GENETIC VARIATION IN RESISTANCE TO FUSIFORM RUST AMONG SELECTED PARENT CLONES OF LOBLOLLY PINE AND THEIR OFFSPRING

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ABSTRACT

Variation in fusiform rust infection among 10 clones of loblolly pine in an industrial seed orchard in South Carolina ranged from 0-92%. In four progeny tests established in different years and locations, full-sib families from these parents also differed significantly in amount of rust infection and tended to reflect the relative susceptibility of their parental phenotypes. Although the average resistance of progenies from superior phenotypes selected in the wild was no better than that of commercial nursery stock, selection of parents on the basis of their clonal performance` in areas of high natural rust hazard would be much more effective.

INTRODUCTION

Fusiform rust, caused by Cronartium fusiforme_Hedgc. and Hunt ex Cum., is a limiting factor to plantation management of loblolly (Pinus taeda L.) and slash (P. elliottii Engelm.) pines in large parts of the southern United States, where environmental conditions favor the development and spread of the disease. Thus, in breeding programs aimed at the genetic improvement of these species, incorporation of resistance is essential. Although extensive genetic variation in resistance has been found in natural populations (Barber 1964, 1966; Kinloch and Stonecypher 1969; Blair 1970), progeny testing has been the only reliable means of evaluating parent selections. Trees superior in growth or other economic traits are usually excluded from clonal breeding orchards if any symptoms of fusiform rust are found, but the efficacy of this selection on improved rust resistance in their progeny is not well known. Rust-free parents generally, but not always, transmitted greater resistance to their offspring than infected trees (Jewell and Mallett 1967; Kinloch and Stonecypher 1969), but accurate phenotypic evaluation of mature trees for rust resistance is difficult at best. The candidate tree is a single unit observed at one point in time, and evidence of previous infection, which most often occurs on branches, is usually lost through natural pruning. Also, candidates are selected from many different stands covering a wide geographic area, where the potential hazard and intensity of the disease varies greatly.

This paper reports **information** on the variation in susceptibility among individual clones of loblolly pine grown in a common environment of high hazard to fusiform rust, and early results on their parent-offspring relationships.

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MATERIALS AND METHODS

Parent trees were selected from mature natural stands of loblolly pine in the lower coastal plain of South Carolina and Georgia. Criteria for selection were phenotypic superiority in growth rate and other traits of commercial importance, and absence of fusiform rust symptoms, though in some stands the incidence of the disease was low or lacking. Scions from selected trees were grafted in the Union Camp seed orchard near Almeda, South Carolina, between 1959 and 1962. There were 6-45 ramets/clone, completely randomized within the orchard. Rust infection on pines in the surrounding area was severe: trees in a plantation established in 1958 within 500 ft. of the orchard were 98% infected, with an average of 7.6 galls/tree.

Candidate trees were bred in the orchard to four tester trees, but insufficient flowering and seed set of some resulted in an incomplete mating design. After growing a year in a nursery, four different plantations of controlledpollinated families were outplanted **in** 1965, 1966, and 1967 on two different sites within a 50-mile radius of Savannah, Georgia. The experimental design was a randomized complete block with 10 trees/plot in rows. In three of the plantations (main tests) there were six replications, and in the fourth (supplementary test) only three replications. The number of different families in each test varied, but 10 families were common to all tests. Only these 10 families are considered in this report. Open-pollinated seedlings of unknown parentage from a commercial nursery were also included in each test as checks.

Orchard trees were examined for fusiform rust symptoms in 1967, and plantation trees in 1969. In the plantations, the unit of analysis was the percentage of trees infected per plot (transformed to arc sin 'percentage equivalents when variance analyses were made). In the clonal seed orchard, galls were counted on every ramet.

RESULTS AND DISCUSSION

Variation in susceptibility to fusiform rust among the 10 different clones was striking, ranging from 0-92% infection and averaging from 0-5 galls/tree (Table 1). Differences of this magnitude in such a relatively small sample of parents demonstrate the great amount of inherent variation that exists among individual genotypes in natural populations of loblolly pine. Nevertheless, the amount of infection observed on the clones was light in comparison to the 98% infection and average of 7.6 galls/tree found in the nearby plantation, established from seed at approximately the same time. This disparity may be associated with differences in the physiological age of the two groups of trees.

Differences in the amount of rust infection among the 10 families common to four progeny tests were also great. For example, in the 1966 (main) test, families ranged from 12-66% infected; in 1967, they ranged from 3-64% infected (Table 2). This degree of variation is typical of young loblolly pine (Barber 1966; Kinloch and Stonecypher 1969; Blair 1970).

Table 1Fusif	orm rust	infection	on	clones	of	loblolly	pine	in	а	seed	orchard	

Clone	No. of	% infection	Avg. no.
designation	ramets		galls/ramet
6	45	0.0	0.0
12	37	10.8	0.1
5	32	18.7	0.3
14	41	29.2	0.4
25	22	31.8	0.5
38	49	42.8	0.6
18	54	64.8	1.0
16	12	75.0	1.6
37	6	88.3	1.1
8	25	92.0	5.0

Table 2.--Fusiform rust infection on 10 controlled-pollinated families common to four different progeny tests, and commercial checks of unknown parentage

		Ye	ear of planting	
	1965	1966	1967 (AT)'	1967 (ST)a
			% Infection	
Avg. of 10 selects	17	43	38	16
Range among selects	5-38	12-66	3-64	7-29
Commercial checks	25	38	21	8

'MT = Main Test

ST = Supplementary Test

Of equal importance was the consistent performance of the families from test to test. Although the total amount of infection among the four tests varied considerably (Table 1), families tended to maintain their relative rankings in degree of susceptibility over all the tests (Table 3). The few important exceptions to this trend all occurred in the plantation with the least amount of infection (1967, supplementary test) and, therefore, probably containing the least reliable data.

Although relatively few parents were common to all tests, parent-offspring relationships were demonstrated quite clearly. The average rank in rust resistance in four tests for each of the 10 families agreed closely with the rank predicted on the basis of the mid-parent values of their parental clones (Table 3).

Table	3Relative	rankings	in	resistance	e to	<u>fusiform</u>	rus	t infec	<u>tio</u>	n of i	10
	controlle	ed-pollina	ated	families	of	loblollv	oine	common	to	four	
		nrogeny				<u></u>					_

progeny	tests

		Rank	a in test year:			
Cross	19 65	1966	1967 ₍ MT) ^b	1967 (ST) ^b		Expected
					rank	rankc
5 x 25	1	1	1	3	1	1
25 x 14	4	3	2.5	1•	2	2
87 x 6	3	2	2.5	6	3	3
87 x 14	5	7	5	2	4.5	7
.8 x 25	2	4	4	9	4.5	4
5 x 8	7	5.5	6	5	6.5	6
.6 x 37	6	5.5	8	4	6.5	9
.2 x 8	9	8	9	7	8	5
.4 x 8	10	9	7	8	9	8
6 x 8	8	10	10	10	10	10

а

b Based on percentage of trees infected.

_MT = Main Test; ST = Supplementary Test.

Based on mid-parent values, computed from Table 1.

These data show that the original selection of parents in the wild was not effective in improving rust resistance in their offspring since unselected stock from a commercial nursery was less susceptible in most cases (Table 2). However, parents were selected over a wide geographic range, and in some areas where the intensity of rust was low, phenotypes for resistance could not be accurately evaluated. Selection on the basis of clonal performance in an area of high natural rust hazard, on the other hand, appears to be a much more effective alternative. This is proposed as a potentially valuable complement to progeny testing.

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