

REDUCTION OF GENETIC BASE BY SIZING OF BULKED DOUGLAS-FIR SEED LOTS

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The laudable desire to produce more vigorous, uniform seedlings has led to widespread sizing of seed in conifer nurseries. Blowing or screening away small seed enhances production of larger, more vigorous germinants. There is little reason to question the practice other than on genetic grounds. The fact that each tree produces cones of a characteristic size has been known since the earliest Douglas-fir seed research in 1917 (1). A study in white spruce (2) has illustrated that reduction in the genetic base would occur with ordinary sizing by weight, practiced with that species. The main question that arises concerning Douglas-fir is, "Are entire families virtually removed from a seed lot population by removing small or light seed?" Beyond this, numerous other questions spring to mind involving the genetic consequences of different methods or degrees of grading seed. Since sizing practices are different in each nursery, the question must be answered in terms of the complete range of seed weights or dimensions.

Fortunately, our laboratory has several large wind-pollinated seed collections of individual trees from local populations. The collection chosen for study was harvested in 1966 from 309 parent trees of Crown Zellerbach Corporation near Vernonia, Oregon, and was

previously reported in some detail(3). We now have 10-year progeny measurements from the collection on six outplanting sites. Another collection, consisting of seed harvested from 15 trees near Sweet Home, Oregon, repeated over three seed crops for which 15-seed samples were weighed. From these collections, most of the preliminary questions regarding sizing effects could be answered.

Procedures

Seed weights from the 15 open-pollinated trees in a natural stand near Sweet Home, Ore., were available, so we could estimate how seed weight from individual trees varies from year to year. The mean of 75 seeds (15 from each of five replications) for each tree was graphed (fig. 1). The 1968 collection was ranked from highest seed weight to lowest, and collection years 1970 and 1971 were graphed over this ranking to show year-by-year variations. Thus, the variable outcome of truncating the array at any seed weight can be shown for families in this sample seed lot. Correlation analyses were used to determine between-year relationships for seed weight.

To determine genetic outcome of seed sizing, seed stores from 309 parent trees collected between April 12 and September 15, 1966, were available. This seed had been

sizing of bulked seed lots to any significant degree eliminates virtually whole families, thus accomplishing unintended reduction in genetic base. Year-to-year variation in family seed weight is appreciable. Relationship of seed size to weight is high, but to 10-year family means is low.

collected from wind-pollinated trees in a 35-year-old Coast Range stand along roads of the 80,000-acre (32,000 ha) Ed Stamm Tree Farm surrounding Vernonia, Ore. Elevations range from approximately 400 to 1,700 feet (120 to 520 m). Cones had been processed in 1/4-bushel (7.6 liters) lots with laboratory-scale equipment. Most of the lots had been cleaned to practically 100-percent full seed, but occasionally lots dropped to 95 percent. A 100-seed sample of each parent had been weighed in 1966. The seed has since been stored in 3 by 5-inch (7.6 x 12.7 cm) envelopes in cold storage at 0° F. Progeny measurements of total height and ground-line diameter were made on six sites in 1976.

As detailed by Olson and Silen (3), the first 99 parent tree numbers represented immature seed that was collected too early in the season. To assure that our population represents only mature seed, parent tree numbers 100 through 309 were used, providing a base population of 210 parent trees. Correlations were computed between seed weight and 10-year growth.

From this base population, 18 seed lots were chosen at random for detailed study. Two subsamples were then removed from each of these 18 seed lots. The

first subsample, consisting of 10 seeds from each lot, was used to determine correlation between seed size (expressed by differences in their flat cross-section diameter) and weight (on an individual seed basis). Seeds were weighed individually to the nearest 0.1 mg on an analytical balance, and seed

cross-section measured to the nearest 0.1 mm using a stereo-zoom binocular microscope and graduated scale eyepiece.

The second subsample consisted of 30 seeds from each lot, measured individually and independently for determining individual seed weights.

This subsample provided means and standard deviations from which cumulated frequency distribution curves for seed size and weight were constructed for 18 families (figs. 2 and 3). Only lot means of size and weight were analyzed for correlation for this subsample.

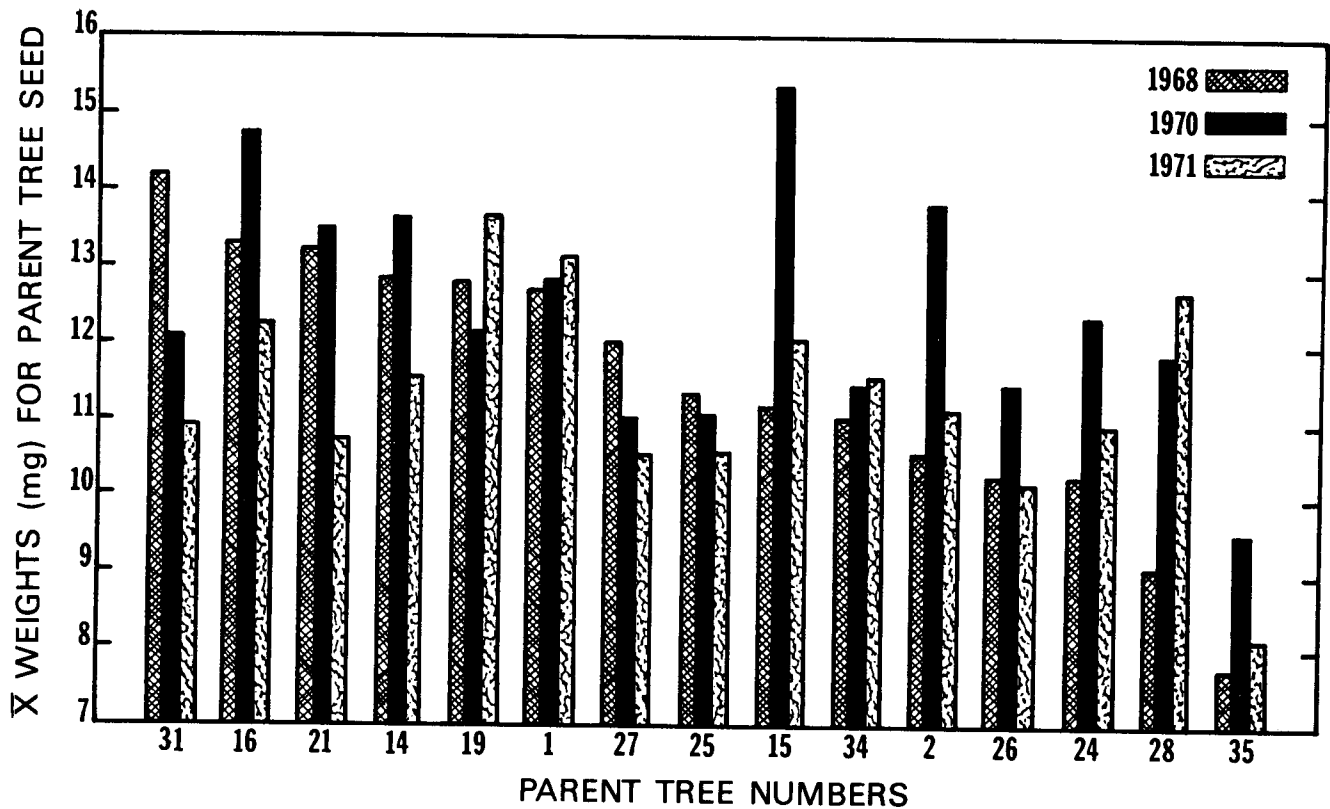


Figure 1.—Comparisons of seed weight for 3 years among 15 parent trees arrayed in descending order of 1968 means.

Progeny growth measurements for the 309 families at 10 years were available based upon performance summarized for the six out-planting sites. These provided data and correlations with seed weight and size. Nursery bed germination measured in 1967 served as data for correlation with seed weight and size.

Results and Discussion

Year-to-year variation in seed weight from our natural stand sample was as large as 40 percent for an individual tree (one tree ranged from 9.1 to 12.7 mg); and half the trees varied more than 15 percent. Figure 1, arrayed in descending

1968 seed weights for the 15 trees, shows considerable variation between years (table 1) and illustrates the gross change in composition of families with any grading of seed by weight. For example, a 50-percent culling rate (below the mean weight of 11.62 mg) in this population would have virtually rejected

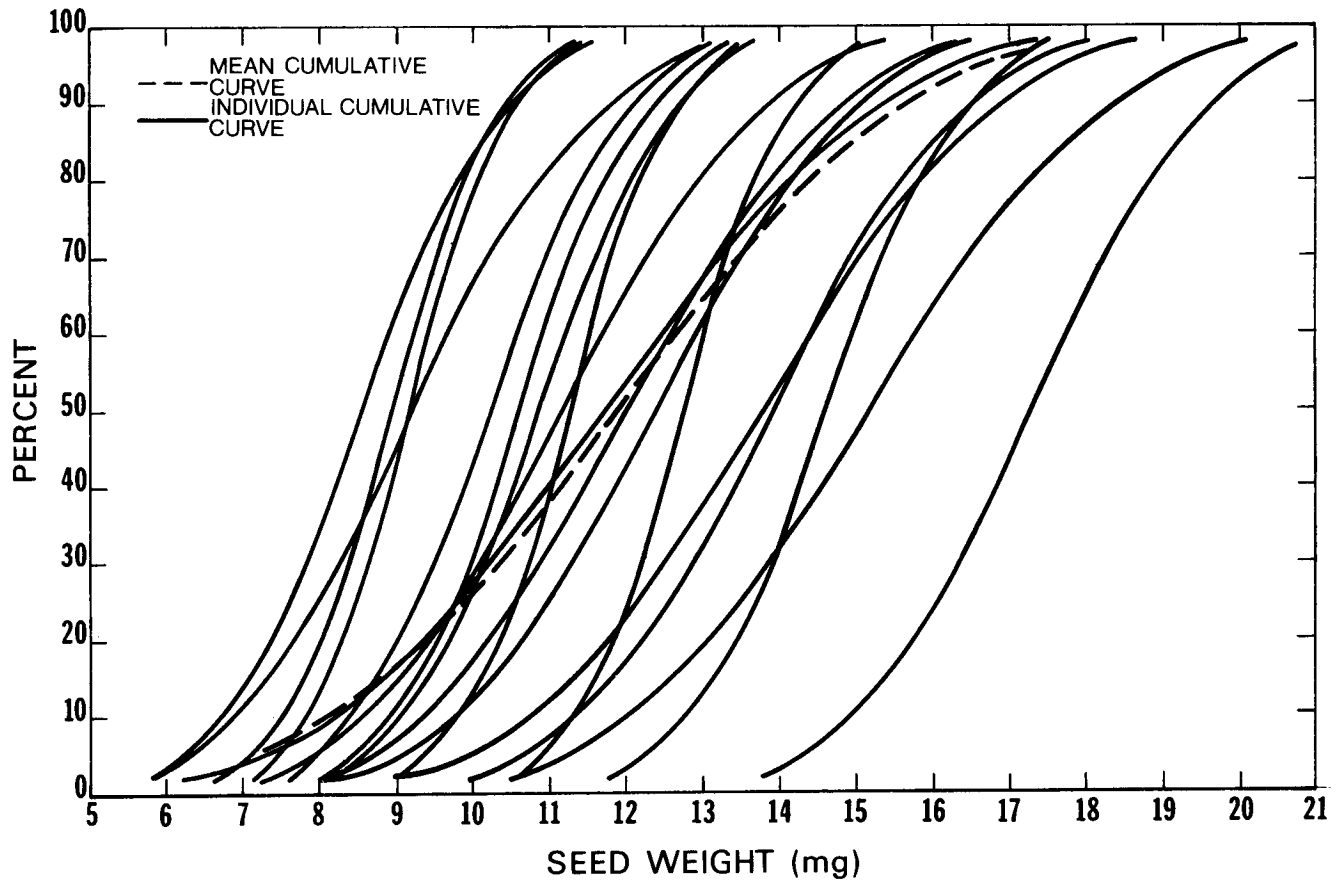


Figure 2.—Cumulative curves for seed weight for 18 Douglas-fir seed lots, and cumulative curve for the mean of same 18 Douglas-fir seed lots.

families 24, 25, 26, and 35 every year, and at least one year's contribution of all families except 14, 16, and 19.

The proportion of such families retained or rejected depends upon their variation around their mean value. The cumulative frequency distributions of seed weight (fig. 2), and seed size (fig. 3), were developed to illustrate this statistic. Both are based upon the 18 samples from which 30 seeds were measured or weighed. These two figures are based upon seed weight and size means and their standard deviations are found in tables 2 and 3. Each figure shows the 18 individual curves as well as that of the sample population.

The percent of any family affected is shown by truncating the figure vertically at any seed weight (horizontal axis). Using the cumulative curve is appropriate for setting a percent of culling. For example, the 50 percent frequency corresponds to the 11.84 mg seed weight and 3.54 mm size on the population curves of figures 1 and 2. Likewise, the mean seed weight or size of any parent corresponds to the 50 percent frequency in tables 2 or 3.

For most families, seed weight and particularly seed sizes cluster near mean values. Variation between family mean values is much greater. For this reason, almost any appreciable culling by size or weight effectively culls families.

The particular randomly chosen 18-tree sample is fortuitous. It has a

slight excess of parentage with heavy seed and contains a greater range of seed weight than average. It serves well to illustrate the consequences of culling.

In this paper, sizing levels of one-third and two-thirds are used for illustrative purposes. The outcome in this sample is that discarding the lightest one-third would effect 16 of the 18 families to varying degrees. Six would lose more than 50 percent, of which three would lose more than 90 percent of their seed. The six families losing more than 50 percent include two of the top five for 10-year progeny height.

Removing two-thirds of the lighter seed in the sample would affect all 18 families differently. Thirteen would lose more than 50 percent of their seed, including 7 of the top 10 for height growth. Eight families would lose more than 90 percent, which includes four of the five top trees in height growth.

The main component of the top one-third families would be more than 50 percent of three families with heaviest seed, none of which now ranks high in height growth.

In this sample the consequences of such sizing procedures are overly dramatic in their effect on

Table 1.—Correlation coefficient values

Comparison	d.f.	Correlation coefficient	
Seed weight by tree from year to year:			
1968 to 1970	13	0.481	
1968 to 1971	13	0.475	
1970 to 1971	13	0.533 ¹	
Relation between seed size and seed weight:			
10-seed subsample (individual seed lots)	179	0.741 ²	
x 30-seed subsamples (seed lots)	16	0.899 ²	
Relationship between seed weight and the following:			
	(sample)		
10-year mean height growth	(18-tree)	16	-0.299
10-year mean height growth	(209-tree)	207	-0.021
10-year mean diameter	(18-tree)	16	-0.017
10-year mean diameter	(209-tree)	207	0.110
Relationship between seed size and the following:			
10-year mean height growth		16	-0.009
10-year mean diameter		16	0.246

¹Significant (.05 level).

²Highly significant (.01 level).

10-year heights. The low correlation coefficients of 10-year heights and diameters on seed weight would indicate no different genetic composition between fractions of the sample (table 1). The proportion of families virtually eliminated from the population by these culling levels can, however, be considered to be fairly typical for most seed lots. The main effect of sizing, thus, is reduction of genetic base.

Another major conclusion of the study (table 1) is that seed weight and size are fairly closely related. To the extent that screening duplicates measuring seed for size, and blowing duplicates grading by weight, both would seem to give comparable grading.

Conclusions

There are four main conclusions:

1. Sizing to any significant degree eliminates a significant portion of virtually whole families.
2. Seed lots from the same parentage collected during different seed years produce different family distributions with sizing. Families represented in nursery beds would vary from year to year, and not be the same as those families from unsized lots.
3. Relationship of size and weight is quite good, whereas

Table 2.—Mean seed lot weights, standard deviations of individual lot weights, 10-year height growth, 10-year diameter, and percent nursery bed germination by parent tree numbers

Parent tree number	x seed lot weight (mg)	Standard deviation	x 10-year height growth (cm)	Ranking by height	x 10-year diameter (mm)	Ranking by diameter
197	17.31	1.83	171.1	16	34.1	14
276	15.19	2.50	180.0	12	37.4	4
182	14.60	1.41	188.8	7	36.2	9
263	13.99	2.00	171.5	15	36.0	10
243	13.84	2.47	159.0	17	33.5	17
178	12.77	1.09	190.0	6	37.2	5
274	12.40	2.08	191.0	4	36.6	6
130	12.00	2.20	185.8	11	33.6	16
162	11.70	2.87	187.2	10	34.9	12
147	11.26	2.04	158.8	18	30.6	18
287	11.18	1.10	196.0	2	38.5	1
190	10.86	1.39	216.5	1	38.1	2
265	10.61	1.12	190.0	5	36.4	7
127	10.25	1.47	187.3	9	36.3	8
141	9.22	1.79	175.3	14	34.1	15
196	9.16	1.04	187.9	8	35.1	11
247	8.95	1.12	194.0	3	37.7	3
213	8.57	1.43	177.0	13	34.8	13
Sample X	11.84	2.38	183.7		35.3	
Population x	10.79	1.56	185.2		36.0	

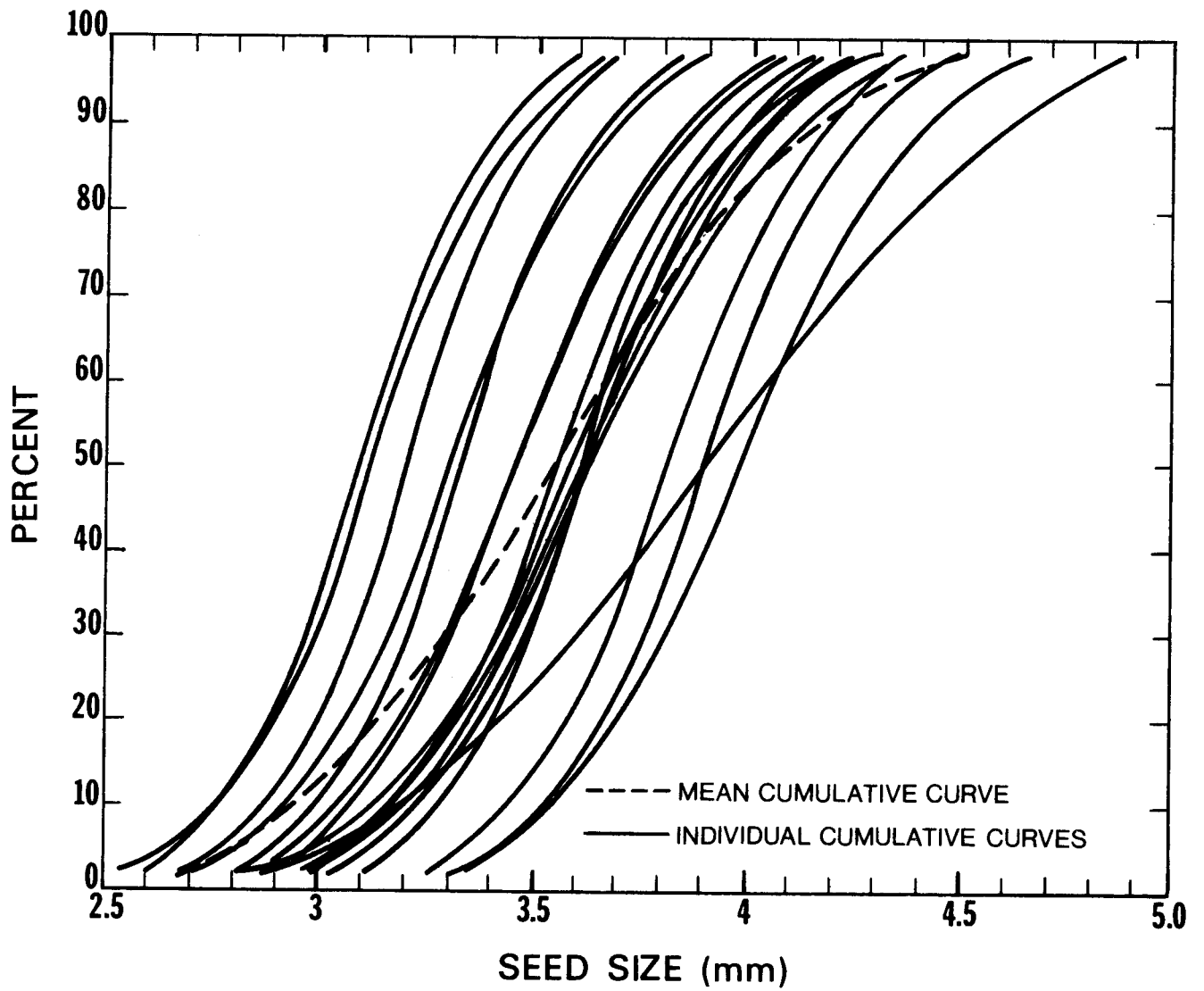


Figure 3.—Cumulative curves for seed size of 18 Douglas-fir seed lots and mean cumulative curve for the same 18 seed lots.

relationship of either to 10-year growth is very poor. Hence, there is no indication here that sizing for heavier seed will result in better trees by age 10.

4. The main known detrimental genetic effect of sizing is a reduction of the genetic base.

Thus, sizing of bulked seed lots is a form of genetic family selection. The need to remove empty and light immature seed from bulked lots has always been recognized as good practice. Some family selection,

however, appears as an outcome of any substantial level of sizing. Such would not occur if sizing were applied to seed of a single parent, the main effect being elimination of small seed from the ends of the cone, or immature seed.

Because our results were so similar to Hellum (2) for spruce, there appears little expectation that sampling of other Douglas-fir races would produce different results. There is likelihood now that other conifers would show similar results.

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Table 3.—Mean seed lot sizes, standard deviation of individual lot sizes, 10-year height growth, 10-year diameter, and percent nursery bed germination by parent tree number

Parent tree number	x seed lot weight (mg)	Standard deviation	x 10-year height growth (cm)	Ranking by height	X 10-year diameter (mm)	Ranking by diameter
197	3.98	.33	171.1	16	34.0	14
276	3.91	.50	180.0	12	37.4	4
182	3.90	.28	188.8	7	36.2	9
178	3.81	.27	190.0	6	37.2	5
190	3.64	.33	216.5	1	38.1	2
130	3.63	.38	185.8	11	33.6	16
263	3.62	.28	171.5	15	36.0	10
162	3.61	.25	187.2	10	34.8	12
243	3.60	.34	159.0	17	33.5	17
147	3.59	.35	158.8	18	30.6	18
274	3.55	.30	191.0	4	36.6	6
265	3.46	.33	190.0	5	36.4	7
287	3.45	.33	196.0	2	38.5	1
127	3.33	.26	187.3	9	36.3	8
213	3.30	.30	177.0	13	34.8	13
196	3.20	.25	187.9	8	35.1	11
141	3.11	.28	175.3	14	34.0	15
247	3.09	.26	194.0	3	37.7	3
x	3.54	.49	183.7		35.3	