

Interactions Between Virulent Isolates of *Cronartium quercuum* f. sp. *fusiforme* and Loblolly Pine Families of Varying Resistance

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ABSTRACT

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Nine half-sib families of loblolly pine seedlings with varying degrees of resistance were artificially inoculated with five highly virulent isolates of *Cronartium quercuum* f. sp. *fusiforme* from diverse geographic areas. Significant differences were found in resistance among the host families. There also were significant differences in infection levels produced by the various rust isolates. All five pine families previously rated as resistant had relatively low levels of infection, but only one was resistant to all five rust

isolates. The two families intermediate in resistance showed adequate resistance to at least one of the rust isolates. These interactions between pine families and rust isolates were statistically significant. The different genetic bases of resistance displayed by these host lines could be utilized in the development of rust-resistant pine seed orchards in specific geographic areas.

Additional key words: disease resistance, fusiform rust, *Pinus taeda*.

Fusiform rust, which is caused by *Cronartium quercuum* (Berk.) Miyabe ex Shirai f. sp. *fusiforme* (Cumm.) Burds. et Snow (1), produces widespread (5,7) and increasingly heavy (9) losses in loblolly (*Pinus taeda* L.) and slash (*Pinus elliottii* Englem. var. *elliottii*) pine plantations. Most plantations in the South contain one of these pines, more often loblolly. Resistance to fusiform rust has been demonstrated in loblolly pine (12), but less than 20 resistant loblolly clones are available for use in tree improvement programs (H. R. Powers, Jr. The development of rust resistant pine selections for the South. [Unpublished abstr.] Southwide For. Dis. Workshop, Atlanta, GA. 1976).

This narrow genetic base is cause for concern when one considers that pathogenic variability is extreme in *C. quercuum* f. sp. *fusiforme* across most of the natural range of loblolly pine. In 1977, rust isolates taken from individual galls within localized areas varied as much in virulence as those collected from different geographical areas, and significant interactions exist between geographic isolates of the fungus and half-sib families of loblolly pine (6). Thus, both resistance in the host and the variation in virulence of the pathogen should be considered in breeding programs.

This paper reports differential reactions among a range of half-sib families of loblolly pine inoculated with virulent isolates of the rust fungus from diverse geographic sources. The results are helpful for planning programs to breed resistant pine clones for use in seed orchards.

MATERIALS AND METHODS

Half-sib families from nine clones of loblolly pine were used in this test. Based on previous inoculation studies, five families were rated as resistant (10-5 [GA], 11-20 [SC], B-5-4 [LA], S-6-5 [TX], and S-4-8 [TX]), two as intermediate (7-56 [SC] and 15-42 [GA]), and two as susceptible (4-R [GA] and 3838-3 [GA]) to *C. quercuum* f. sp. *fusiforme*. Five single-gall rust isolates, collected in 1973, were selected. One gall was from each of the following States: Texas (TX-3), Louisiana (LA-4), Mississippi (MS-1), Georgia (GA-3), and South Carolina (SC-10). The isolate from South Carolina was known to be highly virulent on family 11-20 (SC) (6). The isolates from Georgia, Louisiana, and Mississippi were virulent on a bulk collection of seed from Livingston Parish, LA. Virulence of the Texas isolate was unknown. It was included because two of the pine families were from east Texas.

Spore collections were handled separately and were processed and stored according to the procedures outlined by Roncadori and Matthews (8). To produce inoculum, seedlings of northern red oak (*Quercus rubra* L.) were inoculated with aeciospores from each collection. Basidiospores were harvested 3 wk later from the oak leaves and used in a concentrated spray for pine inoculation (3). Seeds of the half-sib families were germinated and the seedlings were transplanted into flats containing 20 seedlings each. At 4 wk of age the seedlings were inoculated by spraying 8 ml of a suspension containing 50×10^3 spores per ml on each flat as seedlings moved on a conveyor belt under a spray nozzle. Each of the five rust isolates was tested on six flats of 20 seedlings from each of the nine half-sib families. A total of 5400 seedlings were included in the study. Immediately after inoculation the seedlings were placed in a mist chamber and held at 21 C for 24 hr. They were then grown in a greenhouse for 9 mo.

Infection data are based on the number of seedlings with actively growing galls after 9 mo. In the $9 \times 5 \times 6$ factorial design, each flat constituted a replication. Differences among means were examined for statistical significance according to Duncan's multiple range test (2).

RESULTS

Differences in levels of rust resistance among half-sib families, differences among average infection levels caused by the five rust isolates, and interactions between the pine families and rust isolates were highly significant ($P = 0.01$). Average levels of infection ranged from 36% on family 10-5 (GA) to 84% for family 3838-3 (GA) (Table 1).

There was a tendency for levels of infection on families to be highest when a family was inoculated with isolates from an area nearby. For example, family S-4-8 (TX) had relatively high levels of infection when inoculated with western isolates (Texas, Louisiana, and Mississippi). Family S-6-5 (TX) was among the most resistant to all rust isolates except those from Texas and Louisiana. Families 11-20 (SC) and B-5-4 (LA) were resistant except when challenged by isolates from the State of their origin. Two exceptions to this trend were family 10-5 (GA), which was uniformly resistant, and 4-R (GA), which was uniformly susceptible.

Infection levels of the five rust isolates averaged over all nine families were: Georgia 54%, Louisiana 66%, Mississippi 56%, South Carolina 56%, and Texas 58%. Although differences among these averages are statistically significant, they are not considered very meaningful biologically because of the very limited sample of the total population involved, and because of the high rust isolate

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× pine family interaction.

The interaction between host families and rust isolates was also highly significant. The differential reaction of half-sib family 11-20 (SC) to the South Carolina isolate in comparison to all the other isolates (except the unknown Texas isolate) was expected, based on previous infection studies. However, significant interactions were also observed among families S-6-5 (TX), S-4-8 (TX), 7-56 (SC), and 15-42 (GA) in relation to rust isolates from Georgia and Texas (Table 1).

DISCUSSION

The responses of the five resistant families to the five rust isolates were favorable from a disease control standpoint. Infection levels on four of these families, averaged across all isolates, were relatively low. The 55% infection on selection S-5-8 (TX) borders between intermediate and resistant, but it is obviously better than the high infection levels of families 4-R (GA) and 3838-3 (GA).

It is important, however, to examine the effects of each isolate on each family. Family 10-5 (GA) was uniformly resistant, even to the isolates that were highly virulent on 11-20 (SC) and B-5-4 (LA). Apparently, the genetic bases for resistance differ among these three half-sib families. Family 11-20 (SC) was highly resistant, except when challenged with the South Carolina rust, which was included because it was the only isolate that had been found to be virulent on this host family (6). The results with family B-5-4 (LA) were also encouraging, since three of the isolates (Louisiana, Mississippi, and Georgia) were known to be virulent on the bulk seed collections from Livingston Parish, LA. However, only the Louisiana isolate was virulent on this particular half-sib selection. The bulk collections of Livingston Parish seed, which are currently sold in large quantities, obviously contain a wide assortment of genotypes, most of which are relatively resistant to a range of pathogenic isolates. These results demonstrate that at least one rust isolate already exists that is highly virulent on this host selection from Louisiana, as was the case with the South Carolina isolate on family 11-20 (SC). Although it has not yet been demonstrated, the same is probably true for family 10-5 (GA). Selections S-6-5 (TX) and S-4-8 (TX) were most resistant when challenged by eastern rust isolates.

The relatively high infection levels produced by some specific isolates on host families from the same geographic areas indicate that certain rust isolates have adapted to these sources of resistance in the host. For example, the rust isolate from South Carolina represented one gall of ten collected in a localized area in the 1977 study (6). The fact that one highly virulent isolate was obtained among such a limited sample means that there are probably other sources of the rust fungus equally pathogenic on 11-20 (SC) present in that particular area. However, evidence suggests that such genes for virulence are not distributed throughout the range of the pathogen. In the 1977 study, the South Carolina rust isolate was by far the most virulent of 56 rust collections tested against host family 11-20 (SC). The isolate ranking next highest in virulence on this family was from an area in North Carolina which was next nearest to the origin of this host family. It appears, therefore, that genes for virulence tend to build up where their complementary genes for resistance are found, and that while relatively common in these areas, such genes are not frequently found in other regions.

The infection levels on the two intermediate selections, 7-56 (SC) and 15-42 (GA), were approximately the same as those in previous tests. Although background information was lacking on the Texas rust used in this study, these two families were resistant to at least this one isolate. Family 15-42 (GA) also had a relatively low infection level when challenged by the isolate from South Carolina. These results indicate that selections such as 7-56 (SC) and 15-42 (GA) could be used in the development of resistant seed orchards in specific geographic areas. Since the number of resistant clones currently available is limited, this is an important consideration.

Our very limited sample of rust isolates gives no definitive answers about where specific clones could be used in a seed orchard mix. These results, however, do provide some indications as to where potential trouble spots may occur. Obviously, there are rust isolates in South Carolina and Louisiana that are highly virulent on families 11-20 (SC) and B-5-4 (LA), respectively. Families S-6-5 and S-4-8 from Texas showed relatively high infection levels when inoculated with the one random isolate from Texas. Even so, the results indicate that the five resistant families, plus the two intermediates, could be used in a mixture of resistant clones in seed orchards, particularly in western areas. The seed obtained from such a genetic mix should be substantially more resistant than currently available susceptible material. In contrast, it would seem advisable to avoid a heavy dependence on family 15-42 (GA) in Georgia and Louisiana.

The results also emphasized the need to search for additional host selections with resistance to this disease. Material with all types of resistant responses, as described by Miller et al (4) and Snow et al (11), should be incorporated into rust-resistance orchards as soon as possible. Selections with field tolerance should also be included in order to provide the widest possible genetic base. Since forest tree rotations are long, intense selection pressure on the pathogen must be avoided because it could result in the development of highly virulent strains (10).

Four of the five rust isolates we selected already had demonstrated virulence on specific host families. The interactions of these isolates with specific half-sib families are striking. For ease of communication, these rust isolates probably should be referred to as specific "strains". The use of the designation "pathogenic race" becomes complicated since highly inbred host material is usually involved in such host-parasite relationships. However, since most noteworthy races usually are the virulent ones, such as race 15-B of black stem rust of wheat (*Puccinia graminis* f. sp. *tritici*), it should be recorded that strain SC-10 is highly virulent on family 11-20 (SC), LA-4 is highly virulent on B-5-4 (LA), etc. In this way tree breeders can be made aware of specific rust isolates from certain areas that could build up to dangerous levels.

TABLE 1. Infection produced on nine loblolly pine families inoculated with five isolates of *Cronartium quercuum* f. sp. *fusiforme*

Pine family and state of origin	Rust isolate and percent seedlings infected	Host mean
10-5 (GA)	GA (30) ^b MS (34) TX(35) SC(39) LA(41)	36 a ^c
11-20 (SC)	GA(34) LA(38) TX(39) MS(43) SC(71)	45 b
B-5-4 (LA)	SC(29) GA(38) MS(39) TX(48) LA(76)	64 b
S-6-5 (TX)	GA(33) SC(40) MS(43) LA(58) TX(65)	48 b
S-4-8 (TX)	SC(43) GA(46) MS(58) TX(63) LA(65)	55 c
7-56 (SC)	TX(48) LA(61) MS(64) SC(65) GA(68)	61 d
15-42 (GA)	TX(45) SC(46) MS(65) GA(78) LA(88)	64 d
4-R (GA)	SC(80) GA(80) LA(81) MS(83) TX(84)	82 e
3838-3 (GA)	MS(75) GA(78) LA(83) TX(91) SC(92)	84 e

^bNumbers in parentheses are percent seedlings infected.

Means underscored by a common line do not differ significantly according to Duncan's multiple range test, $P = 0.05$.

^cHost means followed by the same letter do not differ significantly at the $P = 0.01$ level as determined by Duncan's multiple range test. Each mean, however, should be evaluated by state since there was a significant family × isolate interaction.

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