SWEETGUM FAMILY SEEDLING SCREENING AND RESPONSE TO STRESS

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Abstract:-- Progeny trials are the traditional method used to select families for use in forest tree breeding. This has proven to be an effective, but slow method. This study examined differences in seedling growth among sweetgum *(Liquidambar styraciflua)* families under different stress regimes, and how these differences might be used in a seedling screening program. Twenty-two open pollinated families from a broad genetic background were used. High and low levels of light, fertility and artificial insect defoliation resulted in significant differences in height growth and volume index (D^2H) among families and treatments, and some two-way interactions. The rank order of families changed under different treatments.

Keywords: *Liquidambar styraciflua,* seedling screening, genotype X environment

INTRODUCTION

Forest geneticists have found that the most reliable method of predicting which families will be the highest yielding is through progeny trials. Progeny tests are typically conducted on good sites with excellent culture to maximize growth and allow the trees to express their genetic potential over a period of years. The trees typically reach one-third to one-half of rotation age, before selections for breeding are made. This method has proven effective, but not rapid. The development of an early screening technique, based on the evaluation of seedlings, would be attractive. To be useful such a technique would not have to rank families precisely, but merely separate them into categories for further study, elimination, or breeding.

Research on the genetic improvement of sweetgum *(Liquidambar styraciflua)* is limited (Webb 1964 Roberds 1965, Johnson and McElwee 1967, Wilcox 1970, Stubblefield 1984). No published research on sweetgum seedling screening has been found. Most studies of sweetgum seedlings have focused on interactions with mycorrhizal fungi (Bryan and Kormanik 1977, Kormanik 1985, Pope et al. 1983).

In this study we examined the seedling growth of sweetgum families under a variety of stresses. Th overall objective was to discover if through the application of stress, family level growth potential could be detected at the seedling stage.

METHODS

Twenty-two open pollinated (half-sib) sweetgum families were used in this research. Families we selected to maximize probable genetic diversity among them by maximizing the range of growth potential as known from *a priori* knowledge, and the geographic range of the families. Sixteen families were from the NC State - Hardwood Research Cooperative clone bank in St. George, SC. The families included six from estimated upper performing families, six from estimated lower performi families and four from the edge of the geographic range of sweetgum. These *a priori* performan rankings were very preliminary, at best. Also, six families with a range of growth potential w provided by Union Camp Corporation.

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Stress treatments were applied immediately after sowing in D40 pots (Deepots 40 ™, 6.35cm dia., 25.4cm deep) in a glasshouse during the summer of 1998, and continued for 157 days (Table 1).

Tablel. Treatments applied to 22 0-P sweetgum families in a glasshouse study of growth potential.

Treatment	Light	Fertility	Defoliation
1	Full	High	None
2	Full	High	75%
3	Full	25% of High	None
4	Full	25% of High	75%
5	30% of Full	High	None
6	30% of Full	High	75%
7	30% of Full	25% of High	None
8	30% of Full	25% of High	75%

The study included three replications and eight sub-sub plots, with seven trees per family grown in each replication per treatment, totaling 3696 measurement trees. Seedlings were free to grow until competition between plants began, when two-thirds of the seedlings were removed; one-third for destructive harvest and analyses, and one-third for field planting. The remaining third were continued in the greenhouse for later measurement, and destructive analysis for component biomass, nutrient and starch allocation (not reported here). Seedling height (+ 1 mm) was measured biweekly throughout the experiment, and root collar caliper (± 1 mm) was measured periodically.

The period of time from thinning (15 weeks post sowing) until the end of the experiment (5 weeks post thinning) was focused on for growth analysis. Prior to this period, growth differentiation among families and treatments was small.

RESULTS AND DISCUSSION

There were significant differences for all treatments and light related two-way interactions in height growth among families (Table 2). All other two-way interactions were not significant. Analyses based on volume growth index showed similar trends, except that not all two-way interactions involving light were significant (Table 2). Comparison of families across treatments, indicated that the limiting factor for each family differed.

There are a number of interesting patterns in family ranking among the eight treatment combinations (Table 3), which represent the range of responses. For example: family 10141 ranked among the top six families in three of the four shade treatments, while ranking among the bottom eight families in three of four sun treatments; family 10021 ranked among the top four families in all the sun treatments, while having mid-range rankings (3 to 12) among the shade treatments; family 10090 ranked among the bottom three families in 6 of the 8 treatments (sun and shade); and family 10095 exhibited great variation in rankings among the eight treatments.

These findings suggest strong genotype X environment interactions for some families, while others are more robust across environments. These differences could be exploited in a seedling screening protocol, potentially accelerating the process of family selection for testing and breeding. As part of the ongoing tree improvement program of the NC State - Hardwood Research Cooperative, this finding will be further tested. The same 22 families are currently included in a series of new NC State - HRC progeny trials across the South. The finding that stressful growing conditions may provide a better screening environment than traditional methods for early testing, may have important implications.

Table 2. Overall (22 families pooled) significance of treatments on growth of sweetgum

Treatment	Volume Index Growth (D^2H), by ANOVA	Height Growth by Repeat Measures ANOVA
Light	***	*
Fertility	***	***
Defoliation	**	***
Family	***	***
Light*Fertility	**	***
Light*Defoliation	ns	*
Light*Family	*	**
Fertility*Defoliation	ns	ns
Fertility*Family	ns	ns
Defoliation*Family	ns	ns

Note: Replication (greenhouse table) not significant overall. *, ** and *** indicate significance at P< 0.05, 0.01 and 0.001 respectively.

Table 3. Volume index ranking of sweetgum families as seedlings under stress regimes.

Full Sun High Fertility No Defoliation	Full Sun High Fertility Defoliation	Full Sun Low Fertility No Defoliation	Full Sun Low Fertility Defoliation	Shade High Fertility No Defoliation	Shade High Fertility Defoliation	Shade Low Fertility No Defoliation	Shade Low Fertility Defoliation
A UC-3	A 10141	A 10021	A 10006	A 10022	A 10024	A 10006	A 10008
A B UC-5	A B 10095	A B 10006	A B 10090	A 10141	A B 10022	A B 10008	A B 10095
A B 10176	A B C 10021	A B 10141	A B C 10034	A B 10139	A B C 10021	A B 10095	A B C 10022
A B 10021	A B C 10024	A B 10139	A B C 10021	A B 10008	A B C 10023	A B C 10024	A B C 10015
A B UC-1	A B C 10006	A B 10008	A B C UC-6	A B UC-1	A B C 10192	A B C UC-4	A B C 10093
A B 10141	A B C UC-3	A B 10034	A B C 10022	A B 10034	A B C 10015	A B C 10022	A B C D 10021
A B 10024	A B C 10090	A B 10023	A B C UC-3	A B 10024	A B C D 10095	A B C UC-3	A B C D UC-2
A B 10192	A B C 10093	A B UC-6	A B C 10093	A B C 10006	A B C D 10176	A B C 10176	A B C D 10006
A B 10139	A B C 10176	A B C 10022	A B C 10095	A B C 10015	A B C D E UC-1	A B C D 10021	A B C D E UC-1
A B 10034	A B C 10139	A B C 10192	A B C UC-5	A B C D 10192	A B C D E UC-4	B C D UC-2	A B C D E 10192
A B 10022	A B C 10034	A B C UC-1	A B C 10023	A B C D 10023	A B C D E 10006	B C D 10023	B C D E 10024
A B 10095	A B C 10008	A B C 10005	A B C 10024	A B C D 10021	A B C D E 10139	B C D 10139	B C D E 10139
A B UC-4	A B C 10022	A B C UC-2	A B C 10192	A B C D UC-2	A B C D E UC-3	B C D 10093	B C D E 10034
A B 10023	A B C 10015	A B C 10024	A B C 10015	A B C D 10176	A B C D E 10005	B C D 10015	B C D E UC-4
A B 10015	A B C UC-1	A B C UC-3	A B C 10008	A B C D 10005	A B C D E 10093	B C D 10005	B C D E 10141
A B 10006	A B C UC-2	A B C UC-5	A B C 10141	A B C D UC-3	A B C D E UC-2	C D UC-5	B C D E 10005
A B 10008	A B C UC-4	A B C 10176	A B C 10139	A B C D 10093	A B C D E UC-6	C D 10141	C D E 10176
A B UC-2	B C 10192	A B C UC-4	A B C UC-1	B C D UC-6	A B C D E 10008	C D 10192	C D E 10023
A B 10005	B C UC-5	A B C 10093	A B C UC-4	B C D 10095	B C D E 10034	C D 10034	C D E UC-5
A B 10090	B C 10023	A B C 10090	B C 10005	C D UC-4	C D E 10141	C D UC-1	D E 10090
A B UC-6	B C 10005	B C 10095	B C UC-2	C D 10090	D E UC-5	C D 10090	E UC-3
B 10093	C UC-6	C 10015	C 10176	D UC-5	E 10090	D UC-6	E UC-6

Note : Same letters preceding familes indate no significant differences between families using a protected LSD mean seperation test.

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