VARIABILITY OF CRONARTIUM FUSIFORME AFFECTS RESISTANCE BREEDING STRATEGIES

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Abstract.--Variable response of open-pollinated slash pine families to diverse inocula indicate extensive pathogenic variability in *Cronartium fusiforme.* Inocula from field-infected members of a resistant slash pine family were more virulent on seedlings of the same parent than inocula representing the general rust population. Hence, the raw material and capacity for shifts in virulence are present. The rates and importance of such shifts are uncertain, but C. *fusiforme* will be subjected to increasing selection pressure as plantings of resistant pines expand. The potential threat of increased virulence must be considered in breeding and deploying resistant pines. Procedures for enlarging the number and variety of resistant selections in seed orchards are suggested.

Additional keywords: *Pinus taeda,* P. *elliottii* var. *elliottii,* virulence, fusiform rust.

Fusiform rust, caused by *Cronartium fusiforme* Hedgc. and Hunt ex Cumm., limits productivity of loblolly *(Pinus taeda* L.) and slash (P. *elliottii* var. *elliottii* Engelm.) pines over much oE their commercial ranges. The disease, largely a curiosity until 1930, has become increasingly widespread and damaging (Dinus 1974). Resistance breeding is a promising tactic for reducing losses to rust (Rockwood and Goddard 1973, Stonecypher et al. 1973), but development and deployment of resistant pines involves some risk. C. *fusiforme* has proven highly variable, and selection pressures imposed by resistant plantings may increase the frequency of virulent forms.

The present paper summarizes available information concerning pathogenic variability and shifts in virulence and suggests means for coping with these problems.

PATHOGENIC VARIABILITY

An early experiment (Snow and Kais 1970) provided the first direct evidence of pathogenic variability in C. *fusiforme.* Two open-pollinated families each of loblolly and slash pine were inoculated artificially with three collections of C. *fusiforme* from each of five widely separated areas. Families considered susceptible in previous field tests proved susceptible

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to all inocula. In contrast, loblolly pines from the resistant family were moderately resistant, on the average, to inocula from all areas but varied in their response to individual inocula from each area. Seedlings from the resistant slash pine family were even more variable in their responses. They were moderately resistant to Texas, Mississippi, and North Carolina inocula but susceptible to those from Alabama and Florida.

Much additional information concerning the occurrence and extent of pathogenic variability has since been accumulated. In three experiments, we evaluated the responses of 14 open-pollinated slash pine families to diverse inocula (Snow et al. 1975). In each experiment the inocula x family interaction was significant. Most families were quite variable in response; they proved susceptible to some inocula and resistant to others. Only four families were susceptible and two families were resistant to all inocula. These results demonstrated variability among inocula from widely separated areas, among inocula from different locations within each area, and also among inocula from individual galls.

SHIFTS IN VIRULENCE

The extensive variability described above is the product of past evolution but more importantly is also the raw material for future change. To the extent that resistant pines are planted, future change will be man-directed, and therein lies the risk. Extensive or repeated planting of pines with only one or a few types of resistance may lead to an increased frequency of virulent forms of C. fusiforme.

Such shifts have been observed in response to the planting of at least one resistant slash pine family, one whose responses proved highly variable in the experiments previously described. In a recent test (Snow et al., in prep.), inocula specific to the particular family--family specific--were collected from nine galls on field-infected members of that family in two open-pollinated progeny tests. Random inocula--samples representing the general rust population--were collected from nine galls on woods-run slash pines outside, but within 1 mile of, the same plantations. Collections from each gall were processed separately and used to inoculate open-pollinated seedlings of the same family.

Two random inocula caused no galls, two others infected only one seedling each, and only one approached the family specific inocula in virulence (fig. 1). With the random inocula, percentages of seedlings with galls ranged from 0 to 54 and averaged only 17 percent. In contrast, average infection over all family specific inocula was 77 percent. This significant fourfold difference indicates that the frequency of forms capable of infecting seedlings of this family was increased. Moreover, variation among family specific inocula was sizable, ranging from 52 to 94 percent. Hence, even further selection seems possible.

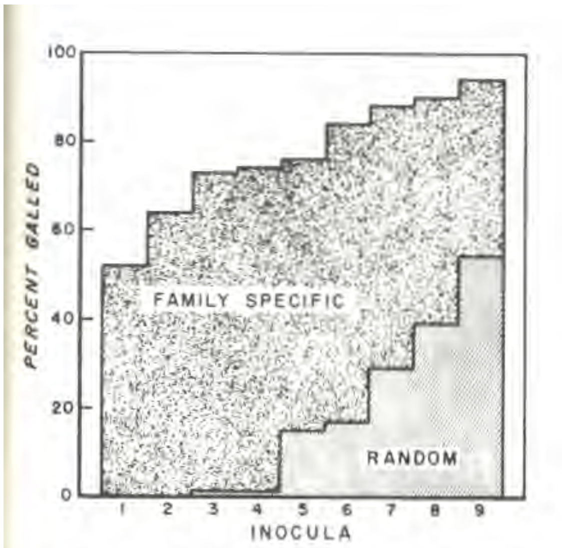

Figure 1.--Percentage of seedlings in a resistant slash family galled 6 months after inoculation with nine inocula from field-infected offspring of the same parent (family-specific) and nine random inocula. Inocula are ranked in order of increasing virulence.

TESTING FOR RESISTANCE

C. *fusiforme,* then, can adapt in response to resistant hosts. Existing plantings of resistant pines are small and scattered. Resistant materials are just now becoming available for extensive use. As the number and area of resistant plantings enlarge, C. *fusiforme* will be subjected to increasing selection pressure. We do not see drastic shifts as imminent, but we do visualize at least gradual erosion of resistance unless the potential for change is considered in resistance breeding programs.

Currently, progenies from rust-free parents are tested either in the field near sites to be reforested or by artificial inoculation with C. *fusiforme* collected from such sites. These procedures identify resistant parents but provide little information about the stability of resistance or different types of resistance.

To acquire such information, we suggest that present testing practices be supplemented. First, the most resistant parents now available should be tested against a broad array of inocula. Minimally, such a array should sample all likely planting sites; for example, all eastern Coastal Plain sites managed by a given agency. Indeed, some agencies have already expanded the number and distribution of their progeny tests. Ideally, the array of inocula should be as extensive as possible. The most desirable parents will be those whose progeny are least variable in their response to diverse inocula. The resistance of such parents is least likely to be overcome by extant virulent forms or to cause future shifts in virulence.

Second, individual resistant families should be tested against inocula from field-infected members of the same families and also against inocula representing the general rust population. Families that respond similarly to family-specific and random inocula seem least likely to provoke selection for increased virulence.

Third, to identify parents with different types of genetic resistance, we suggest cross-inoculation among families that have proven most promising. Inocula should be collected from field-infected members of each family and systematically applied to seedlings of that particular family and all others. This systematic cross-inoculation would indicate if a given set of parents has different genetic bases for their resistance.

The ideal resistance breeding program should utilize a large number of parents, each with one or more types of resistance. Should such parents be few in number, steps should be taken to broaden the genetic base. Selection and testing of new parents must be a continuing process. The primary purpose of continued selection is acquisition of additional resistance genes, but a broad genetic base will facilitate improvement of other traits and will also lessen the probability of encountering problems with yet other pests in the future.

In the absence of more complete information, the above suggestions should enable us to enlarge the number and variety of resistant parents in seed orchards. If resistant pines are to be planted with confidence, however, further research is needed on the genetics of both resistance and virulence. Reactions contributing to resistance must be better characterized and their inheritance patterns quantified. Mechanisms providing for genetic change in C. *fusiforme* as well as maintenance and spread of forms with increased virulence must also be clarified.

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