1. AN INTRODUCTION TO GENETICS

It is unlikely that many breeders think of their role in these terms but you are in fact geneticists! That is, as a cattle breeder your job is to manipulate the gene pool to deliver superior quality genetics to the beef industry for production of the commercial product.

Within any population of animals there is what is known as a normal distribution around the population average. This is illustrated in Diagram 1 and is commonly called a bell curve.

Diagram 1. Population Normal Distribution or ‘Bell Curve’

The concept of a normal distribution is quite simple. It tells us that the majority of animals in the population lie close to average and there are decreasing numbers of animals at the extremes, high or low, in expression of each trait. By knowing which animals differ significantly from average we can select from this group to ‘move’ the population average in the desired direction.

While the shape of the bell curve may differ, the normal distribution of animals’ performance applies to all traits that cattle breeders are interested in.

2. GENETIC IMPROVEMENT

Genetic improvement occurs in a population when the average genetic merit for a trait is moved in a desired direction, eg. weight gain or carcase yield increases, days to calving decreases. That is; when the average of the population is moved, as illustrated by the bell curve in Diagram 2.
Diagram 2. Genetic Improvement is ‘Shifting the Bell Curve’

It should be noted that for some traits the breeding objective may be maintaining the current breed average and endeavoring to minimise variation.

3. **INCLUSION OF TRAITS IN A HERDS’ BREEDING OBJECTIVES**

Before any trait is prioritised into a herds’ breeding objective there are three basic ‘tests’ that it should pass. They are

1. Is the trait of economic importance to the herd (and to your clients)?
2. Is the trait heritable?
3. Can it be measured with reasonable accuracy and at reasonable cost?

If the answer to all three questions is yes then it is reasonable to include it in your selection criteria.

4. **RATE OF GENETIC IMPROVEMENT**

There are three key factors which influence the rate of genetic improvement, or response to selection. They are;

1. the heritability of the trait,
2. the generation interval, and
3. the selection differential.

**Heritability:** The heritability of a trait is the proportion of the difference between animals which can be passed on to their progeny. Traits with a higher heritability are more easily selected for.

**Generation Interval:** The time interval between generations, defined as the average age of parents when their progeny are born. In beef cattle this generally averages around 4.5 – 6 years.

**Selection Differential:** The difference between the average genetic merit of the parents selected and the average of the population from which they come.
In considering these three drivers of the rate of genetic improvement we are considerably restricted as breeders because we cannot change the heritability of a trait and we can do little to reduce generation interval (especially in commercial herds) which leaves us with the selection differential as our primary tool to drive genetic improvement.

5. Genetic Correlation’s

In any animal selection program we must be aware that genetic correlations, or relationships, may exist between traits. The effect of this is that when we select for one trait we are likely to have an influence on another trait, or traits.

Correlation’s are expressed as positive or negative. A positive correlation is when selection for one trait leads to an increase in another trait (eg. growth rate and birth weight). A negative correlation is when selection for one trait leads to a decrease in another trait (eg. marbling and yield).

While the correlated effect is what happens on average in the population (See Table 1) there will be animals which do not conform to the expected correlation. (eg. high growth with below average birth weight). As cattle breeders, these are often highly desirable animals. However, to identify these animals within the population requires all traits of interest to be analysed. See Table 1.

6. Animal Selection

Animal selection is essentially the identification of differences between animals for commercially desired traits and then choosing those animals which have the best overall combination of characteristics to achieve the herds’ breeding objectives.

However, the process is much easier said than done because the differences you identify between animals must be genetic if those characteristics are to be passed on their progeny. You can only take home the genetic component of the desirable attributes you identify in any animal.

How much of the ‘good’ you see in an animal is an expression of genetic merit and how much is a result of the environment? (‘Environment’ being all non-genetic influences.)

A simple example of an environmental effect is the fluctuation in seasonal conditions properties continually encounter. In the bull selling business feeding plays an important role and the confusing effect of ‘environment’ is no more evident than in the multi-vendor sale ring. A bull’s genetic merit is constant irrespective of his condition but unfortunately the market (usually) heavily penalises breeders who do not play by the rules of the ‘feeding game’.

There’s a saying that what you see in an animal is ‘30% breeding and 70% feeding’. While we can argue the exact percentages involved the message is true.

When selecting for a trait we must be conscious that correlation’s, or relationships, exist between many traits. Selection for one trait may have an undesirable effect on another trait (see Table 1).
Table 1. Indicative Genetic Parameters used by Brahman & Other Tropical Breeds
(heritabilities are on the diagonal, genetic correlations are represented as positive (+) or negative (-) as low, medium or high)

<table>
<thead>
<tr>
<th>TRAITS</th>
<th>Milk</th>
<th>BWT</th>
<th>WWT</th>
<th>YWT</th>
<th>FWT</th>
<th>Mature Weight</th>
<th>Scrotal Size</th>
<th>DC</th>
<th>C.Wt.</th>
<th>EMA</th>
<th>Rib Fat</th>
<th>Rump Fat</th>
<th>RBY%</th>
<th>IMF%</th>
</tr>
</thead>
<tbody>
<tr>
<td>Milk</td>
<td></td>
<td>0.08</td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>B. Wt</td>
<td>0.40</td>
<td>+++</td>
<td>++</td>
<td>++</td>
<td>++</td>
<td>+</td>
<td>+</td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>W. Wt</td>
<td>0.17</td>
<td>+++</td>
<td>+++</td>
<td>++</td>
<td>+</td>
<td>0</td>
<td>++</td>
<td>0</td>
<td>-</td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>Y. Wt</td>
<td>0.22</td>
<td>+++</td>
<td>++</td>
<td>+</td>
<td>0</td>
<td>+++</td>
<td>+</td>
<td>-</td>
<td>-</td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>F. Wt</td>
<td>0.39</td>
<td>+++</td>
<td>+</td>
<td>0</td>
<td>+++</td>
<td>+</td>
<td>-</td>
<td>-</td>
<td>+</td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>Mature Wt.</td>
<td>0.39</td>
<td>+</td>
<td>-</td>
<td>++</td>
<td>-</td>
<td>-</td>
<td>-</td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>Scrotal Size</td>
<td>0.40</td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td>+</td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>DC</td>
<td></td>
<td>0.10</td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>C. Wt.</td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>EMA</td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>Rib Fat</td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>Rump Fat</td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>RBY%</td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>IMF%</td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td>0.38</td>
</tr>
</tbody>
</table>

Milk is considered to be genetically independent of all other traits.
No score means the correlation has not been calculated rather than that it is zero.
Carcass traits refer to abattoir carcase traits (adjusted to 300kg) as opposed to scan carcase traits.
Correlation Ranges:  
Low (0 – 20) shown as +/ -
Medium (21 – 60) shown as ++/ - -
High (61 – 100) shown as +++/ - - -
No correlation = 1 or –1.
6. **THE ROLE OF BREEDPLAN IN ANIMAL SELECTION**

An EBV is the best prediction of an animals’ genetic merit that modern technology can provide.

**EBVs are used to differentiate between the genetic and environmental components of an animal.** That is, they can be used to identify the ‘30%’ that you can take home with you.

Of the three factors influencing the rate of genetic improvement selection differential is the key tool as we can do little to influence the heritability of a trait or significantly shorten generation interval, especially in commercial herds.

EBVs play a key role in ranking animals within the breed for a range of traits. This enables breeders to better identifying animals of desired genetic merit to allow selection differential to be exploited and genetic improvement to be sustained and monitored.

7. **HOW DOES BREEDPLAN COMPARE ANIMALS FROM DIFFERING ENVIRONMENTS?**

The most common issue raised about BREEDPLAN is that of how cattle bred in widely differing environments can be validly compared. That is, how does it separate the genetic and environmental components of animals’ measured performance?

This is achieved through genetic linkage.

5.1 **What is genetic linkage?**

Genetic linkage occurs when two or more herds within the breed share common genes. Genetic linkage is created by sires (predominantly) and is developed between herds when common sires have been used, by AI or natural mating, and the subsequent progeny are performance recorded. Specifically, a 200 day (weaning) weight must be recorded in a valid contemporary group.

5.2 **Why is genetic linkage needed?**

One of the strengths of BREEDPLAN is that it enables direct comparison of animals across herds, which are often run under vastly different management, climatic and nutritional regimes. To do this BREEDPLAN must be able to calculate an EBV that is free of non-genetic (environmental) effects on the animal’s performance. Genetic linkage is the tool that allows this to occur. Genetic linkage is essential for BREEDPLAN to perform effectively.

5.4 **A Practical Example**

Consider three herds which have used an AI sire and have its progeny run under equal nutritional conditions as a second sire, and a fourth herd which has not used the AI sire.

<table>
<thead>
<tr>
<th></th>
<th>Herd A</th>
<th>Herd B</th>
<th>Herd C</th>
<th>Herd D</th>
</tr>
</thead>
<tbody>
<tr>
<td><strong>AI (Link) Sire Progeny</strong></td>
<td>340</td>
<td>380</td>
<td>420</td>
<td>--</td>
</tr>
<tr>
<td>Sire W</td>
<td>360</td>
<td>--</td>
<td>--</td>
<td>--</td>
</tr>
<tr>
<td><strong>Home Sire’s Progeny</strong></td>
<td></td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>Sire X</td>
<td>--</td>
<td>380</td>
<td>--</td>
<td>--</td>
</tr>
<tr>
<td>Sire Y</td>
<td>--</td>
<td>--</td>
<td>400</td>
<td>--</td>
</tr>
<tr>
<td>Sire Z</td>
<td>--</td>
<td>--</td>
<td>--</td>
<td>370</td>
</tr>
<tr>
<td><strong>Difference Between Home &amp; Link Sire</strong></td>
<td>+20kg</td>
<td>0</td>
<td>-20kg</td>
<td>??</td>
</tr>
</tbody>
</table>
BREEDPLAN uses the link sire as a reference point from which it looks at the relative performance of other sires. Essentially it is interested in the +20, 0 and –20kg figures which are derived from the actual weights submitted by breeders.

From this example we can reasonably deduce that Sire W is a higher performance bull (for growth to yearling age) than sires X or Y despite the fact his progeny are on average lighter than those by Sires X & Y. However, because there are no progeny by the AI sire in herd D we cannot draw any conclusions about Sire Z.

A point to note from this example is that evaluation of sires is only effective when there are two sires represented in a contemporary group (same sex, similar age and same nutrition & management) of calves.

6. **What contributes to an EBV?**

EBVs are calculated using all information available at the time of analysis from three key areas;

- The animal’s own performance, relative to its peers.
- The performance of all known relatives.
- The relationship (correlation) between traits.

7. **Accuracy of EBVs**

*By definition EBVs are an estimate.* Accuracy, expressed as a percentage, is a reflection of the amount of information available to calculate the EBV.

7.1 **Interpreting Accuracy**

<table>
<thead>
<tr>
<th>Accuracy Range</th>
<th>Interpretation</th>
</tr>
</thead>
<tbody>
<tr>
<td>Less than 50%</td>
<td>EBVs are preliminary and could change as more performance information becomes available.</td>
</tr>
<tr>
<td>50 to 74%</td>
<td>Medium accuracy, usually based on the animal’s own records and pedigree.</td>
</tr>
<tr>
<td>75 to 90%</td>
<td>Medium/High Accuracy, Some progeny information included. It is unlikely that the EBV will change much with addition of more data.</td>
</tr>
<tr>
<td>Above 90%</td>
<td>High accuracy estimate of the animal’s true breeding value.</td>
</tr>
</tbody>
</table>

As a rule, animals should be compared on EBVs regardless of accuracy. However, where two animals have similar EBVs the one with the higher accuracy could be the safer choice, assuming other factors are equal.
8. **EBVs AVAILABLE AND DATA USED FOR CALCULATION**

All traits that can be evaluated in BREEDPLAN are listed below.

### 8.1 Calving Ease Traits EBVs

**Calving Ease Daughters (DTRS - %):** Estimates the genetic differences between animals in the ability of their 2 year old daughters to calve without assistance.

**Calving Ease Direct (DIR - %):** Estimates the genetic differences between animals in the ability of their calves, from 2 year old heifers, to calve without assistance.

DIR and DTRS EBVs are calculated from calving ease scores primarily, but also draw on birth weight and gestation length data.

**Gestation Length (Days):** Estimates the genetic differences between animals in the numbers of days from conception to birth of the calf.

GL EBVs are calculated from calves bred by AI or hand mating, which have known conception and birth dates.

**Birth Weight (kg):** Estimates the genetic differences in calf birth weight.

Birth weight EBVs are calculated from calf birth weights. Calves are weighed on the day of birth.

### 8.2 Weight and Maternal Trait EBVs

**Milk (kg):** Estimates the genetic differences in milk production, expressed as variation in 200 day weight of daughter’s calves.

Milk EBVs are generated from 200 day weights. There is no additional data collection required.

**200 Day Growth (kg):** Estimates the genetic differences between animals in live weight at 200 days of age. Weight taken when calf is between 80 to 300 days of age.

**400 Day Weight (kg):** Estimates the genetic differences between animals in live weight at 400 days of age. Weight taken when calf is between 301 to 500 days of age.

**600 Day Weight (kg):** Estimates the genetic differences between animals in live weight at 600 days of age. Weight taken when calf is between 501 to 900 days of age.

**Mature Weight (kg):** Estimates the genetic differences between animals in live weight at 5 years of age.

MW EBVs are calculated from cow weights taken at weaning. For these weights to analysed the dams must be weighed within a week of their calves having their weaning (200 day) weights recorded.
8.3 Fertility Trait EBVs

**Scrotal Size (cm):** Estimates the genetic differences between animals in scrotal circumference at 400 days of age.

SS EBVs are calculated from scrotal circumference measured between 300 – 700 days of age. Breeders generally take this measure when 400 day weighing is done. Taking the measure at a relatively young age will better identify bulls exhibiting early puberty and scrotal development.

**Days to Calving (days):** Estimates of genetic differences in female fertility, expressed as the number of days from the start of the joining period until subsequent calving.

The herd must be managed under controlled mating periods to be able to calculate DC EBVs.

Data used for EBV generation is bull in and out dates and fate codes (reason) for all cows culled or dying.

8.4 Carcass Trait EBVs

Carcase traits EBVs are generated utilising both ultra-sound scan and abattoir data. Animals are scanned between 300 and 800 days of age.

**Carcase Weight (kg):** Estimates the genetic differences between animals in carcase weight (kg) at 650 days of age.

**Eye Muscle Area (cm²):** Estimates the genetic differences between animals for EMA at the 12/13th rib, in a 300kg carcase.

**Rib Fat (mm):** Estimates the genetic differences between animals for fat depth at the 12/13th rib, in a 300kg carcase.

**Rump Fat (mm):** Estimates the genetic differences between animals in fat depth at the P8 site, in a 300kg carcase.

**Retail Beef Yield Percentage (%):** RBY% is an estimate of the genetic differences between animals for retail beef yield percentage, in a 300kg carcase.

**Intra-Muscular Fat Percentage (%):** IMF% is an estimate of the genetic differences between animals for percent intra-muscular fat (marbling), in a 300kg carcase.

8.5 Other EBVs

**Net Feed Intake (kg/day):** is a trial BREEDPLAN EBV indicating the genetic differences between animals in net feed intake. This EBV is calculated from daily feed intake data collected in feed efficiency tests. This data is adjusted for the energy density of diet (adjusted to 10 MJ ME/kg DM), the weight of the individual animal measured mid-test, and test average daily weight gain of the individual. Animals with lower (more negative) EBVs will have a lower feed intake at the same weight and growth rate than those with higher more positive EBVs.
9.0 BREEDOBJECT

BreedObject is a tool that assists the targeting of a beef breeding enterprise by calculating an optimum mix of EBVs for any given production system. It gives economic weightings to EBVs and calculates a single $Index. This $Index provides a ranking of animals based on all available EBVs to suit a specific production system.

$Index figures are used to predict the average net profit resulting from the use of one sire over another. If we compare a “superior” sire with a $Index of +$50 to an “Inferior” sire with a $Index +$10 for the same breeding system, the superior sire has the potential to produce an additional ($50 - $10) x ½ = $20 per cow joined (half the $Index received from sire and half from dam). Over a working life of a sire (4 years, joined to 40 cows per year) the superior sire would therefore have the potential to generate an additional (4 x 40 x $20) = $3,200 compared to the inferior sire.

Brahman Example.
A Brahman BREEDPLAN $Index has recently been generated and released for a Grass Fed Jap Ox production system.

This is suitable for a self-replacing commercial herd in tropical and subtropical Australia targeting the production of grass fed steers for the Jap Ox market.

The percentage weighting on the different EBVs in the Grass Fed Jap Ox $Index is shown in Figure 1.

<table>
<thead>
<tr>
<th>Milk</th>
<th>200-day Weight</th>
<th>400-day Weight</th>
<th>600-day Weight</th>
<th>Days to Calving</th>
<th>Scrotal Size</th>
<th>P8 Fat Depth</th>
<th>Eye Muscle Area</th>
<th>Retail Beef Yield %</th>
<th>Mature Cow Weight</th>
</tr>
</thead>
<tbody>
<tr>
<td>-1%</td>
<td>-2%</td>
<td></td>
<td>+27%</td>
<td>-41%</td>
<td>+5%</td>
<td>+7%</td>
<td>+5%</td>
<td>+7%</td>
<td>+5%</td>
</tr>
</tbody>
</table>

Figure 1. Percentage emphasis on different EBVs for the Grass Fed Jap Ox $Index.

10. PRODUCER DEMONSTRATION SITES PROVING BREEDPLAN IN THE FIELD

Collinsville, Coastal Qld

Ten Brahman bulls were used by AI over randomly selected heifers. Bulls were selected on 600 Day EBV. The 5 High EBV bulls had an average 600 Day EBV of +27.4 kg. The 5 Low EBV bulls had an average 600 Day EBV of -12.6 kg.

The High EBV bulls average 40kg above low EBV bulls therefore BREEDPLAN predicts the progeny of the high line bulls to weigh 20kg heavier at 600 days. (Because calves will receive half of their genes from their sire we expect half of the 40kg difference to be displayed in the progeny).

<table>
<thead>
<tr>
<th>Results</th>
<th>High EBV Progeny</th>
<th>Low EBV Progeny</th>
<th>Wt. Difference</th>
<th>No. of Progeny</th>
</tr>
</thead>
<tbody>
<tr>
<td>Weaning Wt.</td>
<td>184</td>
<td>178</td>
<td>+6kg</td>
<td>82*</td>
</tr>
<tr>
<td>540 Day (18mth)</td>
<td>279</td>
<td>263</td>
<td>+16kg</td>
<td>78*</td>
</tr>
<tr>
<td>900 Day (30mth)</td>
<td>482</td>
<td>460</td>
<td>+22kg</td>
<td>36**</td>
</tr>
</tbody>
</table>

* = Steers & heifers. ** = Steers only. QDPI/MLA Producer Demonstration Site