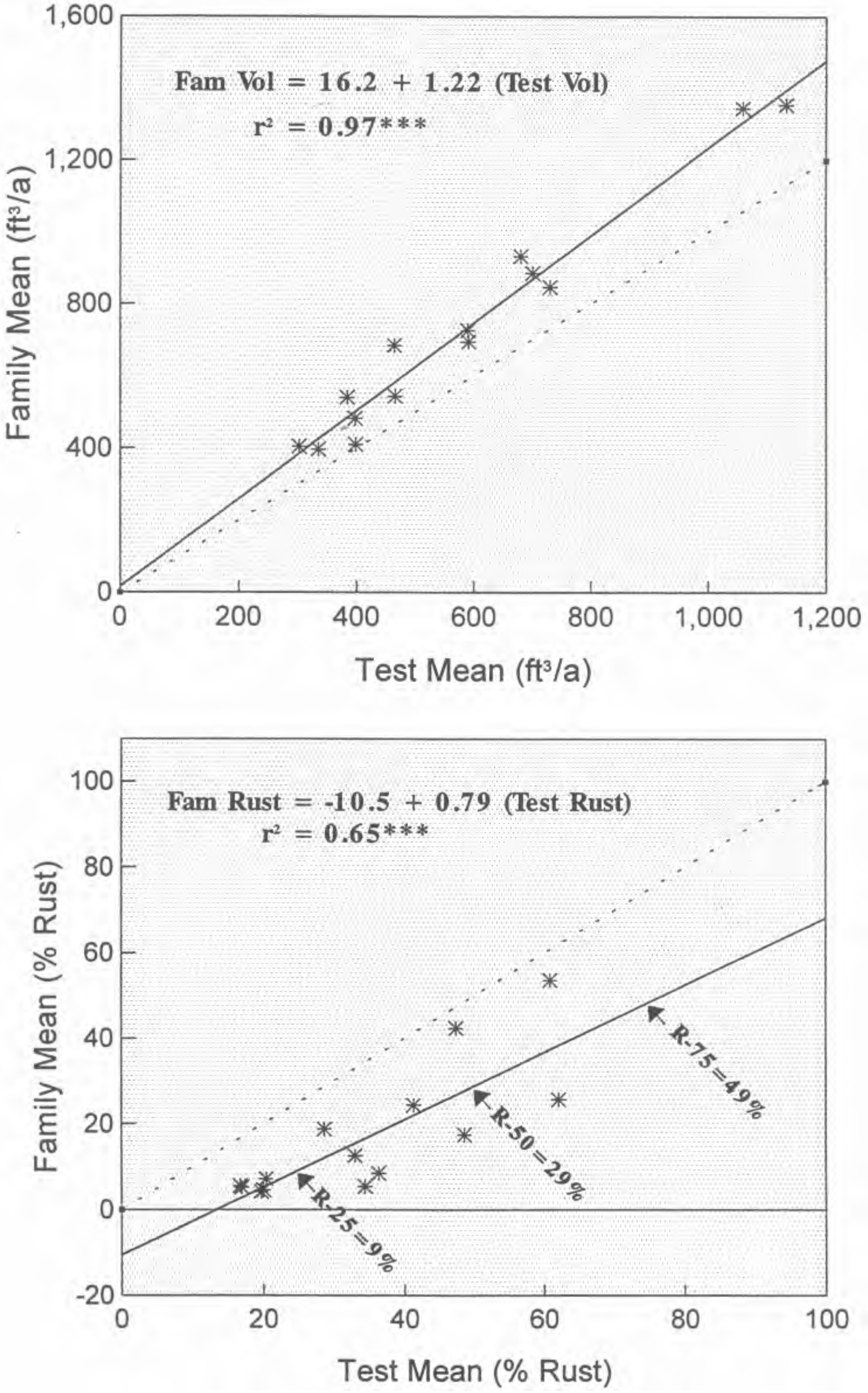


Figure 2. Volume performance (ft^3/acre) for family 11009 (top) and rust performance (bottom) in the 28 trials used in the stability analyses. This is an example of an outstanding family for volume production and rust resistance. (Dashed lines indicate performance of average families).

These rust performance data can be combined with volume predictions from the same trials (McKeand et al. 1997) to guide deployment decisions. Many of these clones are in 1.5-generation seed orchards and are routinely used in regeneration programs in the Gulf Coast and Atlantic Coastal Plain regions. Family 11009 is an excellent example of an exceptional family that combined high volume production (25% above average) and very high rust resistance (Figure 2). This family would be particularly valuable to deploy on the highest rust hazard sites with high predicted volume production.

Although GxE was significant in this population that was tested over a wide range of sites, it should be of relatively little importance in breeding and testing programs. Most of the GxE was due to heterogeneous regressions and not rank change. Testing in relatively few sites with intermediate rust levels should be reliable for predicting rust performance for loblolly pine.

Literature Cited

Li, Bailian and S.E. McKeand. 1989. Stability of loblolly pine families in the southeastern U.S. Silvae Genetica. 38:96-101.

McKeand, S.E., R.P. Crook, and H.L. Allen. 1997. Genotypic stability effects on predicted family responses to silvicultural treatments in loblolly pine. South. J. Appl. For. 21:84-89.

SAS Institute Inc. 1989. SAS/STAT User's Guide, Version 6, Fourth Edition, Vol. 2, Cary, NC. 846pp.