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Sycamore Seedlings From the Nursery -- Not the Same Genetic Composition as the Collected Seedlot[1]

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The genetic composition of bulked sycamore seedlots is altered when smaller or larger diameter seeds are removed. The family composition of seedlings from bulked seedlots is different from the composition of individual family seedlots because families germinate at different rates.

Tree improvement programs stress the importance of controlling the genetic composition of planting stock in order to achieve genetic gain. By collecting seeds from seed orchards, it is possible to control, to some extent, the genetic composition of seedlots. If seed orchard seeds are bulked, the family composition of the resulting seedlings may be different from the average of the original lots. These differences can be caused by seed handling practices and by different germination rates among the families in the bulked seedlot. Removing lighter density seeds from seedlots has improved the germination of the remaining seeds for some species (1, 2). However, studies have also shown that seed sizing can alter the genetic composition of bulked seedlots (3, 4).

Removal of the lighter density seeds of American sycamore *(Plantanus occidentalis)* improves the germination of the remaining seeds (2). Sizing seeds on the basis of density is not a common practice in commercial nurseries, but removing the smaller seeds with slotted sieves is sometimes done. The objective of this study was to determine if the genetic composition of seedlings from bulked seeds can be altered (1) by removal of the smaller seeds using slotted sieves and (2) by families germinating at different rates.

Methods

Sycamore fruits were collected from 10-year-old grafts from the Catawba Timber Co. sycamore seed orchard at Catawba, S. C., in December 1978. Fruits were collected from one ramet of each of 12 clones. The fruits were air-dried for 5 weeks and then broken apart for seed separation and cleaning. Each family seedlot was sorted through a series of slotted sieves into four classes on the basis of seed diameter. The diameter classes were greater than 1 /16 inch (1.59 mm), 1/16 to 1/20 inch (1.27 mm), 1/20 to 1/24 inch (1.06 mm), and less than 1/24 inch. For each family, the weight of seeds in each size class was recorded to determine the percentage of total weight in each size class (table 1).

Table 1—*Seed size distribution by percentage of total weight for 12 open-pollinated sycamore family seedlots*

	Seed size			
Family	<1/24 in.	1/24-1/20 in.	1/20-1/16 in.	> 11/16 in.
	----- *% of total weight* -----			
A	5	9	57	29
B	9	23	62	6
C	9	25	63	3
E	23	36	41	0
F	0	0	44	56
J	7	20	65	8
K	4	16	69	11
Q	14	34	52	0
S	4	14	69	13
U	17	34	49	0
V	0	0	52	48
X	0	0	34	66

The seedlots were subjected to a germination study in the spring after the seeds had been moist-stratified. Fifty seeds from each seed size-clone combination (35 lots) were allowed to germinate in a cup of water for 22 days. The fungicide Ferbam was added to the water to prevent mold buildup. Germination counts were made after 22 days.

Results and Discussion

Seed size distribution differs by family (table 1); therefore, seed sizing can alter the genetic composition of a bulked seedlot. If all seeds smaller than 1 /24 inch were

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removed from a bulked seedlot consisting of equal weights of seeds from the 12 families in table 1, only 3 families would lose more than 10 percent of their total weights. If all seeds less than 1 /20 inch in diameter were removed, families F, V, and X would have no seeds removed, while over 45 percent of the seed weight from families E, Q, and U would be removed. Use of only the largest diameter class would severely restrict the genetic base of the seedlot. Four families constitute 83 percent of the total weight in this size class.

The germination study showed that seeds from different clones had significantly different germination rates (tables 2 and 3). If an equal number of seeds from each of the 12 families were planted, not all of the 12 families would be equally represented in the resulting seedling crop. Seventy percent of the seedlings would be offspring of families E, D, K, U, and S. Families U and S alone would account for 31 percent of the seedlings. It is invalid to assume a bulked seedlot consisting of equal amounts of seeds from each family will produce equal numbers of seedlings from each family.

To keep a seedling crop from being predominantly the offspring of a few individuals, sycamore can be planted by family. In this way, each family seedlot can be sown with regard to its particular germination rate. The seedlings could then be lifted by family and either maintained separately or bulked for outplanting. An advantage of sowing and lifting by family is that families can be matched to sites where they perform best.

Table 2—*Percentage of germination for 12 open-pollinated sycamore family seedlots*

	Seed size				
Family	<1/24 in.	1/24–1/20 in.	1/20–1/16 in.	> 11/16 in.	Mean
	------ *% of germination* ------				
A	—[1]	0	0	2	1
B	4	2	6	—	4
D	20	8	32	—	20
E	14	14	18	—	15
F	—	—	16	2	9
J	10	10	14	12	12
K	—	20	12	24	18
Q	2	4	16	—	7
S	26	22	50	36	32
U	18	28	30	—	25
V	—	—	0	0	0
X	—	—	18	8	13

[1]— = no germination.

Table 3—*Significant family germination differences at P = 0.05*

Family	V	A	B	Q	F	J	X	E	K	D	U	S
Percent	0	1	4	7	9	12	13	15	18	20	25	32
	———	———	———	———	———	———	———	———	———	———		
				———	———	———	———	———	———	———	———	
								———	———	———	———	———

[1] Families underlined by the same line are not statistically different with a probability of 0.05.

Conclusions

Seed size distribution differs by family for sycamore. Because of these distribution differences, removing certain sizes of seeds from a bulked seedlot will alter the family composition of the lot.

Germination rates also differ by family. Sowing a bulked seedlot consisting of an equal number of seeds from various families will produce unequal numbers of seedlings from each family.

The only way to be sure of the genetic composition of a seedling crop is to sow the seeds by family. The separate families can then be bulked to match genotype and site.

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