Genetic Variation in Fusiform Rust Resistance in Loblolly Pine Across a Wide Geographic Range

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Abstract

To evaluate the risk of inadequate testing on relatively few sites, data from a series of 28 trials were analyzed to study open-pollinated families for fusiform rust (caused by *Cronartium quercuum* (Berk) Miyabe ex Shirai f. sp. *fusiforme*) resistance across a wide geographic range in the Gulf Coast and Atlantic Coastal Plains of the southeastern US. Large family differences for rust infection were found, and predicted rust levels at sites where 50% rust infection is expected (i.e., R-50 values) ranged between 22% and 75%. Although family by environment interaction was statistically significant, its variance was small compared to the family variance. Much of the G x E was due to heterogeneous regressions of families across different sites and not family rank change. However, the relatively low r^2 values for the regression of some family means on site rust infection means (i.e., confidence intervals of R-50 values of some families are wide) may be due to interactions of the family's susceptibility/resistance and specific pathogen avirulence/virulence among sites.

Key words: Breeding, *Cronartium quercuum,* genotype by environment interaction, major gene resistance, *Pinus taeda.*

Introduction

Fusiform rust disease, caused by *Cronartium quercuum* (Berk) Miyabe ex Shirai f. sp. *fusiforme,* is the most economically important disease of loblolly and slash pine in the southern United States (Anderson et al., 1986; Kinloch and Stonecypher, 1969; Kinloch and Walkinshaw, 1991; Kuhlman, 1992; Powers et al., 1981). Genetic variation in host resistance expression to the fusiform rust fungus is commonly recognized in both slash and loblolly pine (Barber et al., 1957; Jewell and Mallett, 1967; Kinloch and Stonecypher, 1969; Schmidt et al., 1981; Walkinshaw and Bey, 1981; Powers and Kraus, 1986; Kuhlman and Powers, 1988; Kuhlman, 1992; Kuhlman and Matthews, 1993). Since 1973, the US Dept. Agric. Forest Service Resistance Screening Center in Asheville, NC has evaluated rust resistance in pine families through greenhouse testing (Knighten et al., 1988).

Identification and deployment of pine families with enhanced resistance to fusiform rust across a broad range of sites is critical if the full benefits of resistance breeding programs are to be realized. While genotype x environment (G x E) interactions for both loblolly and slash pine have not been considered highly important by some researchers (Kinloch and Stonecypher, 1969; Hodge et al., 1993), others have suggested that interactions may be consequential only for specific resistant families (Kuhlman et al., 1995). Most breeding and testing programs for loblolly pine evaluate rust resistance in a relatively small number of tests with little or no opportunity to assess genetic variation and patterns of resistance across a full range of rust hazard sites (e.g., areas of differing rust incidence). Likewise, if variation in pathogen virulence is a concern (Snow et al., 1975; Powers et al., 1977; Kuhlman and Matthews, 1993; Nelson et al., 1993; Wilcox et al., 1996), limited testing is inadequate to evaluate G x E interactions related to variation in virulence.

In greenhouse trials, specific host x specific pathogen interactions have been common (Snow et al., 1975; Kuhlman, 1992; Kuhlman and Matthews, 1993; Nelson et al., 1993; Wilcox et al., 1996; Kuhlman et al., 1997; Stelzer et al., 1997). Recent findings that rust resistance in some families may be controlled by one or few genes that can be overcome by specific virulent rust genotypes (Wilcox et al., 1996), further suggests that G x E in field trials needs to be thoroughly examined. Should important G x E interactions exist in field trials, either due to different hazard levels or to differences in rust virulence, testing at a few locations under a narrow range of rust incidence levels may be inadequate.

To evaluate the risk of testing on few sites with loblolly pine, data from a series of trials established in the mid-1970's by members of the North Carolina State University-Industry Cooperative Tree Improvement Program were used to study G x E by estimating response functions for rust resistance for families across a wide geographic range in the Gulf Coast and Atlantic Coastal Plains of the Southeast. Tree breeders rarely use response functions to predict family performance, since most genetics trials are established on relatively few sites. In this study, we expand the work of Li and McKeand (1989) and McKeand and Li (1997) and take advantage of the unique opportunity to analyze rust incidence from a large number of trials located across a range of rust hazards.

Materials and Methods

Details of the experimental design and measurements are in Li and McKeand (1989). Briefly, open-pollinated families from diverse origins were established in a series of randomized complete block design tests, each with six replications of 10-tree row plots of 30 to 50 seedlots. Test trees were evaluated at age 8 years for presence or absence of galls on stems and/or branches (the standard parameter used to assess rust resistance in loblolly pine). There were 43 open-pollinated families established in 28 test locations in the Coastal Plain from southeast Louisiana to eastern North Carolina (*Figure 1*). Each of the 43 families analyzed was planted in at least 6 test sites.

An analysis of variance (*Table 1*) for percent rust infection (percent galled) was conducted on family plot means using the method of Freeman and Perkins (1971). To determine if part of the G x E was due to family differences in their linear response to changes in rust incidence across sites, the G x E (i.e., family x test) sum of squares was partitioned into two components; one contributed by heterogeneous regressions of family mean percent infection on site mean percent infection and another contributed by deviations from linear regression. The heterogeneous regression effect was further partitioned into convergence and non-convergence effects (Eagles et al., 1977; Rehfeldt, 1979) to determine if slopes corresponded to family rank changes at the different sites. The sum of squares for convergence was calculated as:

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Figure 1. – Location of the 28 tests used in the stability analyses for resistance to fusiform rust for 43 OP families of loblolly pine. The three stars with hatched filling represent the three tests specifically referred to in the text: northern is Effingham Co., GA, middle is McIntosh Co., GA, southern is Camden Co., GA. The natural range of loblolly pine is shaded.

$$SS(convergence) = r^2 \times SS(heterogeneous\ regression)$$

where r is the PEARSON product-moment correlation between family stability values and family mean rust performance across all sites. Significant convergence indicates that the intercepts of the family regressions converge at the origin.

The family-mean heritability ($\hat{h}^2_F$) for percent rust was calculated using variance component estimates from the VARCOMP procedure (REML estimates) in SAS (SAS Institute Inc., 1989). Coefficients of the expected mean squares came from the GLM procedure (RANDOM option) in SAS:

$$\hat{h}^2_F = \frac{\hat{\sigma}^2_F}{\hat{\sigma}^2_F + k_1/k_2\ \hat{\sigma}^2_{TF} + \hat{\sigma}^2_e / k_2}$$

Where: $k_1 = 5.7$ and $k_2 = 25.3$ are coefficients on the expected mean squares in *table 1.* Variance components are defined in *table 1.*

Family means from each test were regressed on the site means to determine the genetic stability of rust resistance (FINLAY and WILKERSON, 1963). Rust infection across the tests averaged 39%, ranging from 17% to 74%. To have the largest genetic sample possible representing the mean infection for each location, 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. The estimated slope of each regression (b) is a measure of family stability. Families with a slope not signifi-

Table 1. – Analysis of variance for % rust infection for 43 families of loblolly pine in the 28 trials in the south-eastern U.S. at age 8 years.

Source	d.f.	Mean Square ¹	Expected Mean Squares	Variance Comp. (% of Total)
Test	27	23514.74	$\sigma^2_e + 6.0\ \sigma^2_{TF} + 13.4\ \sigma^2_{B(T)} + 84.4\ \sigma^2_T$	37.6
Block(Test)	151	797.57	$\sigma^2_e + 23.4\ \sigma^2_{B(T)}$	2.6
Family	42	2632.33	$\sigma^2_e + 5.7\ \sigma^2_{TF} + 25.3\ \sigma^2_F$	13.5
Test x Family	589	516.42	$\sigma^2_e + 6.3\ \sigma^2_{TF}$	3.7
Heter. Regr	42	1014.93		
Convergence	1	17050.86		
Non-Converg.	41	623.81		
Dev. from Regr.	547	478.14		
Error	3375	334.43	σ^2_e	42.7
Corr. Total	4184			100.0

Where: σ^2_T = variance due to test, $\hat{\sigma}^2_T = 294.6$
$\sigma^2_{B(T)}$ = variance due to block within test, $\hat{\sigma}^2_{B(T)} = 20.2$
σ^2_F = variance due to family, $\hat{\sigma}^2_F = 105.6$
σ^2_{TF} = variance due to test x family interaction, $\hat{\sigma}^2_{TF} = 28.8$
σ^2_e = variance due to within test experimental error (i.e. block x familiy within test), $\hat{\sigma}^2_e = 334.8$

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

cantly different from 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 display less than average sensitivity to increases in test mean infection levels.

The predicted rust infection that each family 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. The 95% confidence interval around the R-50 values was calculated (NETER and WASSERMAN, 1974, p. 71–73).

Results and Discussion

Highly significant family differences ($\hat{h}^2_F = 0.84$) for rust infection across the 28 tests were found (*Table 1*). Predicted R-50 values (*Table 2*) ranged from 22.4% for family 11010 to 75.3% for family 19016.

The family x test interaction was highly significant in the analysis of variance (*Table 1*) suggesting that G x E for rust resistance could be important. However, the family x test component of variance was only 3.7% of total variation, while the family variance was 3.7 times larger and contributed 13.5% of the total variance. Partitioning of the interaction sums of squares showed that the G x E interaction was largely due to the heterogeneity of family linear response to rust incidence over sites. Nonlinear response of families also contributed a small but significant amount to the total G x E interaction sums of squares.

Slopes of the mean family rust percentage regressed on the mean site rust percentage did not differ significantly from b = 1.0 ($p \leq 0.05$) for 34 of the 43 families indicating average stability for 8-year rust resistance for about 80% of the families (*Table 2*). The relatively high coefficients of determination (r^2) and examination of residuals indicated that the linear models fit the data well. The highly significant G x E interaction sum of squares from the analysis of variance was contributed by about 20% interacting families. Most of the G x E due to heterogeneous regressions was due to convergence of the regressions through the origin, although a small but significant amount of

Table 2. – Open-pollinated loblolly pine families used in stability analyses for fusiform rust resistance with prediction equations [intercepts, slope, and coefficient of determination (r^2)] and predicted rust infection level (R-50) and 95% confidence interval for sites with average infection of 50%.

Seedlot	Origin[1]	# Tests	r^2	Intercept	Slope	R-50(%)	95% Conf. Int. R-50
01014	P,GA	10	0.96	-4.35	1.17+	53.9	42.2 - 65.6
01064	P,GA	13	0.87	-9.84	1.38*	59.0	37.8 - 80.2
01523	P,SC	9	0.90	-2.33	1.24	59.6	36.0 - 83.2
02008	C,VA	12	0.86	-10.09+	1.10	44.8	27.2 - 62.4
02040	C,VA	25	0.84	-2.70	1.26*	60.4	42.3 - 78.5
03007	P,SC	17	0.76	-6.85	0.88	37.0	19.2 - 54.8
03036	P,SC	17	0.93	-9.24*	1.23*	52.1	37.9 - 66.3
04006	C,VA	14	0.92	-5.49	1.29*	59.2	43.2 - 75.2
04018	C,VA	25	0.78	-10.16	1.26+	53.1	29.7 - 76.5
05005	C,SC	13	0.76	-8.18	1.28	55.9	27.2 - 84.6
06009	P,NC	14	0.76	12.30	1.22	73.4	47.7 - 99.1
06020	P,NC	24	0.82	-5.63	1.21+	55.1	35.1 - 75.1
06022	C,NC	8	0.78	-4.11	1.18	55.0	17.2 - 92.8
07002	C,SC	11	0.67	9.90	0.80	50.0	24.1 - 75.9
07034	C,SC	15	0.75	-11.42	1.05	41.3	16.9 - 65.7
07056	C,SC	26	0.80	-4.83	0.93	41.9	25.4 - 58.4
08001	C,NC	25	0.77	-6.48	1.12	49.3	29.5 - 69.1
08059	C,NC	27	0.80	-1.43	1.15	56.3	35.4 - 77.2
08061	C,NC	25	0.90	-10.88**	1.33**	55.7	40.3 - 71.1
08068	C,NC	28	0.81	-4.30	0.96	43.6	27.4 - 59.8
08076	C,NC	22	0.76	-9.59	1.11	45.8	21.6 - 70.0
08102	C,NC	12	0.86	15.84*	1.06	68.9	51.8 - 86.0
08509	C,AL	11	0.70	-3.42	1.36	64.6	37.5 - 91.7
09017	P,NC	15	0.91	-4.83	1.03	46.6	33.4 - 59.8
10002	C,GA	9	0.51	11.57	0.49*	36.3	14.2 - 58.4
10005	C,GA	18	0.58	-1.17	0.75	36.5	12.9 - 60.1
10006	C,GA	11	0.80	-4.70	0.62**	26.1	14.0 - 38.2
10010	C,GA	9	0.64	1.65	0.99	51.3	17.3 - 85.3
10014	C,GA	19	0.79	-0.35	0.92	45.6	28.6 - 62.6
10046	C,GA	10	0.80	-7.79	1.18	51.0	26.9 - 75.1
11009	C,SC	14	0.65	-10.53	0.79	28.9	6.9 - 50.9
11010	C,SC	12	0.58	-10.57	0.66+	22.4	1.4 - 43.4
11016	C,SC	20	0.44	4.27	0.57*	33.0	9.7 - 56.3
11061	C,SC	10	0.79	-16.27	1.17	42.4	14.7 - 70.1
15042	P,GA	19	0.56	2.58	0.62**	33.4	12.9 - 53.9
17004	C,AL	11	0.91	-2.41	1.30+	62.7	46.0 - 79.4
17005	C,AL	7	0.92	-11.72+	1.14	45.0	33.5 - 56.5
17016	C,AL	27	0.86	-0.56	1.20+	59.5	42.0 - 77.0
17019	C,AL	6	0.57+	1.73	0.81	42.4	12.2 - 72.6
17037	C,AL	12	0.80	3.97	1.02	55.1	35.5 - 74.7
19016	C,AL	10	0.80	14.34	1.22	75.3	49.0 -101.6
19017	C,AL	7	0.90	6.11	1.21	66.6	45.3 - 87.9
19024	C,AL	10	0.84	12.74+	1.04	64.9	45.4 - 84.4

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[1]) Origin: Provenance (P = Piedmont, C= Coastal Plain), State Abbreviation

+, *, ** Significantly different from slope = 1.0 or intercept = 0 at $P < 0.1, 0.05, 0.01$, respectively. All r^2 except for 17019 were significant at $P < 0.01$.

variation was due to non-convergence (*Table 1*). This indicates that most families do not change rank over a range of rust infection levels.

Families 01064, 02040, 03036, 04006, and 08061 had stability values significantly greater than b = 1.0 ($p \leq 0.05$). These five families were relatively unstable and would have greater rust infection on higher rust hazard sites compared to families with average stability. Families 10002, 10006, 11016, and 15042 had stability values significantly below b = 1.0 ($p \leq 0.05$) and would not respond as much to high rust infection on high hazard sites as average stability families.

Only three families had an intercept significantly different from zero ($p \leq 0.05$), families 03036, 08061, and 08102. Significant non-convergence indicates that some families have intercepts of non zero. However, 40 of the 43 families in the experiment had intercepts that did not significantly differ from zero. This result has important implications for calculating R-50 values for families that are in relatively few tests. In operational breeding and testing programs, most families are typically planted in only 3 to 5 progeny tests for routine evaluations, and with so few sites, no opportunity exists for direct calculation of R-50 values using regression equations. Typically, check seedlots are used for regression because they are common across many tests (LI et al., 1996). The R-50 for the check seedlot is estimated from regression, and the deviation of family infection from the expected R-50 value for the check seedlot is used to estimate the family R-50. With few exceptions, most families had intercepts of zero, so the calculation should be valid.

Caution must be used when interpreting these prediction equation. Linear regressions were appropriate for the range of rust infection assessed (test means from 17% to 74%) and slightly beyond. However, at rust levels near 100% and for some families at the low rust incidence, the regressions must become non-linear. Rather than emphasizing the intercept for a family, a more valuable measure that falls within the range of the data is R-25, the predicted percentage rust for a family when the site mean is 25%. Conversely, R-75 values are informative for predicting family means for sites with high incidence.

Deployment of Families Across Rust Hazard Sites

Most families were of average stability and performance (b = 1.0 and intercept = 0 at $p \leq 0.05$), suggesting that most loblolly pine families in this study are not exceptionally resistant or susceptible to fusiform rust. Family *07056,* a well-known family for volume production, was in this category. While it was consistently 5% to 10% below the average infection at each site (R-50 = 42%), it did not have exceptional rust resistance.

About one in nine of the families were unstable ($b \neq 1.0$) for rust resistance, e.g., family *08061* (*Figure 2*). This would be a poor family to deploy on high rust hazard sites. It is good on low hazard sites (R-25 = 22%) where resistance is not critical, but it is very unstable (b = 1.33) and would be highly susceptible on the high hazard sites (R-75 = 89%).

Relatively few families had intercepts that were different from zero. One example was family *08102* that had average stability (b = 1.06) but was consistently about 16% to 20% worse than the test mean, no matter what the infection level was (R-25 = 42%, R-50 = 69%, and R-75 = 95%).

Seven families showed good rust resistance at virtually all sites: *10002, 10005, 10006, 11009, 11010, 11016,* and *15042.* These families are very stable for rust resistance (b < 1) and should do well on high hazard sites. Family *11010* (*Figure 3*) appears to be the most resistant family to rust in the population due to its low intercept (–10.57) and high stability (b = 0.66). The estimated R-values for 11010 (R-25, R-50, and R-75) are 6%, 22%, and 39%, respectively. For some families, such as *11016,* resistance should be good, but the r^2 for the prediction equation is low. Although family 11016 was very well tested in 20 trials, there is relatively little confidence (note the wide confidence interval in *table 2*) in predicting its resistance on different sites.

Family *19016* is the best example of an extremely susceptible family to fusiform rust. The R-Values (R-25, R-50, R-75) are 45%, 75%, and 106%, respectively. This family is predicted to get rust when there is no rust in the test (R-0 = 14.4%) and to have more than 100% rust on a 75% rust hazard site, hence the caution of extrapolating beyond the range of our data.

Variation in Rust Virulence?

Although rust resistance for most families is 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). While this could be due to the inherent variation in

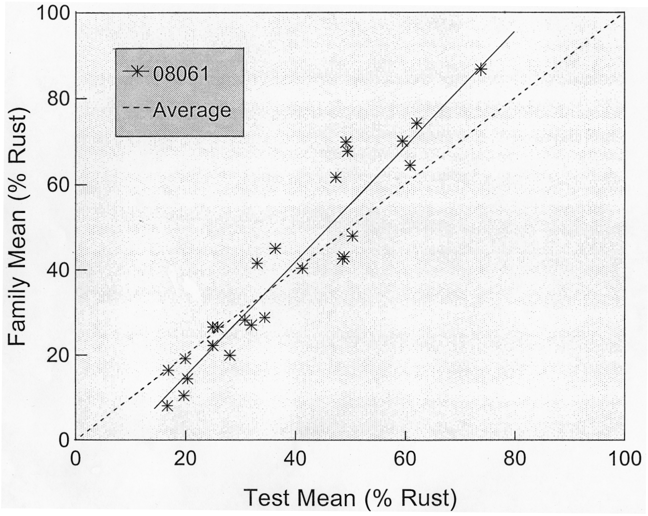

Figure 2. – Regression of family means for family 08061 at each test site on the environmental index (test mean) for percent fusiform rust infection. For family 08061, $b_0 = -10.88$, $b_1 = 1.33$, R-50 = 55.7, and $r^2 = 0.90$.

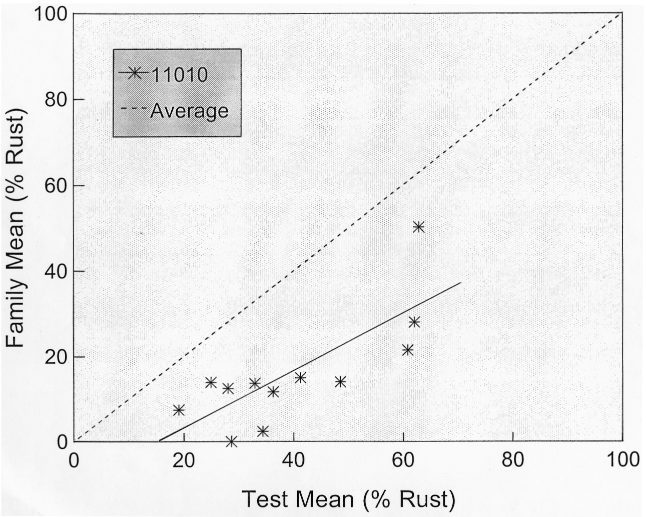

Figure 3. – Regression of family means for family 11010 at each test site on the environmental index (test mean) for percent fusiform rust infection. For family 11010, $b_0 = -10.57$, $b_1 = 0.66$, R-50 = 22.4, and $r^2 = 0.58$.

the likelihood and timing of infection compared to the incremental increase in stem volume, the relatively low r^2 values for the rust regressions suggest more important genotype by environment interactions for rust than for volume. For a highly resistant family like 11010 (*Figure 3*) where the $r^2 = 0.58$, the points that deviate the most from the regression line could be due to the interaction of 11010's susceptibility/resistance and specific rust avirulence/virulence that may differ from site to site (e.g. KUHLMAN et al., 1995).

For each family, we examined the regressions carefully to see if observations that deviated from the regression line were from the same geographic region. No regional patterns of susceptibility or resistance were evident for any family. For example, 11010 appeared to be very susceptible to rust in the McIntosh, GA test, but in tests in Effingham, GA and in Camden, GA, the only other tests in that region, the observed rust level for 11010 was near the predicted rust level. The lack of a broad geographic pattern for differential expression does not preclude the possibility that different virulence strains of fusiform rust exist locally or from site to site.

While previous works (KINLOCH and STONECYPHER, 1969; HODGE et al., 1993) and our current work indicate that G x E interactions were not highly important in field assessments, the same cannot be said for greenhouse inoculation studies. In such tests, specific host x specific pathogen interactions that would be interpreted as G x E in the field, have been frequently observed (SNOW et al., 1975; POWERS et al., 1977; KUHLMAN, 1992; KUHLMAN and MATTHEWS, 1993; NELSON et al., 1993; WILCOX et al., 1996; KUHLMAN et al., 1997; STELZER et al., 1997). In the current study, deviations from the regression line for a given family at a specific site could similarly represent specific interactions where variation in pathogen virulence across sites would be the most obvious explanation for the deviations. It is possible to test this explanation by examining site specific deviations across the current trials for two of the families, 10005 and 10006. Molecular markers (RAPD, Random Amplified Polymorphic DNA markers) for specific resistance genes in these two families have been identified (WILCOX et al., 1996; AMERSON, unpublished data). Assuming adequate levels of infection, co-segregation analysis of the markers and disease phenotypes in these two families at specific field sites can be used to determine if pathogen virulence is differing among sites. Family 10005 is relatively resistant (*Figure 4*), but the deviations around the regression are fairly large ($r^2 = 0.58$) suggesting possible variation in virulence from site to site (e.g. KUHLMAN et al., 1995). Family 10006 is very resistant and has a high r^2 (0.80) suggesting that variation in rust virulence for this family is minimal in the tests considered here.

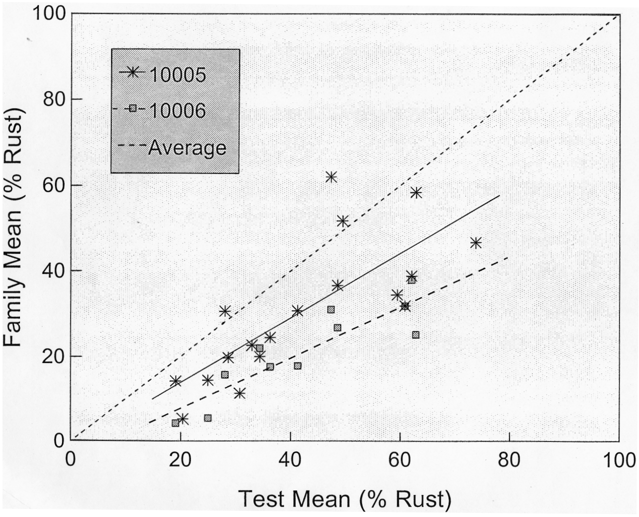

Figure 4. – Regression of family means for families 10005 and 10006 at each test site on the environmental index (test mean) for percent fusiform rust infection. For family 10005, $b_0 = -1.17$, $b_1 = 0.75$, R-50 = 36.5, and $r^2 = 0.58$. For family 10006, $b_0 = -4.70$, $b_1 = 0.62$, R-50 = 26.1, and $r^2 = 0.80$.

Conclusion

Although family by site interaction was statistically significant in this population of loblolly pine tested over a wide range of sites, G x E should be of relatively little importance for most families in breeding and testing programs. Most of the G x E was due to heterogeneous regressions and not rank change. Allowing that a few exceptions (highly deviate sites) may occur, testing in relatively few sites with intermediate rust levels should generally be useful for predicting family rust performance for loblolly pine. Such testing should be adequate to identify families that typically perform at, above, or below expectations for a given hazard rating. However, this generalization does not ensure that local site to site variation will not result in significant infection of resistant families (e.g. KUHLMAN et al., 1995), only that these families are likely to have relatively lower infection on most sites.

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Pressemitteilung

XXI IUFRO Congress 2000

The International Union of Forestry Research Organisations (IUFRO), a renowned international body in forestry research, has entrusted Malaysia to host the prestigious XXI IUFRO World Congress to be held on August 7 to 12, in the year 2000, at the Putra World Trade Centre, Kuala Lumpur. This Congress will see the convergence of 3,000 foreign and local participants, making it the largest scientific congress on forestry to be held in Malaysia, the first developing country ever to host the Congress in the 100 years history of IUFRO.

The theme of the Congress, “Forests and Society: The Role of Research“ was chosen to reflect the increasing importance of research and development in sustainable forest management. The Congress, with the support of the Malaysian Government, will be organised by the Organising Committee headed by Forest Research Institute Malaysia (FRIM).

IUFRO a non-profit and non-governmental international scientific body, was established in 1892. Among the tasks undertaken since its formation have been to promote international co-ordination and co-operation in research and development on various aspects of forest science. IUFRO now has 676 member organisations from 105 countries.

The Congress will cover pertinent issues such as Sustainable Management of Natural Resources, Forest and Society Needs, Changes in Environment and Society, Cultural Diversity in Forest Management and the Global Vision of Forest and Society. A renowned speaker will address each of these topics at the Congress during the keynote addresses.

Apart from keynote addresses, there will be numerous scientific sessions comprising technical paper and poster presentations based on the above theme and issues. Presentations for Scientific Achievement Award, Outstanding Doctoral Research Award and Best Poster Award will also be some of the highlights of the Congress. Commemorative stamps will also be launched.

A one-day In-Congress tour within Klang Valley, related to forestry activities to highlight Malaysia's commitment towards achieving Sustainable Forest Management, would be conducted. For the accompanying persons, special programmes will be organised. Post-Congress excursions will also be organised covering Malaysia and selected neighbouring Asean countries.

For further information, please contact: –
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Website: http://frim.gov.my/iufro.html.

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