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BOTANY

Some Observations in Progeny Tests of Slash Pine in Georgia

In 1950 the Ida Cason Callaway Foundation at Hamilton, Georgia embarked upon a program of Forest Tree Improvement. This was a cooperative project under the technical supervision of the Southeastern Forest Experiment Station (U. S. Forest Service). The project has been concerned primarily with the four major Southern pines (loblolly, *Pinus taeda* L.; longleaf, *P. palustris* Mill.; shortleaf, *P. echinata* Mill.; slash, *P. elliottii* Englem.).

The first open-pollinated progeny were outplanted in the spring of 1952. The progeny test area now covers more than 80 acres and contains about 30,000 trees on which individual records are kept. The progeny are planted in plots varying in size from 10 to 100 trees, depending upon the study and the number available. All studies are replicated so that data collected will be statistically acceptable.

Considerable emphasis has been placed on the work with slash pine because of its rapid growth and widespread use in plantations. In 1956 Georgia nurseries produced 113 million seedlings, 80 million of them slash pine.

Open-pollinated progeny tests have received a great deal of attention in many tree improvement programs because of the ease with which seed can be collected and the tests begun, and because they represent a great saving initially in work and time over the use of progeny from controlled pollinations. This saving of one and one-half to two years in time is probably much more important in the South where juvenile growth is rapid and the nursery phase of the program involves only one year.

The real value of these open-pollinated progeny tests is still unknown, as is detailed information on controlled pollination tests for most characters of economic importance in forestry. It is hoped that these open-pollinated tests will provide sufficient information for selection of trees to be used in breeding programs and to be propagated for use in commercial seed orchards.

Observations and data analyses are concentrated along three lines of interest: growth-rate, form, and disease resistance. Differences among various lots have been readily detected, many of them being statistically significant in each of the three categories.

Growth-rates have been determined by height measurements. Differences become apparent at an early age, sometimes even in the nursery bed. At four years in the field, differences as great as 32 percent (6.99 feet vs. 9.26 feet) are present among lots.

Form is a difficult characteristic to measure. On this young material the attempt has been to evaluate only crown-width. Expressed as the ratio average crown width/height, the values range from about 0.33 to 0.43 at four years of age. The contrast among groups in the field is often quite striking.

Southern fusiform rust (*Cronartium fusiforme*) is the only disease of importance for which an evaluation of the progeny under test is possible. Under field conditions the infection rate varies according to season. The best lots show infection rates of 30 percent compared to 77 percent in the poorest. Another test planted the following year shows 19 vs. 48 percent in the same lots. Seed furnished from plantations in Australia have given progeny with high infection rates. The rust fungus is not present in that country and a selection for resistance to the disease could not be made. A wide range in infection is noted between open-pollinated progeny of individual select trees but these average much below the control lots from commercial seed and seedlings.

At present there are not sufficient economic data available to base a decision as to the relative importance of these characters. There is no single progeny group which is best in all characters rated, but several appear which are very good in all. These trees which are good all-round parents will be those used immediately in seed orchards. The

individuals excelling in only one or two and being poor in the others will be useful only for breeding purposes.

The data from these early progeny tests will serve as a basis for improving techniques of progeny testing and for refining selection methods so that the fullest values from the forest genetics program now underway may be achieved.