15. Breeding Program Design Principles

Julius van der Werf and Brian Kinghorn

Learning objectives

On completion of this topic you should be able to:

- Understand the issues involved in breeding program design
- Predict rates of genetic improvement for breeding programs
- Design and compare alternative breeding programs

Key terms and concepts

- The breeders equation
- Selection Accuracy, Selection Intensity, Generation Interval
- Open Nucleus schemes

Introduction to the topic

Animal breeders aim to bring about genetic change in their livestock, with a view to increasing profitability, ease of management and sustainability. This involves a large number of issues, which can be classified into three groups:

- **Objectives to target:** This relates to asking 'Where to go?', whereas Tools and Strategies below relate to 'How to get there?' Breeding objectives describe the type of animal that we might want to develop, or, more commonly, describe the utility of marginal genetic changes in each trait of commercial value. However, there is increasing concern about loss of genetic diversity, both within and between breeds, and this needs to be accommodated in our objectives and breeding methods.

- **Tools to exploit:** The animal breeder's toolkit includes performance and pedigree recording systems, novel reproductive techniques, information from genetic markers, knowledge of population genetic parameters, and genetic evaluation systems. These tools cost money and the cost benefit of applying them can be evaluated.

- **Strategies to adopt:** This relates to the design of breeding programs. In terms of implementing breeding programs, the main components are deciding which animals to use as parents, and in what combination to mate them. These are the driving elements of both selection theory and crossbreeding theory. Other strategy decisions involve data recording (pedigree, trait performance and DNA test information), and the use of novel reproductive and gene transfer techniques.

15.1 Tactical design of breeding programs

All breeding programs are driven by "action decisions" on:

- Which animals to use for breeding
- How to allocate mates

Together, these constitute mate selection. The only other key action decision area is how to allocate measurement effort – both trait measurement and genotyping of genetic markers.

Animal breeding programs can be very complex, with many decision issues, as shown in Table 15.1.

We currently tend to accommodate these by implementing separate sets of rules. Each of these sets is known to be appropriate on its own, but the best way to combine them in a real breeding program is often unclear. They can however be handled simultaneously using **Mate Selection**.

Table 15.1 Animal breeding issues.

Issue	Comment
Selection value	As indicated by Estimate Breeding Values
Inbreeding	Avoid loss of merit and genetic variance
Crossbreeding value	Breed differences and heterosis
Connection	Comparing animals from different groups
Assortative mating	Elite matings, giving longer term gains
Measurement strategies	trait recording, pedigree recording, progeny testing; recording of (commercial) crossbred progeny, multi-stage selection
DNA testing	Increasing breeding value accuracy based on genomic prediction
Parameter estimation	*e.g.* heritability - good for longer term gains
Reproductive. manipulation	AI, MOET, IVF, sexing, cloning etc.
Running costs	No. of breeding females, semen costs, etc.
Inbreeding	Maintaining genetic diversity
Risk	Staying in business
Breeding objectives	Probably most important of all.

When we do mate selection, the design of the breeding program emerges, purely as a function of the resulting action decisions – the selections and mate allocations made. Topic 19 on Total Genetic Resource Management gives more detail on this. This is a tactical view on program design (see also Kinghorn (2011).

We can also take a rules-based view. This approach is useful in modeling and comparing alternative breeding programs in order to decide a good strategy. Researchers and consultants often use a strategic approach, e.g. whether it is cost effective to measure feed intake, whether or not to use DNA testing, whether progeny testing is beneficial, or whether to use more young sires in the breeding nucleus. For day to day decision making it is more relevant to use tactics, i.e. make decisions that use the prevailing opportunities in a best possible way (see topic 19).

15.2 Rules-based design of breeding programs

Optimizing breeding programs involves choosing the best possible outcome from alternative programs for a given genetic resource in a given production system (market & environment). For each program it is required to predict rates of genetic gain and inbreeding.

To predict rates of genetic gain we use the <u>breeder's equation</u>

Response = <u>Selection intensity * Selection Accuracy * Genetic SD</u>
Generation Interval

Or: response per year = $\dfrac{i_m r_{IAm} + i_f r_{IAf}}{L_m + L_f} \sigma_A$

[1]

Where i = selection intensity, r_{IA} = selection accuracy, σ_A is the genetic standard deviation (e.g. for overall merit: SD of breeding objective), L = generation interval and subscripts m and f refer to males and females.

Besides obtaining genetic change, the breeders also wants to think about the future and maintain some genetic diversity. There are various aspects that need to be balanced:

1) Selection accuracy versus generation interval

   Short generation intervals are good for fast progress, but young breeding animals have lower EBV accuracy

2) Selection accuracy versus selection intensity

   Money available for testing (either performance or DNA) can be used to test a few animals accurately, or to test more animals with lower accuracy. For example, testing fewer young bulls but giving them more test progeny.

3) Selection intensity versus generation interval

   Selecting fewer animals for breeding each year and keeping those longer (e.g. see exercise with AGES in GENEUP.

4) Selection intensity versus inbreeding.

5) The relative emphasis in selection for multiple traits

6) Cost versus benefits

Compared with genetic evaluation (BLUP, mixed models), less attention is usually devoted to designing an optimal breeding program. There are a number of procedures and theories to predict outcomes of breeding programs, but rarely are they optimized in an integral manner. This may be partly due to the complexity and diversity of issues (see Table 15.1)

Any breeding program has to find the right balance between investment in information and obtained rates of genetic improvement in the wider population. It was already pointed out by Robertson and Rendel (1950) that "the apparent lack of connection between an animals' breeding value and its phenotype led many to advocate more complicated methods for judging genotype". They proposed a progeny testing scheme for dairy. The use of artificial insemination (AI) along with the fact that the main traits are sex limited has led to progeny testing becoming prevalent in dairy breeding systems.

Another important breakthrough in breeding program design was the proposal of closed nucleus breeding schemes where selection of young animals based on less accurate breeding values could give accelerated rates of improvement (Nicholas and Smith, 1983). In their case, a new design was proposed to use more optimally the emerging technology of artificially increased female reproductive rate, through multiple ovulation and embryo transfer (MOET, see topic 16). The significance of the paper was that it highlighted the importance of the balance between generation interval and selection accuracy and that this should be optimized, possibly leading to selection of young animals based on less accurate information. Although MOET nucleus schemes seem to achieve the opposite effect to progeny testing schemes in terms of accuracy (r) and generation interval (L), - they reduce both r and L - both developments have demonstrated that the ratio r/L needs to be optimized and that the optimum can be critically affected by new breeding technologies. It is easy to see how selection based on DNA information will affect this ratio as it provides scope for obtaining more information about breeding value early in life, thereby changing the optimal balance toward shorter generation intervals. Therefore, genomic selection is likely affect again the optimal design of breeding programs (Schaeffer, 2006).

The nucleus scheme is a dominant feature in animal improvement programs. Economically, the important feature of nucleus schemes is that investment in measuring a limited number of animals can greatly benefit genetic improvement of a much larger commercial population. Bichard (1971) referred to this as the "selection-multiplication overhead".

Breeding program designs are strongly affected by reproductive rates of the species (compare plants, fish, poultry, sheep, cattle). Reproductive rates can often be boosted artificially (see topic 16) but that may not always be cost effective. But in any case, there is a almost always a pyramidal structure where the genetic improvement of a population is the results of measurement and selection in a small part of that population.

15.3 Optimizing selection in a single tier

The simplest representation of a breeding program is a single tier where breeding males and females are replaced by their offspring (figure 15.1). As many more females are needed, the selection intensity on the female side is usually lower than in the male side. The module AGES in GENUP allows to explore single tier selection, and predict responses per year for a given reproductive rate of males and females. The module assumes selection on individual phenotype, hence selection accuracies are the same for males and females, therefore optimizing

$$\frac{i_m+i_f}{L_m+L_f}\, h^2{}_P.$$

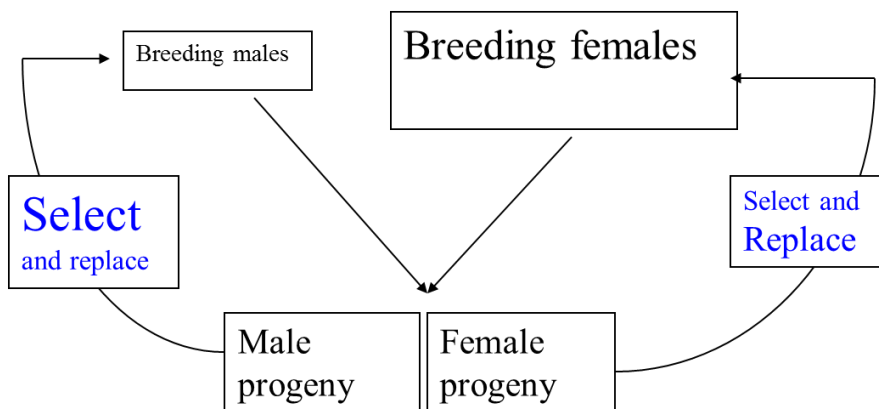The module demonstrates optimization of age structure as in point 3) in the previous section.

Figure 15.1 Illustrations of a single tier breeding scheme

The situation modeled in AGES assumes that once selected, a breeding animal stays in the herd or flock until it is culled for age. This has been termed 'progeny selection'. A more optimal structure is achieved with 'parent selection' where breeding animals compete for each other across age classes, i.e. older breeding animals will be culled if there are more competitive younger breeding animals. In the lecture on BLUP properties, we saw that BLUP breeding values can be compared across age class, and that selection on BLUP automatically optimizes selection over age classes, and therefore it optimizes generation interval. An example of this is illustrated in Figure 15.2, showing that if younger animals get more accurate EBV (e.g. due to genomic information), they are more likely going to be selected as breeding animals, therefore reducing generation interval. Therefore, selection response according to the breeder's equation is optimized under BLUP selection. This is short term response and does not account for inbreeding.

Figure 15.2 Distribution of EBVs for age classes 1 and 2.

Top: Accuracies of EBV for age class 1 is 0.4 and for age class 2 it is 0.8. Of the selected parents (to the right of the truncation line) 27% is from age class 1 and 73% is from age class 2.

Bottom: Accuracies of EBV for age class 1 is 0.7 and for age class 2 it is 0.8. Of the selected parents (to the right of the truncation line) 54% is from age class 1 and 46% is from age class 2.
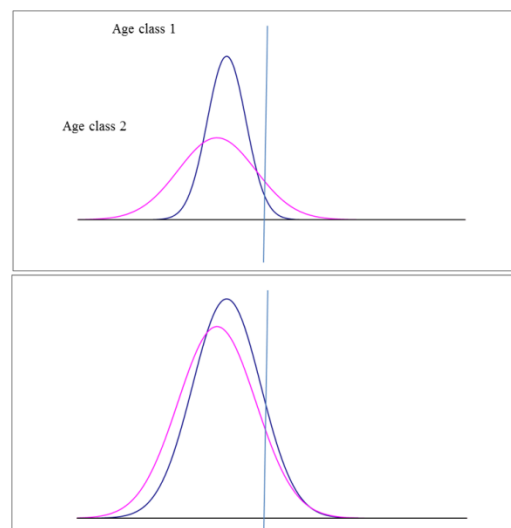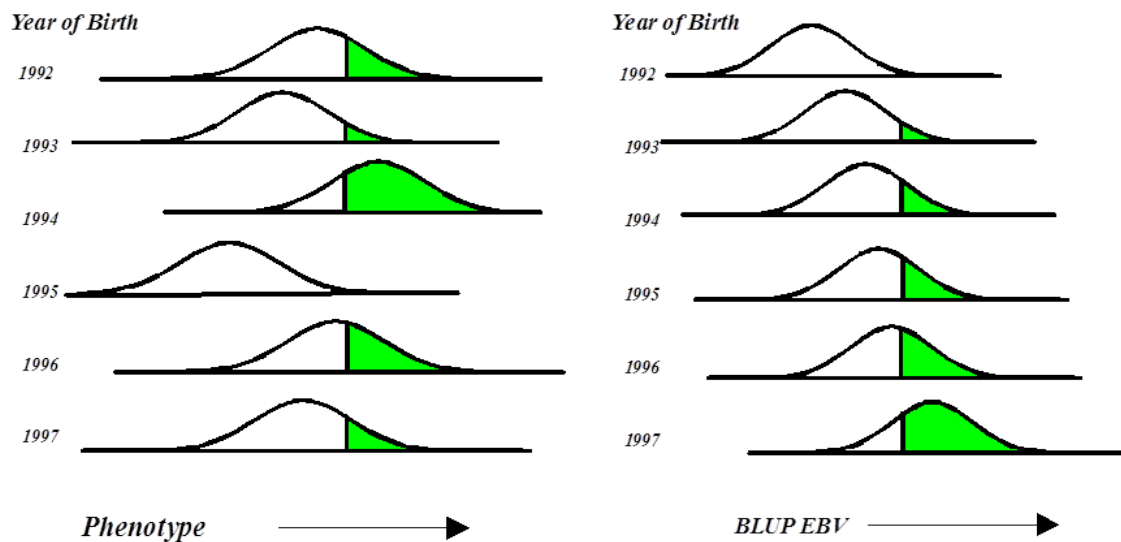
Fig. 15.3 Selection across age classes is facilitated by BLUP. BLUP accounts for genetic trend

Another illustration how BLUP helps to select across age classes is depicted in Figure 15.3. The figure mainly illustrates how BLUP accounts for year effects and for genetic trend. In the Figure, the various age classes have all the same spread of values, hence the same index accuracy. In reality, younger animals have lower accuracy of index values, narrowing their distribution, resulting in fewer of them selected compare d to the figure.

For a give age structure, the response can be predicted as follows:

Assume a breeding objective with a multi-trait selection index to optimize selection for various traits. The selection index framework will be able to calculate selection accuracy for overall merit for a given set of trait measurements. It also allows prediction of genetic change for each trait. If the standard deviation of the multi trait breeding objective is σ_H, and the predicted selection accuracy is r_{IH} the standard deviation of the index will be $r_{IH}\sigma_H = \sigma_I$ The predicted rate of genetic progress per year would be

$$\frac{i_m + i_f}{L_m + L_f} \quad I \qquad\qquad [2]$$

It is likely that males and females, as well as animals from different age classes, have different information and therefore different σ_I. Therefore, the predicted response will be a weighted average of the section differential over age classes. If we write the selection differential $S = i . \sigma_I$ then formula [2] can also be written as

$$\frac{S_m + S_f}{L_m + L_f} \qquad\qquad [3]$$

And for each sex, S is an average of the selection differentials in each age class. These depend on the selection intensity, which follows from the proportion selected from that age class, and the standard deviation of the index pertaining to that age class.

Applying this to the example in Figure 15.2: The example assumes 10 animals are selected out of 100, 50 in each age class. Assume a genetic trend of 0.2/year and σ_H = 1.
In the top, the proportion selected are 2.7/50 = 5.4% and 7.3/50 = 14.6%, hence selection intensities are 2.03 and 1.57., hence S_1 = 2.03*0.4 + 0.2 =1.01 for age class 1 and S_2 = 1.57*0.8 = 1.26 for age class 2, giving a weighted average S of 1.19.
In the bottom the proportion selected are 5.4/50 = 10.8% and 4.6/50 = 9.2%, hence selection intensities are 1.72 and 1.79., hence S_1 = 1.72*0.7 + 0.2 = 1.40 for age class 1 and S_2 = 1.57*0.8 = 1.44 for age class 2, giving a weighted average S of 1.42.

15.4 Nucleus breeding schemes

An industry can contain millions of animals. It is not worth including them all in a breeding program due to measurement costs, recording costs, and lack of proper control.   The solution is to concentrate effort on relatively few elite breeding units (or nucleii) at the top of a pyramid structure, and disseminate the superiority to the whole industry (Fig. 15.4).

For example, there could be 50,000 breeding ewes in sheep studs. If they produce 50,000 progeny per year and 40% of the male lambs from the studs is sold as breeding stock to the multiplier tier, giving 10,000 rams per year. If 50% of flock rams is replaced every year, the total number of flock rams would be 20,000, serving 1 million flock ewes in the multiplier level.   The same multipliers will hold for rams sold from the multiplier to the commercial flocks.
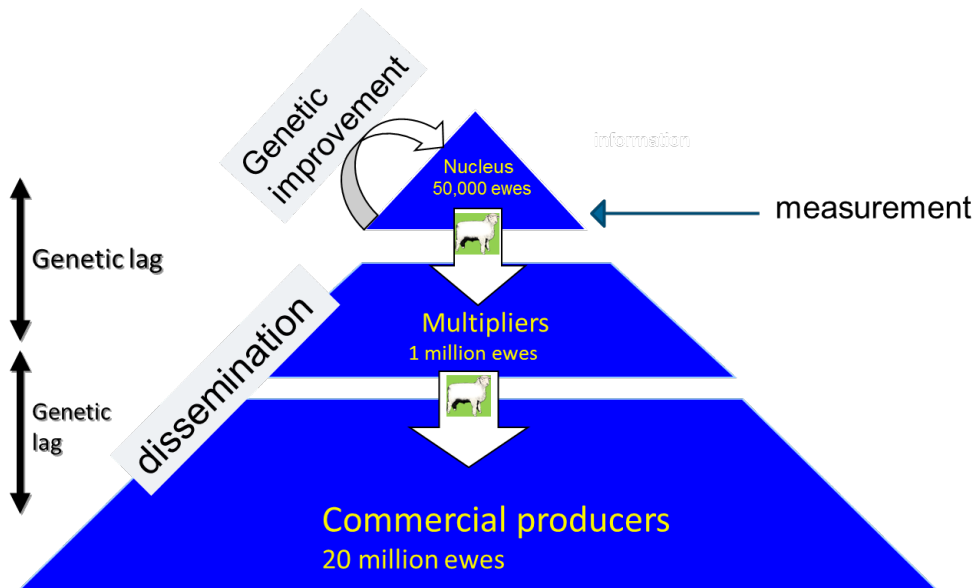

Figure 15.4 Illustrations of a 3 tier breeding schemes.

Things to note about Figure 15.4

- Measurement takes place only in the nucleus. This is only a small group of animals as a proportion of the whole population

- Due to measurement and selection, the nucleus improves gradually over time. As a result, the other tiers will improve as well, and at the same rate, provided they purchase breeding material from the tier above.

- The rate of improvement is the same in all tiers. If a lower tier obtains average sires as well as dams from the tier above, they would be one generation behind. If the lower tier only buys rams, they will be 2 generations behind, i.e. the genetic lag is 2 generations.

Closed nucleus breeding schemes

Closed nucleus schemes are closed in that no breeding stock are imported into the top level, or tier. In reality, there is usually a fair bit of migration between different flocks and herds in the top one or two tiers. Closed schemes have evolved in most animal industries, driven largely by market forces. Here are some key properties of closed schemes:

1. Selection effort is only permanently effective in the nucleus - any temporary changes in lower tiers are diluted by importation from the nucleus (Figure 15.5).
2. Nucleus breeding objectives impact on the whole scheme.
3. If lower tiers buy average rams (and no ewes) from the tier above, they will lag behind the tier above by 2 generations (about 7 years in sheep) of selection response (Bichard, 1971).
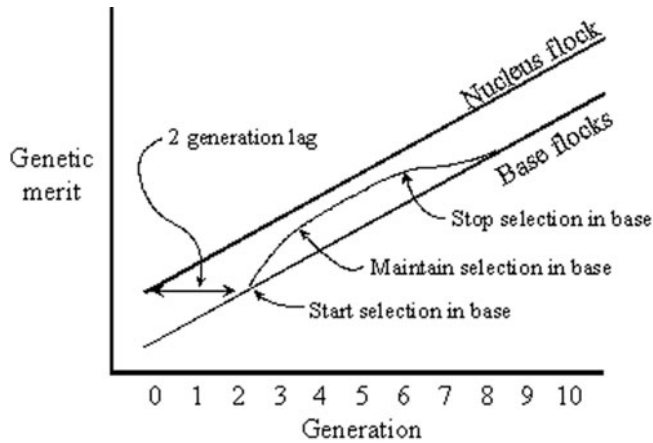
Figure 15.5 Selection response in a 2-tier closed nucleus scheme. The base lags about 2 generations behind the nucleus. Any selection effort in the base needs to be maintained just to keep a non-increasing advantage. Opening the nucleus will give more sustained returns from selection in the base.

Open nucleus breeding schemes

Stock in the base tier(s) can have higher EBV's than nucleus stock that would have otherwise been selected. This is most true for animals of low fecundity, such as ewes, as illustrated in Figure 15.6.

These high-merit base ewes can be migrated up to be bred in the nucleus, giving an open nucleus scheme. This pushes the nucleus to progress more quickly, and this benefits the whole scheme as the base will move as fast as the nucleus after things have settled down. Overall response in open 2-tier schemes is 10 - 15 percent faster than in closed schemes when optimal design is applied: about 10% of the population in the nucleus and about 50% of nucleus mated ewes born in the base (James, 1977).
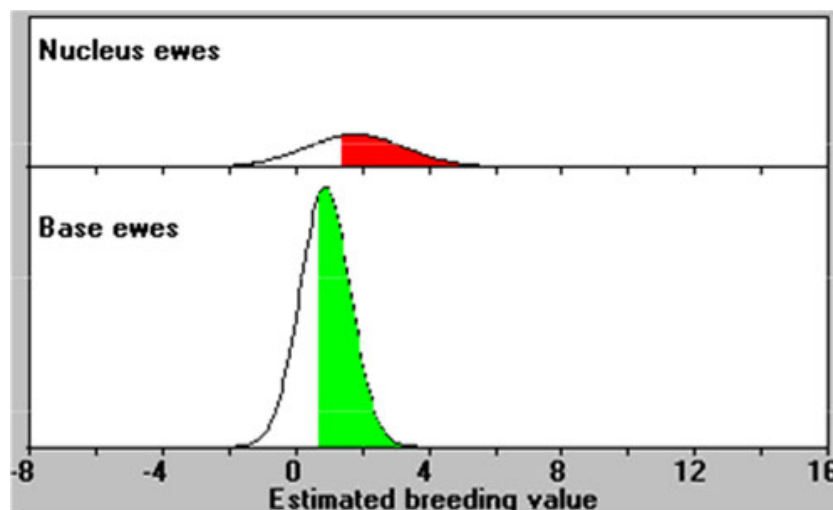

Figure 15.6 In closed nucleus schemes, the best base ewes are better than the worst selected nucleus ewes (the shaded areas represent ewes selected into their flocks of birth). This means that the base flocks can contribute ewes to the nucleus to make faster genetic progress for the nucleus.

Figure 15.7 illustrates migration in a 2-tier open nucleus scheme at generation 4. The scale is in units of across-flock dollar EBV's. The best animals are used in the nucleus, including animals born in the base, the next best are used in the base, and the rest are culled. With selection across flocks on EBV, as in Figure 15.7, migration rates are optimal. They change as the breeding program progresses, and as random chance plays a role in where and when the best animals are born.
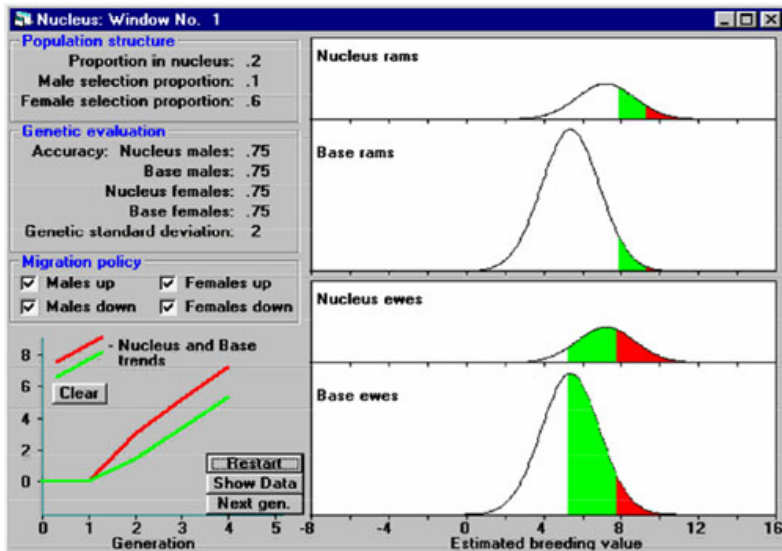

Figure 15.7 Migration in an open nucleus scheme, as illustrated in the module NUCLEUS under GENUP.

Different measurement strategies in nucleus and base

A major use of nucleus schemes is to avoid or reduce measurement costs in lower tiers. The example in Figure 15.5 does not reflect this - selection accuracy ($r_{\hat{A}A}$) was 0.75 for nucleus and base stock. Increased (or decreased) accuracy can be achieved by measuring more (or less) traits as selection criteria for the index or using more (or less) information from relatives. As $r_{\hat{A}A}$ increases, $\sigma_{\hat{A}}$ increases ($\sigma_{\hat{A}} = r_{\hat{A}A}\sigma_A$), and the distributions of EBV widen, as shown in Figure 15.8.

Figure 15.8. The relationship between amount of measurement made and the width of EBV distributions.

If the only information available is the animals' tag numbers, then there is no power to identify superior (or inferior) animals and there is no variation in EBV's.

If GFW is known, there is some power - and yet if FD is of key importance in the objective, then this power is obviously limited. Animals of exceptional breeding value are difficult to identify as the most important trait is not measured.

As more information is gathered, there is more power to identify animals of low and high breeding value, and the EBV distribution widens.

Information from relatives also helps here, as in the
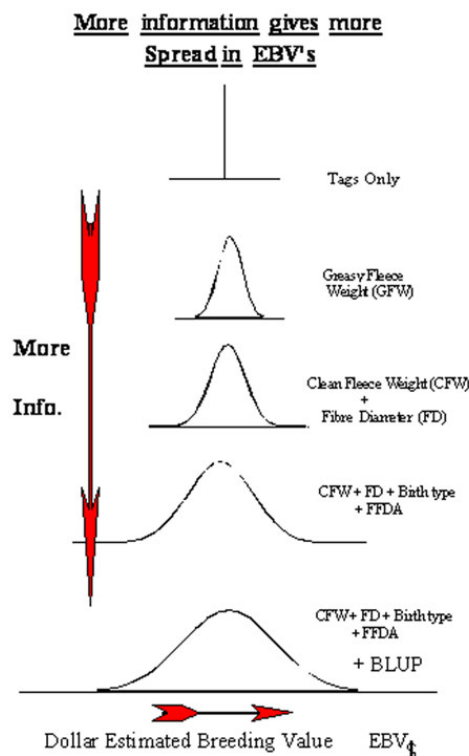
distribution at the bottom of Figure 15.6 which includes BLUP genetic evaluation.

Figure 15.9 shows what happens in an open nucleus breeding scheme when there is a different amount of information gathered in the nucleus and base flocks.

Notice that higher accuracy in the nucleus ($r_{\hat{A}A}$ = 0.75 versus 0.375 in the base) is reflected in a wider distribution of EBV's - the more accurate the EBV's the more power to identify animals of high or low dollar breeding value. This in turn affects the average superiority of parents, migration rates and overall response to selection.
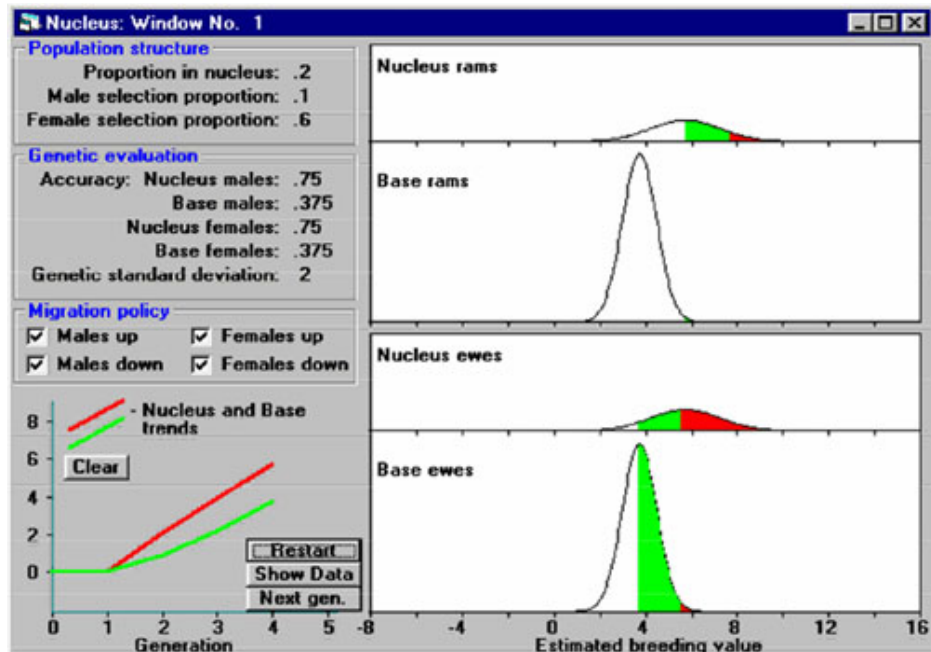

Figure 15.9. Migration in an open nucleus scheme when less measurement, and therefore less accurate selection, is made in the base flocks.

Why do open nucleus schemes perform better?

A simple answer to this question is evident from the examination of Figures 15.7 and 15.9. Use the best stock to make the elite nucleus move quickly then let the rest of the population enjoy the benefits. There can be some increased lag between the tiers, but this is compensated for quite quickly.

However, this can be viewed from a different angle. Assortative mating (mating best to best) gives extra response due to increased genetic variation in the next generation. We could simply do this across the whole population, but the open nucleus system does it at just two or three levels (tiers), with generally random mating within tiers. However, the open nucleus design has an added advantage - knowing the source of an animal (the tier of its birth) tells us something about its likely genetic merit even if we do not know its pedigree or its measurements. Each tier contains many animals, and therefore "tier means" for given traits constitute high quality information - they are highly heritable. In simple nucleus schemes we measure animal merit as deviations from flock mean (regressed by heritability, as in the Topic 2 on Principles of EBV's). If we add these to flock-of-birth genetic means we get simple estimates of across-flock EBVs. This flock mean is like the mean of a big family. Thus, in the absence of normal pedigree information, we get an added boost in overall selection accuracy through use of this crude but effective "family" information.

This extra information about genetic merit is essentially redundant in the face of full pedigree information. This means that we could capture all the benefits of an open nucleus scheme by using pedigree information to select on BLUP EBV's, and mating assortatively. In this case there would be no need to migrate ewes - as long as we could generate all desired matings by migrating semen between flocks.

Geographically diffused nucleus schemes

As suggested in the last section, we can enjoy the full benefits of an open nucleus scheme without nominating one flock or herd to be the nucleus. We can create the elite 'nucleus' matings in the flocks of birth of the female partners, with migration of semen to these flocks. This relies on good pedigree information, without which we lack the useful information about the tier of birth that a simple open nucleus scheme manages to exploit.

Geographically diffused nucleus schemes are in fact very common. The classical four-pathway dairy breeding design, as described below, is in fact a geographically diffused nucleus design

Design of dairy breeding programs

Dairy breeding programs are a somewhat special case in the design of breeding programs, as they have a *4-pathway* structure. The 4-pathways structure has mainly arisen from the progeny testing practice. As progeny testing is expensive, obviously not all male dairy calves are progeny tested. Only those with high EBVs are progeny tested, where the EBV is based on parent average EBV. To achieve more efficiency, the very best dams are mated to the best bulls, giving higher EBV for resulting progeny based on parent average. These 'best to best' mating are elite matings, as opposed to normal matings to create progeny to replace dairy cows in normal herds. So in fact, the 4-pathway system is not different from a 2 tier nucleus breeding scheme, where the elite matings are those in the nucleus, and the normal matings are those in the commercial tier.

Also the dairy industry was relatively advanced in taking up new technologies, such as use of BLUP, AI and other reproductive technologies and genomic selection. It is therefore an interesting case to study when it comes to the effect of new technologies on breeding program design.

Dairy breeding is characterized by

- high degree of data recording, typically about 70% of commercial farms participate in milk recording schemes
- widespread use of AI, about 95% of all calves are born through AI.

The combination of widespread herd recording and AI, i.e. using sires across many herds, provides a good structure for genetic evaluation. EBV's of both bulls and cows are comparable over different herds. Of all livestock industries, the use of information provided by EBV's is most widely accepted in dairy.

4-pathway structure

Up to 70 percent of the cows in a national dairy population can be served by very few progeny tested sires (maybe 5 to 10) - the rest being used for progeny test matings. Note that:

a) This means that a lot of effort can be made to ensure that these few bulls are as good as possible.

b) Progeny testing candidate bulls is nevertheless very expensive.

From a) and b) it is clear that effort is warranted ensuring that candidates for progeny testing are the best available - this is done by setting up **elite matings** on a contract basis:

So there are two types of matings:

- Elite matings to breed young bulls for progeny testing, e.g. the top 5 AI bulls time the top 2% of breeding females ("bull dams") in contract matings. The females born in these elite matings have usually a high chance to become bull dams themselves.

- Normal matings to produce replacement females for the commercial herds: (normal AI bulls time the top70% cows within each herd.

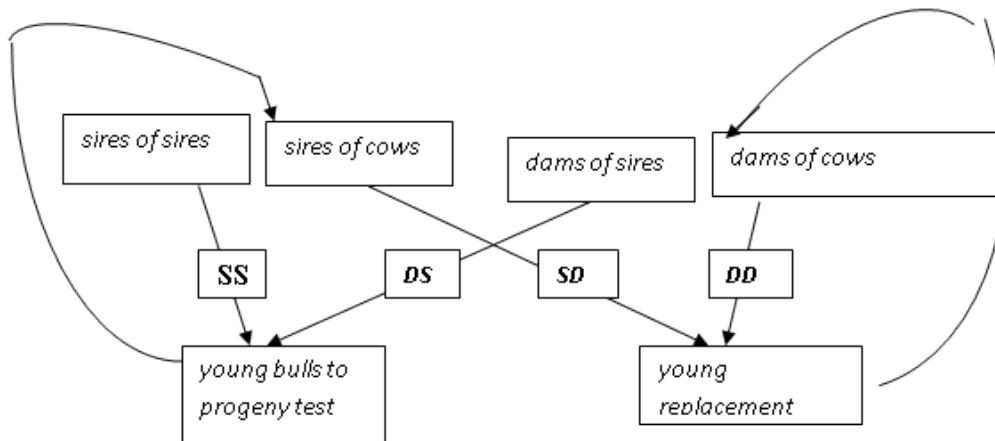But in a sense this is simply an open 2-tier structure of a breeding program.

Figure 15.10. Diagram of a 4-pathway dairy breeding program.

Economic evaluation of breeding programs

The ability to model breeding programs becomes an important part of strategic decisions about investment. The first question could be: is it cost effective to invest in breeding programs? How much can we afford to invest in measurement? Is it cost-beneficial to measure certain traits that are expensive to measure (e.g. a computer scan of whole carcass, eating quality taste panels, or feed intake). With new technologies similar questions are being asked: what is the cost-benefit from implementing genomic selection?

Assume a certain breeding program where the predicted rate of annual genetic gain is dG, which is expressed in monetary value, e.g. $2/head. This figure can be calculated using equations [2] or [3] in this topic. It assumes that the economic values are expressed on a 'per head' basis, which could be per breeding female, or per animal sold (for slaughter). As genetic improvement is incremental and cumulative, the increase in merit after t years will be t.dG. The benefit for the whole population will be N.t.dG, where N is the total number of animals in the population expressing the improvement. If the cost of running the program is equal to C, the the benefit in year t will be N.t.dG – C. To assess costs and benefits, it is appropriate to discount future benefits. Money earned in the future will be of less value due to discounting. The discount factor for year t is $(1/r^t)$, where r is the discount rate is equal to the nominal interest rate, corrected for inflation. So the benefit in year t in net present value (NPV) will be equal to

$$(N.t.dG – C).(1/r^t).$$

The benefit over time of this breeding program is illustrated in Table 15.2 and Figure 15.11. In the example it is assumed that dG = $2/head, N=20 million and costs are 0.5 million. This is based on the structure in Fig 15.4, assuming a measurement cost of $10 per breeding ewe in the studs. These are figures, pretty close to those for sheep in Australia. You can see that the 0.5M investment per year is easily earned big by large and cumulative value of genetic gain. For example, in year 10, the benefit from genetic improvement is $180M whereas the annual investment is only 0.5M.

Table 15.2. Genetic mean, benefit of genetic improvement and NPV of investing in genetic improvement in each of 20 years after commencement.

| year	Genetic Mean ($)	Benefit (M)	Cost (M)	discount factor	NPV (M$)
1	0	0	0.5	1.00	-0.50
2	1	20	0.5	0.95	18.57
3	2	40	0.5	0.91	35.83
4	3	60	0.5	0.86	51.40
5	4	80	0.5	0.82	65.40
6	5	100	0.5	0.78	77.96
7	6	120	0.5	0.75	89.17
8	7	140	0.5	0.71	99.14
9	8	160	0.5	0.68	107.96
10	9	180	0.5	0.64	115.71
11	10	200	0.5	0.61	122.48
12	11	220	0.5	0.58	128.34
13	12	240	0.5	0.56	133.36
14	13	260	0.5	0.53	137.62
15	14	280	0.5	0.51	141.17
16	15	300	0.5	0.48	144.06
17	16	320	0.5	0.46	146.37
18	17	340	0.5	0.44	148.12
19	18	360	0.5	0.42	149.38
20	19	380	0.5	0.40	150.18
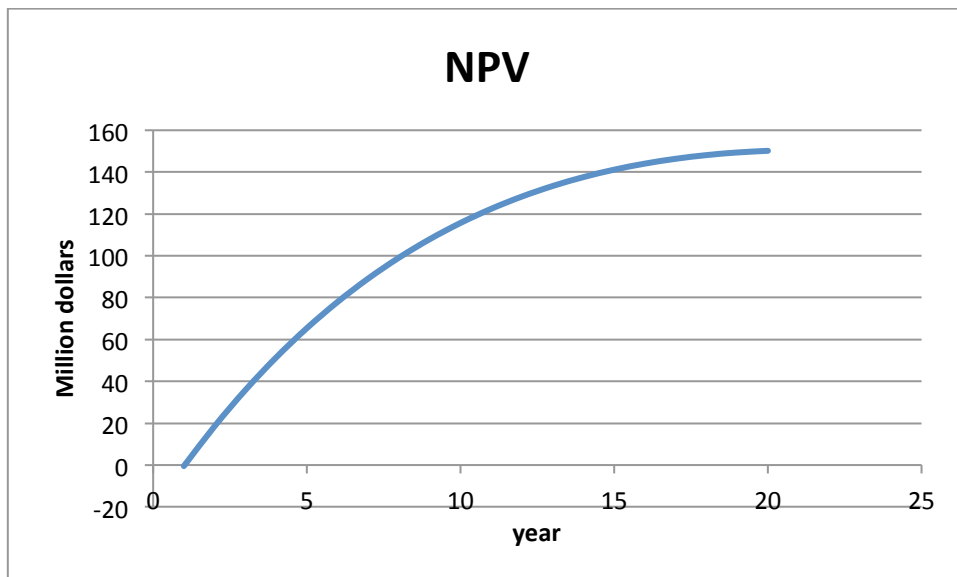
Figure 15.11 Graph showing the NPV of a genetic improvement program over the next 20 years, assuming a cost of 0.5M/year, a rate of improvement of $2 per year and improvement expressed in 20M sheep

We can follow the same principles when comparing 2 breeding programs. For example, one with and one without genomic selection. Suppose the extra gain due to genomic selection is 10%, i.e. dG is now $2.20/head. Assume the cost is now 2.5 million dollars per year. The NPV for the 2 strategies are compared in Fig 15.12
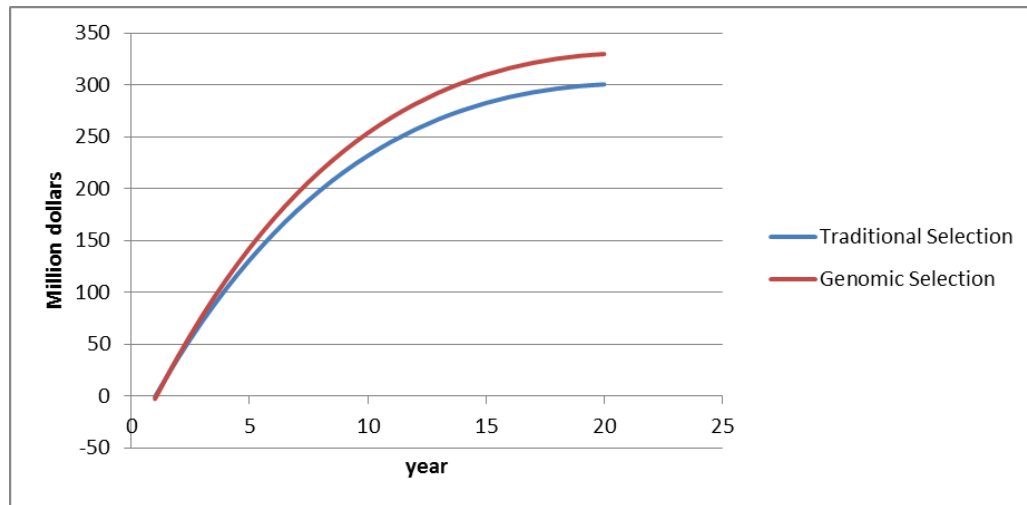

Figure 15.12. Graph showing the effect of genomic selection on industry wide NPV of a genetic improvement program over the next 20 years, assuming a cost of $0.5M for noGS and 1.65$M for GS, a rate of improvement of $2 per head per year under noGS and $2.20 under GS and improvement expressed in 20 million sheep

The example shows that investment in breeding programs is highly lucrative because 1) genetic improvement is incremental and cumulates over years, and 2) due to the multiplication factor in the 3 tier design, an investment in a small number of nucleus animals bring about benefit in many commercial animals. Even a potentially large investment of genomic selection is cost effective.

The economic assessment as presented above has a number of caveats. It is a cost-benefit analysis at an industry level, as if there was a complete integration between tiers, and the investors also reap the benefits. In reality this is not the case. It is up to the breeders to invest in measurement and technology, whereas the commercial producers reap the benefit. There would be a sharing of benefit if the breeders increase the price of seed stock according to the increased value of genetic improvement. In reality, that may be difficult. In the example, where stud breeders sell a total of 10,000 rams per year, the increase in ram price would have to be thousands of dollars over the next 20 years. So for an individual breeder, cost benefit considerations could be quite different than those at a whole-of industry level.

A more conservative approach could be to only value benefits in the second tier, i.e. for the direct clients of the stud breeders. In that case, the genetic improvement of stud rams is only valued in its direct offspring. The multiplication factor would be much lower. For example, consider a commercial operation with 10,000 ewes, needing 100 rams per year. This could be supplied by a stud breeder using 500 rams (selling 40% of his stud born males as rams to the commercial). Figure 15.13 shows the NPV for the stud breeder, assuming he shares the benefits equally with the commercial level (hence the graph would look the same for the commercial operation). It will take at least 10 years before the initial investment in genomic testing pays off and becomes more profitable than traditional measurement of phenotype. In the GS scenario he would have to increase his ram price with about $200 more over 20 years. If te stud breeders captures less than 50% of the benefit, his perspective to invest in a relatively expense technology such as genomic selection would look even more bleak, even though the technology delivers a clear industry wide benefit..
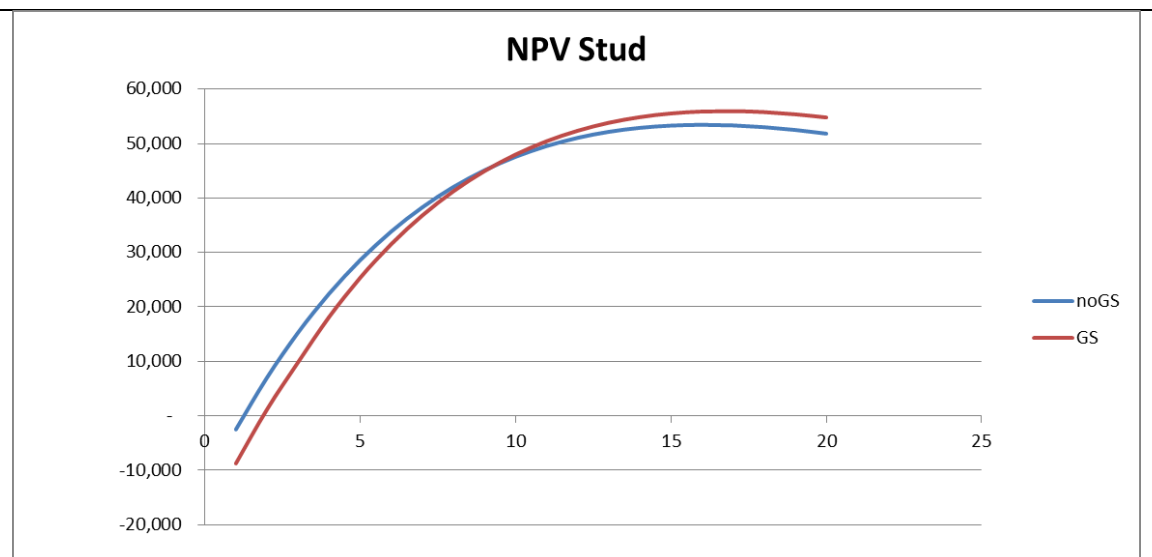
Figure 15.13. Graph showing the effect of genomic selection on NPV for an individual stud breeder of a genetic improvement program over the next 20 years, assuming a cost of $5k for noGS ($10/head) and $16.5k for GS (only males genotyped for $50/head), a rate of improvement of $2 per head per year under noGS and $2.20 under GS and improvement expressed in 10,000 sheep

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Summary

There are many issues in animal breeding, which can be classed into 3 different groups: Objectives to target, Tools to exploit and Strategies to adopt.

There are two key approaches that can be used by animal breeders to bring about genetic changes in livestock by addressing these issues. These are the Tactical approach and the Rules-Based approach. The first is to make operational decisions (see topic 18). The second is to model alternative breeding programs for more strategic decision making.

Selection on BLUP breeding values across age classes optimizes age structure and an optimal strategy would implement BLUP selection along with inbreeding management (see topic 17)

Animal populations have a pyramid structure of the breeding program such that few animals can be measured and many can be improved. Measurement and selection takes place in the breeding "nucleus" in the top tier of the pyramid, and commercial or base herds in the bottom tier. In some industries there are multiplier tiers in the middle.

Nucleus breeding schemes can be closed where no new animals are imported into the nucleus or open where the better animals from the tiers below the nucleus are migrated up to the nucleus for inclusion in the breeding program.

Economic evaluation of alternative breeding programs can help assess the cost and benefit of investment in breeding programs. If breeders cannot capture the full benefit of genetic improvement for the whole industry, they have less incentive to invest in expensive breeding technologies (such as genomic selection).

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Glossary of terms

Assortative mating	Mating can be assortative with respect to a certain genotype (e.g. individuals with genotype AA tend to mate with other individuals of genotype AA) or phenotype (e.g. tall individuals mate with other tall individuals)
Closed nucleus breeding scheme	No new individuals are introduced into the nucleus breeding scheme
Elite matings	Breeding the best with the best. A form of assortative mating
Open nucleus breeding scheme	The best individuals from lower tiers of the pyramid structure can be migrated up into the nucleus breeding scheme if the genetic merit of these individuals would accelerate genetic gains in the population
Pedigree[1]	A record of the ancestry of an animal
Selection accuracy[1]	The correlation between the selection criterion (eg an index) and the breeding goal
Progeny testing[1]	A comparison of animals (and subsequent selection amongst them) based on the performance of their progeny

[1] Glossary terms taken from Simm (2000).