



Beef cattle

recording and selection



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For application to specific circumstances, professional advice should be sought.

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Introduction

This book is one of a series produced by the Queensland Beef Industry Institute, Beef Genetic Improvement Project (QBGIP). The QBGIP is an extension project of the Queensland Beef Industry Institute (QBII) aimed at encouraging beef producers to increase the use of objective measurements for making selections in their breeding programs.

Our aim has been to provide information on basic genetics and in particular, BREEDPLAN and GROUP BREEDPLAN technology as a selection tool. Included is a summary of results from several producer demonstration sites using bulls of various Estimated Breeding Values (EBVs) and the subsequent financial benefits. We have endeavoured to provide an overview of on-farm computer aided selection packages and the benefits of BREEDOBJECT as a single breeding value for the selection of animals. It includes a brief discussion of the application of molecular technology to the breeding and identification of animals.

This book is designed to assist all beef producers, both seedstock and commercial. We encourage producers to gain confidence and skills in buying bulls and using the technology to make continuing genetic progress in their herds, despite unfavourable seasonal conditions. Furthermore, we hope that this report becomes a valuable source of BREEDPLAN information for all in the beef industry.

The other books in this series are 'Bull Selection', 'Breeding for Profit' and 'Female Selection and Management in Beef Cattle'. 'Bull Selection' reviews all aspects of objective selection of bulls. 'Breeding For Profit' examines the various options open to beef producers in developing the breeding programs required to meet specific market options, within the limitations of their respective environments. 'Female Selection' provides producers with a practical guide to making the best selection decisions to improve the female component of their herd.

This publication is a companion to, and overlaps with, the 'BREEDPLAN user manual' produced by Agricultural Business Research Institute (ABRI) and Animal Genetics and Breeding Unit (AGBU) staff. A further related publication is 'Industry Validation of Current and New Traits for BREEDPLAN' (1996) Project Number UNE.030.

For further advice, contact the QBGIP State Coordinator Dr Mick Tierney (07) 33629563 Brisbane, your local QBII Beef Extension Officer, or Mr Richard Apps, Tropical Cattle Technology Services (07) 49276066.

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1

Basic genetic selection

This section provides an overview of the genetic make-up of animals, and how this forms the foundation of all selection practices. It will assist those who are searching for a reason behind the often difficult decisions made when relating live animal characteristics to the selection process. Genetic selection uses animal differences and progresses as a result of the ability to select the most desirable animals for use as parents of the next generation.

The individual cells of all animals are controlled by genes: strings of protein molecules joined in a distinctive patterns. Many genes are linked to form a chromosome. Chromosomes are found in pairs within the nucleus of each cell.

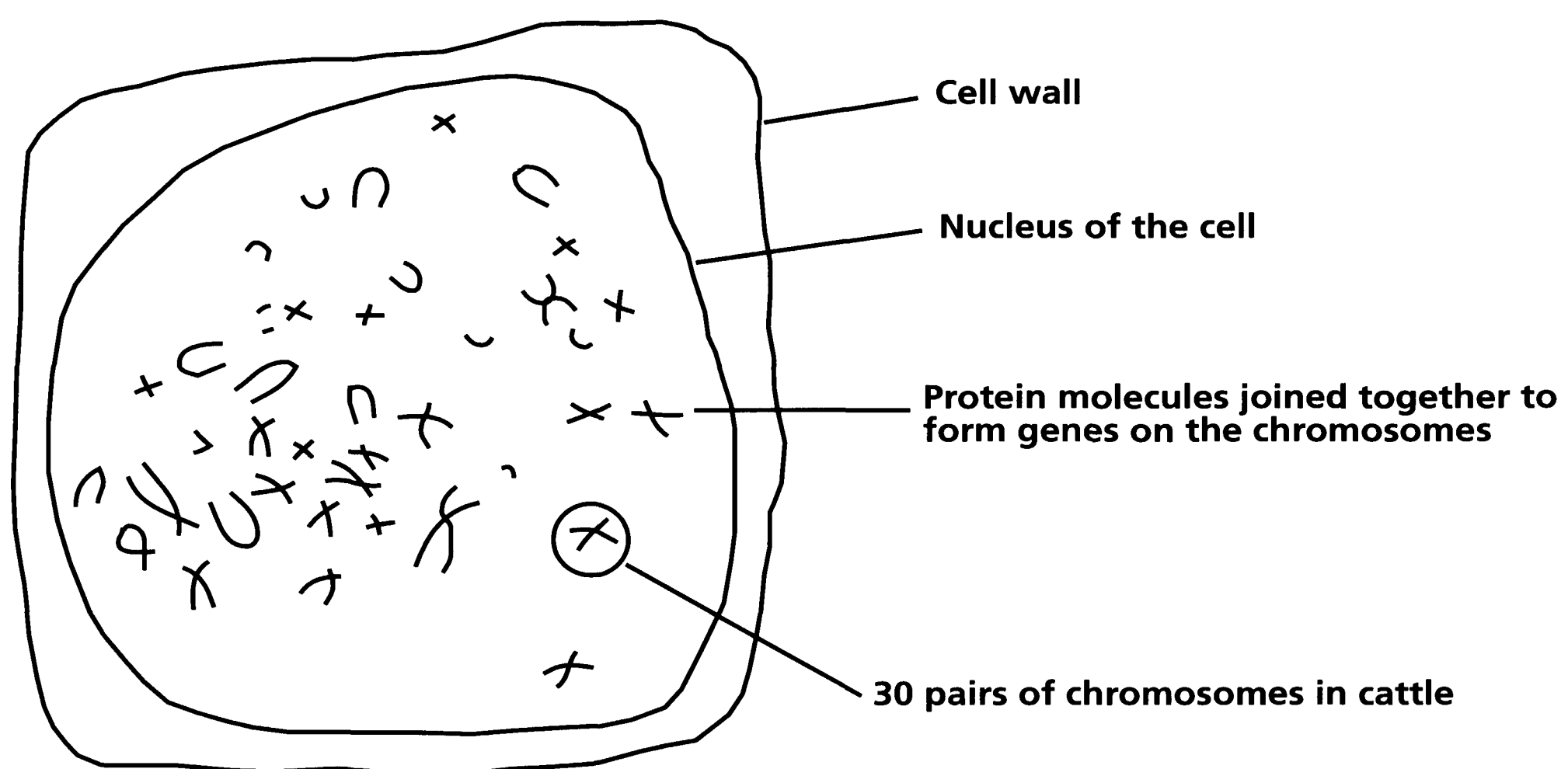


Figure 1. Individual cells of cattle with the full complement of genetic material have a nucleus containing 30 paired chromosomes

Different species have different numbers of chromosomes. Cattle have 30 pairs of chromosomes, as shown in Figure 1, while humans have only 23 pairs. Genetic characteristics are controlled by single pairs or many pairs of genes.

The appearance and performance of an animal is largely determined by its genes. 'It's all in the genes', refers to the animal's genetic make-up or genotype. The extent to which an animal achieves its genetic potential is determined by its environment—all the external factors that have influenced that animal from conception to the present.

Single gene action

Characteristics controlled by a single pair of genes include such traits as coat colour in Shorthorn cattle, and polledness. For single gene characteristics animals can be divided into discrete classes and are easy to identify and quantify. Figure 2a shows gene types for coat colour represented as either 'big r' (R) for red, or 'little r' (r) for white.

From this single pair of genes three colours are possible: red, represented by RR; white, represented by rr; and roan, as Rr. If one gene of a pair is dominant over the other, then the characteristic will always be expressed when one dominant gene is present, irrespective of the other gene. If red or white were dominant, then roan would not exist and there would only be two, not three colour types from the single pair of genes.

Figure 2b shows dominance for polledness, where PP and Pp are polled and pp (two recessive genes) is horned. If both parents are horned, the progeny breed true-to-type, but if both parents are polled and carry the recessive gene, they will breed 25% horned offspring.

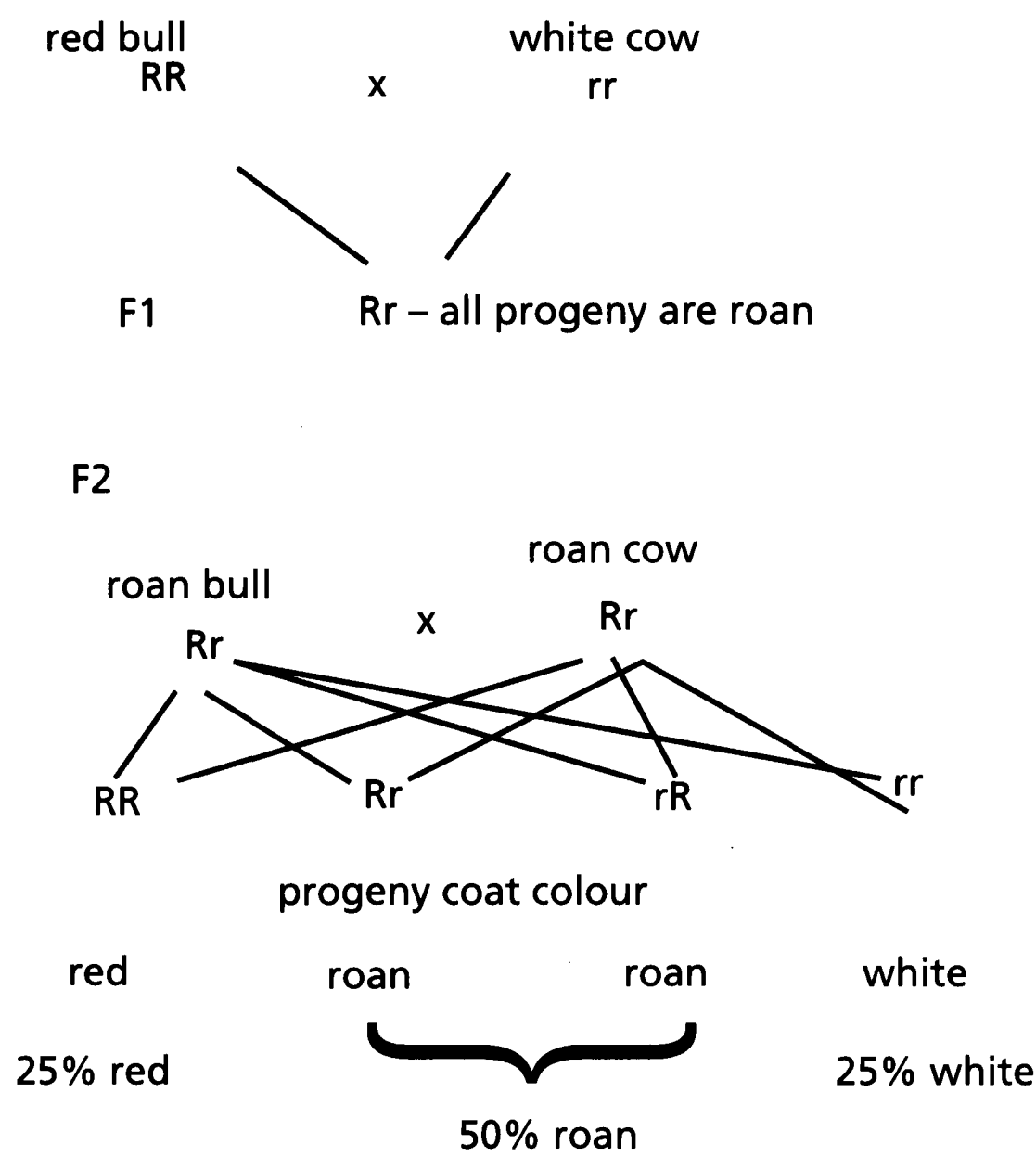


Figure 2a. Single gene action: no dominance.

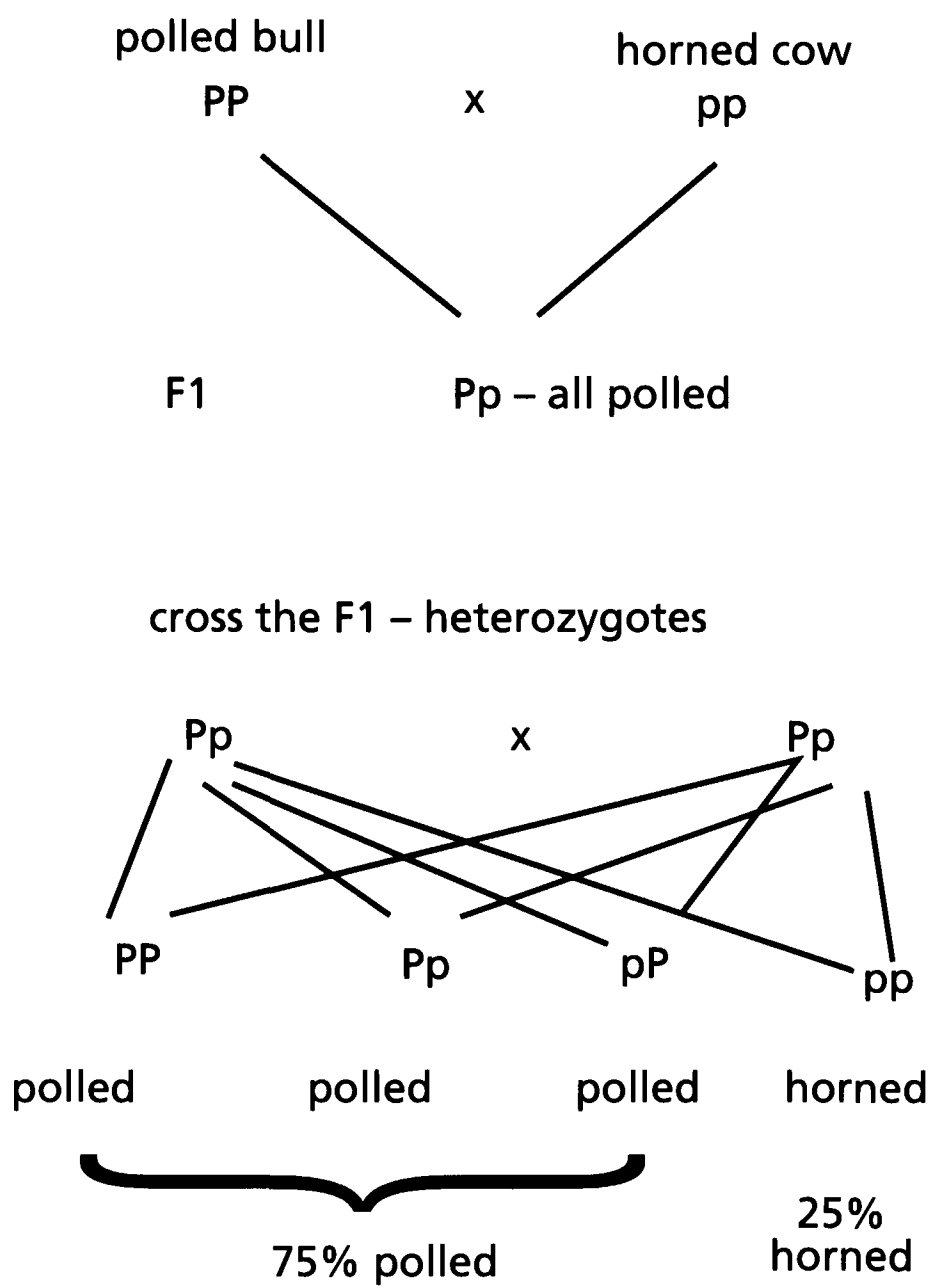


Figure 2b. Single gene action: dominance.

Population distribution

Various characteristics of a group of animals can be represented in a population distribution graph. The population distribution from a single gene pair (without either gene being dominant) is shown in Figure 3. The animal types; red, roan and white represent the possible gene combinations, and therefore the types.

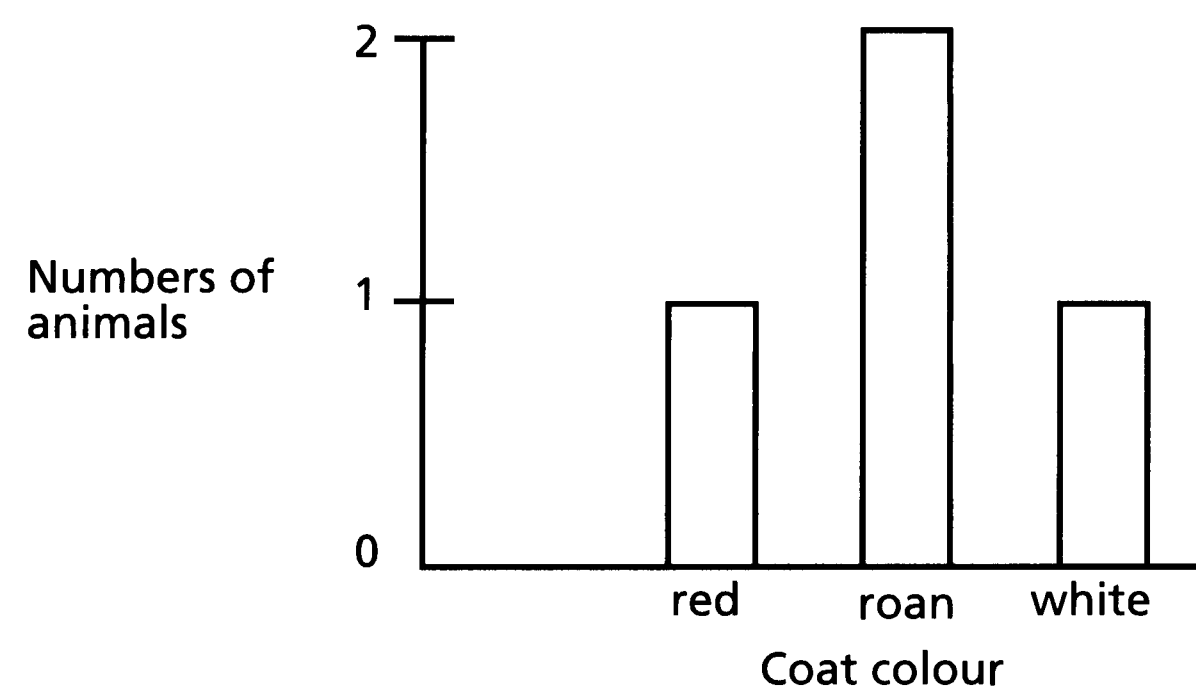


Figure 3. Population distribution from the second generation (F2) of a single pair of genes, using coat colour in shorthorn cattle.

Multiple gene pair interactions

As the number of gene pairs that influence a trait increases, so do the number of types, for example, two pairs of genes can produce five coat colours. The population distribution for a characteristic which is controlled by two gene pairs is shown in Figure 4. With five coat colour types, the colours red and white are still the minority of the group with true roans the largest of the population groups. There are now two more groups of intermediate numbers on each side of the roan colours, and of the intermediate population number.

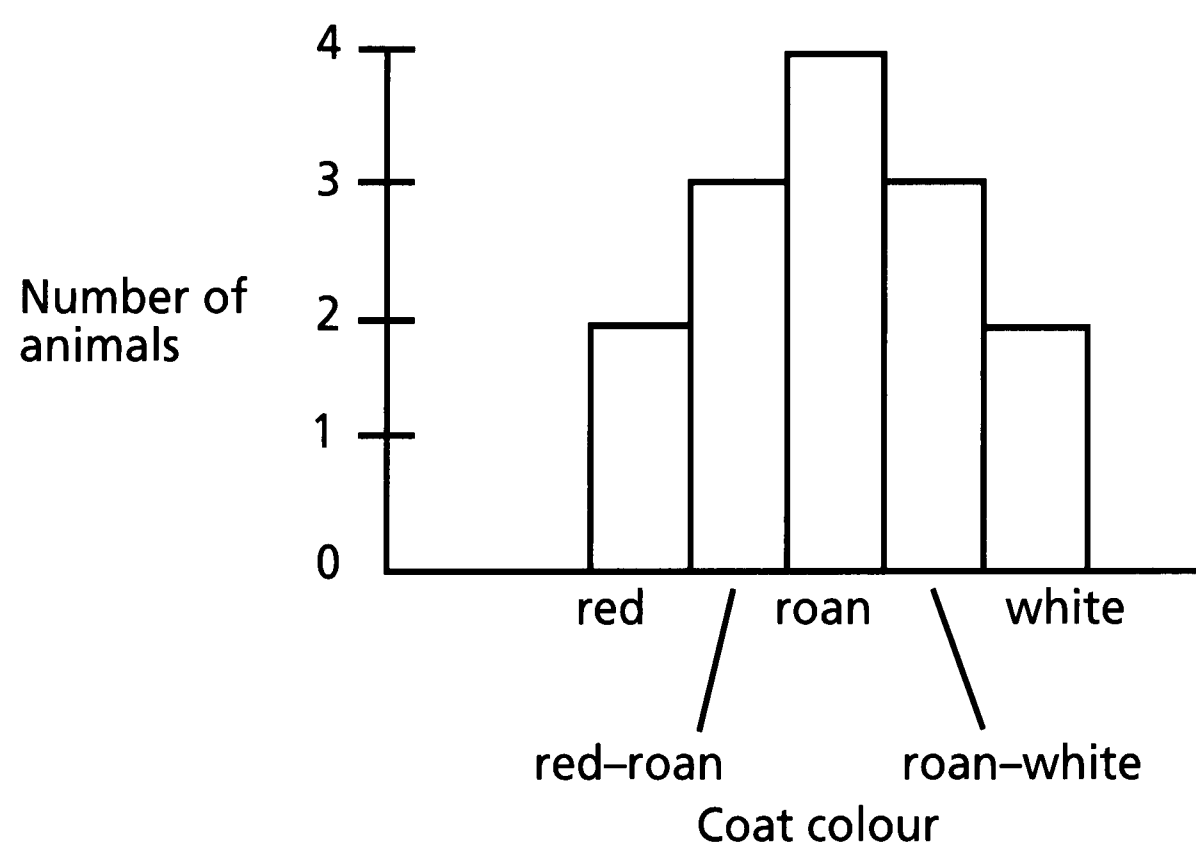


Figure 4. Population distribution for a two pair gene interaction.

As the number of gene pairs (n) increases then the number of types increases by a factor of twice the number of gene pairs plus one ($2n+1$). It becomes increasingly difficult to classify animals into discrete types. With 12 gene pairs affecting a trait, there would be 25 discrete classes for the trait.

Genotypic and phenotypic relationships

The phenotype (P) of an animal is the measured, or observed, performance of that animal. It is determined by the genotype (G) of the animal (the genes the animal carries) and the environment (E), the many external factors that the animal has been exposed to from conception to the time of measurement. These factors include feed, parasites, temperature and disease. This is usually expressed as $P = G + E$.

Environmental effect

In the case of production characteristics, the environment will interact with the character differences and lead to overlap of adjacent genetic classes. The combination of a large number of gene pairs and the effect of the environment will cause a merging of genetic types and the population begins to be represented as a 'continuous' distribution rather than a series of identifiable types. A continuous distribution of a characteristic is shown in Figure 5.

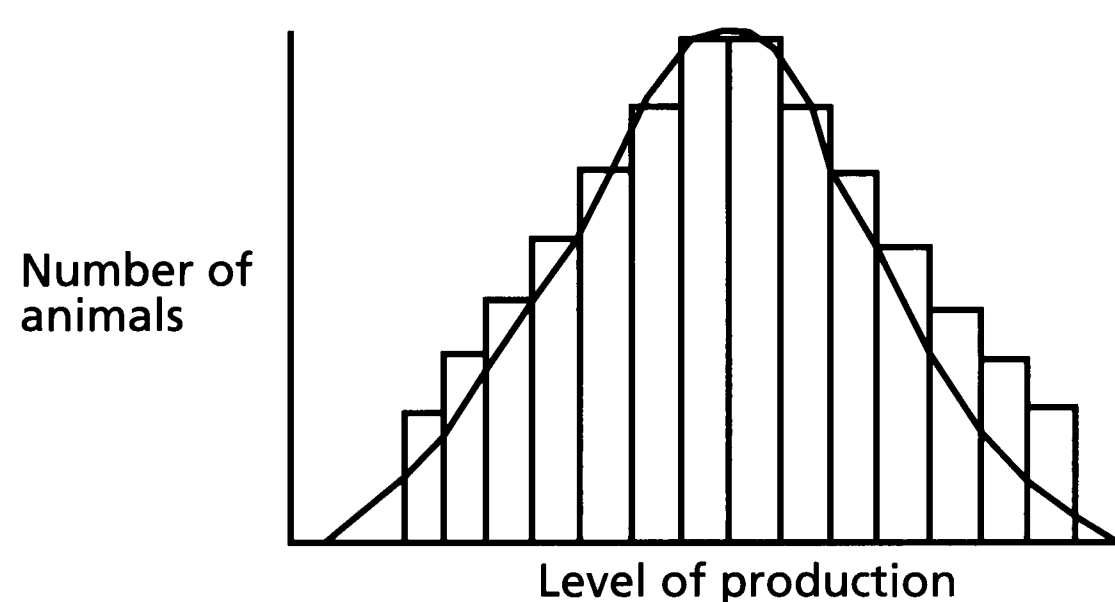


Figure 5. Production distribution from a large number of gene pairs.

This normal distribution, or bell curve, pattern is seen where characteristics are controlled by many pairs of genes. Virtually all the economically important characteristics for beef production are controlled by large numbers of gene pairs and are therefore expressed as normal distribution curves (Figure 6).

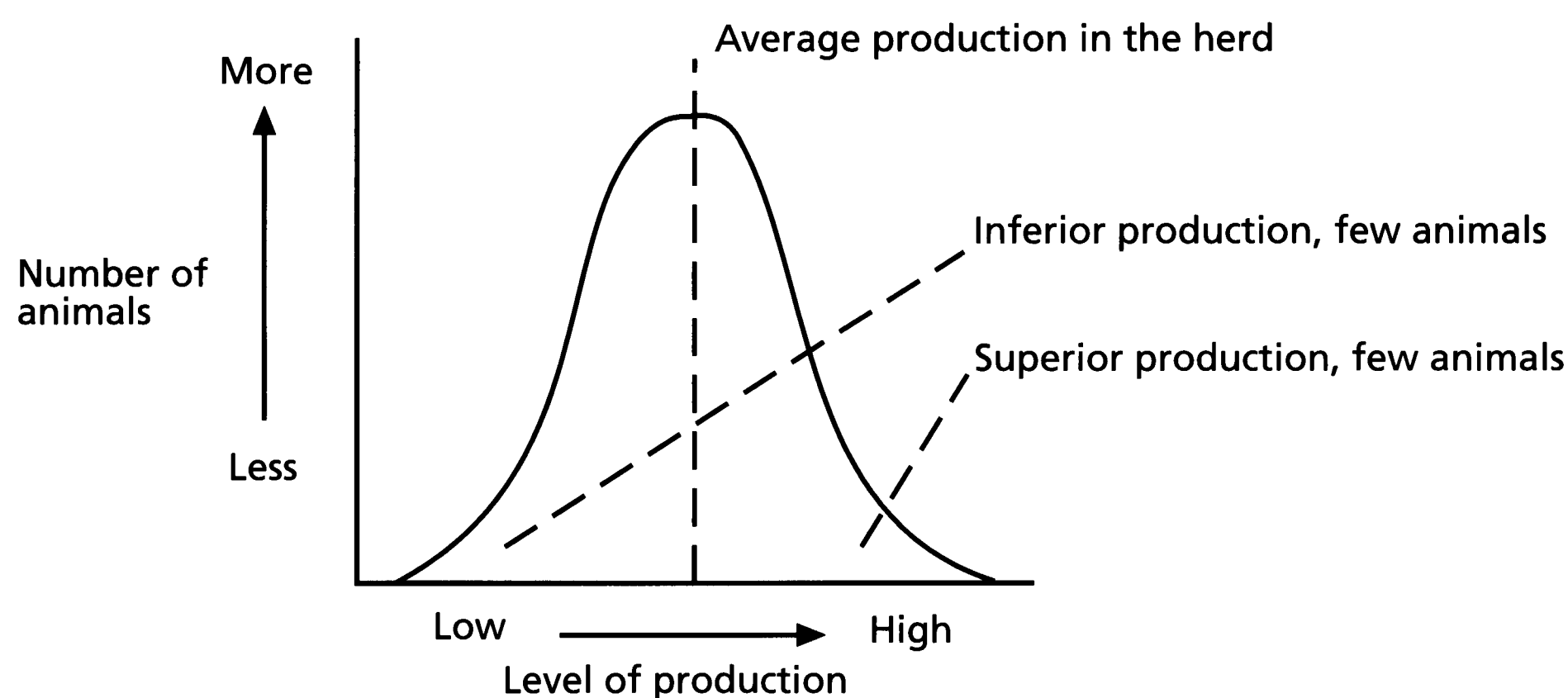


Figure 6. Normal distribution curve for multiple gene interactions.

The major features of the normal distribution curve are the average (or mean) production of the population and the variation within the population as shown by the spread or range in performance of individuals.

The average growth rate for a group of cattle on reasonable pasture, for example, may be 0.5 kg liveweight gain/day. The mean production will occur at the peak of the population distribution curve. A large proportion of the cattle will produce between 0.45 and 0.55 kg/day.

For the same group of cattle, the most productive animal may have a growth rate of 0.9 kg liveweight gain/day and the worst may have a growth rate of 0.1 kg/day. The number of animals that produce at these extremes will be very small in number.

The next generation

When faster-growing sires and dams are selectively mated, the progeny will, on average, produce better than the original population. The distribution will be similar to the original population, but the distribution curve will be based around a higher mean, or average. A comparison of the two generations can be seen in Figure 7.

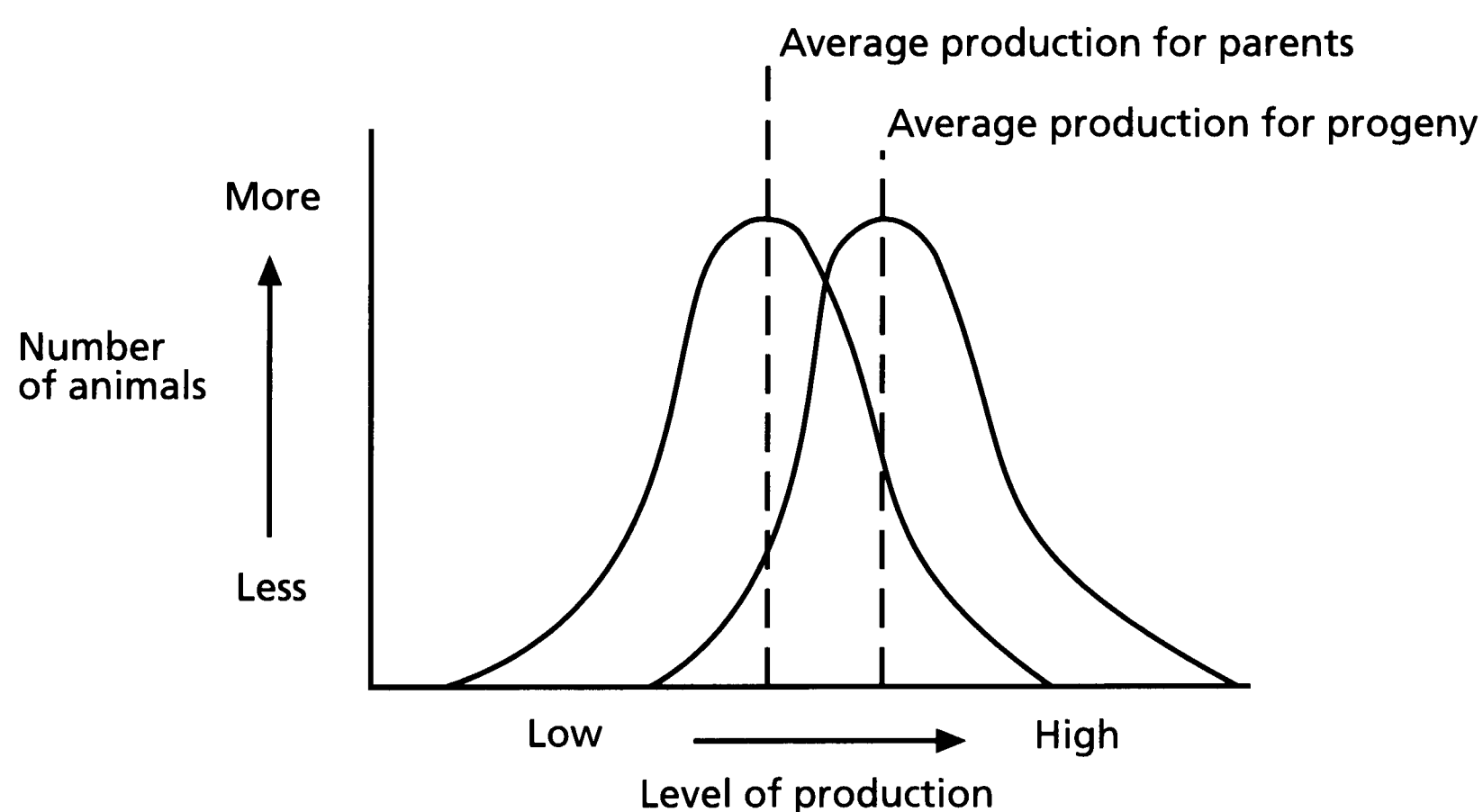


Figure 7. The production distribution curves for parents and progeny.

Correlated genes

Another factor to consider is that selection for one desirable trait may have 'side effects' on other economical traits. The most obvious example in cattle selection is when selecting for growth rates. High growth rate is desirable because it allows animals to reach target market weights as young as possible. However one of the 'side effects' of high growth is that high-growth animals often have large birth weights, causing an increased incidence of dystocia (difficult birth). This is an undesirable side effect caused by the genetic correlation between birth weight and later growth.

This effect occurs in many traits. If selection for an increase in one trait causes an increase in another trait, the traits are positively correlated. Where selection for an increase in one trait causes a decrease in another trait, they are negatively correlated. Positive and negative correlations can have desirable or undesirable effects. An example of a correlated trait with a desirable effect occurs in fertility, where selection of bulls with large scrotal circumferences will lead to the production of daughters of above average fertility. Selection for increased growth rate can lead to an undesirable increase in birth weight.

Correlations can range from +1.0 (perfectly correlated in the same direction) to 0.0 (no correlation) to -1.0 (perfectly correlated in the opposite direction).

Genetics of the sex of an animal

The sex of an animal is determined by a single chromosome that contains a multitude of genes. The chromosomes of males and females are the same except for one pair called the sex chromosomes. In mammals, the female sex chromosome pair is termed XX, while the male chromosome pair is XY. (In birds the XX combination gives males while the XY combination gives females).

When forming sex cells — ova for females and sperm for males — the chromosome pairs split in half so that each parent provides half the genetic material. This means that in mammals each egg or ova produced by the female will contain an X (or female) chromosome. However, male mammals, will produce two types of sperm — one containing the X (or female) chromosome and the other containing the Y (or male) chromosome.

Genetic defects

Genetic defects are characteristics that make an animal less than optimally suited for its intended role. For example, a steer with a genetic potential for low growth rate could be said to have a genetic defect for growth rate.

The more usual definition of genetic defects is traits which have a detrimental effect on an animal's survival and/or ability to grow and reproduce. Often these defects are caused by single recessive genes which must be carried in pairs before their effect is expressed, that is the animal must inherit a copy of the recessive gene from each of its parents. Such traits include umbilical hernia, which is sometimes seen in calves at birth and Pompes Disease in Brahman cattle. For these traits to be expressed the calf would have received one recessive gene for the trait from each of its parents. Lethal genes are genetic defects, which cause the death of an embryo, fetus or animal.

2

Principles of selection

Breeding programs are developed with a number of objectives in mind. The principal objectives should ensure that the cattle function efficiently under the environment in which they are grazed and that they profitably meet the required market specifications.

To do this, producers must clearly define the current and expected market requirements for which they produce cattle and set out their breeding objectives. This process implies that producers have a detailed knowledge of the performance of their existing turn-off animals, including the percentage of animals conforming to specification. These breeding objectives define the characteristics for selection in a breeding program, and the relative selection emphasis that should be given to each of these characteristics. Selection based on genetic differences alone is more effective in achieving long-term goals than mixing genetic differences with environmental influences.

The potential gains that can be made in a herd through selection are permanent and cumulative. More rapid progress is made in genetic selection when fewer traits are used for selection. Selection using traits that are positively related to one another will result in improvement in one as selection pressure is placed on the other, without diminishing the performance of the trait. For negatively correlated traits, selection for one trait will result in a decrease in performance of the other trait (see correlated genes page 5).

Measurement of performance is necessary to maximise genetic gain in the beef industry. It will not replace visual assessment for traits such as structural soundness, but is to be used in association with those assessments.

What traits should be included?

To be included in a genetic improvement program a trait must meet four basic criteria, it must be:

- economically important
- measurable
- reasonably heritable
- characterised by variability in the population.

Economic value

All traits used in selection must be economically important, that is, they must produce increased economic returns for the producer. In addition, in most instances breeders will be attempting to achieve improvement in more than one trait simultaneously. Additional traits included in a selection program usually decrease the rate of improvement in each individual trait. It is best to concentrate selection on fewer traits, each with high economic value.

Economic importance can mean different things to different producers. For the commercial beef producer, probably the most important traits economically; are growth rate, fertility, and carcase quality.

Measurable

Objective measurement of beef cattle performance traits, enables the producer to compare the traits irrespective of season, bias, year or environmental effects, and allows the calculation of estimates of genetic merit. Liveweight is easy to measure and was a logical first choice for most of the animal growth research involving genetic improvement programs.

Growth rate is easily measured and highly heritable. In the early development of the National Beef Recording Scheme (NBRS), evaluation was based on weight ratios that compared individual animals according to their growth rates or weights at particular ages. The first estimated genetic differences between animals were calculated for growth rate.

Relative to growth, fertility traits are more difficult to measure. Emphasis initially was on two relatively easily measured fertility traits: scrotal circumference in bulls and days-to-calving in cows. Since then, measurements of calving ease and gestation length have become available.

Some carcase attributes are now measurable and therefore included in the genetic analysis of carcase weight (Cwt), eye muscle area (EMA), rib and P8 rump fat, intramuscular fat percent (IMF%) and retail beef yield percent (RBY%). The measures of these attributes come from ultrasound scanning or abattoir carcasses.

Heritable

Heritability (h^2) is the proportion of the measured variation between animals attributable to genetic differences between them. The variation that is not genetic is due to numerous environmental factors, including nutrition, management and disease.

The higher the heritability of a trait, the greater the proportion of the parental genetic merit passed on to the offspring. Most of the growth traits in beef cattle have a heritability of between 30% and 50%. This means that of the measured differences in growth rate between animals in a group, 30–50% are due to genetic factors and 50–70% to non-genetic or environmental factors.

Carcase traits generally have heritabilities of between 30% and 55% for the combined direct and maternal components. The heritability of scrotal circumference is in the range 30–50%, while for serving capacity it appears to be 15–30%. Female fertility traits tend to have much lower heritabilities of between 5% and 20%. This means that fewer of the measured differences between animals for fertility are due to genetic differences, and so the rate of improvement in a genetic improvement program will be slower than for the other traits. Heritability estimates from trial groups, for some of the important traits of beef cattle are shown in Table 1.

Table 1. Heritability estimates for some traits in beef cattle in temperate and tropical environments.

Trait	Heritability description	Heritability% (BREEDPLAN)*	
		Temperate (AA)	Tropical (BR)
Reproduction			
conception	low	0–5	5–20
days-to-calving	low	0–10 (7)	0–10 (9)
calving ease (heifers)	low–medium	15–50	na
semen quality	low–medium	25–40	6–44
scrotal circumference (18 months)	medium–high	20–50 (39)	28–36 (40)
serving capacity (18 months)	low–high	15–60	na
maternal ability	medium	20–40	na
gestation length	medium	15–25 (21)	(21)
Conformation and growth			
body length	medium	25–45	na
chest girth	medium–high	25–55	na
wither height	medium–high	30–50	na
birthweight	medium	35–45 (39)	35–45 (46)
milk yield	medium	20–25 (10)	(4)
weaning weight	medium	20–30	3–50
200-day weight	medium	(18)	(28)
weight gain — birth to weaning	medium	25–30	16–40
yearling gain (pasture)	medium	30–45	20
400-day weight	medium	(25)	(37)
18 month weight (pasture)	medium–high	40–50	30
600-day weight	medium	(31)	(43)
mature cow weight	high	50–70 (41)	25–40 (39)
dry season gain	medium	na	17–30
wet season gain	low	na	18
Carcase			
carcase weight/day of age	medium	25–45 (36)	(36)
rib Fat (12/13th rib)	medium	(27)	(27)
P8 rump Fat	medium–high	29 (28)	18 (28)
intramuscular fat (IMF%)	medium–high	15 (22)	30 (22)
eye muscle area (EMA)	medium	20–25 (23)	(23)
dressing percent	medium–high	15	37
tenderness	high	4–25	16–30
retail beef yield (RBY%)	high	29 (36)	36 (36)
yield % carcase weight	high	49	52
Other traits			
cancer eye susceptibility	medium	20–40	na
eyelid pigmentation	high	45–60	na
temperament	medium–high	25–50	25–50
tick resistance	medium	na	20–42
worm resistance	medium	na	25–36
buffalo fly resistance	medium	na	20–30

* – BREEDPLAN heritability values for AA (Angus) and BR (Brahman).
na – (not available)
Sources: (a)Hammond, K. (ed.) (1981) (19XX), Selecting Beef Cattle for Maximum Production in the 80s, AGBU, UNE.
(b) Davis, G.P. (1993) Genetic Parameters for Tropical Beef Cattle for Northern Australia. *Aust. J. Agric. Res.*, **44**, pp. 170–198. (c) Robinson, DL., Ferguson, DM. & Skerritt, JW. (1998) Genetic Parameters for Beef Tenderness, Marbling and Yield. *Proc. 6th World Congress Genet. App. Livestock Prod.*

Variation in traits

With greater variation in a trait there is more scope for change by selection. Some traits vary much more than others and even if a trait has a low heritability, a large variation may mean that changes can be made. Most traits that are governed by more than one gene fit a normal distribution. A normal distribution for traits is a pattern of distribution for which the majority of animals are close to the mean (or average) while away from the mean there are fewer animals (Figure 8).

A trait with a large variation will have a lower, wider curve (more animals further from the mean), while a trait with small variation will have a higher, narrower curve (more animals close to the mean). If we select 10% of

animals in each case, then the distance from the mean will be greater for a trait with the larger variation. Distances from the mean for small and large variations (x_1 and x_2 respectively) are shown in Figure 8.

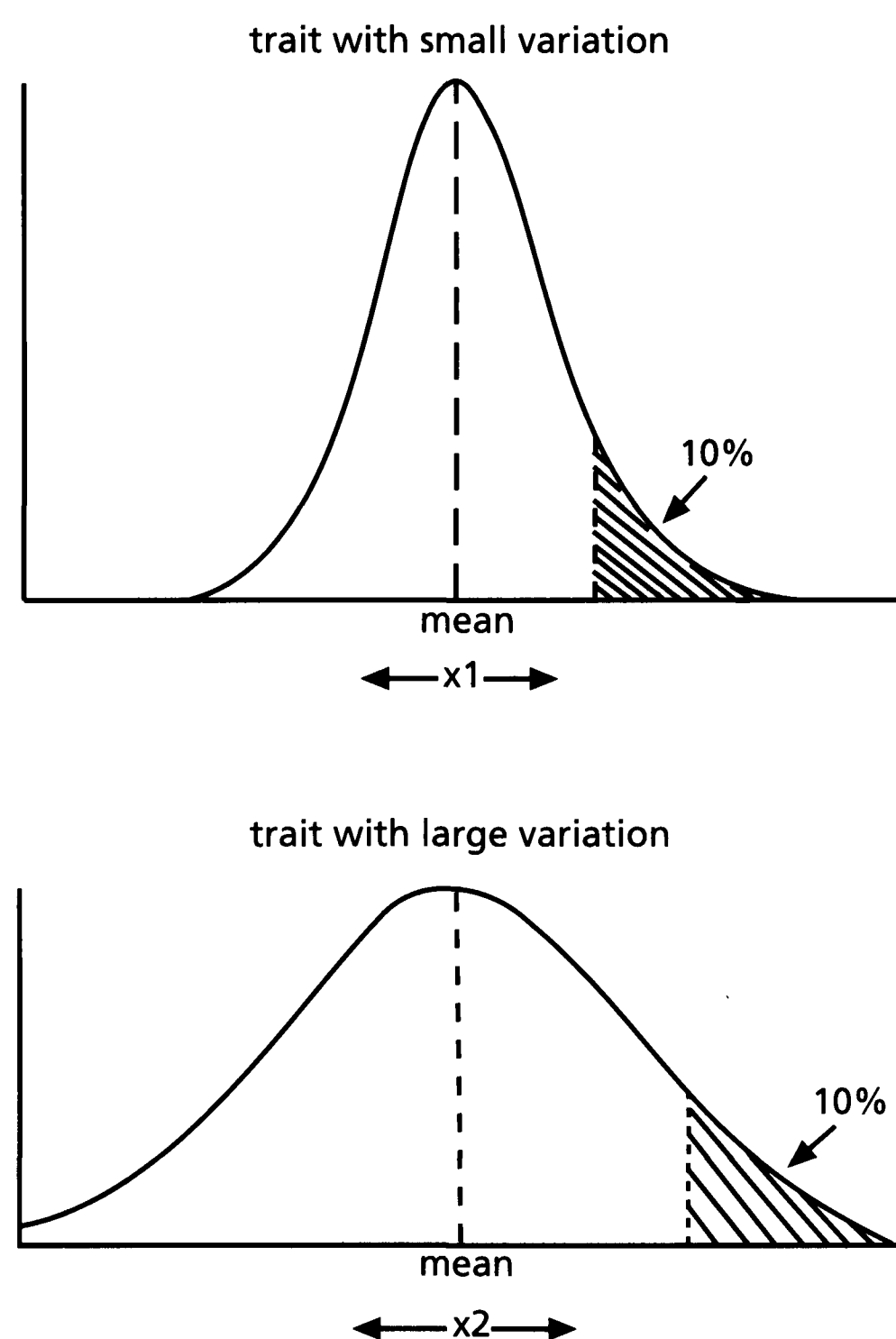


Figure 8. Normal distributions for traits with large and small variations.

Establishing breeding objectives

The first and most important step in planning a balanced breeding program is to establish a clear set of breeding objectives. Defining the breeding objectives of a beef enterprise requires a clear measure of the current performance of the herd for all beneficial traits and comparing this with the customer requirements or the chosen market. Steps providing a progressive approach toward meeting these objectives include:

- listing the traits of economic importance;
- listing the customer's requirements;
- listing future herd production targets — set realistic targets for important traits;
- listing the herd's current performance — objectively measure the herd's performance;
- listing breeding goals — traits requiring special emphasis;
- listing selection criteria — the means of achieving the above goals;
- prioritising the selection criteria — 'weighting' the relevant traits.

Influencing rate of change

The rate of change in an individual trait will be influenced by the heritability of the trait, the amount of variation present in the trait, the selection intensity, the generation interval and the level of inbreeding. It can be independent of the rate of change in other traits.

Heritability

As discussed above, the heritability of a trait is the proportion of the measured differences between animals that are due to genetic differences between them. This determines the extent to which the superiority of selected parents will be passed on to their progeny.

Intensity of selection

Intensity of selection is related to the proportion of animals selected from a group. If we select a large proportion of animals, as is normal when selecting replacement heifers, the advantage of the selected group over the mean of the group (usually referred to as the selection differential) will be small. By contrast, when selecting bulls using measured traits (Figure 8), we can generally select a smaller proportion of animals, with the advantage that the selected group will have greater average performance than the average of the total group. The proportion selected and hence the intensity of selection is affected by a number of factors relating to herd management, such as generation interval, variation in performance for a particular trait and the bull percentages used.

Generation interval

Generation interval is defined as the average age of the parents in a population at the time that their offspring are born. A short generation interval means that selected animals are mated in the herd sooner and so the rate of response to selection is faster. However, a compromise is needed, as a short generation interval also means that animals are mated at a younger average age, and hence the number of replacements needed each year is higher. Therefore, at shorter generation intervals, the selection intensity is lower than at longer generation intervals.

Inbreeding

Inbreeding is the mating of animals that are closely related. It generally has a deleterious effect on many production characteristics. This is particularly important if the level of inbreeding increases rapidly. If the rate of increase in inbreeding is slow, selection can be made to eliminate undesirable types and low producers. Inbreeding may be of particular significance in the formation of new breeds for which the original gene pool needs to be large enough to allow undesirable types to be culled. As a rule of thumb, avoid active inbreeding, that is, deliberate matings of sires to daughters, half sisters or dams. For herds where initial inbreeding is low and active inbreeding is avoided, the economic effects of inbreeding are likely to be small.

Linebreeding is the strategic use of inbreeding to improve traits found in one family line. While this may improve some traits, it may be detrimental to other traits. An 'inbred' animal in one herd may effectively be an 'outcross' if used in another.

3

Selection methods

Selection is the process of determining which animals will be used as parents in the herd to produce genetically superior progeny. As the beef industry places greater emphasis on producing cattle that meet specific market requirements, it is essential that selection be aimed at achieving this goal. Clearly defining the breeding objectives for a beef enterprise requires the producer to objectively describe the targeted markets, recognise the environmental constraints associated with the breeding property and objectively describe the performance of the existing herd sires and the performance of the animals currently turned off to the targeted markets. The manager can then identify sires by focussing on the traits needed to achieve this objective. The greater the number of traits used in selection, the more difficult and slower it is to meet the breeding goals in relation to all traits.

By selecting animals that are genetically superior for these traits, the herd will make permanent gains that accumulate from year to year. In measuring the performance of an animal for any trait, that performance, or phenotype, is a combination of its genetic potential and the non-genetic (environmental) factors affecting the animal. Only the genetic potential of an animal is passed on to the progeny; so selection should be based on trying to accurately identify the true genetic potential of the animals in the herd.

Visual selection

Selection in the beef industry has traditionally been based on visual appraisal. This has been satisfactory in the past and has resulted in some of the differences in performance that are currently seen both between and within breeds. The greater the heritability of a trait, the closer visual assessment approaches genetic assessment.

For some traits, such as colour or horns, visual selection is quite adequate. For other traits such as temperament and structural soundness, visual assessment is frequently the only evaluation method available. Visual assessment is most effective for traits that are easily assessed on an 'all or none' basis and are controlled by one, or a few, pairs of genes. However, for traits such as growth, carcass and fertility, selection based on objective measured assessment is far more accurate than visual selection.

Weight ratios

Weight ratios have been used successfully and are valuable if the herd is too small to effectively use the process and benefits of a more complex genetic analysis or would not fit the overall property management. Ratios compare animals of similar ages within the same management group and environment for a particular trait. If selection is based on ratios, progress is likely to be slow and variable because of the impossibility of selection across management groups, ages, years, etc. The animals are compared using 100% as the average and all animals are compared to the average and reported as greater than, equal to or less than 100% (i.e. individual animal performance is converted to a percentage, relative to the average performance of the group which equals 100%). The ratio is an index showing both the relative ranking of animals within a group and the magnitude of individual differences.

Weight ratios are a useful device for rapidly revealing the relative ranking of individuals within a group. The ratio is calculated by relating individual performance to the group average. For instance if a group’s average yearling weight was 300 kg and individual animals at the extremes of the population had yearling weights of 390 kg and 210 kg, the weight ratios would be calculated as demonstrated below.

weight	210 kg	300 kg	390 kg
calculation	(210 kg/ 300 kg) x 100%	(300 kg/ 300 kg) x 100%	(390 kg/ 300 kg) x 100%
ratio	70%	100%	130%

Average performers have ratios of 100% and ratios above or below this indicate above or below average performance. A ratio of 130% indicates that the animal is 30% above average.

Corrections and adjustments of records

For accurate weight ratios, individual records have to be adjusted for known environmental influences, such as age of dam, so that legitimate comparisons can be made between animals within a single management group. These adjustments cannot be achieved subjectively with eye appraisal. An example of correcting for various weights follows.

Standard 200-day weaning weight

Comparisons can be made only within groups of animals treated in the same way with narrow ranges in age, generally no greater than two months. Otherwise nutritional and other environmental differences will have an influence that cannot be accounted for in the comparison. Weights are adjusted to a standard age and ratios are then applied to these differences. Calves are weighed when the average age is about 200 days. Weaning may take place at this weighing or some time after it. The standard 200-day weight is calculated as follows:

Actual daily gain = $\frac{\text{Weaning weight} - \text{birth weight}^*}{\text{Age in days}}$

Standard 200-day weight = (Actual daily gain x 200) + birth weight*

*If birth weights are unavailable, a standard weight for particular cattle types (e.g. 32 kg) may be substituted.

Age of dam corrections

Older cows generally rear better calves than younger cows because of the better milk supply and mothering instincts they provide. Calves produced by older cows appear to be better than they are genetically, because of the more favourable maternal environment. To make comparisons between calves and the age of their dams, the calf performance has to be adjusted according to these maternal influences.

After adjusting to a standard 200-day weaning weight, these weights can be further adjusted for age-of-dam effects. These will vary across breeds and environments.

Adjusted 200-day weaning weight

Correcting the standard 200-day weight by the age of dam factor, produces the adjusted 200-day weight used to evaluate calf performance within same-sex groups. Formulae for making these adjustments are outlined below.

adjusted 200-day weight = standard 200-day weight x age of dam adjustment

average adjusted 200-day weight (av. adj. 200wt) = sum of all adjusted 200-day weight records within a management group/total number of animals within the group

A ratio is then calculated for each animal:

$$\text{ratio} = (\text{adjusted 200-day wt} / \text{av. adj. 200-day wt}) \times 100\%$$

Later weights

Age-of-dam effects have a declining influence in the post-weaning period. The strength and duration of this influence varies with breeds, the management practices imposed by the breeder and the environment, but generally appears minimal by 18 months of age. Successful selection for increased final weight is likely to be accompanied by some increase in birth weight and this may result in undesirable increases in the incidence of dystocia. If birth weights are known it is recommended that they be subtracted from the final weight before calculating final weight corrected for the animal's age. This effect will be greater at a younger age.

Weights can be adjusted to a standard age, 400 or 600 days for example. This is necessary because the animals in a herd will be at different ages at weighing.

To calculate the adjusted 400-day weight:

$$\text{adj. 400-day wt} = \frac{\text{adjusted 200-day wt} + (\text{actual wt} - \text{actual weaning wt}) \times 200}{\text{No days between weighings}}$$

To calculate the adjusted 600-day final weight:

$$\text{adj. 600-day wt} = \frac{\text{adjusted weaning wt} + (\text{actual final wt} - \text{actual weaning wt}) \times 400}{\text{No days between weighings}}$$

A less accurate but simpler calculation (which ignores birth weights, maternal influence and management groups) for 600-day weights is: (600-day weight/age in days) x 600

BREEDPLAN

Weight ratios can only allow accurate comparisons within groups of animals on a property under similar management and born within a relatively short period of time of each other. Analysis methods now exist to refine the measured performance assessment to accurately reflect the genetic potential of the animals across management groups and environmental differences, and to allow the incorporation of information from an animal's relatives. These methods have led to the development of BREEDPLAN and GROUP BREEDPLAN as selection tools in the beef industry.

BREEDPLAN is a world-class evaluation system produced by the ABRI. It estimates the genetic, or breeding value of an animal using a number of measurements made at various stages of the animal's life and the performance of its relatives. BREEDPLAN reports estimates of genetic merit as estimated breeding values (EBVs) for each trait.

EBVs are predictions of relative genetic merit, not measures of the observed differences between animals. There is no magic in BREEDPLAN. As breeders use it they become more interested in how it functions and their questions become more complex. The following section provides a description of how BREEDPLAN works and why the EBVs may not reflect the differences observed in the calves on a particular property.

BREEDPLAN predicts breeding values for animals based on the differences in performance among animals in a group. Animals in a group must have had equal opportunity to perform otherwise the predictions will be biased.

While EBVs are reported in the unit of original measurement, for example growth traits in kilograms (kg), scrotal size in centimetres (cm) and days-to-calving (days); the EBVs are relative to each other at a particular end point. The EBVs are calculated in relation to a genetic base for the herd, which is set from a particular year or range of years.

GROUP BREEDPLAN is simply a BREEDPLAN analysis which includes many herds of the one breed. GROUP BREEDPLAN allows across-herd genetic evaluation of cattle from herds which are linked genetically and have been recorded with BREEDPLAN. It utilises all relationships and valid progeny records in a group of herds while BREEDPLAN is restricted to within-herd records.

BREEDPLAN features

- BREEDPLAN uses all information on all known relatives in the herd since the first year of recording.
- BREEDPLAN adjusts for special matings (e.g. mating best bulls to best cows) to provide unbiased estimates of EBVs.
- BREEDPLAN adjusts for the previous selection at weaning when assessing later weights. For example, if half of one sire's and a quarter of another sire's progeny are castrated, or culled at weaning this is taken into account when these sires are ranked on later weights.
- BREEDPLAN pre-weaning (200-day weight) performance results are split into the effects of growth genes and milk genes. Since they both affect pre-weaning growth and are largely independent of each other, this feature is useful for producers vitally interested in younger age of turn off production systems.
- BREEDPLAN makes use of additional growth information. For example, 400-day weights are also used to help predict 600-day weight genetic merit more accurately and vice versa.
- BREEDPLAN makes valid comparisons possible between all animals in the herd across the years of recording. This means that the best of all potential breeding stock can be chosen for future breeding.
- BREEDPLAN provides an estimate of both genetic and environmental trends year by year for each recorded trait. Cattle producers can assess if the improvements in the herd (increased weaning weights each year, for example) are due to genetic advancement or simply to better feed.

BREEDPLAN separates GxE differences

A question frequently of concern to breeders is, 'How does a computer in Armidale know the differences between animals in different herds, paddocks, years and countries etc?' This question is commonly asked in relation to BREEDPLAN, particularly in the context of whether or not the ranking of bulls in GROUP BREEDPLAN in southern Australia will be the same in northern Australia.

Other questions for which answers remain incomplete, in relation to growth for example include: In the case of growth, are there different genes controlling growth in southern Australia to those that control growth in northern Australia? Alternatively, are there characters that affect the expression of growth in northern Australia that do not affect it in southern Australia? We do not yet have the complete answers to these questions.

Producers particularly concerned about this should select animals recorded in an environment similar to their own.

If future evidence shows that there are differences in the ranking of bulls in the north and south, this could easily be rectified by running separate GROUP BREEDPLAN analyses for each environment or by making adjustments for the different environments. In the meantime, its better to continue to run a single analysis for all environments as this allows more bulls to be evaluated with greater numbers of progeny and therefore with greater accuracy.

If bull buyers have doubts about the applicability of results from outside their region they should select their bull requirements from those bulls that have been reared and evaluated in a similar environment to their own and use a GROUP BREEDPLAN analysis.

These points provide the key to the power of BREEDPLAN. Valid comparisons can be made between all animals in a herd, not only those run together. BREEDPLAN continues to build up a picture of the genetic potential of each animal. It uses the genetic linkages between management groups in a herd, or across herds from one year to the next as more progeny become available and additional growth information on existing animals is recorded (for example, 400-day and 600-day weights). Breeders can observe the genetic progress that they are making. The following is a simplified version of how BREEDPLAN accounts for environmental differences between paddocks and years and GROUP BREEDPLAN accounts for differences between herds.

- HERD 1:** Progeny of **Sire A** have 600-day weight average of 580 kg
Progeny of **Sire B** have 600-day weight average of 590 kg
- HERD 2:** Progeny of **Sire A** have 600-day weight average of 620 kg
Progeny of **Sire C** have 600-day weight average of 610 kg

Therefore, within each herd the deviations from the average are:

Herd 1	Sire A	- 20 kg
Herd 1	Sire B	- 10 kg
Herd 2	Sire A	+ 20 kg
Herd 2	Sire C	+ 10 kg

The average deviation of **Sire A** over both herds is: (+20 kg) + (-20 kg) = zero.

If we assume that **Sire A** has been mated to cows of equivalent genetic merit in both herds, the deviations from the base should be the same in both herds. Thus, the difference in performance of the progeny of **Sire A** in the two herds is due to environmental effects.

Therefore, to bring the progeny of **Sire A** in **Herd 1** up to the overall average, we need to add 20 kg to account for the environment. The same environment has affected the progeny of **Sire B** in **Herd 1**, therefore 20 kg must also be added to the average deviation of **Sire B** in **Herd 1**. Similarly, 20 kg must be taken from the average deviations of the progeny of **Sire A** and **Sire C** in **Herd 2**.

The new deviations are:

Herd 1	Sire A	0
Herd 1	Sire B	+ 10 kg
Herd 2	Sire A	0
Herd 2	Sire C	- 10 kg

These are the deviations we would expect if all the progeny had been run in the one environment. The deviation would then be multiplied by the heritability to give the EBV value.

BREEDPLAN separates milk and growth

Consistent with the G x E discussion, a preliminary explanation is required to describe the mechanism used in separating these two traits.

In this example, two calves have the same adjusted 200-day weight of 300 kg compared to the group average of 260 kg — no information is available on previous performance of the sires or dams. If no other information is available, BREEDPLAN assumes that about half the difference in 200-day weight is due to milk production of the dam and half is due to inherent growth potential, i.e. of the 40 kg extra 200-day weight, 20 kg is attributed to superior growth and 20 kg is attributed to superior milking ability of the dam.

EBVs for 200-day weight and 200-day milk are calculated as follows for each calf (Estimated Breeding Values are discussed in detail on page 19):

EBV = weight due to growth x heritability; or 20 kg x 0.12 = +2.4 kg

EBV = weight due to milk x heritability; or 20 kg x 0.14 = +2.8 kg

The extra growth due to milk reflects the cow’s genetic potential for milk, so only half of the EBV is inherited by the calf. The cow’s EBV for milk is +2.8 kg and the calf’s EBV for milk is +1.4 kg

	200-day milk EBV (kg)	200-day growth EBV (kg)
Calf A	+1.4	+2.4
Calf B	+1.4	+2.4

At 400 days Calf A weighs 400 kg and Calf B weighs 380 kg compared to an average of 360 kg. This indicates that Calf A has higher inherent growth potential than Calf B. With this extra information BREEDPLAN reassesses the amount of extra weight at weaning allocated to growth and milk production of the dam. A likely reassessment of the EBVs would be:

	200-day milk EBV	200-day growth EBV	400-day EBV
Calf A	+0.2	+4	+12
Calf B	+2.6	+2	+6

Note that the superior growth of **Calf A** after weaning has indicated that a higher proportion of the extra weaning weight was due to growth and a lower proportion to milk production of the dam. Hence the change in the EBVs for 200-day milk and 200-day growth for **Calf A**. The reverse effect has occurred for **Calf B**. If milk EBVs for the dams from previous calvings were available, this would be used to refine the EBV.

BREEDPLAN allows for selective mating

BREEDPLAN can adjust for selective mating, such as mating some sires to selected females, provided there is some background information on the cows from previous calves. An example to demonstrate this follows:

In Group 1 a sire with an EBV of +40 kg for 200-day weight is joined to the top cows in the herd which have an average EBV of +20 kg for yearling weight. The average expected EBV for the progeny group is +30 kg.

If an animal weighed 20 kg more than the rest of the group, its EBV would be (weight x h²) or 20 kg x 0.3 = +6 kg plus the expected average for the group. The sire’s EBV would therefore be (20 kg x 0.3) + 30 = +36 kg.

In Group 2 the same sire was joined to a group of cows with average EBVs of 0 kg. The average expected EBV for the group of progeny is the mid-parent value of +20 kg. The EBV for an animal which was 20 kg heavier than the group would be $20 \text{ kg} \times 0.3$ plus the group mean of 20 kg, that is, $(20 \text{ kg} \times 0.3) + 20 = +26 \text{ kg}$.

Although each sire was 20 kg heavier than the average of his contemporary group, the animal bred from the superior group of females gets a higher EBV.

4

Estimated Breeding Values: EBVs

Within-herd BREEDPLAN reports refer to the genetic merit in one herd only. Each herd has a separate base from which its EBVs are calculated. Therefore, BREEDPLAN EBVs from one herd cannot be compared with those from other herds. Comparisons of animals in different herds of a breed can only be made if all the herds involved take part in the breed's GROUP BREEDPLAN analysis which requires adequate genetic linkage — preferably two or more sires used in two or more herds.

EBVs are reported as a positive or negative value from the herd base, in actual measurement units, for example kg for growth, cm for scrotal circumference and days for gestation length and days-to-calving.

If information is available, BREEDPLAN version 4.1 currently determines breeding values for the following traits.

Growth traits:

- birth weight (if recorded)
- growth to 200 days
- maternal or milk to 200 days
- 400-day weight (yearling)
- 600-day weight (final)
- mature cow weight.

Fertility traits:

- scrotal size or scrotal circumference
- days-to-calving
- gestation length (Group BREEDPLAN only)
- calving ease; direct and maternal (Group BREEDPLAN only).

Carcase traits:

- carcase weight (Cwt)
- eye muscle area (EMA)
- fat depth (RIB)
- fat depth (RUMP)
- retail beef yield percentage RBY%
- intramuscular fat percentage IMF%.

Fixed base

EBVs are expressed as positive or negative deviations from a base which is set to zero for a fixed time or period. This period is set to a year or between a range of years for the trait being analysed. Each analysis has an independent and unique fixed base. Previously, the base was fixed using the first 200 records for each trait recorded, that is, the average of the first 200 records is zero. All EBVs are calculated as deviations from this base and if genetic

progress is being made in the herd, the EBVs will change over time. The relative differences between EBVs are more important than the actual values which are dependent on where the base was set.

Crossbred EBVs

BREEDPLAN version 4.1 has been developed to produce EBVs using a calculation to include both direct and maternal components of heterosis (hybrid vigour) - the genetic benefit gained by crossing two or more breeds of animal. As the mating of two animals within the same breed (purebred animals) is assumed to have no heterosis, the crossbred animals are adjusted to the purebred equivalent (with the heterosis benefit removed) based on average heterosis estimates for that cross.

Growth EBVs

Birth weight EBV

Recording birth weight is an option but is not essential in BREEDPLAN. If recorded, the weight should ideally be taken immediately or at least within a few days of birth. Birth weight is associated with an animal's weight at later ages; in general, calves which are heavier at birth tend to be relatively heavier at later weighings. An EBV for birth weight is not available unless the calf's birth weight or that of a number of its relatives has been measured. Note that the EBV is for birth weight, not calving ease. If dystocia is a problem in the herd and excessive birth weight is contributing to the problem; the following will aid in better selection decisions:

- weigh calves at birth and use the EBVs for birth weight from sires and dams in your joining decisions;
- evaluate a sire's potential to produce calves of low birth weight by examining the EBV for this trait (the lower the EBV, the lighter the calves);
- consider direct and maternal calving ease and calving ease as an associated trait to minimise dystocia (see page 22).

200-day growth and 200-day milk EBVs

For growth related traits, BREEDPLAN, provides information about:

- 200-day growth — calf weighed between 81 and 300 days of age;
- 200-day milk — body weights measured between 81 and 300 days of age.

The 200-day weight (the measure of pre-weaning gain) is derived from four sources:

1. the calf's inherent growth potential;
2. the dam's merit for milk production, milk quality etc;
3. performance of all known relatives e.g. sire, dam, brothers and sisters;
4. the environment in which the calf was reared.

BREEDPLAN splits the 200-day growth and milk and calculates separate EBVs for the 'growth' and 'milk' genes (see also page 17). Note that the estimate in kilograms is not the yield of milk of the dam, but the growth weight in the calf due to milk and other factors in the dam. Thus, it is an indirect measure of the 'milk' of the dam expressed in kilograms of calf

weight at 200 days. It is the potential of that animal for increased milk production and should be used for the selection of replacements, when the contribution of the dam through her milk is important in the progeny for particular markets.

Each time a 200-day weight is recorded it adds information to the EBVs for growth and milk of all relatives of the particular calf, for example the EBV of its dam for growth and milk, the EBV of its sire for growth and the EBV of the maternal grandsire for milk and growth.

An EBV for milk of a calf is simply a calculation of the average of its sire and dam's EBVs for milk and is called a mid-parent value or average. It is not until females have progeny and males have daughters that have weaned calves, that the EBVs for milk will change from the average of their parents' EBVs.

The heritability of 200-day milk is about 8%, which means that genetic progress in this trait will be slow. Conversely, the heritability for 200-day growth is about 20%, which enables greater opportunities in improved growth following selection using this trait. EBVs for milk are smaller in magnitude than those for growth, even though both are expressed in the same units — kilograms of growth at 200 days. Because EBVs for milk are less heritable than growth EBVs, milk EBVs are more likely to fluctuate as new information is added relative to growth.

Using 200-day EBVs for growth and milk

Within-herd

The pre-weaning estimate of direct growth (200-day growth EBV) should be used in selection to increase weaner weights and greater positive milk genes for selection of replacement heifers to modify their milk production. Therefore, to improve the milking ability of a herd, consideration should also be given to the 200-day MILK EBV in sire selection.

The bull buyer

The vealer producer should give priority to the 200-day growth EBV, especially if using a terminal sire system. Similarly, consideration should be given to positive milk genes when using the bull to breed replacement heifers with superior maternal value. Conversely, when the nutritional contribution to production is limiting, then additional milk may be undesirable and may cause lower reproductive rates in the breeders. The calf's individual potential for 200-day growth may be more desirable than the provision of additional milk. The older an animal is when marketed; the less the benefit from extra milk from the dam, as seasonal variation has a greater effect than extra milk.

400-day yearling weight EBV

This EBV covers records of calves weighed between 301 and 500 days of age. A projected EBV for yearling weight is predicted using the 'average growth curve' for the animal type, until weaning weight is recorded. Very few animals actually grow to this 'average'. Once yearling weight is recorded it is used to update the yearling weight EBV. This EBV is most useful for selection in yearling production systems in which cattle are sold some months after weaning.

600-day final weight EBV

Final weight EBVs are computed for growth and recorded between 501 and 900 days of age. It is an estimation of an animal's ability to continue to grow to an older turnoff age.

Mature cow weight

Mature cow weight is defined as the cow's weight recorded at the same time as her calf is weaned. The mature cow weight EBVs are estimates of the genetic differences in weights between cows at weaning during their first four calves, starting at no later than five years of age. Mature cow weight EBVs for sires are based on weights recorded from their daughters (following weaning of their calves) plus the correlations that exist between cow weight and earlier growth performance. Mature cow weight EBV values can be used to influence the mature size of the females in the herd, and thus, the nutritional requirements of the herd. This can also affect female fertility in times of reduced or poor feed quality. Smaller mature cow weight is often associated with lower overall growth potential.

Reproduction EBVs

Scrotal size (circumference)

The scrotal size EBV is adjusted to 400 days. An animal with a greater scrotal size EBV will on average produce male progeny with relatively larger scrotal circumferences and daughters that reach puberty at an earlier age. The sons with larger scrotal size will on average have a greater daily and total sperm production, which can be associated with increased fertility. There is also a positive relationship between scrotal size and days-to-calving of the female progeny.

Days-to-calving

This EBV is an estimate of the genetic differences between cows for the period from when the bull is placed with the breeder females to calving. A female with a shorter days-to-calving EBV tends to be one that reaches puberty earlier as a heifer, returns to oestrus earlier after calving and conceives early in the joining period. A lower days-to-calving EBV value indicates greater opportunity for the cow to conceive within any one mating period. Cows that do not calve are given a 'penalty' figure. These EBV values for bulls are based on the performance of their daughters and female relatives.

Gestation length

Gestation length is available only when the conception date is known, that is, in the case of artificial insemination. Gestation length is one component of days-to-calving and indicates that an animal with a more negative EBV will have a shorter pregnancy, more time to go back in calf relative to females with a larger EBV, and potentially a smaller calf than had it been carried for a longer term.

Calving ease

This is a relative EBV indicating the degree of difficulty experienced by the dam at birth. The direct calving ease EBV is an indication of that animal's ability to calve easily. Its components include gestation length and birth weight. Calving ease maternal is the EBV associated with the daughter's ability to calve. A larger positive value for both direct and maternal calving ease EBVs, is a desirable selection option.

Carcase EBVs

Five carcase EBVs are available based on live animal ultrasound scan measurements taken by accredited scanners and actual carcase data. These are eye muscle area, rump fat depth, rib fat depth, IMF% and RBY%. Extra data collected at abattoir, (including hot carcase weight, marble score, meat colour, fat colour and meat pH) can be stored on the database. The EBVs are expressed in terms of a 300 kg dressed steer carcase weight and measured between 300 and 800 days of age with a preference for measuring at less than two years old. The 300 kg carcase weight was chosen as the standard as it is a reasonable compromise between domestic, Korean and Japanese market specifications. Further EBVs will be added if requested by industry and when the appropriate research has been completed.

Carcase weight

These EBVs are estimates of the genetic differences between animals' untrimmed hot carcase weight at 650 days of age and are based on abattoir carcase weight records.

Fat depth

This can be readily measured at the 12/13th rib site and the P8 rump site on a standard 300 kg carcase. The measure at the 12/13th rib has a genetic correlation of 0.9 with P8 fat and is utilised in the multi-trait model to refine the EBV for P8 fat. Fat depth has a negative relationship with RBY%.

The genetic variation in fat depth is relatively small but may still be very significant in a marketplace where the fat depth of turn-off animals is important through specification and weight, fat and \$ value/kg 'grid trading'. Most of these measurements are taken on yearling bulls and yearling heifers with an average fat depth of 5mm. The actual differences in heavy steers and heifers could be much greater than the EBVs indicate. Producers wishing to market leaner turn-off animals can select for lower fat values.

EMA

Eye muscle area is measured in cm² at the 12/13th rib on a standard 300 kg carcase. Eye muscle area and fat measurement are used in the prediction of RBY% from a live animal or carcase. The correlation with muscle score is higher for EMA adjusted for age only. Larger positive eye muscle area EBVs are associated with higher carcase yield and often with leaner carcasses.

Retail beef yield percent (RBY%)

The major reason for measuring either fat depth or eye muscle area is to predict the yield of meat from the live animal or carcase. Equations have been developed for the within-breed calculations of RBY%. These include the components of age, liveweight, fat depth and eye muscle area; fat depth having a greater influence than eye muscle area. RBY% can be used to increase the yield of retail cuts for carcasses, within the set weight ranges imposed by the processing industry for carcasses for specific markets.

IMF%

This is a measurement of the percentage of fat within the 'eye muscle' and similar to the AUSMEAT 'marbling score' reported at slaughter. The 'marbling score' is a subjective assessment of intramuscular fat. IMF% is based on the 300 kg standard carcase. Larger positive IMF% EBVs are important in the selection of sires producing progeny for the markets that

require increased amounts of marbling in the carcasses. This EBV is calculated from the ultrasound scanned live animal data, overseas genetic evaluation marbling expected progeny differences (EPDs) and abattoir carcass measures.

Future carcass EBVs There is increasing demand from consumers for improved carcass quality. Tenderness is the continuous focus of research primarily through the Meat Quality Cooperative Research Centre (Beef CRC), where there is potential development of an EBV for this trait.

Additional EBVs to be developed

A number of herds have been subject to research that may form the basis of future BREEDPLAN evaluations. New traits include the following.

Feed efficiency

Net feed intake EBVs can be used to predict the differences in feed consumption among progeny of different sires adjusted for differences in their growth performance. Net feed intake is sometimes referred to as residual feed intake (RFI), net feed efficiency (NFE) or net feed conversion efficiency (NFCE). A negative net feed intake EBV is preferred.

Other traits. A number of traits are being analysed according to the demand for them from the various breed societies. For new traits to be included and analysed they must be recorded and be available for analysis, in the same way as any other previously discussed traits, such as 400-day weight. Because any new trait is analysed by BREEDPLAN, there is no implication that it will meet the criteria of 'economic importance' or assist the commercial producer to meet market specifications and increase farm profitability. Depending on the breed society, traits available for analysis include the following.

Animal length records:

- heart girth
- hip height
- hip width
- hip to pin
- hip to shoulder
- hock to dewclaw
- shoulder to pin
- pelvic height and pelvic width.

Conformation records:

- leg score
- foot score
- sheath score
- navel thickness score
- prepuce score
- eye pigmentation score (left and right eyes)

- eye setting score
- teat size.

Temperament records:

- flight speed
- temperament score.

Parasite records:

- tick score.

The effect of correlated traits

Correlated traits are those that have an effect on other traits in either a positive or negative manner. A change in the value of one trait can influence the performance in another trait even though there may be no direct selection made by the breeder for the alternative trait.

Table 2 summarises the heritabilities and covariances for a tropical cattle breed. It is an indicator of some of the relationships BREEDPLAN uses when calculating EBVs. The correlations show the inter-relationships and potential effects of one measured trait on another. Correlations between traits play an important part in the calculation of EBVs for traits that are not actually measured on the animal itself at the time of calculating the EBVs. It is the correlated effects and the influence of an animal’s relatives that allow BREEDPLAN to calculate EBVs, for 600-day weight for example, when an animal’s weaning weight is submitted. However, actually measuring the animal gives a more accurate EBV and allows animals to be identified that ‘bend the growth curve’and makes them more suited to the breeding program.

Table 2. Correlations between traits for a tropical cattle breed shown as positive to negative, nil and low to high.

Trait	Gest Len	Birth wt	200 wt	400 wt	600 wt	Mat wt	Carc wt	Rib Fat	P8 Fat	EMA	RBV%	IMF%	SS	DC	200 Milk
Heritability	L	H	L	M	H	M	M	L	L	L	M	L	H	V	V
Gest Len		L	-V	-V	-V										
Birth wt			-V	M	M	L	L						V		
200 wt				H	H	M	M	-V	-V		-V	-V	V		
400 wt					H	M	H	-V	-V	V	-V		V	-V	
600 wt						H	H	-V	-V	V	-V		V	-V	
Mat wt							M						V	-V	
Hfr P8							V	H	H	V	-M	L			
Hfr Rib							V	H	H	V	-M	L			
Hfr EMA							M			H	L	V	V		
Hfr IMF								L	L		-L	H			
Bull P8							L	H	H		-L	L			
Bull Rib							V	H	H		-L	L			
Bull EMA							M	V	V	H	L	-V	V		
Bull IMF								V	V		-V	H			
Carc wt								-V	-V	V	-V	V	V		
Rib Fat									H		-L	L			
P8 Fat											-L	L			
EMA											M	-V			
RBV %												-L			
SS														-V	

Heritabilities: V = very low (<15%), L = low (<30%), M = medium (<40%), H = high (40%+)
Correlations: V = low (<0.2), L = low (<0.4), M - medium (<0.6), H = high (0.6+),
'-' indicates negative correlation, blank = 0
DC = days-to-calving, SS = scrotal size

Consider two animals that have been weighed at 400 days. Their EBVs after 400-day weights are analysed as:

	400-day weight (kg)	600-day weight (kg)
Animal A	+10	+15
Animal B	+10	+15

When the animals are weighed at 600 days, **Animal A** has an adjusted weight of 520 kg and **Animal B** an adjusted weight of 490 kg; the group average is 460 kg. With the addition of the 600-day weight information, BREEDPLAN recalculates the EBVs for 600-day and 400-day weights. The superior performance of **Animal A** after 600 days of age gives it a higher 600-day EBV and also causes a slight increase in its EBV for 400-day weight. The reverse effect occurs for **Animal B** because of the genetic correlation between 400-day and 600-day weights.

EBVs after 600-day weights are included in the analysis:

	400-day weight (kg)	600-day weight (kg)
Animal A	+12	+20
Animal B	+8	+10

The influence of an individual’s relatives on its EBVs

Consider two animals with the same 400-day adjusted weight of 380 kg compared to a group average of 350 kg. If there were no information on the genetic merit of the parents or other relatives, the animals would have the same EBV for yearling weight. However, if information already existed on the parents, such as their own performance or that of other progeny, the parents’ EBVs will influence those of their progeny. An example follows to illustrate this point.

The parents of **Animal D** have EBVs of +20 and +10 for 400-day weight and the parents of **Animal E** have EBVs of +4 and +2. In other words, the parents of **Animal D** are genetically superior to the parents of **Animal E**. Given this information the EBVs for yearling weight would be adjusted to something like:

Animal D	+12
Animal E	+8

Although these two animals had the same individual performance, the superior genetic background of **Animal D** suggests that his progeny would probably be slightly superior to the progeny of **Animal E**. This is indicated by the EBVs of **Animals D** and **E**. There is likely to have been some random environmental influence acting on their individual 400-day weights, e.g. gut fill or sickness.

The following is another example of how relatives influence the EBVs of an individual. **Animals F** and **G** (the same weight relative to the average of their management group), are by different sires, but the dam of **Animal F** had an EBV of +12 and the dam of **Animal G** had an EBV of +4. The impact of the progeny on the EBVs of their sires would be such that the EBV of the sire mated to the low EBV dam of **Animal G** would get a greater boost in EBV than the sire mated to the dam of **Animal F** with the higher EBV.

Accuracy and EBVs

There are benefits in knowing the reliability of EBV estimates and the likelihood they will change with the addition of more performance information about the animal or its relatives. Accuracy is expressed as a

percentage and is calculated from the number of performance records that are available for each trait on the animal itself, as well as its progeny and relations (Table 3). The higher the accuracy the greater the confidence we have that the EBV is an accurate estimate of the bull’s true breeding value, and the less chance of it changing as more information becomes available.

An accuracy of less than 55% indicates that no direct information is available about the animal (assuming $h^2 = 30\%$). Information may come from relatives rather than direct observation or from a correlated trait. An EBV with this level of accuracy should be considered a preliminary estimate only and could change considerably up or down as more substantial information becomes available.

Table 3. Accuracy values for a trait ($h^2 = 30\%$) when additional performance records are added to an EBV.

Performance measured on:	Accuracy (%)
individual	55
individual + 10 PHS + 2 MHS	61
individual + 20 PHS + 4 MHS	64
10 progeny	67
32 progeny	85
55 progeny	90
individual + 10 progeny	74
individual + 20 progeny	82
individual + 45 progeny	90

PHS: paternal half sibs or other calves by the same sire,
MHS: maternal half sibs or other calves by the same
sire.

Therefore, EBVs for yearling bulls without progeny recorded are calculated from the record of the bull and/or its relatives. The accuracy of these EBVs will be in the range of 40 to 75%, with the higher accuracy EBVs reflecting a greater depth of information from relatives. The EBVs of sires with recorded progeny are more accurate and more stable than the EBVs of bulls without progeny. Progeny information is a better estimate of a bull’s breeding value than the individual’s performance. These EBVs will range in accuracy from 75% to 99%, the higher accuracy EBVs reflect a greater number of progeny and/or the availability of daughters’ progeny records.

Examples of how accuracies affect EBVs

As more information becomes available about an animal, particularly once progeny information comes to hand, the EBV changes to reflect the more accurate estimate of the animal’s breeding value. An example of how EBVs can be expected to change is shown in Table 4. For example, an EBV for 400-day weight, with an accuracy of 75% will have a range of 10 kg, meaning that with the addition of more performance information it can be expected to change by up to ± 10 kg (one standard deviation), in either direction, about 65% of the time. If the EBV is +30, then it could fall within the range of +20 to +40 (30 ± 10 kg). If the accuracy was 99%, then the change to be expected from the addition of more records is much smaller and the expected EBV would be within the range of +28 to +32 (30 ± 2.0 kg).

Table 4. Likely changes in EBVs associated with a range of accuracies for a trait with $h^2 = 30\%$.

	Accuracy %											
EBV	20%	40%	55%	60%	65%	70%	75%	80%	85%	90%	95%	99%
birth wt (kg)	2.7	2.6	2.0	1.9	1.8	1.7	1.6	1.4	1.3	1.0	0.7	0.3
200-day wt (kg)	12.8	11.9	8.0	8.0	7.0	7.0	6.0	6.0	5.0	4.0	3.0	1.0
400-day wt (kg)	16.2	15.1	13.0	12.0	12.0	11.0	10.0	9.0	8.0	7.0	5.0	2.0
600-day wt (kg)	21.8	20.4	16.0	16.0	15.0	14.0	13.0	12.0	10.0	9.0	6.0	3.0
milk (kg)	9.0	8.4	6.0	6.0	5.0	5.0	5.0	4.0	4.0	3.0	2.0	1.0
mature cow wt (kg)			25.0	24.0	23.0	21.0	20.0	18.0	16.0	13.0	9.0	4.0
scrotal size (cm)			1.1	1.0	1.0	0.9	0.9	0.8	0.7	0.6	0.4	0.2
days-to-calving (d)			5.3	5.1	4.8	4.5	4.2	3.8	3.3	2.8	2.0	0.9
gestation length (d)			2.0	1.9	1.8	1.7	1.6	1.4	1.3	1.0	0.7	0.3
calving ease			4.7	4.5	4.2	4.0	3.7	3.3	2.7	2.4	1.7	0.8
carcase wt (kg)			12.0	11.0	11.0	10.0	9.0	9.0	7.0	6.0	4.0	2.0
rib and P8 fat (mm)	1.2	1.1	1.6	1.5	1.4	1.3	1.2	1.1	1.0	0.8	0.6	0.3
EMA (cm ²)	2.8	2.6	2.4	2.3	2.1	2.0	1.9	1.7	1.5	1.2	0.9	0.4
IMF%			0.7	0.6	0.6	0.6	0.5	0.5	0.4	0.4	0.3	0.1
RBY%			1.1	1.0	1.0	0.9	0.8	0.8	0.7	0.6	0.4	0.2

BREEDPLAN reports

BREEDPLAN will produce reports for:

- all sires who have had progeny recorded during the total recording period
- active cows
- calves (divided into a heifer report; a bull report and a steer report)
- the herd’s genetic and environmental trends.

Genetic trend report

This report shows the genetic progress for various traits from year to year. The tabular presentation shows the average performance in the herd by trait, year to year.

Environmental effects report

This report records averages for animals, with genetic effects removed, so that it is possible to assess the effect of management changes.

Reproduction reports

There are genetic differences in fertility between animals that are worth exploiting. Environmental factors such as disease, feeding and management are also important in determining the reproductive level of the herd. Performance records established within a herd can be used to select or cull animals. A number of reproduction reports are produced in BREEDPLAN. While these do not report genetic differences they are still useful indicators of herd performance.

Calving spread report

Calving spread is a good indicator of reproductive efficiency in herds with a controlled joining. Compact calving can lead to higher profits. The calving spread report shows the calving spread of the herd and the distribution of birth dates of progeny for individual sires.

The age at first calving report

Age at first calving (in years) for all recorded dams is provided as part of the dam's report. This is a measure of early reproduction by heifers and can aid decisions about which young cows to select.

Average calving interval

Average calving interval (in days) is included in the dam's report. By culling cows with poor average calving intervals (more than 365 days) the reproductive performance of the herd can be improved, as long as bull fertility and nutrition are satisfactory. The current status of cows is shown too. In the dam's report an asterisk (*) identifies all cows that calved within 12 months of the most recently recorded calf.

Future developments

Across breed EBVs

Analysis of GROUP BREEDPLAN EBVs across a number of breeds is possible with version 4.1. This comparison of EBVs across a number of breed societies will require approval from the participating breed societies and an appropriate reporting base and criteria for those EBVs. Current research by the Beef CRC will provide valuable across breed performance data of mutual interest to directly compare the performance of participating breeds. All individual animals must be directly linked to their 'pure breed' base.

5

GROUP BREEDPLAN

GROUP BREEDPLAN extends the BREEDPLAN concept across herds and uses a common base for all animals in a breed analysis. Sire summary lists for sires of individual breeds with sufficient progeny numbers is a major outcome of the GROUP BREEDPLAN analysis. Trait leader lists rank sires in EBV order for each trait and are not necessarily the best guide to the superior sire as they imply that the animals with the highest EBV are the ones that should be selected. A single breeding objective (see chapter 9) is most desirable as it combines the market requirements, herd performance and individual breeding values.

GROUP BREEDPLAN analysis requires all common sires in the participating herds to be identified (by breed society accepted identification) in order to establish the necessary links between animals and across herds.

Importation of genetic solutions

EBVs are referred to differently in different countries and have different bases according to the country of origin. One such genetic evaluation is the Expected Progeny Difference (EPD). GROUP BREEDPLAN analyses will use imported solutions such as EPD files. The effect of importing solutions from overseas evaluations will depend on the number of animals, the traits which have solutions and their accuracy. The relative ranking of overseas animals in the country of origin will be used as the starting point for the local analysis. As the imported genetics gains more performance information recorded in the local genetic analysis, GROUP BREEDPLAN will start to take more notice of local information.

Breeds in GROUP BREEDPLAN

In 1999, data for a GROUP BREEDPLAN analysis were available for the following thirteen breeds:

British breeds

Angus
Hereford and Poll Hereford
Murray Grey
Shorthorn
South Devon

European breeds

Charolais
Limousin
Simmental

Tropical breeds

Belmont Red
Brahman
Droughtmaster
Santa Gertrudis

An interest has been expressed in conducting a GROUP BREEDPLAN analysis for the Braford, Brangus and Wagyu breeds.

Use of logos in catalogues and advertisements

Two stand-alone logos are available for use in advertisements and catalogues. The standard BREEDPLAN logo shown below may be used by all herds actively recording in BREEDPLAN. The breed specific GROUP BREEDPLAN logo may be used only by those herds that have been included in a GROUP BREEDPLAN analysis for their breed and therefore have GROUP BREEDPLAN EBVs for their cattle. Examples of logos for BREEDPLAN, *Bos taurus* and a tropical breed follow.



6

Selecting animals using EBVs

A sound recognition of the environmental constraints under which the animal must perform is essential prior to the selection of any animal. The market requirements both in the short term and foreseeable future are the breeder's targets. An objective realisation of the performance of the existing herd is necessary to identify any obvious shortcomings in the ability of the herd to meet market requirements. Selection of animals using the various traits must recognise the change that is required for the existing herd to best meet market requirements. Single trait selection allows rapid progress in that trait, but may not be beneficial to the entire herd. Similarly, using multiple-trait selection may result in slower progress in any one trait but will result in more effective progress of the herd in the direction of the market requirements, if objective, planned breeding is considered. In this respect, many producers are unsure whether to use a highly positive EBV or on occasion use an animal with a negative value for a trait/s in their herd.

Valuing bulls in selection

A producer once said, 'Buying a bull with the aid of EBVs can be like picking a bull after having checked out all his progeny and relatives'. The EBV can be used to estimate the relative prices that could be paid for bulls in a sale. For any particular trait, the performance of the progeny of two bulls under comparison will be half the difference in the EBVs of the bulls. This is because progeny only receive half their genes from each parent, and so only half the breeding value of each parent is passed on to the progeny. It must be stressed that this expected difference in progeny refers to the average difference expected over a large number of animals and will not apply exactly to each animal. In addition, bulls influence many more progeny than any female in the herd and therefore have a greater effect on the future performance of the females in the herd.

In this simplified example two bulls are compared which have individual 400-day growth EBVs of +40 and +16, and are to be used for four years in a herd of 50 females with a weaning rate of 80%. The difference in the 400-day growth performance of the progeny would be expected to be 20 ($40/2$) less 8 ($16/2$) which gives 12 kg at 400 days. Assuming that they have similar fertility, they will produce 160 progeny each, resulting in 1920 kg of extra liveweight from the higher EBV bull. Using a liveweight value of \$1.10/kg for the progeny at 400 days of age, the extra value of the higher EBV bull would be \$2304. This is based on the value of slaughter progeny alone and does not consider the value of improvement in the genetic merit of the breeder herd.

Selecting bulls to meet particular needs

Undue emphasis on any one trait (such as 600-day weight) is not without potential detriment to the overall performance of the herd. A preferable option is to use BREEDOBJECT to collectively assess the value of a number of traits. Currently BREEDPLAN provides EBVs for five growth traits. The growth traits of interest to northern cattle breeders are 200-day milk, 200-, 400- and 600-day growth. EBVs from BREEDPLAN can be used to select or buy bulls to improve different production systems. For example, growth figures for five bulls are shown in Table 5: Which sires would you choose?

Table 5 . EBVs for several growth traits for five bulls.

Sire	Birth weight	200-day milk	200-day growth	Yearling weight	Final weight
1	-1	+5	+10	+30	+45
2	+2	+2	+14	+25	+28
3	+5	-8	+16	+40	+50
4	+2	+10	+10	+25	+30
5	+1	0	+10	+28	+40

Buyer 1 has a herd of Brahman crossbred cows with no calving problems. The producer wants a sire to produce fast-growing weaners for sale and does not keep heifers. The most likely choice would be *Sire 3*.

Buyer 2 primarily sells vealers and does not retain any heifers, choosing to buy in replacements. The breeder places most emphasis on EBVs for weaning, while trying to avoid large birth weights. The most likely choice is *Sire 2*.

Buyer 3 sells vealers but also breeds his own replacement heifers. The breeder thinks that increasing the level of milk production in the herd would be profitable. *Sire 4* is the most likely choice because of its emphasis on milk and early growth rate.

Buyer 4 wants to increase yearling and final weights, avoid calving difficulty and slightly increase milk production. The main product is steers and the breeder retains replacement heifers. The most likely choice would be *Sire 1*.

Buyer 5 is straightbred animals in a harsh environment where cows with high EBVs for milk are slower to rebreed. The breeder wants to maintain the current levels of birth weight and milk production while increasing growth rate in the cattle. The most likely choice would be *Sire 5*.

The five buyers above choose five different bulls to match their situation. Different types of animals are needed to fit the various performance levels of existing herds and suit the range of market requirements in the beef industry.

Selecting females

Female selection can be based on the EBV’s for 200-day milk, 200-, 400- and 600-day growth, days-to-calving, calving ease (maternal) as well as the information reported for age of first calving and inter-calving interval. The mature cow weight EBV will assist in monitoring the mature size of the breeding cows.

Negative EBVs

Under certain circumstances negative EBVs, for example, for milk, birth weight, and gestation length in a harsh environment, may be desirable.

If dystocia is a problem in a breed or herd, consideration could be given to purchasing bulls with negative or low-positive EBVs for birth weight. This would tend to reduce or maintain current birth weights. Low-positive to negative gestation length EBVs are also alternatives in selection that overcome dystocia and are desirable. However, care should be taken to ensure that birth weights are not reduced to an extent where subsequent growth rate is decreased or calf survival threatened. Similarly, bullock producers might not be concerned if EBVs for 200-day milk were not high, provided the EBV for final weight was high.

7

Performance recording — using BREEDPLAN

Producing EBVs that are close to the true breeding value of the animal in as short a period as possible, should be the aim of all BREEDPLAN users. Inadequate attention to detail and poor management practices can result in inaccuracies. Conversely, good breeding practices enable quick identification of superior animals and the ability to rapidly progress the herd toward the market specifications chosen. BREEDPLAN can be readily implemented within your herd to add the improved benefits of selection for traits independent of environmental effects.

BREEDPLAN requirements

Identification

A method of permanent and unique individual identification (ID) is required for all recorded animals.

Herd Size

There is no restriction on the number of animals in a herd but if it has fewer than 30 cows, the progeny should be born as close together as possible to get effective comparisons. Using GROUP BREEDPLAN sires will provide a more accurate basis for evaluations.

Breed description

To allow the BREEDPLAN analysis to correctly allow for the effects of heterosis, it is essential that the breed description of all animals in the herd is accurately reported.

Mating Groups

Single-sire joined herds or those using Artificial Insemination (A.I.) have an advantage if both parents of all calves recorded are known and identified. The value of BREEDPLAN for multiple-sire joining herds is substantially reduced. Progeny of multiple-sire matings can be DNA parentage tested to effectively provide the benefits of single-sire mating. If this is not possible, all sires in multiple-sire groups should have similar EBVs.

Recording a herd on BREEDPLAN

The minimum requirements for recording a herd on BREEDPLAN are to:

- have single-sire mating or multiple-sire matings with either progeny being DNA fingerprinted, or groups of sires with similar EBVs;
- have a unique and permanent identification for each animal;
- record birth dates;
- mother-up;
- weigh calves at weaning and on at least one other occasion prior to 600 days of age.

There is also provision to record a birth weight and one or more measures for:

- 200-day weaning weight
- 400-day yearling weights
- 600-day final weights
- scrotal size at 400 days.

In addition breeders can record:

- dates that the bull is placed in the herd and subsequently removed
- calving ease
- artificial insemination date
- mature cow weight when weaning the calf at approximately 200 days
- carcase traits.

Existing performance recorders are already using these processes and all pedigree breeders are using some of them for breed registration. More than three post-birth weights will incur extra charges upon analysis.

Birth weight measurement

EBVs for birth weight will only be estimated if weights are supplied by the breeder. If collecting birth weights is too difficult or a breeder considers that birth weight information is not important, it is not necessary to record it. However, in breeds where difficult births are regarded as a problem, breeders should consider recording birth weights, so that more complete information can be supplied to potential purchasers.

Accuracy of birth dates

Birth dates are like all other information in BREEDPLAN; the more accurate the better. Even if births can only be recorded once each week, this will be sufficiently accurate to correct the subsequent weights back to a common age and to divide the herd according to birth date periods for analysis.

Management groups in BREEDPLAN

If some animals have been treated differently, eg. by having different pasture quality or worm treatments, then that fact must be identified. If this is not done, environmental differences will be incorrectly attributed to genetic differences. Thus, if there is any suggestion that some animals have been treated differently in any way, they should be recorded as separate management groups.

Examples for which animals should be recorded in separate management groups include:

- sick calf or calves as compared to healthy calves;
- grain fed calves as compared to paddock calves;
- calves reared in a 'tough' paddock as compared to those in 'good' paddocks;
- calves given growth promotants as compared to calves not given growth promotants;

- pregnant heifers as compared to non-pregnant heifers;
- different stages of pregnancy for heifers (weighing should occur before joining and definitely before two months of pregnancy);
- spayed heifers as compared to non-spayed heifers.

There are also a number of management groups which are automatically applied in the BREEDPLAN analysis. These cover such things as herd, year of birth, sex, breed, number in birth, birth status, birth date periods and weigh date. As many animals as possible should be weighed on the same day or at least under the same conditions of time off feed.

While all weights are adjusted to a standard age (200, 400 or 600 days), only calves born within 45 days of each other are compared in the analysis of the 200-day weaning trait. This 45 day age-slicing within the analysis does not carry through to the later weights. Hence, calves separated for comparison at 200 days (45 day slice) may be directly compared at 400 days or 600 days where the age-slicing is extended to 60 days.

Correct recording of management groups is one of the cornerstones of BREEDPLAN. To correctly identify genetic differences between animals, it is essential that comparisons are only made between groups of animals kept under identical management conditions. When joining BREEDPLAN, breeders are strongly advised to discuss their management group structure with their local QBGIP team member or ABRI staff.

Inaccurate recording affects EBVs

The accuracy of EBVs depends very much on the accuracy of the data supplied. However, because EBVs are determined from many measurements and the comparison of that animal's measurement with the group average, the heritability of that trait and correlated traits, inaccuracies in recording will have less effect under BREEDPLAN than under other evaluation systems. An animal's EBV depends not only on its own measurements, but also on information from its parents, progeny and other relatives. Thus, incorrect information on one animal will be partially corrected by other information in the system. The analysis also has acceptable range 'checks' within the analysis, and any large deviations will be 'flagged' and identified for subsequent detailed checking by the owner.

The same applies to deliberate attempts to put incorrect information into the system with the intention of gaining commercial advantages.

Including a herd in GROUP BREEDPLAN

Herds must be actively enrolled in BREEDPLAN, usually through the relevant breed society and will preferably have at least two or three years of calving records. The herd will need to have adequate linkage with other herds. As a rule of thumb each herd should try to record a total of about 30 calves by one or more link sires to be linked to other herds. A link sire is a sire whose progeny have been recorded in two or more herds taking part in the GROUP BREEDPLAN analysis.

To achieve a well structured breeding program, the calves from link sires should be directly compared with calves from other sires used in the herd. Ideally two link sires will be used to produce a minimum of 15 calves each. This may be achieved in either one year or, for small herds, over more than one year or calving season. Some linkage may already exist in a herd if sires

have been used from other herds that are already in a GROUP BREEDPLAN analysis for that breed. The use of link sires enables an estimation of the environmental differences between years, paddocks, management groups and herds.

Benefits and costs

For breeders of registered or commercial cattle, performance recording will contribute to future returns. Current costs for a herd of 200 cows are equivalent to approximately the value of one steer per year.

The information base for the herd will grow each year as more information is added, and will also expand as BREEDPLAN is enhanced to include other ranking and measures.

In addition to the benefits of improved husbandry that result from keeping and using accurate records, case studies show that commercial cattle producers have increased the average annual yearling weight of surplus stock by 3–5 kg/yr by using an effective performance-recording and selection program. This means that by the tenth year of this program, surplus commercial cattle could be 50 kg heavier and bring approximately \$40–50 per head extra.

BREEDPLAN costs: March 1999

Most BREEDPLAN costs are now administered through the respective breed societies using their independent approach to the integrated pedigree system. There may therefore be some variation in the individual costs. The following serve only as an indication of the relative costs:

	\$
Initial enrolment	100.00
Annual membership renewal	100.00
Processing costs (birth wt plus three post-birth wts recorded) per calf	4.20
Processing past records (calves born prior to current calf crop) per calf	2.10
Extra weights (after 3 post-birth wt) per weight	1.10
Scan data/calf/observation date (2 fats, EMA and IMF%)	1.30
Mature cow weights/cow/observation date	0.50
EBVs copied to diskette	15.00
Additional copies of the BREEDPLAN report	25.00
Processing herd ancestry report (within-herd pedigree relationships)	60.00–150.00

There is a \$0.20 discount for data supplied electronically (on diskette or by email) and free of errors. Processing costs cover three sets of data submitted, and three BREEDPLAN runs. Additional runs will cost \$25.00 plus 60 cents per calf for which new data has been submitted. Past records refer to old performance records which may not have been recorded with BREEDPLAN but which are to be added to the herd file. Note: No charge is made for processing empty cows or cows whose calf died at or shortly after birth.

8

Practical application of EBVs

A number of beef producers are confident in the value of BREEDPLAN as their selection tool. Other producers would like evidence of achievable gains and the benefits of EBVs in increasing the profitability of a beef enterprise. Using BREEDPLAN, any profit increase obtained in one generation is passed on to the next generation, so that the gains and associated profits are cumulative. By contrast, when feeding a supplement to cattle, or when using a hormonal growth promotant in order to get increased growth rate, improved results occur only in treated animals. The next generation must have repeated treatments and incur the financial costs, in order to get the same improvement.

With genetic improvement, each successive generation receives the gains from the previous generation; cost free. Furthermore, the bull with extra genes for growth (higher EBVs for the particular market characteristic) will pass these genes on to all progeny each year, while the bull is in the herd and not just the immediate year of use, as is the case with supplementary feeds and hormonal growth promotants. Resources often decline over time and do not accumulate like the gains obtained by improved genetic selection.

Economics of using EBVs

Herd bull replacement is a major cost for cattle breeders. Costs per calf are increased by lowered bull fertility, reduced cow fertility and bull deaths. Bulls have a major influence on the future performance of the herd. A superior bull can increase herd performance and decrease risk taking; while a poor performance bull can adversely affect future production and increase the manager's risks.

What are the benefits from buying better bulls?

Better bulls may have superior genetic worth as indicated by their EBVs, or they may have a better physical phenotypic performance which is beneficial for their immediate performance, although only a portion of that benefit is passed on to the progeny. The purchase of bulls with better fertility, growth and carcass performance enables the breeder to achieve:

- more calves per bull;
- progeny that grow faster and have desirable carcass traits;
- future breeders that will produce more valuable offspring;
- animals that repeatedly meet market specifications.

All these advantages compound to minimise the risk to the beef producer and increase the enterprise's profitability.

Potential gains

One method of examining the potential long term gains through the selection of sires with the aid of BREEDPLAN has been identified using a herd production computer model. This herd model used a commercial herd of

1000 adult equivalents (equivalent to a 450 kg dry animal) in central Queensland to estimate the effect of mating bulls with 600-day weight EBVs in the top 10% of the breed, on the resultant profitability of the herd.

A summary of the calculated response (Table 6) shows that the use of bulls with high EBVs for 600-day weight increased the annual gross margins by 6.4, 7.6 and 8.3% after 5, 10 and 15 years respectively. This increase in gross margin could be achieved while running fewer cattle, leading to greater sustainability of the enterprise. The gross margins referred to here are based on the assumption that there has been no change in feed efficiency associated with the improvement in growth rate.

Table 6. Profitability of using bulls with high EBVs for 600-day weight.

Annual income and costs	Years after start of selection				
	0	5	10	15	20
Gross income (\$)	192 600	205 200	207 700	209 100	213 054
Less direct costs (\$)	11 100	12 200	12 300	12 500	12 645
Gross margin (\$)	181 500	193 000	195 400	196 600	200 409
Total Adult Equivalent	1 361	1 332	1 295	1 271	1 253
Gross margin per head (\$)	133	145	151	155	160

Source: Burrow, H.M. & Rudder, T.H. (1991), Increased profit through selection of zebu crossbred cattle for growth rate in the tropics, *AAABG 9th Conference, 24–27 June 1991*, pp. 186–189.
Gross income is income generated by the herd, less bull purchasing costs. Direct costs include animal health, supplementation and transportation costs.

Examples of producers’ experiences using BREEDPLAN

Producer demonstration sites were conducted at Collinsville, Clermont, Aramac, Goondiwindi and Mundubbera to show how producers can select bulls based on EBVs and use these with confidence in various environments.

North Queensland — Brahman sires, progeny differences at ‘Birralelee’

At a cattle property ‘Birralelee’ near Collinsville, northern Queensland, bulls were selected from the Australian Brahman Breeders Association GROUP BREEDPLAN Sire summary. The selection criteria used were:

- only bulls that were structurally sound
- bulls similar to those commonly used (because of either high EBVs or good eyeball)
- the difference was maximised between the average of the highs and average of the lows
- use as high as possible EBV accuracy data.

Progeny from the mating of higher compared with lower 900-day EBV Brahman bulls (average +27.4 EBV versus -12.6 EBV respectively) resulted in bulls selected having a +40 kg difference in EBVs. The result of the matings was for an advantage to the higher EBV bulls to the extent of 5.5 kg at weaning, 16 kg at 18 months of age and 22 kg at 30 months of age (Table 7).

Table 7. Demonstration of higher and lower EBVs from Birralelee .

Progeny age	No. animals	Higher EBV progeny	Lower EBV progeny	Weight advantage
Weaning weight	82	183.5	178	+5.5 kg
18 month weight (heifers & steers)	78	279	263	+16 kg
30 month weight (steers only)	36	481.5	459.7	+21.8 kg

For the live export trade at a market price of \$1.20/kg live animal, the following list shows the advantage of progeny from higher EBV sires over lower EBV sires. In this example there are 40 progeny or 20 steers per bull per year and a five year functional life of the bull.

Weight of progeny at 18 months	16 kg
benefit per head at \$1.20/kg live weight	\$ 19.20
benefit per bull (20 steers) per year	\$384.00
benefit per bull per 5 year life	\$1920.00
benefit per herd (700 steer progeny over 5 matings)	\$67 200.00

Central Queensland — Belmont Red sires and progeny differences at ‘Bendemeer’

At ‘Bendemeer’ near Clermont, Jap Ox steers sired by higher growth performance bulls return \$47.00 per head, or a 10% premium, over progeny of lower growth sires (tables 8 and 9). In the higher EBV group, 35 out of 40 carcase sides were graded Jap Ox to attract the optimum price, while only 17 out of 40 were so graded in the lower EBV group. Heifer progeny from the higher EBV growth bulls returned an extra \$12.00 per head over lower EBV sired progeny, when sold on the domestic market.

Table 8. Average liveweight (kg) and average daily weight gain (kg/d) of ‘Bendemeer’ progeny.

Group	200–day weight steers and heifers	600–day weight steers and heifers		900–day weight steers and heifers	
	Average liveweight (kg)	Average Liveweight (kg)	Average daily weight gain (kg/d)	Average liveweight (kg)	Average daily liveweight (kg/d)
High EBV	187	456	0.52	585	0.56
Low EBV	190	434	0.46	548	0.50
Control	193	448	0.50	593	0.56

Table 9. ‘Bendemeer’ steer carcase report (20 steers per group) sold to Japanese Market* for 1 July 1996.

	Carcase weight (kg)	Dentition (teeth)	Price (\$/kg)	Value (\$)	EMA (cm²)	Fat P8 (mm)
High EBV	326.3	3.4	1.49	487.18	81.5	13.2
Low EBV	301.8	3.8	1.45	436.96	80.5	12.4
Control	327.6	3.6	1.47	484.07	86.7	10.7

* = (premium \$1.50/kg)

Central Queensland — Belmont Red sires and progeny differences at ‘Swanlee’

At the cattle property ‘Swanlee’ near Aramac in north-western Queensland in desert spinnifex country, higher and lower EBV Belmont Red bulls were mated to Braford cows. The progeny from the matings showed an advantage to the higher EBV bulls. In draft 1, the benefit was 14 kg to the higher EBV bulls at 600 days and 22 kg as turn-off animals for Jap Ox (Table 10). In the second draft of progeny, the benefit was 22 kg at 600 days of age and 24 kg as turn-off animals.

Table 10. Average weights (kg) for two drafts of progeny from high and low EBV Belmont Red sires.

	Branding	Weaning	400 days	600 days	Turn-off
Draft 1					
High EBV	113	146	251	362	564
Low EBV	115	147	250	348	542
Draft 2					
High EBV	88	179	338	358	556
Low EBV	76	166	320	336	532

Combined selection for growth plus fertility

Santa Gertrudis. A Santa Gertrudis breeder at ‘Marrett’ near Goondiwindi mated two bulls to 34 three-year-old cows in 162 ha over a period of 12 weeks. The bulls were selected for their fertility and weight ratios (i.e. the relative weights of the bulls compared to the average of all bulls for that year). The calves were assigned to their sire using DNA fingerprinting and all calves were weighed at weaning. Details on the progeny of the two bulls is shown in Table 11.

Key results were:

- the total weaning weight of all calves by their respective sires is 5447 kg greater for the bull of higher growth rate and fertility. This difference equates to about \$6500 at \$1.20/kg;
- the difference in calf output was 26 versus 7 calves for the high versus low fertility bulls;
- the average growth rates were 277.7 kg versus 253.4 kg for the high versus low growth rate bulls.

Table 11. Comparison of total weight (kg) of progeny of two bulls at weaning.

Bull ID	Age	Wt ratio %	SS cm	% Norm	Serving capacity			No. of calves	Total wt kg	Av. wt kg.
					Int.	Mnts.	Serv.			
O90	08–11–93	+25.7	36.5	92	10	2	3	26	7221	277.7
O60	11–11–93	+6.7	31.5	90	9	9	1	7	1774	253.4

Age = Bull’s age in days, Wt. Ratio % = weight ratio relative to the group average, % Norm = Percent normal sperm, Int = number of interest in restrained test female and false mounts, Mnt = number of mounts, Serv = number of effective serves independent of mounts.

Belmont Red. Similarly, a Belmont Red breeder at ‘*Narayen*’ near Mundubbera mated three 12 month old bulls to 87 cows of various ages in a 800 ha scrub paddock for a 12 week period. The bulls were again selected on their fertility and weight ratio. The calves were assigned to sire using DNA testing and were weighed at weaning. Details on the progeny of the two bulls is shown in Table 12. Key results were:

- the total weight of calves weaned on the one day from high versus medium versus low fertility and growth rate sires was 9360 versus 6035 versus 1276 kg respectively;
- the difference in weaner weight between the high growth — high fertility and low growth — low fertility equates to about \$9700 at \$1.20/kg liveweight;
- the average weights of the progeny were relatively consistent with the weight ratio and EBVs of their sires.

Table 12. Comparison of total weight (kg) of progeny of three bulls at weaning.

Bull ID	Age	400–day wt ratio	400–day EBV	SS. cm.	Serving capacity			No. of calves	Total wt kg	Av. wt kg.
					Int.	Mnts.	Serv.			
95–26	8/08/94	112		26.5	1	8	4	43	9360	217.6
95–155	27/09/94	101	4.0	23.5	0	1	0	29	6035	208.1
95–39	19/08/94	86	11.0	25.5	3	0	0	6	1276	212.6

Thus at the two sites, the extra income from using high-growth — high-fertility bulls compared with low-growth — low-fertility bulls was \$6500 at Goondiwindi and \$9700 at Mundubbera. This clearly demonstrates the financial advantages of using high-fertility and high-growth bulls in multiple-sire herds.

Breed Society trends

Figure 9 shows genetic trends experienced by many of the breed societies in BREEDPLAN. This demonstrates the progress made within-breed for selection for growth rate and carcase traits.

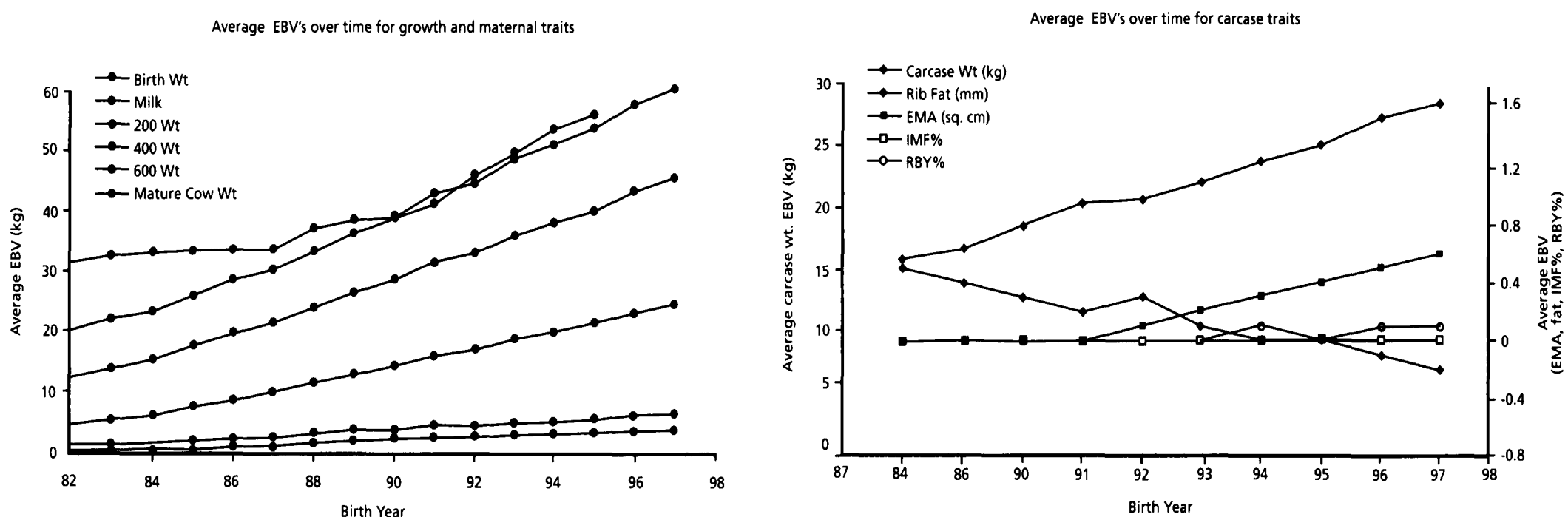


Figure 9. Genetic trends are published by various breed societies. These average EBVs are for the performance recorded Angus population (Angus GROUP BREEDPLAN Report, Autumn 1999).

9

Recording systems

In addition to the manual data collection sheets available from ABRI for BREEDPLAN users, several herd recording software packages are available. Basic spreadsheet and database formats are also used. These programs vary in their ability to transfer data to ABRI for further BREEDPLAN analysis. 'Herd Magic' and formerly 'Ag-Vantage Beef', were used in many breed societies for recording and transferring breed society pedigree information for the stud registers.

Integrated Pedigree Systems

Integrated pedigree systems is the integration of BREEDPLAN performance data with the pedigree system of the various breed societies. Each breed society system varies slightly in the traits recorded and the registration of the animals under comparison. Recording of performance data in association with the pedigree information streamlines data collection with correct animal identification, enables effective 'linkage' of sires and enables better data analysis across the breed.

Software programs

The following is a very brief description of relevant animal breeding and performance software packages, which have varying degrees of compatibility with BREEDPLAN as summarised in Table 13. This list, compiled in April 1999, may not be complete as animal performance software is frequently modified with changing technology. No responsibility is taken by the authors for the compatibility of each program with BREEDPLAN requirements.

Beef Stud is a DOS-based program designed for the management of a beef cattle stud. It records the relevant information for each animal including progeny and, if required, weight. The earlier version of this module was a finalist in the 1987 Royal Agricultural Show (NSW) Software Competition. New facilities include a pedigree trace, facilities to record all aspects of animal management such as weights, inoculations, dipping, treatments and drenching. It contains a check system for cross-matching; especially useful for avoiding the mating of particular animals under various management conditions. The program contains a module for the transfer of data to the industry standard system.

Possum Gully Software — Breeder's cattle records has been designed to record and analyse the main aspects of the cattle breeding herd for the commercial beef producer. The program records carcase information for individual animals as well as like-treated groups. A cow file records data for each cow showing tag number, dam, sire, age, current season joining details (natural or AI), calving group, pregnancy status and expected calving date. A history of all previous calves is also stored, including 200-day ratios. The calf file (automatically cross-referenced to the cow file) records calf birth details. Weight gains, 200-day and 400-day ratios can be calculated and carcase feedback from the abattoir can be entered.

Chandelle Pastoral CATTLE-BOSS (Cattle-Pro) is a Windows 95 livestock recording and analysis program for beef cattle breeders. CATTLE BOSS will provide five generation pedigrees and also maintain embryo, AI records, scanning data and carcass feedback. Data entry can be through individual or multi-entry data fields and electronic interface with cattle scales. Weight gain, breeding, health treatment, calving histories, paddock treatment histories, mob and group records are available. A quality assurance component is also incorporated in this program and it is ABRI and BREEDPLAN compatible.

Practical Systems — CATTLE PLUS is a Windows-based, herd recording and analysis software package designed for the modern commercial and registered beef producer. Individual animals, either bred or purchased, are entered into the program with optional details on sire, dam, previous pedigree history, breed type, colour, etc. Animals are grouped by mob, management group, paddock and property. There are 28 pre-designed reports for easy selection. Additional features include transfer of weights from electronic scales, import of EBVs on disk, automatic crossbreed tracking, multiple-sire group joinings, unlimited user-defined traits to assist selection, yard sheets (for on-the-spot data recording), undo facility (for incorrectly entered data) and a quality assurance recording section. CATTLE PLUS offers a breed compatible stud version.

Farmanager Systems — Genesys is a recording program for individually identified stock. The program is activity driven, has separate methods for recording matings, births, measurements and entries as groups of animals. The animal cards hold two tag numbers or names, sex, date of birth, sire, dam, breed, group, descriptive code, evaluation and pictures of the animal. Pedigrees can be generated and unlimited measurements of each animal recorded.

Wilga Park Software Systems — FARMMASTER is a total property recording system for livestock, paddock, cropping and rainfall recording. The livestock section covers all aspects of livestock husbandry, weight gains, sales, purchases, stock movements, paddock carrying capabilities and stock totals.

Herd File is a simplified recording DOS-based program for the beef or dairy cattle industry for herds that are not studs. This software records relevant information on individual animals.

Genie Herd Management is extremely easy to use, manages local weight ratios, herd and group EBVs using graphical and numerical outputs. It allows any cow to be joined to any bull as well as the usual herd recording features. The program determines average calving interval, gestation length, calf weights and EBVs and can handle any number of herds or groups of animals.

Saltbush — Herd Magic is a detailed Windows compatible software computer package used by breed society members and is designed to help record vital information on the breeding herd, efficiently and accurately. It reports four generations of pedigree, calculates on-farm performance records, has a marketing module and a wide range of traits can be recorded and analysed.

Data recorded on the computer on farm is readily transferred to ABRI for BREEDPLAN analysis and is then able to be transferred back onto the farm-computer with updated EBVs. There are a number of comprehensive reports available that enable the production of marketing reports, on-farm performance analysis, and the opportunity for customised reports. Service is

provided under an agreement with ABRI for staff support if any difficulties are experienced in using the software. *Herd Magic* for Windows replaces *Ag-Vantage Beef*.

Pinpoint is a paddock recording package which relates aerial photographs of properties to paddock management. Within this management system, groups of cattle and the individuals within the group can be identified with limited pedigree and mating information.

Prism software (On Farm Software–Beef) is primarily a herd management system, although it allows a broad range of management, breeding, animal movement and financial information to be recorded and analysed. An important feature of this package is the provision for feedlot data and carcass feedback information, recorded for individual animals and groups.

Stock Traka software, from Aleis International, is a comprehensive information package that complements their electronic identification system for stock management. As well as capturing identification numbers and animal weights, Stock Traka software records information on feed, drenching, health and progeny. Data can be entered manually or electronically. The software can be used to produce a range of reports including profit and loss reports for each animal or group of animals.

Shep Herd Management is a Windows-based, herd recording program for stud and commercial breeders and is available in two versions either for non-users of EBV data or those who obtain EBV data on disk from ABRI. While not requiring BREEDPLAN membership, users will gain full benefit by using or inputting BREEDPLAN data for all animals. Individual animal identification with pedigrees, date of birth, growth information, joining, calving, sales, purchases, carcass and all relevant EBVs are available. A range of animal, paddock and client reports can be produced.

Generic enterprises — STUDBOOK allows the breeder to store comprehensive genetic information on individual animals and performance rating in meaningful terms. It includes an extensive range of reports.

Spreadsheets and databases are very versatile for tabulated data recording. Although very basic, they can be customised to record the specific details required by the breeder and be as simple or as complex as is required to record on-farm, feedlot and abattoir data. They are not readily compatible with BREEDPLAN and are therefore less desirable for long term benefits.

Winsoft–Beef Production System provides individual animal records, EBV results, weight gains, calving records and pedigree charts. Reports include weight gain comparisons (including offspring of each bull), expected calving dates and veterinary treatment records.

Table 13. Roles and operating systems for the various herd recording software packages.

Software	BREEDPLAN compatible	Breeding component	Individual animal details	Calculation wt ratio	Operating system			
					MS-DOS	Windows	Mac	Hard disk
Beef Stud	*	*	*		*			
Breeder's cattle records	*	*	*	*	*			*
CATTLE-BOSS	*	*	*	*		*	*	*
Cattle Plus	*	*	*	*		*		*
Farm Manager -Genesys		*	*			*	*	*
W. Park Software -FARMMASTER				*	*			*
Herd File		*	*		*			
Genie Herd Management		*	*	*		*		
Saltbush Herd Magic	*	*	*	*		*		*
Pinpoint		limited	limited			*		*
On Farm Software		*	*	*	*			*
Shep Herd management	*	*	*	*		*		*
Stock Traka	*	*	*	*		*		*
Generic enterprises -STUDBOOK		*	*	*	*	*		*
Spreadsheets			*			*	*	
Winsoft-Beef Production System		*	*	*	*			*

*system facility

10

BREEDOBJECT: A single selection EBV

Whether selecting animals on visual traits alone, or in combination with EBVs and visual selection, the breeder makes intuitive decisions about the relative value of a range of traits including growth rate, scrotal size, structural soundness, eye pigmentation and carcase quality. These economic values depend on the market supplied and the performance of the current herd (as discussed on page 7).

The cattle industry has a history of seeking maximum performance for individual traits such as maximum weight, maximum height or maximum muscle. Discerning cattle breeders believe that they should be breeding for an optimum rather than a maximum. Breeding for an optimum is another way of saying that selection should be balanced across all traits. BREEDOBJECT is designed to help breeders establish their assessment of this balance, and to provide a simple selection procedure. This computer software package is designed to allow breeding objectives to be developed and utilised on a customised basis, so that breeders retain control of their economic destiny.

BREEDOBJECT is a computer software package that can help breeders make these important decisions more objectively and more accurately. It is a selection tool enabling bull breeders and bull buyers to:

- suggest the relative weightings that should be applied to the measures or EBVs that are available for use in selection
- rank animals for their overall breeding value for a given market application.

It can also predict the genetic changes that will occur in a herd if a particular set of weightings are applied to selection, to compare alternative selection strategies and for testing how sensitive any strategy is to a change in market requirements or prices.

BREEDOBJECT involves three key elements:

- breeder supplied production and cost estimates for commercial beef production which are the basis for arriving at the breeder's own required 'balance' between traits i.e. the breeding objective;
- the measurements or EBVs available to a breeder through BREEDPLAN or GROUP BREEDPLAN;
- a description of the inheritance of all the traits in the breeding objective, including the genetic correlations between all traits and measurements.

BREEDOBJECT analyses are currently available to the beef industry through accredited users of the package. For further information contact your local QBGIP member or ABRI at Armidale.

11

Molecular genetics

Molecular genetics focuses on the building blocks or components, at a cellular level, that determine the characteristics observed in the live animal. They are the components that make one animal perform differently from another for the range of traits available to breeders, and are indirectly selected for when one animal is selected for breeding relative to another.

The Building Blocks: DNA

DNA is the basic genetic component of each cell and can be identified using 'markers'. These markers provide a means for assessing the genetic merit of an animal for various traits. A major application is that it allows selection of sires for carcass and meat quality traits without performing a progeny test or slaughtering the bull. Such markers must be shown to be associated with major genes affecting those traits.

Gene markers

Trait measurements are being analysed with the DNA marker information to detect major genes. More than 70 traits are currently being investigated in work by CSIRO. This research covers a range of traits such as carcass quality, parasite and heat resistance, and growth in the dry season under nutritional stress.

Impact on the beef industry

The outcomes of this research include predictive markers for growth and meat quality traits, new ways of selecting cattle at a young age to meet nominated market specifications, and an understanding of how individual genes control growth and development in cattle. Thus, if there are markers that can predict whether an animal has genes such that its progeny will have a high degree of muscling and a heavy carcass weight, the animal can be selected at an early age as a future parent.

DNA markers illustrate variation at the gene level. The marker status of an animal can be assessed from conception when the genetic make-up of an animal is fixed. However, under the right circumstances the DNA markers provide the critical information on traits which are difficult or expensive to measure. To enable this, the location of the genes must be known and DNA markers which can be used for prediction must be available.

DNA fingerprinting applied in the beef industry

Genetic identification using DNA markers allows the identification of the unique attributes of each animal in order to develop the relationships between progeny and parents. Therefore, parentage and paternity testing relies on two basic principles:

- the detection of genetically inherited markers that remain the same throughout the animal's life
- the knowledge that all animals possess two copies of every gene (or marker).

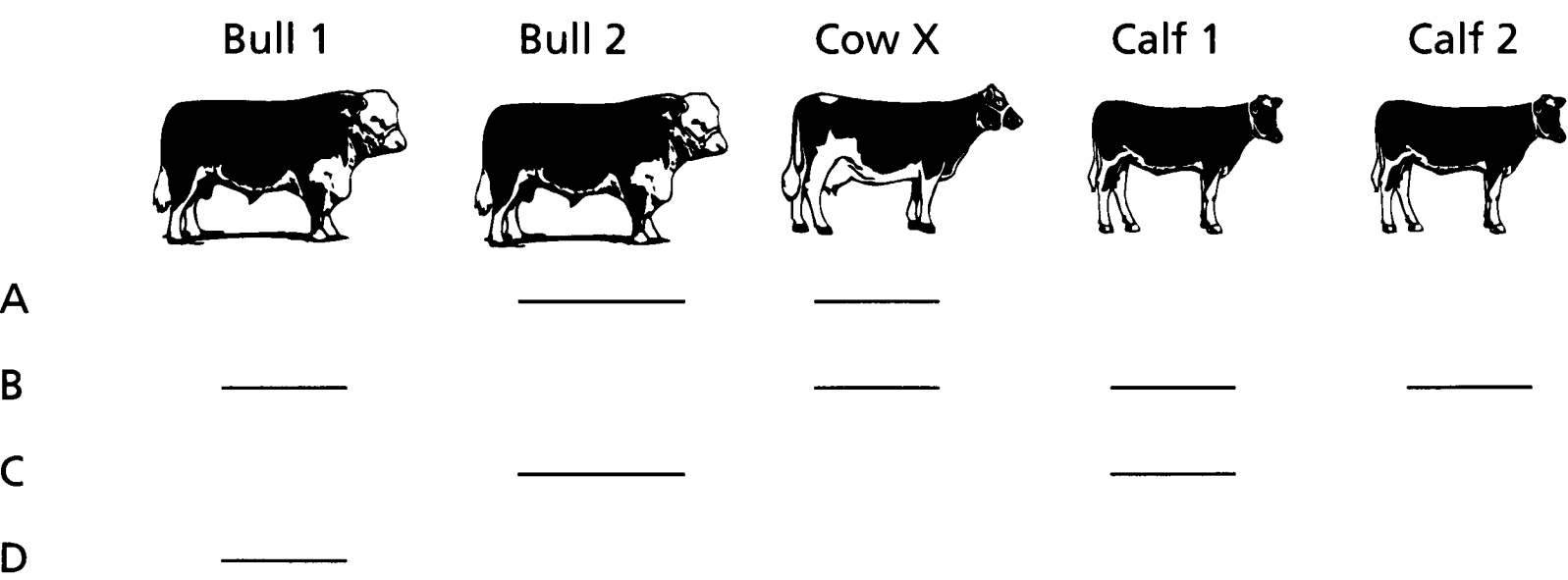
One marker is inherited from the sire and the other from the dam. This provides the foundation for parentage and paternity testing. If one copy (or variant) of a genetic marker is present in a calf but absent in both alleged parents; then the calf must be excluded as the offspring of that mating.

Parentage and paternity tests work by exclusion since no test can positively identify the parents of an animal. Testing can exclude a sire or dam as a possible parent, or an offspring can be excluded as being possible from a nominated mating or parent and these exclusions are absolute. However, parent-progeny relationships can never be proven with complete certainty. At best, a particular parent has an extremely high probability of being the parent of a particular offspring.

The process of DNA fingerprinting requires DNA to be extracted from a tissue sample. Blood tissue is preferred as it is easier, and therefore cheaper, to extract DNA from blood samples compared to samples such as semen, muscle and hair follicles.

How it works

The results of five samples (two bulls, one cow and two calves) tested with one DNA marker are illustrated in Figure 10. Variants of this DNA marker (labelled A, B, C, D) appear as distinct bands. Every animal displays one or two bands. Animals with one band have inherited the same variant from each parent (both bands being in the same position), whereas those with two bands have inherited a different variant from each parent.



Variants of the DNA marker appear as distinct bands shown as ‘_____’.

Figure 10. Illustrated results of one DNA marker tested using samples from two bulls, one cow and two calves.

Calf 1 qualifies as the offspring of **Cow X** and **Bull 2** because it has one band in common with each of these potential parents (band B in common with **Cow X** and band C in common with **Bull 2**). If this calf still qualifies after analysis of 11 such markers there is a greater than 99% chance that this calf is the offspring of **Cow X** and **Bull 2**. **Calf 1** does not qualify as the offspring of **Cow X** and **Bull 1** because its band C is not found in either of these potential parents. This example highlights how the testing of only one parent (e.g. the bull) reduces the power of the test. If **Cow X** had not been tested, **Calf 1** would qualify as the offspring of both **Bull 1** and **Bull 2** since **Calf 1** shares a band in common with both of these bulls.

Accuracy and expectations.

The ‘accuracy’ of a parentage or paternity test is the test’s ability to detect an incorrect parentage or paternity. The overall accuracy of a parentage or paternity evaluation is determined by two factors:

1. the number of genetic markers examined (as more markers are examined accuracy increases, but not linearly, so a compromise must be reached between achieving a reasonable accuracy at an affordable cost);

2. the degree of variation that exists for each genetic marker (more accuracy is achieved if the genetic markers used show a large degree of variation).

Marker variation is reduced when animals are closely related and differs markedly between cattle breeds. Variation, and therefore accuracy, is reduced in those cattle breeds with smaller gene pools. Improved accuracy may be expected in *Bos indicus* breeds as compared to *Bos taurus* breeds.

A commercially viable DNA-based parentage or paternity test requires the identification of groups of markers (three or four markers per group) that can be tested simultaneously and that show a high degree of variability across different cattle breeds. Currently a standard set of 11 DNA markers tested in three separate marker groups are used for DNA fingerprinting. Extra groups of markers are available if further resolution is required. The combined results of all 11 markers produce a DNA profile for each animal. The chances of any two animals having the same profile lies somewhere between three in 10 million to three in 100 billion, depending on the breed.

Parentage versus paternity. The standard set of 11 DNA markers were evaluated in 12 breeds of cattle and were able to detect around 99% of incorrect parentages. This figure varied from 98.5% in Poll Herefords to 99.9% in Brahmans, with the accuracy in all other breeds tested being over 99%. When used for paternity analysis alone (i.e. only the sire and calf are tested), accuracy is reduced to 88-99% depending on the breed.

Multiple-sire joinings. In situations using more than one bull and not testing the dams, the paternity accuracy given above is reduced in proportion to the number of bulls used. One can expect around 90% of calves to be assigned to a single sire if 10 bulls are used in the mating group. These accuracy figures are further reduced if animals in the mating group are related.

Applications in the beef industry

For the stud industry, DNA-typing offers greater accuracy than blood-typing for similar costs. Blood-typing and DNA fingerprinting are distinct tests and the results are not interchangeable. That is, the blood-typing results of parents cannot be used to parentage-verify a calf that has been DNA typed and not blood-typed.

For commercial breeders DNA-typing offers a new and powerful test for collecting information on animals and for enhancing genetic improvement through the selection of progeny that meet market specification and perform well for other traits. It is envisaged that the identification of markers for traits of economic importance will also facilitate the selection of superior animals in the future.

The power of DNA fingerprinting is not absolute and it is important that realistic expectations are placed on the test. As no test works by positive identification, and it is not economically feasible to test animals through an unlimited number of markers, the value of the test to each individual producer will vary according to the demands placed on it.

12

Abbreviations

ABRI	Agricultural Business Research Institute
AGBU	Animal Genetics and Breeding Unit
AE	Adult equivalent (450 kg dry cow equivalent)
AI	Artificial insemination
CRC	Cooperative Research Centre for the Cattle and Beef Industry (Meat Quality)
Cwt	Carcase weight
DC	Days-to-calving
DNA	Deoxyribo nucleic acid
DPI	Department of Primary Industries, Queensland
EBV	Estimated breeding value
EPD	Expected progeny difference
EMA	Eye muscle area
EMY	Estimated meat yield
ID	Identification
HCW	Hot carcase weight
IMF%	Intramuscular fat percent
QBII	Queensland Beef Industry Institute
QBGIP	Queensland Beef Genetic Improvement Project
RBV%	Retail beef yield percent
SS	Scrotal size or scrotal circumference

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Beef Cattle Recording and Selection is a timely, valuable aid for the management of beef enterprises by stud and commercial breeders alike.

Identification of individual animals and the recording of various beef cattle traits have rapidly increased in importance as part of the management of profitable, efficient beef enterprises. Management of effective beef herds depends on an understanding of genetics, objective measurement and sound genetic selection decisions.

This book provides an overview of basic beef cattle genetics, recording of the various production traits reported in GROUP BREEDPLAN and the basic principles of planned breeding and selection in practice. Results of several producers' experiences are included to show the benefit of BREEDPLAN Estimated Breeding Values (EBVs).

Traits currently available with EBVs include:

- Birthweight
- 200 day growth
- 200 day milk
- 400 day weight (Yearling)
- 600 day weight (Final)
- Mature cow weight

Fertility traits

- Scrotal size (SS)
- Days to calving (DC)
- Gestation length (GROUP BREEDPLAN only)
- Calving ease (GROUP BREEDPLAN only)

Carcase traits

- Carcase weight (Cwt)
- Eye muscle area (EMA)
- Fat depth (rib and rump P8)
- Retail beef yield % (RBY%)
- Intramuscular fat % (Marbling IMF%)

Three other valuable references in this series are available in an easy-to-understand style for primary producers, agribusiness, beef cattle breeders, teachers and students of beef production. They are:

Bull Selection

Breeding for Profit

Female Selection and Management in Beef Cattle

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