REDUCTION OF GENETIC BASE BY SIZING OF BULK DOUGLAS-FIR SEEDLOTS

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ABSTRACT

Investigation of family differences in seed sizes and weights of 309 parent Douglas-fir (Pseudotsuga menziesii (Mirb.)Franco) trees shows that 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 low to 10-year family means.

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 f has illustrated reduction in the genetic base would occur with ordinary sizing by weight practiced with that species. The main question that arises with Douglas-fir is, "Are entire families virtually removed from a seed lot population by removing small or light seed?" Beyond this question, numerous others 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.

1 Willis, C.P. 1917. Incidental results of a study of Douglas-fir seed in the Pacific Northwest. J. For. 15:991-1002.

2 Hellum, A.K. 1976. Grading seed by weight in white spruce. Tree Planters' Notes, USDA Forest Service, Washington, D.C. (winter), p. 16-23.

In addition to these viability tests there are two other important tests for measuring seed quality. The moisture test is essential in order to assure that seeds are of low enough moisture to place in storage. Seeds at a low moisture content will store well at high temperatures without loss of quality. High moisture seeds however, will rapidly loose their viability at warm temperatures. Power failures do occur in storage, also temperatures do fluctuate. Therefore it is essential that seed moisture be monitored and kept low.

Seed weight is used primarily to calculate sowing rates, however, there may be positive correlations between seed weight and seed quality.

In summary, there are numerous laboratory tests which can and should be used to evaluate seed quality. These tests may be used to evaluate seed quality at any stage of collection, processing, or storage.

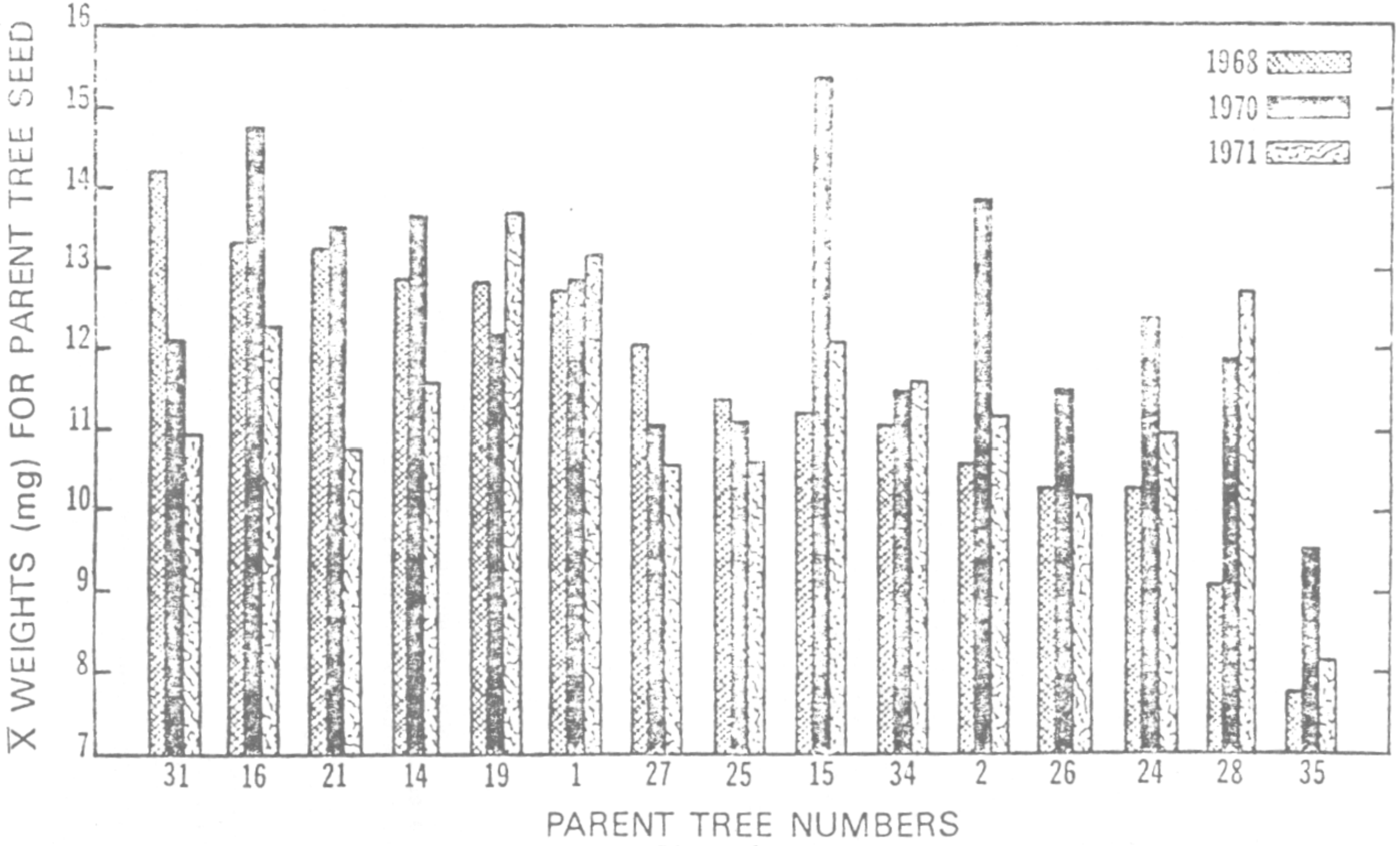

Figure 1
Comparisons of seed weight for 3 years among 15 parent trees arrayed in descending order of 1968 means.

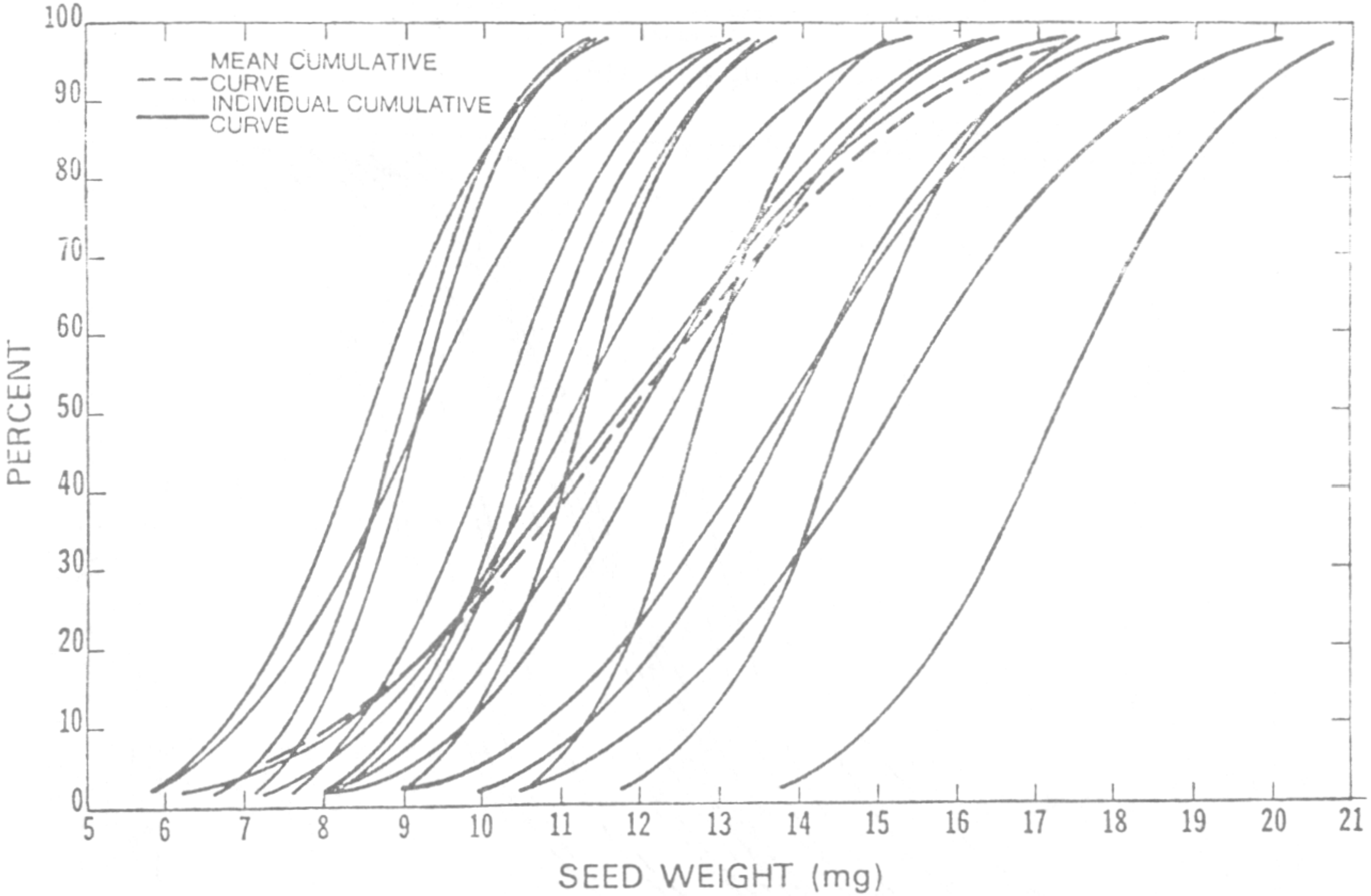

Figure 2
Cumulative curves for seed weight for 18 Douglas-fir seed lots, and cumulative curve for the mean of same 18 Douglas-fir seed lots.

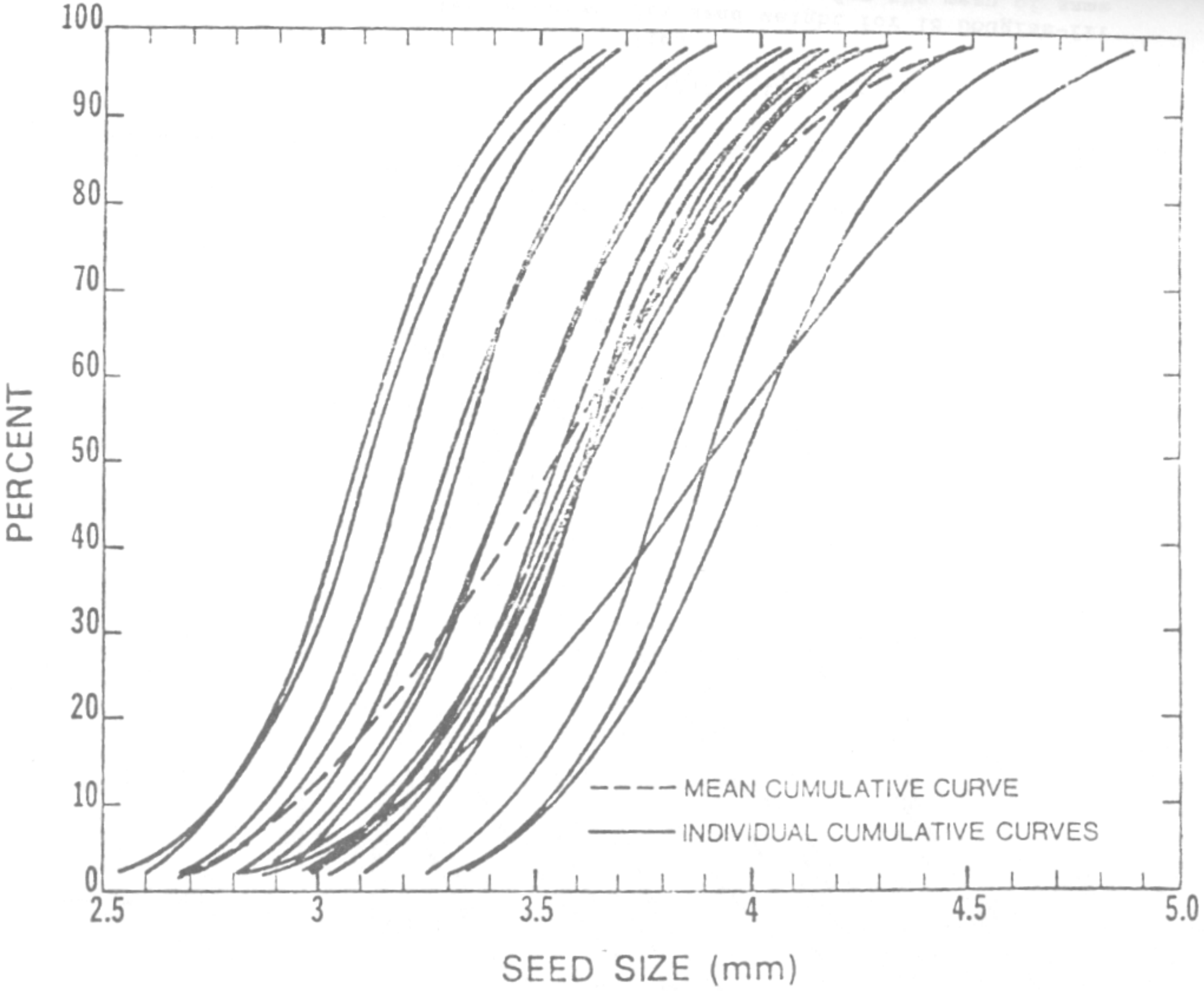

Figure 3
Cumulative curves for seed size of 18 Douglas-fir seed lots and mean cumulative curves for same 18 Douglas-fir seed lots.

As detailed by Olson and Silen 3/, the first 99 parent tree numbers represented immature seed which 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 catpuuted between seed weight and 10-year growth.

Fran 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 nearest 0.1 mg on an analytical balance, and seed cross-section measured to nearest 0.1 nm using a stereo-zoom binocular microscope and graduated scale eyepiece.

The second subsample consisted of 30 seed from each lot measured individually and independently of determing individual seed weights. This subsample provided means and stand 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.

Progeny growth measurements for the 309 families at 10 years were available based upon performance summarized for the 6 outplanting sites. These provided data and correlations with seed weight and size. Nursery bed germination measured in 1967 serves 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 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 in figure 2, and seed size in figure 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.

Table 1.--Correlation coefficient values

Comparison	sample	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*
Relation between seed size and seed weight:			
10-seed subsample (individual seed lots)		179	0.741**
$\bar{x}$ 30-seed subsamples (seed lots)		16	0.899**
Relationship between seed weight and the following:			
10-year mean height growth	18-tree	16	-0.299
" " " "	209-tree	207	-0.021
10-year mean diameter	18-tree	16	-0.017
" " "	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

* Significant (.05 level).

** Highly significant (.01 level).

Table 2. --Mean seed lot weights, standard deviations of individual lot weights, 10-year height growth, 10 year diameter, by parent tree numbers

Parent tree number	$\bar{x}$ seed lot weight	Standard devi-ation	$\bar{x}$ 10-year height growth	Ranking by height	$\bar{x}$ 10-year diameter	Ranking by diameter
	mg		cm		mm	
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 $\bar{x}$	11.84	2.38	183.7		35.3	
Population $\bar{x}$	10.79	1.56	185.2		36.0	

Table 3—mean seed lot sizes, standard deviations of individual lot sizes, 10-year height growth, 10-year diameter, by parent tree number

Parent tree number	$\bar{x}$ seed lot size	Standard deviation	$\bar{x}$ 10-year height growth	Ranking by height	$\bar{x}$ 10-year diameter	Ranking by diameter
	mm		cm		mm	
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
	3.54	.49	183.7		35.3	

By truncating the figure vertically at any seed weight (horizontal axis), one sees the percent of any family affected. Use of 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 1/3 and 2/3 are used for illustrative purposes. The outcome in this sample is that discarding the lightest 1/3 would affect 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.

Re owing 2/3 of the lighter seed in the sample would differentially affect all 18 families. 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 1/3 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 is overly dramatic in its effect on 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 fiat 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 seen 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 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 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.