

# 15. Breeding Program Design Principles

Brian Kinghorn

## Learning objectives

On completion of this topic you should be able to:

- Understand the two approaches to animal breeding implementation: the Tactical Approach and the Rules-Based Approach

## Key terms and concepts

- Mate Selection constitutes Action Decisions - luckily, these are relatively simple. They address animal breeding issues which are complex.
- Animal populations have a pyramid structure, with breeding actively concentrated at the top.
- Open Nucleus schemes benefit from mating best to best in elite matings.

## 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.
- **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. Source: Kinghorn, (2006).**

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	e.g. progeny testing; multi-stage selection
Quantitative Trait Loci	Detection and use of QTL and 'major genes'
Parameter estimation	e.g. heritability - good for longer term gains
Lifetime value	For ongoing harvesting and reproduction
Reproductive. manipulation	MOET, IVF, sexing, cloning etc.
Running costs	No. of breeding females, semen costs, etc.
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. See also Kinghorn et al. (2002).

This is a tactical view on program design. We can take a step further back and take a rules-based view.

## 15.2 Rules-based design of breeding programs

The rules-based approach to design of breeding programs involves rules that we might derive, such as, for example:

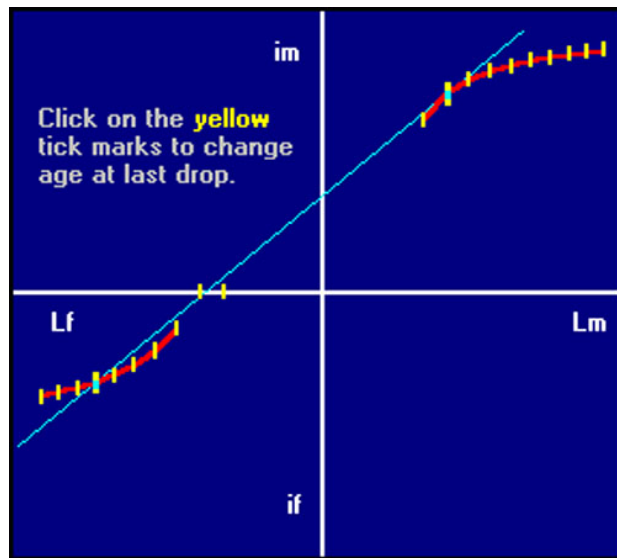
- Cull females at 8 years of age
- Select breeding animals across all age groups on BLUP EBV
- Assortatively mate selected males and females

These rules are usually derived by optimising predictions of rates of genetic gain and inbreeding. For example we can optimise the simple formula for response per year:

$$R_{yr} = \frac{i_m + i_f}{L_m + L_f} h^2 \sigma_P \quad \text{or} \quad R_{yr} = \frac{i_m + i_f}{L_m + L_f} r_{AA} \sigma_P$$

.... by changing a range of parameters, such as culling ages, which affect the elements of these equations. GENUP module AGES uses the following figure (Fig. 15.1) to show the relationship between selection intensity,  $i$ , and generation interval,  $L$ , for each sex, given the prevailing population structure and parameters. Run Ages to find how the slope of the blue line reflects selection response per year.

Figure 15.1 The relationship between selection intensity ( $i$ ) and generation interval ( $L$ ) for each sex as given by the GENUF module AGES. Source: Kinghorn, (2006).



### 15.3 Nucleus breeding schemes

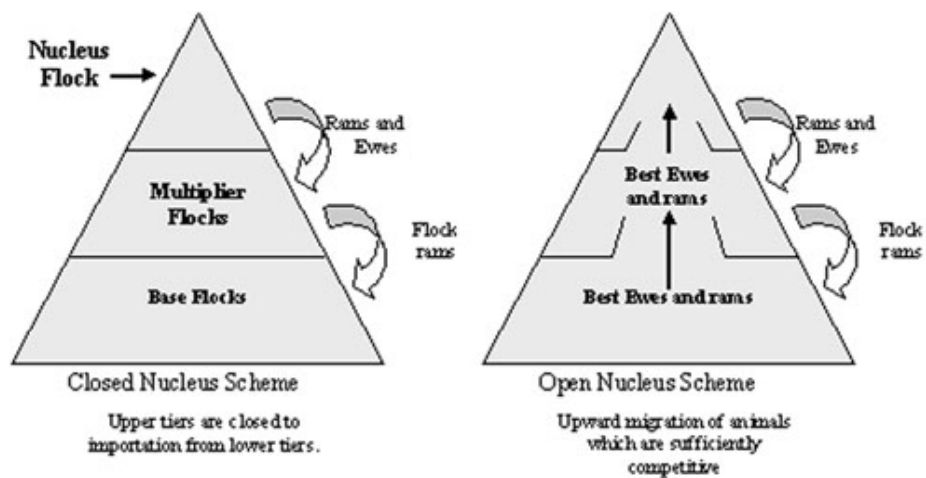
Recall that breeding programs are driven by action decisions on:

- which animals to use for breeding
- how to allocate mates

These constitute mate selection. This covers all animal breeding issues except measurement and genotyping decisions. Mates can be allocated across flocks (or herds etc.) and breeds, as well as within flocks. A sufficiently powerful mate selection algorithm could set up optimal nucleus breeding schemes “automatically”. However, we will consider the Rules-Based approach here.

### Nucleus breeding systems and breeding pyramids

Figure 15.2 Illustrations of closed and open nucleus breeding schemes. Source: Kinghorn, (2006).



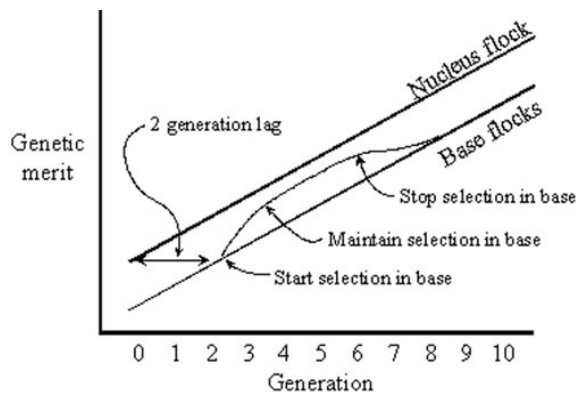
An industry can contain millions of animals. It is not worth including them all in a breeding program due to measurement costs, recording costs, and lack of proper control. The solution is to concentrate effort on relatively few elite breeding units (or nuclei) at the top of a pyramid structure, and disseminate the superiority to the whole industry (Figure 15.2).

## 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 15.3).
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 15.3 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. Source: Kinghorn, (2006).**



## Open nucleus breeding schemes

Stock in the base tier(s) can have higher EBVs 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 15.4.

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 15.4 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. Source: Kinghorn, (2006).

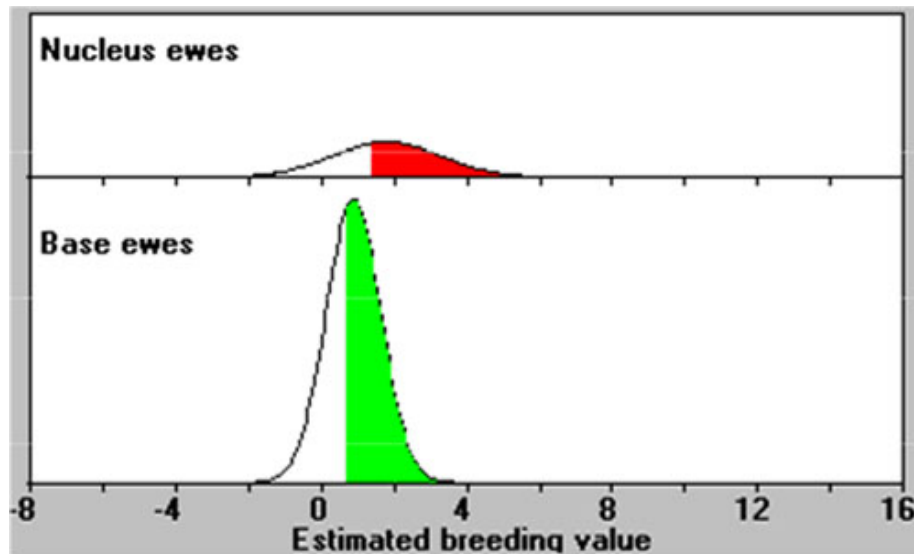
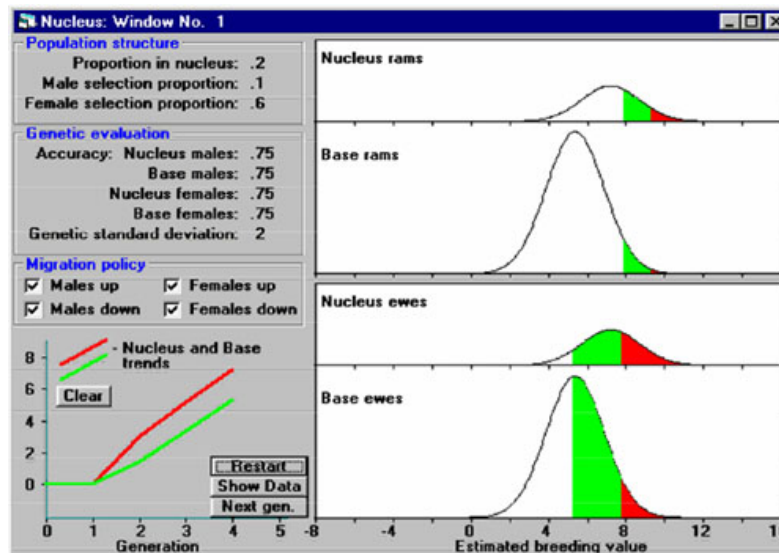


Figure 15.5 illustrates migration in a 2-tier open nucleus scheme at generation 4. The scale is in units of across-flock dollar EBVs. The best animals are used in the nucleus, including animals born in the base, the next best are used in the base, and the rest are culled. With selection across flocks on EBV, as in Figure 15.5, migration rates are optimal. They change as the breeding program progresses, and as random chance pays a role in where and when the best animals are born.

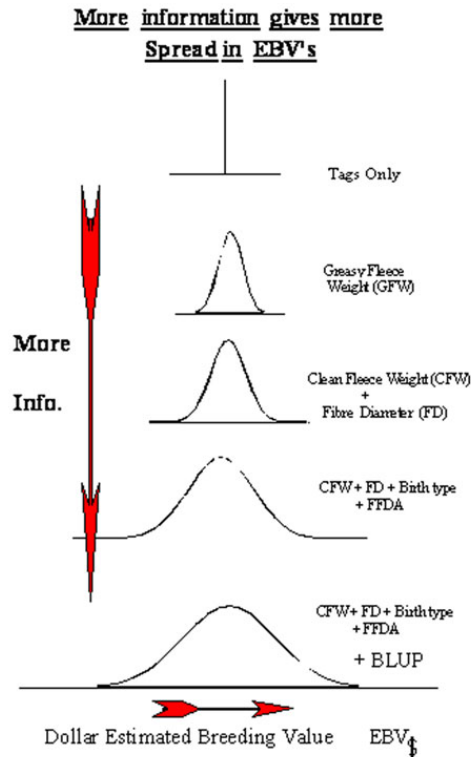
Figure 15.5 Migration in an open nucleus scheme, as illustrated in the module NUCLEUS under GENUP. Source: Kinghorn, (2006).



## 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 ( $r_{AA}^{\hat{}}$ ) 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  $r_{AA}^{\hat{}}$  increases,  $\sigma_{\hat{A}}$  increases ( $\sigma_{\hat{A}} = r_{AA}^{\hat{}} \sigma_A$ ), and the distributions of EBV widen, as shown in Figure 15.6.

**Figure 15.6. The relationship between amount of measurement made and the width of EBV distributions. Source: Kinghorn, (2006).**



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 EBVs.

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.

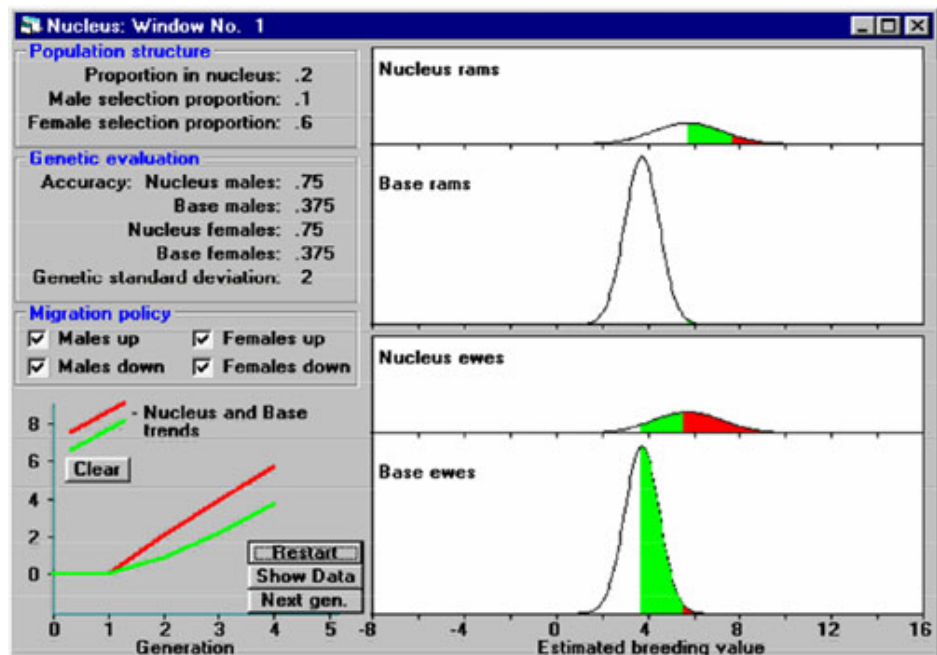
As more information is gathered, there is more power to identify animals of low and high breeding value, and the EBV distribution widens.

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

Figure 15.7 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 ( $r_{AA}^{\hat{}} = 0.75$  versus 0.375 in the base) is reflected in a wider distribution of EBVs - the more accurate the EBVs 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 15.7 Migration in an open nucleus scheme when less measurement, and therefore less accurate selection, is made in the base flocks. Source: Kinghorn, (2006).



## Why do open nucleus schemes perform better?

A simple answer to this question is evident from the examination of Figures 15.5 and 15.7. 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 EBVs). 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 EBVs, 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. Also the dairy industry was relatively advanced in taking up new technologies, such as use of BLUP, AI and other reproductive technologies. It is therefore an interesting case to study when it comes to the effect of new technologies on breeding program design.

Dairy breeding is characterised 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. EBVs of both bulls and cows are comparable over different herds. Of all livestock industries, the use of information provided by EBVs 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:

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

Elite matings:	males to breed males	x	females to breed males	... maybe 10 <sup>3</sup> cows
	[ mm	x	fm ]	
Normal matings:	males to breed females	x	females to breed females	... maybe 10 <sup>6</sup> cows
	[ mf	x	ff ]	



Normally we have two pathways for selection improvement - males and females. In this case we have four pathways, males to breed males (mm), females to breed males (fm), males to breed females (mf) and females to breed females (ff):

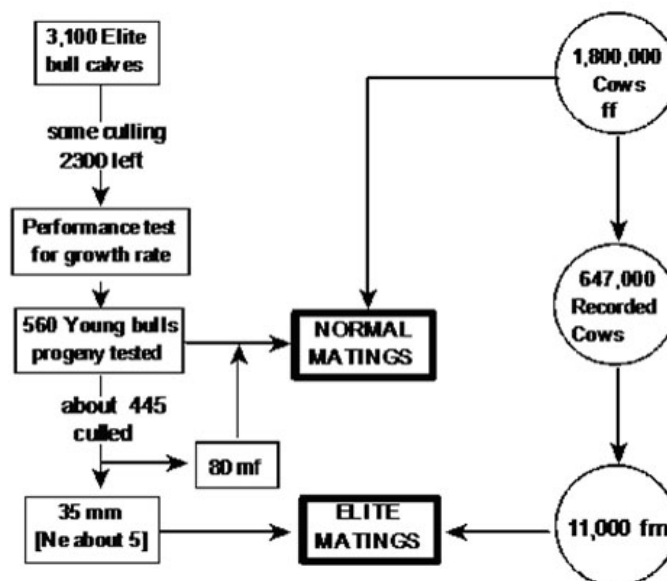
Elite matings:	mm: 2 to 5 top progeny tested sires.  best cows selected on index, contract mated with mm semen to produce young bulls for progeny testing.
Normal matings:	second best (but acceptable) progeny tested sires, plus young bulls for progeny testing. Of course available mm semen is also used here.  ordinary cows, used for ordinary matings plus progeny testing.

Note that this is very similar to a 2-tier open nucleus scheme - with elite matings forming the nucleus and normal matings forming the base. The only differences are that the nucleus is very small in relation to the base, it is also geographically diffused over herds, and no sires are born in the base.

### A typical dairy breeding program

Here is an outline of a typical dairy breeding program (Figure 15.8). It is based on dual purpose Simmentals in Germany.

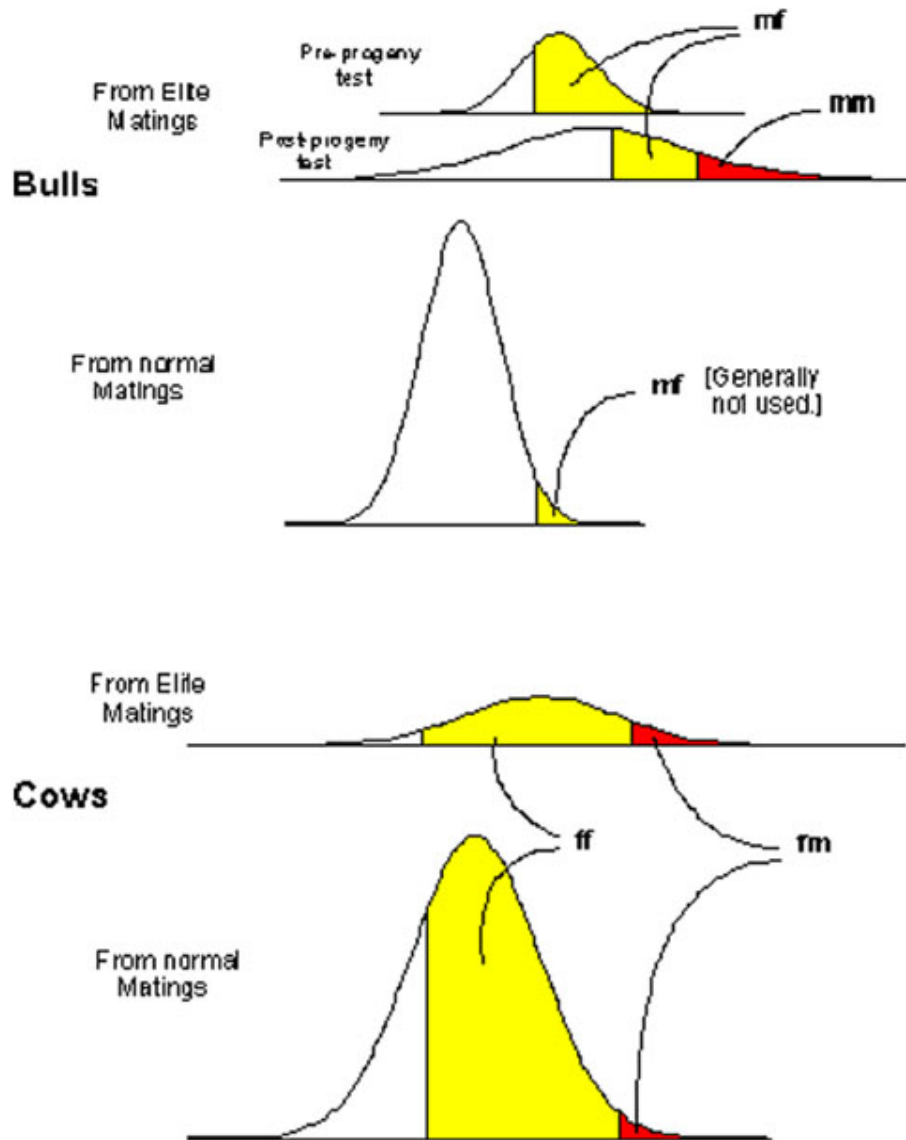
Figure 15.8. A typical dairy breeding program. Source: Kinghorn, (2006).



### Genetic merit in the 4 pathways

Figure 15.9 shows a different type of illustration of a purebreeding 4-pathway dairy cattle breeding structure. The scale is in units of estimated breeding value. For each sex, progeny out of elite matings are in the upper distribution (which is split pre- and post-progeny testing for bulls) and progeny out of normal matings are in the lower distributions. Numbers of animals are reflected by volume of distributions, but the diagram cannot be drawn to scale because of the very small proportion of elite matings. The accuracy of estimated breeding values in each distribution is reflected in the width of the distribution, this being highest for progeny tested sires. Bulls out of normal matings are generally not used in dairy cattle. The four pathways are males to breed males (mm) males to breed females (mf) females to breed males (fm) and females to breed females (ff).

Figure 15.9 Purebreeding 4-pathway dairy cattle breeding structure.  
Source: Kinghorn, (2006).



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## Readings



The following readings are available on CD

1. Kinghorn, B.P. 2000, 'Key issues in breeding program design', Chapter 11 in *Animal Breeding – Use of New Technologies*, Kinghorn, B.P., van der Werf, J.H.J. and Ryan, M. (eds.), The Post Graduate Foundation in Veterinarian Science of the University of Sydney, pp. 141. ISBN 0 646 38713 8.
2. Kinghorn, B.P. 2000, 'Nucleus breeding schemes', Chapter 12 in *Animal Breeding – Use of New Technologies*, Kinghorn, B.P., van der Werf, J.H.J. and Ryan, M. (eds.), The Post Graduate Foundation in Veterinarian Science of the University of Sydney, pp. 151. ISBN 0 646 38713 8.
3. Mortimer, R. 1999, 'Centre Plus, Breeding for the Customer of the 21<sup>st</sup> Century', Proceedings of the Association for the Advancement of Animal Breeding and Genetics, vol. 13, pp. 90-93.
4. van der Werf, J. 2000, 'Design of dairy breeding programs', Chapter 13 in *Animal Breeding – Use of New Technologies*, Kinghorn, B.P., van der Werf, J.H.J. and Ryan, M. (eds.), The Post Graduate Foundation in Veterinarian Science of the University of Sydney, pp. 159. ISBN 0 646 38713 8.

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## Activities



Available on WebCT

## Multi-Choice Questions



Submit answers via WebCT

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Available on WebCT

## Assignment Questions



Choose ONE question from ONE of the topics as your assignment. Short answer questions appear on WebCT. Submit your answer via WebCT

## Summary



Summary Slides are available on CD

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.

Animal populations have a pyramid structure which generally consists of 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.

## References

- Bichard, M. 1971, 'Dissemination of genetic improvement through a livestock industry', *Animal Production*, vol. 13, pp. 401-411.
- James, J.W. 1977, 'Open nucleus breeding schemes', *Animal Production*, vol. 24, pp. 287-305.
- Kinghorn, B.P., Meszaros S.A. and Vagg, R.D. 2002, 'Dynamic tactical decision systems for animal breeding', *Proceedings of the 7th World Congress on Genetics Applied to Livestock Production*, vol. 33, pp. 179-186. [CD-ROM communication n° 23-07. ISBN 2-7380-1052-0]
- Simm, G. 2000, *Genetic Improvement of Cattle and Sheep*. Farming Press, Miller Freeman, UK.

## 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 <sup>1</sup>	A record of the ancestry of an animal
Selection accuracy <sup>1</sup>	The correlation between the selection criterion (eg an index) and the breeding goal
Progeny testing <sup>1</sup>	A comparison of animals (and subsequent selection amongst them) based on the performance of their progeny

<sup>1</sup> Glossary terms taken from Simm (2000).