

## NUMBER OF DAUGHTERS TO 'PROVE' A BULL

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## INTRODUCTION

Minimum number of daughters to be recorded for any bull to declare it 'good' or 'bad' in any breeding program is very important especially where resources are limited and recording for important traits like milk yield is still debated. This is also a frequently asked question by the planners when any field recording project is to be launched. Basic concepts of selection (Khan, 1997) and an overview on recording dairy animals in Pakistan (Khan, 1998b) were previously presented. An attempt is made here to explore the issue of optimum genetic gain and accuracy with reference to performance testing in the genetic improvement programs.

## The genetic gain

The genetic progress or the genetic gain in any trait is usually considered in terms of per unit time i.e., per year. The equation for the genetic gain ( $\Delta G$ ) per year is as follows:

$$\Delta G/\text{year} = (\text{Accuracy} \times \text{Intensity} \times \text{Genetic variation}) / \text{Generation Interval}$$

The 'accuracy' in the above equation is correlation between the estimated breeding values and true breeding values and is determined by how well the genotype is predicted by the phenotypic measures used for selection. For any breeding program the value chosen would come from the four genetic selection paths i.e. sire to sire, sire to dam, dam to sire and dam to dam. For individual animals, for most of the quantitative traits, we hardly have the opportunity to select them directly on their genotypes. Thus the effectiveness of selection is determined by the information available. The accuracy would measure the degree of confidence when breeding value or transmitting ability is talked about. Other than the information available, heritability of the trait would affect it. Less information is needed to obtain a given degree of accuracy as heritability increases. For traits which are lowly heritable such as mastitis resistance and productive life, more information would be required (more records on an individual e.g., more daughters per bull) to reach a certain accuracy level as compared to traits such as milk yield which are mediocre in terms of genetic control.

Maximum value for accuracy would be 100% while minimum value would be square root of heritability and may be as low as zero. Although such a trait won't be considered for genetic selection. Hansen (1993) reported that progeny test programs designed to produce accuracies of 75 to 80% for milk yield would produce accuracies of 50 to 60% for traits like somatic cell score. Relationship between heritability and accuracy is presented in Fig. 1.

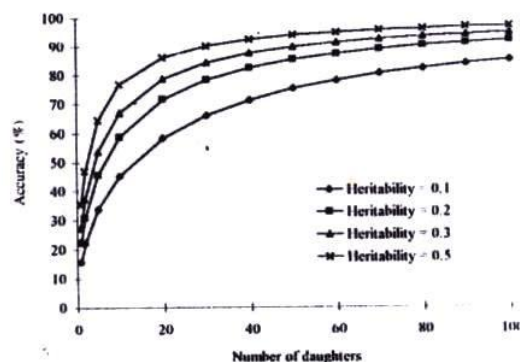


Fig. 1: Effect of heritability on the accuracy for different number of daughters of a bull.

The 'intensity' is the selection differential expressed in phenotypic standard deviation units. Number of animals available for culling mostly determine it. Because in most of the dairy herds, few females can be culled for voluntary reasons, most of the progress comes from the very intense selection on the sire side. Fig 2 represents the selection intensity factor at various levels of percentage selection. Sire of young sires are most intensely selected (top 1-5%) and are the main source of genetic improvement in any trait. Dam selection is usually very mild. Young sampling sires usually are in this range also. Within herd selection is usually the weakest and usually never more than 30% of cows culled from a herd on the basis of traits of economic importance. Ahmad *et al.* (1993) has discussed this issue for buffaloes in Pakistan pointing out that selection for economically important traits like milk yield is very weak.



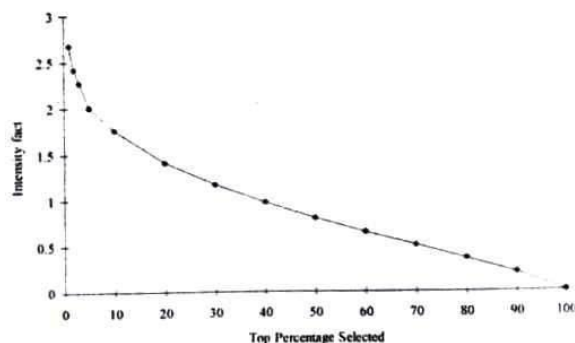


Fig. 2: Selection intensity and the factors associated with it.

The 'genetic variation' (usually measured in terms of genetic standard deviation) is a measure of the variation of breeding values for the trait considered. It is determined by the frequency and effect of the alleles which control it and is usually nearly constant for a given population and trait but can be improved by reduction in the environmental variation through better recording etc. As traits vary widely in phenotypic variation and their genetic control also varies, genetic standard deviation has a very wide range. The percentage variation for age at first calving and first lactation length is 15-20%. First lactation milk yield and calving interval vary some 30-35% while traits like first dry period has a very high variation of 60% (Khan *et al.*, 1997). The genetic standard deviation for milk yield (250 kg) for buffaloes is less than half of the values reported for Holsteins.

The 'generation interval' is the average age of the parents when offsprings are born. It can be reduced for all the four paths of selection by for example reducing the age at first calving in females, reduction in the calving intervals and efficient data collection, processing and feed back for selection. Production of quicker sire summaries for example has been one way to reduce the generation interval by making the newly selected bulls available to the farmers. Canada and the United States now publish official sire summaries four times a year as compared to once a year few years back. Some countries (such as Denmark) even publish eight times a year (Cassell, 1998). In our situation, where generation interval is

quite large especially for buffaloes (7.4, 6.6, 9.6, 6.9 years, respectively for the four selection paths viz., sire to sire, sire to dam, dam to sire, and dam to dam; Khan, 1997a), reduction in age at first calving and service period would be a priority research area in this regard.

Out of the four components of genetic gain the genetic variation is usually fixed at least at a shorter span of time horizon. The generation interval is always tried to be minimum. It is the accuracy and intensity that need to be balanced for optimum gain because if we want to be more accurate (i.e. more number of daughters per sire) this would decrease the number of sires that can be tested resulting in decreased selection intensity and vice versa.

#### Optimising genetic gain

Suppose that 1000 daughters can be recorded. First extreme situation can be 100 daughters per bull (i.e. 10 bulls to be tested). In the second situation, 10 daughters can be recorded for every bull (i.e. 100 bulls to be tested). Now if the requirement of the breeding program, is to retain only five bulls (depends on the number of services required, rearing and collection/storage facilities etc.), the genetic gain would almost be double in second as compared to the first situation. The optimum daughters superiority (175 kg) would however, come at an intermediate accuracy of 25 daughters per bull and selection intensity of 1 out of every 8 bulls tested (Table 1). The genetic standard deviation used in the estimation is according to Khan (1997a).

#### Distribution of daughters

Apart from the number of daughters per bull, their distribution across various herds also affects accuracy. Fig. 3 represents the accuracy for sire proofs for traits like milk yield when daughters of bulls were distributed in a single herd or across different herds. The heritability assumed in calculating the values for accuracy is 18% (Khan *et al.*, 1997a) and an environmental correlation (due to similar treatment to daughters of the same bull as compared to the daughters of the other bulls) of 0.05 among daughters in the same herd. It may be mentioned that some systems (like that in the United States) assume such a correlation to be 0.14 for calculating accuracy values for Holstein bulls. Because such an estimate is not available for our species such as buffaloes, a lower value was assumed in drawing these trends. If such a correlation was higher, the accuracy values would be lower.

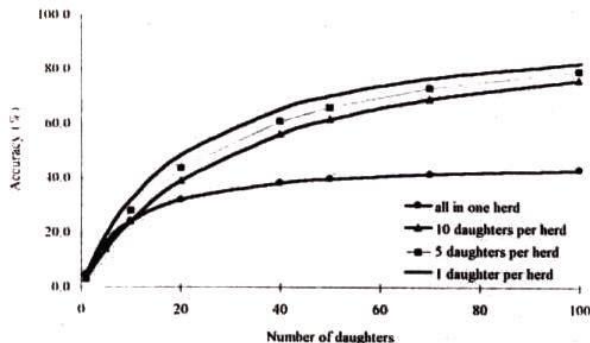


Fig.3: Accuracy of sire proofs for traits like milk yield when daughters are in one or several herds.

Defining herd or more precisely herd-year-season (contemporaries) would still be a very important issue in making valid comparison among bulls. The issue has previously been discussed for Sahiwal cattle (Khan *et al.*, 1997b) and Nili-Ravi buffaloes (Khan *et al.*, 1997c). It was concluded that although, four or five season scenarios were better (in terms of error variance of the fitted model) than the two season scenarios, very low number of daughters for a given herd-year-season subclass warranted the use of fewer seasons for animal model evaluation of the two species in our set up of small herd size.

#### Other terms for accuracy

For beef cattle breeding programs, the term accuracy is still being widely used (Zoolinger, 1996) to as a measure of confidence that a user should have in the breeding value of an individual for a specific trait. For dairy cattle evaluation programs however, the term 'reliability' has replaced the term accuracy which was used to replace repeatability in the 70's. The sire summaries now have REL (for reliability) for Predicted Transmitting Ability (PTA) of any sire. The value of REL of course would vary for different traits for a particular animal because even with the same number of records available the traits may have different heritabilities. For animals with no records or progeny information the reliability is one-fourth the

sum of parent reliabilities. While for animals with more information sources, reliability is calculated from daughter equivalents. The daughter equivalents provide a common unit to measure the information contributed by various sources.

#### a) Reliability for cows

Daughter equivalents are calculated depending on the source of information and the level of reliability (Table 2). These in turn can be used to calculate the reliability on the individual in question. Example:

Consider that the following information is available for a cow.

Relative	Information available	Daughter equivalent
Self	3 lactation records	7.8
Daughters	First with 1 lactation record	1.0
	Another with 3 lactation records	1.5
Parents	Sire with 70% REL	
	Dam with 30% REL	4.7
Total daughter Equivalents		15.0

REL of the cow =  $n/(n+14) = 15/29 = 52\%$

where, n equals to daughter equivalents while 14 is the function of the heritability of the trait.

#### b) Reliability for bulls

Similar daughter equivalents contributed to a sire by daughters are calculated for sires. Assuming for example that each daughter has one record, a dam with known breeding value, and a large number of management group mates that does not include paternal half sisters, the formula for calculating daughter equivalents is  $1/[.16 + (.84/d)]$ , where d is the number of daughters. For daughters in the same herd, daughter equivalents for sire with 50 daughters would be 5.6 as given in Table 3.

For beef sires where traits are expressed by the sires themselves also, the level of accuracy increases but at a lower rate as compared to the dairy sires where for traits like milk yield, only female relatives provide all the direct information. The following example (Table 4) indicates how accuracies are related to progeny number and relatives. If the only information available is a bull's own performance for one trait with a heritability of 30%, the accuracy will be about 55% (i.e., 100 times the square root of 0.30). If the information is available on the 10 paternal half-sibs also, the level of accuracy would reach 67%. An additional information on 2 maternal half-sibs would increase the accuracy to 77%.



Reliabilities or accuracies are usually expressed in percentages. A confidence range can also be built around the breeding values or transmitting abilities to show the level of confidence in them assuming normal distribution and variation in the transmitting abilities in the given population for a particular trait. For higher accuracies such an interval would be very narrow while for lower accuracies, range would be wider. For buffaloes such a confidence ranges or intervals (68 and 95%) are presented in Table 5.

The above table shows the 68% confidence range for a bull with PTA for milk of +200kg and with 40 daughters distributed across various herds is around 95 kg. The confidence range is one standard deviation from the mean. In other words there is a 68% probability that that when he has thousands of progeny, his PTA for milk will fall within the range +105 to +295 kg. If we want to be more sure (95%) however, his PTA would be between +11 to 389 kg. If his all daughters were in the same herd, the range would further widen. Actually when bulls are progeny tested, the random nature of gene transmission plays its role making it difficult to know the bull's true genotype. Enough 'sample halves' of a bull's genes can tell his entire genetic make up. If the 'sample halves' are few we have a wider guess and if they are many, we are quite confident in guessing. The confidence range won't tell us what genes a bull will transmit. Instead, it tells how accurately PTA predicts what those genes really are.

#### Acceptable level of accuracy

After reading the above discussion regarding accuracy, it might come to mind that is there any acceptable level of accuracy. There is no exact cut point or a magic number as an answer but because all tested sires can not be reported/summarised, for dairy sires, 70% is a usual cut point below which the inclusion of a sire in sire summaries would be doubtful. Cows would usually have lower accuracies because of less records on them but sire summaries or equivalently cow summaries are not prepared, individual farmers or association may have their comparative ranking. For beef sires, a Simmental sire has to have an accuracy value of at least 30% for 400-day growth to qualify for publication in the National Sire Summary (Anonymous, 1991). Such restrictions have gone better in the recent past. The Angus group for example, have chosen 80% as a minimum level of accuracy for herd book sires to be included in their annual report (Anonymous, 1997). For our situation, a value around 30% may be acceptable for buffalo or cattle bulls in the start of such an effort because comparison with Holstein bulls where 99% accuracy

is not a very unusual accuracy, won't be realistic. The number of daughters per bull are few and herds involved in these efforts are limited (Khan, 1998).

Ideally, animals with a high transmitting ability and a high accuracy be selected. But it is not always possible. The relative importance of transmitting ability and the accuracy should thus be realised. Farmers are encouraged to select bulls on the basis of their breeding values (or transmitting abilities) for the traits they are doing business for. Accuracy should not be the criteria for such a selection because progeny's phenotype is not determined by the accuracy rather it is the breeding values of the parents. The role of accuracy is the confidence or the risk with which future animals can be predicted to be in a certain range. Bulls with high reliabilities can be used more heavily as compared to bulls with lower values of accuracies because as more information accumulates, the prediction for their transmitting abilities may change. Funk (1990) suggested that a bull with reliability of > 85% should be used to get 25% pregnancies in a herd. For reliabilities between 75-85%, maximum usage should be 20% while bulls with < 75% reliabilities, maximum usage should be 15%.

Another way of looking at it would be to decide the level of probability at which we expect the difference among sires to be significant. Suppose it is 5% and further suppose that we want to test the superiority of 10% above the mean. For trait such as milk yield which has a coefficient of variation of 35% (Khan *et al.*, 1997), number of minimum daughters (n) required would according to Basu, (1985) be:

$$n = (t_{0.05} \times 35 / 10)^2 = (1.96 \times 3.5)^2 = 47 \text{ daughters per bull}$$

Raising the superiority level from 10% to 15% would result in the minimum number of daughters required per bull to be 21. Similarly, if variation can be reduced through uniform management of the daughters etc., the number of daughters required for a certain level of accuracy can be further reduced.

Thus, to declare a bull 'good' or 'bad' many aspects need to be looked into. Number of daughters along with their distribution across herds would determine the accuracy. This would depend on the genetic control of the trait and its repetition in subsequent lactations. Acceptable level may vary according to the breeding structure of the populations and the recorded population. For smaller populations an optimum number has been suggested to be 20 to 30 daughters per bull tested after random mating of test bulls. For larger populations, 50 or more daughters have been suggested by Schmidt *et al.* (1988).

Table 1. Comparison of daughters' superiority for different combinations of selection<sup>1</sup>.

No. of bulls tested	No. of daughters per bull	Bulls selected	Accuracy	Selection intensity	Genetic $\sigma$ (kg)	Average daughter superiority (kg) <sup>2</sup>
5	200	1/1	0.96	0.00	250	0
10	100	1/2	0.93	0.80	250	93
20	50	1/4	0.88	1.27	250	140
<b>40</b>	<b>25</b>	<b>1/8</b>	<b>0.85</b>	<b>1.65</b>	<b>250</b>	<b>175</b>
50	20	1/10	0.76	1.76	250	167
100	5	1/20	0.63	2.06	250	162

<sup>1</sup>For evaluation of 1000 tested daughters when 5 bulls are needed per year<sup>2</sup>Average daughter superiority = Accuracy x selection intensity x  $\frac{1}{2}$  genetic  $\sigma$ 

Table 2. Daughter equivalents contributed to cow reliability by various information sources.

Relative	Information available	Daughter Equivalents
Parents	Sire with 70% REL & Dam with 30% REL	4.7
	Sire with 99% REL & Dam with 50% REL	8.3
	Sire with 99% REL & Dam with 99% REL	14.0
Self	1 lactation record	4.7
	3 lactation records	7.8
	5 lactation records	9.0
Daughters	1 lactation record	1.0
	3 lactation records	1.5
	5 lactation records	1.7
Son	1 daughter with 1 lactation record	0.2
	10 daughters in 10 herds, each with 1 lactation	1.8
	50 daughters in 50 herds, each with 1 lactation	4.4
	Evaluation with 99% REL	7.0

Wiggans and VanRaden (1989)

Table 3: Daughter Equivalents contributed to a sire by daughters in the same herd.

No. of daughters in herd	Daughter equivalents (n) contributed to sire
1	1.0
2	1.6
5	2.9
10	4.0
25	5.1
50	5.6
100	5.9

Wiggans and VanRaden (1989)

Example: For 50 daughters, REL =  $n/(n+14) = 5.6/(5.6+14) = 0.29$  or 29%

Table 4: Accuracy of estimated breeding values for a trait with heritability of 30%.

Information available	Accuracy (%)
Individual	55
Individual + 10 PHS + 2 MHS	61
Individual + 20 PHS + 4 MHS	64
10 Progeny	67
Individual + 10 PHS + MHS + 10 Progeny	77

PHS = paternal half-sibs (Hughes, 1997)

MHS = Maternal half sibs

Table 5. Confidence intervals (CI) for Predicted Transmitting Abilities (PTA) of bulls for milk yield in buffaloes\*.

No. of daughters	One daughter per herd		All daughters in the same herd	
	68% CI (kg)	95% CI (kg)	68% CI (kg)	95% CI (kg)
1	125	250	125	250
5	123	245	123	247
10	118	237	121	243
20	109	219	118	237
40	95	189	115	231
50	89	178	115	229
70	80	160	114	227
100	71	141	113	225
500	35	69	111	221

\*Standard deviation of PTA's was assumed as 125 kg (Khan *et al.*, 1997)



## CONCLUSIONS

The procedures available for evaluating dairy bulls may be modified to be used in our production set up. The genetic improvement programs are resourceintensive requiring sustainable efforts. As sire selection programs are being debated in terms of their suitability, the infrastructure requirements and methods of their evaluation (Khan, 1998a), the procedures to maximise the genetic gain be considered by the planners before finalization and execution of these efforts. Although, there is no hard and fast number, twenty five or more daughters seem reasonable to declare a bull good or poor for traits like milk yield, with a reasonable accuracy. Better pedigree information would help along with the distribution of daughters across various management groups. Failing to meet certain assumptions would however, require more daughters to reach a similar value of accuracy. Further more, to best utilise the resources, optimum genetic gain should be the objective.

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