SCREENING LOBLOLLY PINE FOR ADAPTABILITY TO DEEP PEAT SITES: A SEEDLING STUDY OF TWO EDAPHIC SEED SOURCES FROM EASTERN NORTH CAROLINA

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Abstract.--A study has been initiated to screen for adaptability of loblolly pine to excessively wet, deep organic soils in eastern North Carolina and to investigate the use of seedling root characteristics as morpho-physiological indicators in early genetic evaluation. The study consists of 1) field trials to compare a broadly adapted Coastal Plain seed source with a seed source that originated on the deep organic soils in Tyrrell County, North Carolina and 2) a seedling study of the two edaphic seed sources. The results of the seedling study are given. Edaphic seed source differences are slight but considerable variation exists among open-pollinated families from each seed source. Several families exhibited differential genetic response to soil types. An alternative to a separate breeding program for deep organic sites is suggested.

Additional Keywords: Family by soil interaction, *Pinus taeda,* deep peat and Coastal Plain.

As tree improvement efforts intensify in response to the dwindling land base availability for forestry and to the increasing demands for fiber products adaptability to physiologically difficult sites becomes of critical importance (Bridgwater and Stonecypher 1978). Greater understanding of genetic variation in root response to environmental factors may prove essential to the production of high yield forests on these marginal sites and provide potential physiological indicators for early genetic evaluation (Long 1973, Cannell, et al 1979). The excessively wet areas in the Coastal Plain of North Carolina are an example of marginally productive loblolly pine (*Pinue taeda* L.) sites.

At present, several companies own forest land in the lower Coastal Plain that include areas of excessively wet, deep peat soils. The flat uniform topography and good growth potential are definite advantages but the **excess** water and heavy understory vegetation are serious drawbacks to all aspects of intensive forest management (Terry and Hughes 1975). Better logging technology has made harvesting these sites profitable and increased the demand for well-adapted planting stock. Despite improved silvicultural practices, broadly adapted Coastal Plain loblolly often exhibit poor growth, survival and increased susceptibility to windthrow on the deep organic sites (Anonymous 1971, Stonecypher, et al. 1965). In anticipation of a need for genotypes that are adapted to these sites, loblolly pine selections from the Tyrrell County deep peat areas were made in the late 1950's and were grafted into a production seed

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orchard. Since then, two other seed orchards have been established that include these genotypes. These orchards are the principal source of loblolly pine seeds for the deep peat sites in eastern North Carolina. Genetic differences between the Tyrrell County seed source and the more widely planted Coastal Plain seed sources have not been demonstrated.

The objectives of this study were 1) to determine the extent of the genetic differences that may exist between a broadly adapted Coastal Plain seed source and the Tyrrell County deep peat seed source and 2) to screen for seed source(s) or families that are adapted to organic soils.

METHODS

Experimental Materials

The seeds for the study were collected from two rogued first-generation loblolly pine seed (Pinus taeda L.) orchards in North Carolina. The deep peat source came from the first wet-site seed orchard established by Westvaco in 1959. Seeds were collected from eleven clones to represent what is operationally planted on deep peat soils. The Coastal Plain seed source **was represented** by seeds collected from eleven selected clones in Weyerhaeuser Company's North and South Coastal High (Wood) Density seed orchards. Each of these clones was grafted from select trees that grew on poorly drained mineral soils.

Experimental Procedure

The experiment was conducted in the North Carolin State University phytotron glasshouse at a day/night termperature regime of 26°/18°C. The experimental design was a split-plot with four replications, four soil-water treatment combinations, two seed sources and eleven open-pollinated families within each seed source. There were four seedlings per family-treatment combination in each replication. Watering regimes were the main plots. The soil medium used to simulate the deep organic soils was a 4:1 peat-vermiculite mix. The mineral soil was simulated with a 3:1 river sand-peat mix. Dolomitic lime was added in equal amounts to each medium; soil samples at the time of mixing indicated a pH of 7.00 for sandy soil and 6.2 for the peat. These pH values are not representative of those characteristic of the poorly drained mineral and organic soils of the North Carolina Coastal plain. These sites typically have pH values of 3.0 - 4.0. Higher pH values were maintained to reduce mycorrhizal development, a potential source of uncontrolled variation in this experiment. The bulk densities of the sandy medium and the peaty medium were 1.35 and 0.38 g/cc, respectively. Filled seed were weighed to obtain an estimate of mean seed weight by family. The seeds were soaked in distilled water, stratified for 30 days at 2°C and germinated in a germination chamber at 25°C. We used *a* priori knowledge of family germination rates to stagger sowing dates so that seeds from all 22 families germinated within a 5-day period in order to minimize age differences at harvest. Each germinant was transplanted into a quart-size milk carton the same day the radicle emerged to avoid damage to the embryonic root. Seedlings were doused weekly with Benomyl®, a broad-spectrum fungicide. A high-phosphate nutrient solution, Plant Starters (9-15-45), was applied once weekly for three weeks before harvest. Seedlings were watered twice daily until 35 days after germination when the root systems of seedlings designated to receive the waterlogging regime were submerged in water for five days and were watered twice daily. Seedlings in the "dry" regime were watered once daily until harvest. At age 60 days all seedlings were harvested and their root systems were rinsed free of soil.

Variables

1. Seed weights: Mean seed weights were determined for each family.

2. Total dry weights: Each seedling was dried at 70°C for 24 hours and weighed to the nearest milligram.

3. Number of first-order lateral roots: Each root system was floated in water and all lateral roots longer than 10 mm were counted.

4. Total root length: Total root length was tallied using a grid system (Bohm 1979). A grid with 169 half-inch squares was taped to the bottom of a shallow glass dish filled with water. The root system was spread out in the dish and anchored with glass sides. Each square intersected by a root *was* counted. Repeatability of the method was highly correlated (0.89) and it was highly correlated (r = 0.89) with total root length.

5. Shoot-root ratios were calculated using logarithms because seedling growth increases exponentially (Russell 1979, Salisbury and Ross 1979). Shoot-root ratios are log (shoot dry weight)/log (root dry weight).

Statistical Analyses

Seed weights were poorly correlated with the other variables (Table 1). Therefore, no adjustment for seed weight was necessary in the analyses that followed. All computations were performed on plot means using Statistical Analysis Systems (SAS Institute 1979).

TABLE 1. Correlation coefficients among mean family seed weight (SW) shoot-root ratio (SRRATIO), total root length (TRL), number of first-order laterals (LAT), and total dry weights (TDW).

	SRRATIO	TRL	LAT	TDW
SW	-.04	.02	-.04	.09
	.27[1]	.59	.14	.004

[1] probability of a greater F value

RESULTS

Response to water regimes was small and statistically nonsignificant for all of the traits except number of lateral roots. Seedling morphological differences were largely due to genetic and edaphic factors (Table 2).

Shoot-root ratio, total dry weight and total root length were highly influenced by soil type; soil constituted the largest single source of variation. Seed sources, *by* contrast, were statistically significant at least at the .05 level for shoot-root ratio, total dry weight and first-order lateral roots but accounted for less than 2.5% of the total variation associated with each of the traits. Families within seed sources were statistically significant for all traits measured in the study. Families by soil interaction was a significant source of variation at the 95% confidence level for shoot-root ratio, total dry weight and for total root length.. Spearman's rank correlation coefficients were calculated for each of these three traits to determine if the interaction resulted from families rank change on different soils. Only the correlation coefficient fur shoot-root ratio (r_s = 0.45) was significantly different from zero at the 95% confidence level. 8

TABLE 2© Means of total dr weight (TDW) number of first-order lateral roots (LAT), shoot-root ratio (SRRATIO) and total root length (TRL).

Source of Variation	TDW	LAT	SRRATIO	TRL
	(m^g)	(number)	(log shoot D.W. root D.W.)	**score**
Seed Source				
Deep Peat (DP)	267*	25.4*	.58*	64.9
Coastal Plain (CP)	277	26.6	.57	64©6
Soil				
Peat (P)	313	25.9	.59*	74.0*
Sand (S)	229	26.1	.55	55.6
Water				
Wet (W)	277	25.2*	.58	64.0
Dry (D)	266	26.8	.56	65.5
Families				
Maximum Value	331	30	.61	74
Mean	270*	26*	.57*	64*
Minimum Value	216	23	.50	55
Spearman's rank correlation coefficient	.24		.45*	.15

*Differences were statistically significant at least at the 95% confidence level.

[1] Spearman's rank correlation coefficient calculated for those traits with significant (a = .05) family by soil interaction.

DISCUSSION

Coastal Plain and deep peat seed sources were not genetically distinct in the two test environments. Although the seed source effects were statistically significant for shoot-root ratio, total dry weight and the number of first-order lateral roots the mean differences accounted for 2.5% or less of the total variation in this study. There was no evidence of interaction **between seed** source and soil or water regimes. If the seedling traits are reliably correlated with later field trial performance then the **seed** source differences are of negligible importance in a tree improvement program unless the differences are compounded annually over rotation.

As an alternative, breeding and selection efforts among families should receive more emphasis than seed sources **alone since** variation among families is considerably greater. Half-sib family blocks or a subset of orchard families which are particularly responsive to the silvicultural and edaphic conditions specific to deep peat sites could be planted instead of bulked **seed** lots from an edaphic seed source. This approach would allow the tree breeder to capitalize on genotype by site interaction without the expense of a separate breeding program (Bridgwater and Stonecypher 1978) and is under consideration as an operational practice by Weyerhaeuser in North Carolina (R. G. Campbell, pers. comm. 1981). Additional test environments are necessary to **examine** the full scope of family by soil interaction but the differential **genetic response exhibited** by several families for the traits total dry weight and total root length warrants a closer look at the opportunities for exploiting adaptability to **specific** site conditions.

SUMMARY

Differences between Coastal Plain and Tyrrell County deep **peat seed** sources are small and do not exhibit adaptation to sandy or peaty soil types. Open-pollinated families from both seed sources showed differential **genetic response** to soil types which could be exploited to provide well-adapted planting stock for the deep organic sites in eastern North Carolina. A separate breeding program is not recommended for the deep organic sites in North Carolina at this time.

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