Keys to genetic progress

Variation, intensity of selection

Genetic improvement requires variation, otherwise selection would be a game.

Some of the variation must result from genetic differences: genetic variation

Of course only the best must be selected

The extent to which selection will add to genetic improvement depends on the intensity of selection, whether the best 1 of 10, the best of 5 of 10, the best 9 of 10 or some other fraction is selected.

Which cows are best?

Usually the record of the cow is of major importance, of course several records provide more accuracy.

The knowledge that close relatives of the cow have high records would slightly increase confidence in it.

Thus the number and the kind of records on cow and its relatives determine the accuracy of selection.

Three factors that determine the genetic progress per generation

1. genetic variation
2. intensity
3. Accuracy and
4. Generation interval (years per generation)

$$genetic\ gain/year = \frac{accuracy\ X\ intensity\ X\ genetic\ variation}{years\ per\ generation}$$

Accuracy

Accuracy is defined as the correlation between the prediction of genetic value and true genetic value of the animal, which ranges from 0% to 100%.

Perfection in predicting the genetic value of dairy cows is impossible to obtain.

If enough daughters of a bull are considered, his true daughter superiority, a measure of half his genetic value, can be predicted nearly perfectly.

heritability

- Accuracy also depends on fraction of the differences in cows caused by genetic effects and the fraction caused by other effects. The fraction caused by genetic differences is called heritability.
- If all deferences are genetically determined, heritability is 100%, that means an animals apearance or records perfectly measure its genetic value

heritability

- In general, as heritability increases, the accuracy of predicting the genetic value of a cow from her records and the records of her relativesalso increases.
- Estimates of heritability for milk production vary from 20% to 40%. A value of 25% is commonly used. The heritability of fertility is however, much lower - 0% to 10%.
- Progress by selection is much more likely for milk yield or type than for fertility

heritability

- Heritability is defined as the fraction of the total variance that is genetic variance. In another words «Heritability is the degree of genetic variation inside of the phenotypic variation in a population»
- The remainder of the variance (total variance- genetic variance) is defined as environmental variance.

heritability

$Px = Gx \quad + Ex$ where;

Px is the phenotypic measurement of trait x,

Gx is total genotypic contribution of the animal in Px

Ex is contribution to Px by all other factors (collectively called environmental effect)

Ussually the assumption is made that genotypic value and environmental effects do not influence each other.

heritability

If the G’s for each cow could be measured, then variance of G’ could be calculated

$h^2 = \frac{\sigma^2 G}{\sigma^2 G + \sigma^2 E} = \frac{\sigma^2 G}{\sigma^2 P}$

Heritability can not be negatif; $h^2 = 0$ if $\sigma^2 G = 0$

Which means all the animals have the same genetic value for a trait.

$h^2 = 1$ if $\sigma^2 E = 0$ and $\sigma^2 G \neq 0$, which happens if the environmentel effects make the same contribution to each record

Genetic progress

The genetic standart deviation used in calculating genetic progress is σG, the square root of $\sigma^2 G$

$\sigma^2 G = h^2 \sigma^2 P$

$\sigma G = \sqrt{h^2 \sigma^2 P}$

The square root of heritability times the phenotypic or overall standart deviation.

Estimating heritability

G is can not be calculated, then heritability must be estimated indirectly

Relationship between records of relatives is proportional to the relationship between relatives.

The measure of relationship between records is ***covariance.*** The *symbol for this is* σ_{xy}*, w*here x and y may be two traits or two relatives (x= doughter, y=dam)

Estimating heritability

For example, the relationship between non inbred doughters and dams is 1/2. This is logical since the doughter will receive one-half her genoype and genetic value from her dam.

The environment is of course not inherited. Thus the covariance between records of doughter and dam can be shown to equal one-half the genetic variance.

Estimating heritability

σ^2 can generally be estimated rather easly from covariance between records of relatives. Computing a covariance is no more difficult than computing a variance. The only difference is that instead of squaring the deviation from the average for one trait, the product of the deviations from their respective averages is taken:

$$\sigma xy = \frac{\Sigma^{N}{}_{i}\,(\mathrm{x}_{\mathrm{i}} - \mu_x)\,(yi - \mu_y)}{N}$$

$$= \frac{(x_1 - \mu_x)(y_1 - \mu_y) + (x_2 - \mu_x) + \cdots .. + (xN - \mu_x)(yN - \mu_y)}{N}$$

or $s_{xy} = \frac{\Sigma^{N}{}_{i}\,(\mathrm{x}_{\mathrm{i}} - x)\,(yi - y)}{N-1}$

Estimating heritability

$$\sigma xy = \frac{\Sigma^{N}{}_{i}\,(\mathrm{x}_{\mathrm{i}} - \mu_{x})\,(yi - \mu_{y})}{N}$$

$$= \frac{(x_1 - \mu_x)(y_1 - \mu_y) + (x_2 - \mu_x) + \cdots .. + (xN - \mu_x)(yN - \mu_y)}{N}$$

or $$s_{xy} = \frac{\Sigma^{N}{}_{i}\,(\mathrm{x}_{\mathrm{i}} - x)\,(yi - y)}{N-1}$$

In this case x_i represents a record on relative x and y_i represents the record on corresponding relative y; i refers to the spesific pair of relatives.

Estimated breeding value (EBV)

Use of more than one record on a cow and records of its relatives improves accuracy if the records combined in a way that maximizes the accuracy of predicting genetic value.

The selection index procedure called EBV, provides a «best» estimate of the genetic or breeding value of a cow.

The procedure is complicated if records on many relatives are used. The records of a cow are actually about as accurate as using records of many relatives. Even one record on the cow is sometimes sufficient.

Estimated breeding value (EBV)

If the cow has no record, the proof of her sire gives a good indication of her genetic value. If records of more relatives are used accuracy is increased only slightly. Use of all possible relatives results in accuracy of less than 75%.

The situation is different when evaluating bulls. Nearly perfect accuracy of predicting a bull’s genetic value can be achieved if enough doughters in many herds are analyzed.

Intensity of Selection

Intensity of selection can have a substantial effect on genetic progress. A breeder cannot be as selective with cows as with bulls because not enough heifers are available for replacements. But there can be intense selection of dams to be mothers of young bulls, as well as intense selection of bulls based on daughter records.

Table 1 gives the intensity factors for various persentages of selection. If the intensity factors are to apply, selection must be exactly according to the estimated genetic value. The intensity factor increases at a faster rate as the persentage selected declines

Table 1. Factors associcted with intensity of selection

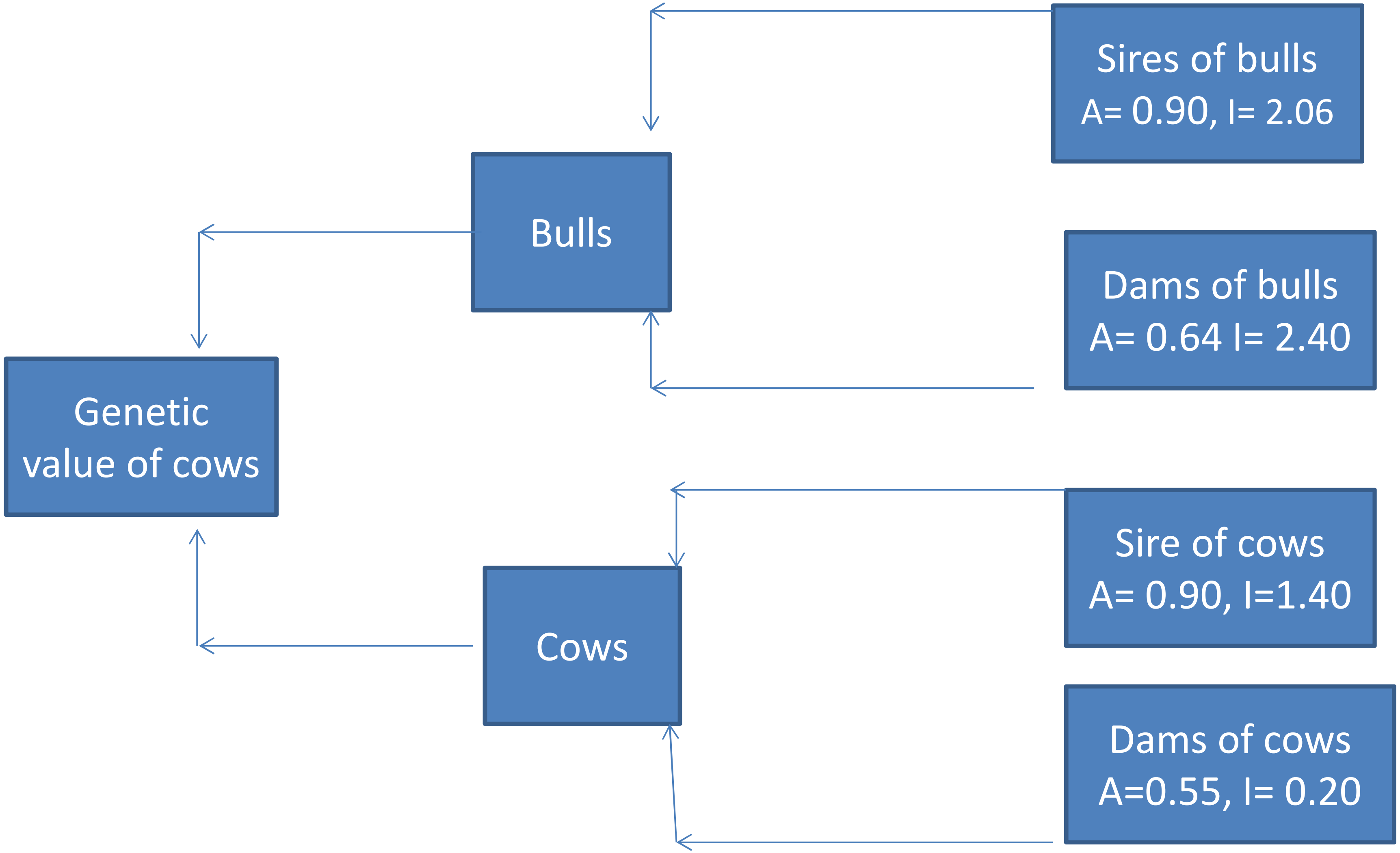
Select top percentage	Intensity factor	Comments
100	0.00	
90	0.20	Usual level for selecting cows in a herd
85	0.27	
75	0.42	Max. Level for selecting cows in a herd
70	0.50	
60	0.64	
50	0.80	Usual range of selecting dams of natural service and A.I. Young bulls. Usual range for selection of bulls out of young bulls sampled
40	0.97	
30	1.16	
20	1.40	
10	1.75	
5	2.06	Range of selection of dams of young bulls to sample in A.I. Also possible range of selection of sires of young bulls to sample A.I.
4	2.15	
3	2.27	
2	2.42	
1	2.67	

Selection intensity X selecting bulls

Since genetic progress is proportional to the product of accuracy and intensity factors, some estimate can be made of the relative importance of four sources of selection for genetic improvement as seen in figure 1.

The selection intensity factors demonstrate how much more intense selection can be for bulls than for cows except for selection of dams to produce sons.

Figure 2. typical accuracy and selection intensity values under A.I condutions for each of the four sources of vgenetic superiorty



Sires of bulls
A= 0.90, I= 2.06

Bulls

Dams of bulls
A= 0.64 I= 2.40

Genetic value of cows

Sire of cows
A= 0.90, I=1.40

Cows

Dams of cows
A=0.55, I= 0.20

Genetic standart deviation

Genetic variation is very important. If there are no genetic differences among animals, there will be no genetic progress no matter how intense the sellection.

Some traits have little genetic variation, others have considerable variation. Fortunately, there are relatively large genetic differences among cows with regard to milk production. The measure commonly used, the genetic standart deviation.

The genetic standart deviation is related to the heritability and overall variation.

Generation

Generation interval influences the amount of progress per year. The shorter the generation interval, the more progress per year. The generation interval is different for bulls and cows. For cows it averages approximately 5 to 6 years, if all heifers were saved for replacements the minimum would be 4 years.

With the bulls the problem is one of waiting for a progeny proof. This takes 4 years. And plus one year which between the time the bull is born and the time he is used. Practically 5 year.

Table 2. Average heritability estimates for some traits

Trait	Heritability
Milk or fat yield	0.25
Final type classification score	0.25
Longevity	0.05
Rate of maturity	0.05
Measure of fertility	0.05
Mastitis incidence	0.20
Milking qualities	0.25
Mature size	0.40
Fat, protein, nonfat solids test	0.45-0.55