

BEEF BULL GROWTH RATE EVALUATION PROCEDURES

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Procedures for estimating the breeding value for average daily gain of beef bulls across breed and across test groups are described. The estimates are best linear unbiased predictions taking into account breed, test group, paternal half-sibs and heritability. Breed differences based on Canadian test stations indicate that Angus gain approximately .05 kg/day less, Shorthorn about the same and Charolais .25 kg/day more than Hereford, with these differences fairly similar for all provinces. The use of evaluations across groups is compared with evaluations within group, considering the differences between large sample and small sample selection and the accuracy of estimating breeding values across groups relative to within groups. Expected genetic progress was found to be similar for across- and within-group selection procedures for fixed tested population size with an advantage for selection across groups for groups with many sires, especially for small numbers of bulls selected. Evaluations across groups can be more flexible, allowing for selection both within and across groups.

Les auteurs décrivent une méthode d'estimation de la valeur génétique de taureaux de type de boucherie pour le gain moyen quotidien. Les estimations, déterminées entre diverses races et entre divers groupes d'essai, sont des prédictions linéaires sans biais de variance minimum tenant compte de la race, du groupe d'essai, des demi-frères paternels et de l'héritabilité. Les différences de race, basées sur les stations d'essais canadiennes montrent que les Angus gagnent approximativement 0.05 kg/j de moins, les Shorthorn à peu près autant et les Charolais 0.23 kg/j de plus que les Hereford, les différences étant sensiblement égales dans toutes les provinces. Les évaluations inter-groupes ont été comparées avec les évaluations intra-groupes en ce qui a trait aux différences entre un grand et un petit échantillon, et à la précision l'estimation de relative de la valeur génétique inter-groupes par rapport à l'estimation intra-groupes. Le gain génétique attendu a été le même pour les méthodes de sélection inter et intra-groupes dans le cas de groupes de population fixe. La sélection inter-groupes semble avantager les groupes comptant de nombreux taureaux, surtout quand il s'agit de sélectionner un petit nombre de taureaux. L'évaluation inter-groupes peut être plus souple et permettre la sélection à la fois dans un groupe et parmi plusieurs groupes.

Performance testing of beef bulls is carried out to bring about genetic improvement in growth rates of feedlot cattle. The key requirements for improvement are testing a very large number of bulls and having many bulls measured under similar conditions. A testing structure with many groups, each containing several bulls, is necessary to

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make possible both accurate and intensive selection.

Selections are often made both within and across groups, but evaluations are often made that are only appropriate for selection within groups. The purpose of this paper is to describe an evaluation procedure for selection across groups and to compare the expected genetic progress in growth rate

resulting from selection across groups with that from selection within groups.

ACROSS-GROUP EVALUATION PROCEDURES

Comparisons across groups or herds are usually impossible because of one or more of the following reasons: small numbers per group, variable breed representation per group, and within-breed genetic differences per group.

Various procedures might be considered to make across-herd or group comparisons. The most direct is to test all the bulls from several herds together. Alternatively, random samples of herds could be tested together and the results used to rate the herd. This would be appropriate only for the concurrent test animals within the herd since the following year's calves would often be by different sires. The procedure described here is the use of standard test procedures and calculations for large numbers of groups. Only groups meeting minimum requirements for numbers of sires and bulls per sire are used. The requirements are designed to minimize sampling genetic differences between groups.

Standard test procedures could be carried out for groups in which

1. A minimum specified number of sires are represented with a minimum number of bulls per sire.
2. All bulls in a group are treated alike and standard procedures followed.
3. Start of test and end of test weighings are supervised.

Standard procedures could be

1. Age of all bulls at start of test should be relatively similar (for example between 190 and 265 days).
2. All bulls should be given a 28-day warm-up to offset pre-test environment. This has largely been achieved in station tests, as a very low phenotypic correlation between growth rate on test and starting weight after warm-up has been found by Wilton et al. (1973) and Batra and Wilton (1972). Similar adjustment periods would be necessary for within-herd tests.
3. Test period length should be 140 days.
4. Growth rate evaluations should be computed by a standard procedure.

Across-Group Models

A complete model for growth rate must be specified to determine evaluation procedures.

The model used here is:

$$w_{ijkl} = \mu + b_i + g_j + s_{ijk} + p_{ijkl} + e_{ijkl}$$

Where w_{ijkl} = average daily gain (ADG) on test record

μ = overall mean of all groups in a specified year

b_i = constant common to all bulls of the i^{th} breed

g_j = constant common to all bulls tested in j^{th} group

s_{ijk} = random sire effect of the i^{th} breed whose progeny appear only in the j^{th} group

p_{ijkl} = random bull or progeny effect of the k^{th} sire within the i^{th} breed and j^{th} group, and

e_{ijkl} = random error effect with each record

with s , p , and e having mean zero and variances σ_s^2 , σ_p^2 and σ_e^2 , respectively. A linear additive model should be appropriate, since previous research has indicated no changes of variance with changes in mean (Wilton and Batra 1972).

Accounting for Breed Effect

Simultaneous solutions could be obtained for all effects after a specified period of time. However, it is often necessary to provide immediate evaluations, which would be done after each group has completed test. In this event, there are often not enough bulls of various breeds to accurately eliminate breed effects. A common breed adjustment based on *a priori* breed difference estimates could be used as long as breed differences were similar for each group. Studies of the interaction of breeds and location (representing different groups) using data from B.C., Alberta, Saskatchewan, Manitoba, Ontario and the Maritimes, as described in Table 1, indicated no significant interactions existed on a practical basis. Approximately 1% of the total sums of squares were explained by interaction (Table 2).

Breed differences were fairly consistent from location to location (Table 3). A common breed adjustment appears reasonable, although it would not exactly remove all breed effects from each group. One of the largest differences is the superiority of Charolais over Hereford in Ontario relative to that in Alberta, a difference of .3 kg/day rather than .2 kg/day. Comparisons of Charolais sires might be different by .1 kg/day from these two provinces if tested mainly with

Table 1. Numbers per subclass (N) and means for average daily gain for four breeds in several locations

Location	Year	Angus		Hereford		Shorthorn		Charolais	
		N	Mean (kg)	N	Mean (kg)	N	Mean (kg)	N	Mean (kg)
Manitoba	71	17	1.35	136	1.34	23	1.28	45	1.59
	72	27	1.36	74	1.41	25	1.33	29	1.62
	73	29	1.36	110	1.47	20	1.43	45	1.67
Alberta	71	54	1.17	74	1.28	10	1.23	38	1.41
	72	50	1.16	64	1.15	15	1.12	43	1.41
	73	45	1.25	59	1.22	10	1.26	28	1.46
Maritimes	71	11	1.01	40	1.12	12	1.13	1	.97
	72	9	1.03	33	1.14	4	1.18	1	1.35
	73	13	1.24	35	1.26	7	1.28	6	1.50
British Columbia	71	18	1.24	29	1.15	10	1.23	5	1.51
	72	25	1.42	34	1.30	5	1.26	20	1.49
	73	42	1.26	20	1.20	2	1.38	18	1.59
Saskatchewan	71	30	1.26	129	1.26	14	1.37	20	1.53
	72	44	1.21	104	1.34	25	1.30	14	1.57
	73	44	1.38	183	1.40	38	1.44	5	1.73
Ontario	71	33	1.22	144	1.36	18	1.32	39	1.76
	72	27	1.20	180	1.34	33	1.30	53	1.67
	73	62	1.32	209	1.38	45	1.40	69	1.68

Table 2. Analysis of variance for average daily gain for group tested bulls†

Source	df	MS (kg/day) ²	F	R ² (%)
Location‡	5	1.73	62.86**	5.70
Breeds§	3	3.49	126.88**	6.91
Groups/location 1	2	0.64	23.18**	.84
Groups/location 2	2	1.10	40.09**	1.46
Groups/location 3	2	0.16	5.78**	.21
Groups/location 4	2	0.48	17.31**	.63
Groups/location 5	2	0.62	22.57**	.82
Groups/location 6	23	0.51	18.62**	7.77
Location × breed	15	0.13	4.71**	1.28
Residual	2,975	0.03		

**P < 0.01.

†Model: $y_{ijkl} = \mu + p_i + b_j + (pb)_{ij} + g_{ik} + e_{ijkl}$ In which p is location; b is breed (Angus, Hereford, Shorthorn, Charolais); g is group within location (usually year); and e is a random effect associated with the l^{th} observation within the k^{th} group, distributed $N(0, \sigma_e^2)$.

‡Location, Manitoba, Alberta, Maritimes, B.C., Saskatchewan, Ontario.

§Breeds, Angus, Charolais, Hereford, Shorthorn.

Table 3. Breed[†] differences for average daily gain (kg/day) on a within location basis[‡]

Location	No. of bulls	($\hat{A}-\hat{H}$)	($\hat{S}-\hat{H}$)	($\hat{C}-\hat{H}$)
Manitoba	580	-.06±.02§	-.06±.03	.22±.02
Alberta	490	-.03±.02	-.02±.03	.20±.02
Saskatchewan	650	-.05±.02	+.03±.02	.26±.03
British Columbia	228	+.08±.03	+.08±.05	.29±.04
Maritimes	172	-.08±.03	+.02±.04	.17±.06
Ontario	1002	-.09±.02	-.03±.02	.30±.01

[†]A, Angus; H, Hereford; S, Shorthorn; C, Charolais.

[‡]Breed differences estimated from separate analyses within each location.

Model: $y_{ij} = \mu + b_i + g_j + e_{ijk}$ with terms defined in Table 2.

§Standard error of difference.

Herefords. This would, however, not have a major influence on selecting the superior bulls (say those gaining more than one standard deviation above average or .2 kg/day above average). Breed adjustments based on the differences below would appear suitable.

Breed	b_i
Hereford	.00
Angus	-.04
Charolais	+.25
Shorthorn	.00

These are based on the analysis of the data just described and presented in Table 4. Since Herefords are most numerous in test groups, Herefords would appear to be the most suitable base.

Development of Evaluations

The model for an adjusted record would then be:

$$(w_{ijkl} - b_i) = \mu + g_j + s_{ijk} + p_{ijkl} + e_{ijkl}$$

Using this model, first with records on Hereford, Angus, Shorthorn and Charolais, the development of an evaluation procedure applying the general procedures described by Henderson (1973) is as follows:

Let $z_{ijk} = (w_{ijkl} - b_i)$, a breed-adjusted average daily gain record. Assume that

$$E(s_{ijk}) = E(p_{ijkl}) = E(e_{ijkl}) = 0 \text{ for all } i, j, k$$

$$E(\text{all crossproducts}) = 0$$

$$\text{Var}(z_{ijk}) = \sigma_s^2 + \sigma_p^2 + \sigma_e^2$$

$$h^2 = \frac{\sigma_s^2 + \sigma_p^2}{\sigma_s^2 + \sigma_p^2 + \sigma_e^2} = .50$$

$$\text{and all } n_{ijk} \text{ (number of records per bull)} = 1.$$

Since $\sigma_s^2 = 1/4 \sigma_G^2 = 1/4 (\text{additive genetic variance})$,

$$\sigma_p^2 = 3 \sigma_s^2$$

$$a = \sigma_e^2 / \sigma_s^2 = 4$$

$$\alpha = \frac{\sigma_p^2 + \sigma_e^2}{\sigma_s^2} = 7$$

$$q = \sigma_e^2 / \sigma_p^2 = 1.333 \dots, \text{ and}$$

$$\gamma = \sigma_p^2 / \sigma_s^2 = 3.$$

In order to simplify the calculations assume that

1. Breed adjustments have not changed $\sigma_z^2 = \sigma_s^2 + \sigma_p^2 + \sigma_e^2 = \sigma_w^2$.

2. Sires are represented in one and only one group. This assumption is not valid, but should have little, if any, effect on evaluations within groups, and probably a small bias in comparisons across groups. This assumption is imposed strictly for computational reasons. If there were considerable cross-classification of groups and sires and if data from several groups were available simultaneously, a different model and procedure would be more appropriate.

Table 4. Analysis of variance and breed differences in average daily gain based on a model including breed and group[†]

Source	df	MS (kg/day)	F	R ² (%)
Breeds	3	8.68	309.44**	17.16
Groups	38	0.94	33.36**	23.44
Residual	2,990	0.03		

Breed differences (kg)

$$(\hat{A}-\hat{H}) = -.05 \pm .01$$

$$(\hat{S}-\hat{H}) = .00 \pm .01$$

$$(\hat{C}-\hat{H}) = +.25 \pm .01$$

[†]Model: $y_{ijk} = \mu + b_i + g_j + e_{ijk}$ with terms defined in Table 2.

3. Sires are unrelated individuals, and non-inbred.

Re-writing the model in matrix notation,

$$y = Xb + Z_s u_s + Z_p u_p + e$$

$$E(y) = Xb$$

$$E \begin{bmatrix} u_s \\ u_p \\ e \end{bmatrix} = \begin{bmatrix} 0 \\ 0 \\ 0 \end{bmatrix}$$

$$\text{Var} \begin{bmatrix} u_s \\ u_p \\ e \end{bmatrix} = \begin{bmatrix} I\sigma_s^2 & 0 & 0 \\ 0 & I\sigma_p^2 & 0 \\ 0 & 0 & I\sigma_e^2 \end{bmatrix}$$

Note that since all $n_{ijk} = 1$, $Z_p = I$.

To minimize the errors of prediction using linear unbiased predictors the equations to solve would be

$$\begin{bmatrix} X'X & X'Z & X'Z \\ Z'_sX & Z'_sZ_s + Ia & Z'_sZ_p \\ Z'_pX & Z'_pZ_s & Z'_pZ_p + Iq \end{bmatrix} \begin{bmatrix} \hat{b} \\ \hat{u}_s \\ \hat{u}_p \end{bmatrix} = \begin{bmatrix} X'y \\ Z'_sy \\ Z'_py \end{bmatrix}$$

The vector $\hat{b}$ contains solutions to the group effects (differences). To solve for $\hat{b}$, solve for $\hat{u}_p$ in terms of $\hat{b}$ and $\hat{u}_s$, then substitute into the previous two sets of equations

$$\hat{u}_p = (Z'_pZ_p + Iq)^{-1} (Z'_py - Z'_pZ_p\hat{u}_s - Z'_pX\hat{b});$$

but $Z_p = I$, so

$$\hat{u}_p = I(l/(l+q)) [y - Z_s\hat{u}_s - X\hat{b}].$$

Now substituting into $\hat{b}$ and $\hat{u}_s$ equations and simplifying gives

$$\begin{bmatrix} X'X & X'Z_s \\ Z'_sZ & Z'_sZ_s + Ia \end{bmatrix} \begin{bmatrix} \hat{b} \\ \hat{u}_s \end{bmatrix} = \begin{bmatrix} X'y \\ Z'_sy \end{bmatrix}$$

$$\text{where } \alpha = \frac{a(1+q)}{q} = 7.$$

Thus, no change (except in the ratio added to the sire by sire diagonal coefficients) is made in the sire and group equations, since each progeny has only one ADG record. Due to the nested structure of sires within groups, $\hat{u}_s$ can be absorbed into the $\hat{b}$ equations to yield the following results

$$\hat{g}_i = \frac{\left(y_{i..} - \sum_j \frac{n_{ij}y_{ij}}{n_{ij} + \alpha} \right)}{\left(n_{i.} - \sum_j \frac{n_{ij}^2}{n_{ij} + \alpha} \right)} = \frac{\sum_j \frac{n_{ij}y_{ij}}{n_{ij} + \alpha}}{\sum_j \frac{n_{ij}}{n_{ij} + \alpha}} = \frac{\sum_j \frac{y_{ij}}{n_{ij} + \alpha}}{\sum_j \frac{1}{n_{ij} + \alpha}}$$

where n_{ij} is the number of progeny of the j^{th} sire in the i^{th} group. This estimate of the group effect is a weighted average of sire averages.

Working backwards,

$$\hat{s}_{ij} = \frac{y_{ij} - n_{ij}\hat{g}_i}{n_{ij} + \alpha} = \frac{n_{ij}(\bar{y}_{ij} - \hat{g}_i)}{n_{ij} + \alpha}$$

which is a regressed deviation from the group estimate of the mean. A bull's breeding value within a group is

$$\hat{s}_{ij} + \hat{p}_{ijk} = \frac{y_{ijk} - \hat{g}_i + q\hat{s}_{ij}}{1 + q}$$

The complete across-breed evaluation is then $b_l + \hat{s}_{ij} + \hat{p}_{ijk}$ for bulls of the l^{th} breed (Angus, Charolais, Hereford or Shorthorn). This evaluation is the best estimate possible of each bull's breeding value.

For bulls of other breeds and crosses, the across-breed evaluation can be approximated as $\frac{1}{1+q}(w_{ijkl} - \hat{g}_i)$. This gives the estimated breeding value based on the deviation of the original average daily gain record expressed as a difference from the best estimate of the group mean. An exact estimate could be obtained as soon as breed differences could be estimated. An allowance of approximately 3–5% because of heterosis could be made for crossbreds (Preston and Willis 1970).

This method of evaluating bulls has the following advantages:

1. Each evaluation has the smallest prediction error variance possible of all linear type evaluations, and is unbiased.

2. Information on half-sibs is incorporated. This is done directly from the model specified and requires very little extra computing. Although comparisons with a reduced model have not been made, simple comparisons based on procedures described by Van Vleck (1974) for including half-sibs in evaluations of bulls indicate increases in accuracy or correlation of true breeding value with the evaluation (r_{TI}) of 2% for 5 and 4% for 10 half-sibs.

Measuring the Accuracy of Evaluation

The accuracy of estimating a bull's true breeding value is shown in Table 5, assuming each sire had an equal number of progeny within a group. The accuracy increases rapidly until the number of sires per group approaches 10. The formula for calculating r^2_{TI} for any bull, using the described procedure, is:

$$r^2_{TI} = \frac{\left((1+\gamma) - \frac{(n_{ij}+\gamma)}{k_1c} + \frac{q(n_{ij}+\gamma)}{k_1} - \frac{q(n_{ij}+\gamma)n_{ij}}{k_1^2c} \right)}{(1+q)(1+\gamma)}$$

Table 5. Accuracy of evaluation of individual bulls (r_{Ti}) for various compositions of groups

No. of bulls per sire	No. of sires per group								
	1	2	3	4	5	6	7	8	9
1	.0	.50	.58	.61	.63	.65	.65	.66	.67
2	.40	.58	.63	.65	.66	.67	.68	.68	.69
3	.46	.60	.64	.66	.67	.68	.69	.69	.69
4	.49	.62	.65	.67	.68	.69	.69	.70	.70
5	.51	.62	.66	.68	.69	.69	.70	.70	.70
6	.52	.63	.66	.68	.69	.70	.70	.71	.71
7	.52	.63	.67	.68	.69	.70	.70	.71	.71
8	.53	.64	.67	.69	.69	.70	.71	.71	.71
9	.53	.64	.67	.69	.70	.70	.71	.71	.71
10	.54	.64	.67	.69	.70	.70	.71	.71	.71
20	.55	.65	.68	.70	.71	.71	.72	.72	.72

where $\gamma = \sigma_p^2 / \sigma_s^2 = 3$

$q = \sigma_e^2 / \sigma_p^2 = 1.333 \dots$

$$c = \sum_j \left[\frac{n_{ij}}{n_{ij} + \alpha} \right]$$

$\alpha = 7.0$

n_{ij} = number of progeny of the
 j^{th} sire in the i^{th} group

$k_j = n_{ij} + \alpha$

The confidence interval (CI) for a bull's evaluation could be simply computed by adding and subtracting

$$t \times \sigma_{T/I=10} \text{ which equals}$$

$t \sqrt{(1-r_{Ti}^2) h^2 \sigma_e^2}$ where t is Student's t at some probability level, $\sigma_{T/I=10}$ is the conditional standard deviation of breeding values given that a particular evaluation (I_0) has been found, and other terms are as previously defined. This figure could be reported along with each bull's evaluation. However, it will probably be very similar for all bulls in a group, and even for all bulls in groups of some specified minimum size.

Minimum Group Size

Genetic differences between any two group solutions can be rather large depending on the number of sires in each group and the number of bulls per sire. For example, two groups each with two sires and two sons per sire may differ markedly if the two sires in one group are genetically superior to the two sires in the second group. By chance occurrence the first group may have had a much better than average representation of sires and bulls than the second group. These kinds of differences can be lessened by having a certain number of sires per group and a certain number of bulls per sire. The differences between any two group solutions can be written as

sened by having a certain number of sires per group and a certain number of bulls per sire. The differences between any two group solutions can be written as

$$\hat{g}_1 - \hat{g}_2 = \frac{\sum_j \left(\frac{y_{ij}}{n_{ij} + \alpha} \right)}{\sum_j \left(\frac{n_{ij}}{n_{ij} + \alpha} \right)} - \frac{\sum_k \left(\frac{y_{ik}}{n_{ik} + \alpha} \right)}{\sum_k \left(\frac{n_{ik}}{n_{ik} + \alpha} \right)}$$

Now the variance of a particular solution is

$$\text{Var}(\hat{g}_1) = \sum_{j=1}^m \left(\frac{n_{ij}^2 \sigma_s^2 + n_{ij} \sigma_p^2 + n_{ij} \sigma_e^2}{(n_{ij} + \alpha)^2} \right) \cdot \frac{1}{c^2}$$

Using only the genetic contribution and assuming two groups of the same size,

$$\text{Var}_G(\hat{g}_1 - \hat{g}_2) = 2 \sum_{j=1}^m \left(\frac{n_{ij}(n_{ij} + 3) \sigma_e^2}{4(n_{ij} + \alpha)^2} \right) \cdot \frac{1}{c^2}$$

where m = number of sires per group, and

$$c^2 = \left(\sum_j \frac{n_{ij}}{n_{ij} + \alpha} \right)^2$$

Notice that when $m=1$ and $n_{ij}=1$, $\text{Var}_G(\hat{g}_1 - \hat{g}_2) = 2\sigma_e^2$.

The percentage of σ_e^2 remaining for various combinations of m and n_{ij} is shown in Table 6, and in Fig. 1 for one bull per sire.

Decreases in variation become less at approximately 25% of σ_e^2 (Fig. 1). With 25% of the genetic variance remaining, the genetic sampling difference between two minimum-sized groups would be $\sqrt{.25 \times .03 \text{ (kg/day)}^2} = .09 \text{ kg/day}$. This could be reduced to less than .05 kg/day by going to no more than 10% of the genetic variation. This would require, for example, 20 sires with one bull per sire or 8 sires with five bulls per sire, in each group.

Table 6. Percent of genetic variance remaining in the difference between two groups

No. of sires per group	No. of bulls per sire					
	1	2	4	8	16	30
1	200	126	88	68	60	55
2	100	62	44	34	30	28
3	66	42	30	22	20	18
4	50	32	22	18	14	14
5	40	26	18	14	12	11
6	33	21	15	11	10	9
7	29	18	13	10	8	8
8	25	16	11	9	7	7
9	22	14	10	8	7	6
10	20	12	8	6	6	6
15	13	8	6	5	4	4
20	10	6	4	3	3	3
40	5	3	2	2	1	1

Genetic differences between groups for reasons other than sampling might also exist. Selection of calves going on test would be one such reason. However, the bias in evaluations should be small, since the correlation of weight at start of test with ADG on test is low.

COMPARISONS OF SELECTION WITHIN AND ACROSS GROUPS

The advantages of selection across groups are increased selection intensities through large

sample rather than small sample selection and through increased possibilities for selection. In a fixed testing population and a fixed number of bulls selected, large sample selection results in higher selection intensities than small sample selection (Table 7). For example, selecting the top bull from a group of 20 in 10 different groups (small sample selection) would be only 90% as effective as selecting the top 5% of all 200 bulls (large sample selection). The difference is most pronounced for small numbers of bulls selected per group. The difference becomes less as numbers of bulls selected increases, especially if group sizes are large.

The increases in selection intensities can be offset by inaccuracies in eliminating group effects. The ratio of within-group to across-group accuracies (r_{TI} 's) can be determined by dividing the within-group or simple r_{TI} values calculated as described by Van Vleck (1974) by the values in Table 5. The simple r_{TI} values for evaluating a bull using information from that individual plus from half-sibs are .707 for the individual alone and .713, .717, .721, .724, .726, .728, .730, .732, .733 and .742 for the individual and 1, 2, 3, 4, 5, 6, 7, 8, 10 and 20 half-sibs, respectively, assuming a heritability of .50. The within-group r_{TI} 's are not changed by changing numbers of sires per group, since the group effect does not need to be eliminated. The ratio of annual expected genetic progress from within- to across-group selection is the product of the ratios for selection intensity and r_{TI} 's, since the genetic standard deviation and generation interval are constant, i.e.,

$$\frac{\Delta T \text{ within}}{\Delta T \text{ across}} = \frac{i \text{ within (small)}}{i \text{ across (large)}} \times \frac{r_{TI, \text{ within}}}{r_{TI, \text{ across}}}$$

where ΔT is expected annual genetic change in growth rate and i is selection intensity.

The comparisons depend on numbers of bulls per sire and on numbers of sires per group (Table 8). Groups that minimize genetic sampling variance would usually include several sires, so the expected genetic progress from selection within and across group would usually be fairly similar. Selection across groups is advantageous when small numbers of bulls are selected, especially in groups with many sires and few bulls per sire. Selection within groups is advantageous when larger numbers of bulls are selected in groups with higher numbers of bulls per sire and fewer sires. Procedures of beef bull evaluation appear to be relatively unimportant in determining rates

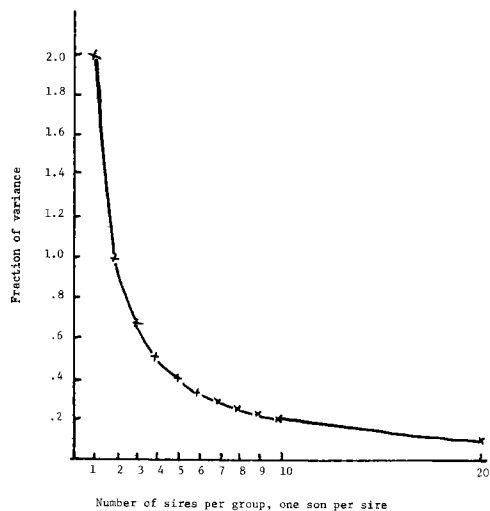


Fig. 1. The effect of number of sires per test group on the genetic variance of differences between groups.

Table 7. Ratio of small sample to large sample selection intensities for varying sample (test group) sizes

No. of bulls tested per group	No. of bulls selected per group									
	1	2	3	4	5	6	8	10	20	50
8	.86	.90	.91	.91						
10	.88	.91	.92	.92	.93					
12	.89	.92	.93	.93	.94	.94				
15	.90	.92	.94	.94	.95	.95	.95			
20	.90	.93	.95	.95	.96	.96	.96	.96		
50	.90	.94	.96	.97	.97	.97	.98	.98	.99	
100	.91	.95	.96	.97	.98	.98	.98	.99	.99	1.00
500	.92	.96	.97	.98	.98	.98	.99	.99	.99	1.00
1,000	.93	.96	.97	.98	.98	.99	.99	.99	.99	1.00

of genetic progress, especially relative to total numbers of bulls tested, which greatly increases selection intensities for either within- or across-group selection.

A potential advantage of evaluations across group is that selection possibilities could be increased. This would most likely be of interest to artificial insemination units who might wish to select accurately amongst bulls tested in several different groups. They would be able to obtain a fixed, usually small, number of bulls from a larger number of bulls, increasing selection intensity. Selection across groups could also avoid any reductions in genetic variability and increases in inbreeding levels that could arise from selection within groups.

Evaluations across group provide flexibility, since they can be used for selection both within and across group. The use of evaluations across group as described could be useful for specific cases such as selection of a small number of bulls, selection from groups with many sires and few bulls per sire, and selection from a larger total number of tested bulls, while still being useful for selection within groups.

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Table 8. Ratios of estimated genetic progress from selection within groups relative to selection across groups

Sires	Bulls/ sire	Bulls/ group	No. of bulls selected									
			1	2	3	4	5	6	8	10	20	50
2	4	8	1.00	1.05	1.06	1.06						
4	2	8	.94	.99	1.00	1.00						
8	1	8	.92	.96	.97	.97						
2	5	10	1.03	1.06	1.07	1.07	1.09					
5	2	10	.95	.98	.99	.99	1.00					
10	1	10	.92	.95	.96	.96	.97					
2	6	12	1.03	1.06	1.07	1.07	1.08	1.08				
3	4	12	.99	1.02	1.03	1.03	1.04	1.04				
4	3	12	.97	1.00	1.01	1.01	1.02	1.02				
6	2	12	.95	.98	.99	.99	1.00	1.00				
12	1	12	.93	.96	.97	.97	.98	.98				
2	10	20	1.03	1.07	1.09	1.09	1.10	1.10	1.10	1.10		
4	5	20	.96	.99	1.01	1.01	1.02	1.02	1.02	1.02		
5	4	20	.95	.99	1.01	1.01	1.02	1.02	1.02	1.02		
20	1	20	.92	.95	.97	.97	.98	.98	.98	.98		
5	10	50	.94	.98	1.01	1.02	1.02	1.02	1.03	1.03	1.04	
5	20	100	.95	.99	1.00	1.01	1.02	1.02	1.02	1.03	1.03	1.04
20	5	100	.92	.96	.97	.98	.99	.99	.99	1.00	1.00	1.01

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