Genetic evaluation for the beef industry in Australia

H-U. Graser[A,B]*, B. Tier*[A]*, D. J. Johnston*[A] *and S. A. Barwick*[A]

[A]Animal Genetics and Breeding Unit (a joint venture of NSW Department of Primary Industries and
The University of New England), The University of New England, Armidale, NSW 2351, Australia.
[B]Corresponding author. Email: hgraser@une.edu.au

Abstract.   Genetic evaluation for beef cattle in Australia has been performed using an animal model with best linear unbiased prediction since 1984. The evaluation procedures have evolved from simple to more complex models and from few to a large number of traits, including traits for reproduction, growth and carcass characteristics. This paper describes in detail the current beef cattle genetic evaluation system 'BREEDPLAN' used for the Australian beef cattle industry, the traits analysed and underlying models, and presents a short overview of the challenges and planned developments of coming years.

Additional keywords: carcass, growth, phenotypes, reproduction, selection indexes.

Introduction

Genetic evaluation of beef cattle using best linear unbiased prediction (BLUP) methods was first introduced in Australia in 1981 (Graser and Hammond 1985), initially for a 2-trait sire-maternal-grandsire model. The genetic evaluation system has now evolved to a multi-trait system involving growth, reproduction and carcass traits and is based on the so called animal model (Quaas and Pollak 1980). This evaluation system, known as BREEDPLAN, has been continuously updated since 1984, with developments presented repeatedly during those years (Graser *et al*. 1995; Johnston *et al*. 1999; Nicol *et al*. 1985). The most recent version (4.3) of BREEDPLAN was released in 2004. This paper describes the underlying models, methods used and latest developments in genetic evaluation for Australian beef cattle, and briefly considers some new challenges.

Performance records

Genetic evaluation for the Australian beef industry is mainly based on performance records and pedigrees collected by individual seedstock breeders on a totally voluntary basis. No formal control or audit is performed by the breed societies on individual breeders. However, most breeds do have quality assurance schemes (e.g. random pedigree DNA verification) and before analysis, extreme records within a contemporary group are identified and removed until verified by the breeder. For some traits, data are only accepted when recorded by accredited professionals. These traits currently include ultrasound scan traits and linear structural traits. Breeders in Australia receive no direct financial support to record performance. Commonly, performance data is channeled through breed societies to the National Beef Recording Scheme (NBRS),

operated by the not-for-profit company 'Agricultural Business Research Institute' (ABRI), at the University of New England, Armidale, NSW. Recorded animals do not have to be registered but all animals must have a known birth date. Data from crossbred animals can be recorded through a number of breed databases. Data from large research projects involving animals of known breeds and pedigree are also used. These data are commonly recorded by research technicians and provided free of charge to the breed societies. For example, most of the available feed intake and abattoir carcass data in the national database have been collected in research projects, such as those of the Cooperative Research Centre (CRC) for the Cattle and Beef Industry (Upton *et al*. 2001). Breed societies and their breeders contribute in-kind resources and sometimes cash to these research projects.

Breeders from 24 Australian beef cattle breed societies submitted performance data in 2003–04. The numbers of phenotypic data used in analyses are published by the individual societies. A list of all breed societies with links to their internet site can be found at http://breedplan. une.edu.au/, under 'links'. For most breeds an across herd genetic evaluation is performed at least once a year, with some of the larger societies having up to 3 evaluations. In some cases the analyses combine data across breed societies (e.g. Hereford and Poll Hereford), and in 11 analyses, phenotypic data from Australia are combined with phenotypic data from overseas, mainly New Zealand. In the near future, evaluations will become more frequent.

Models for evaluation

Genetic evaluation is performed on a breed-by-breed basis using the BREEDPLAN analytical software developed

by scientists at the Animal Genetics and Breeding Unit (AGBU). Single herd evaluation is possible but not requested by many breeders, as most herds have sufficient genetic linkage to other herds, through the use of artificial insemination (AI) sires, to enable across-herd analyses.

The 2 separate analyses performed are (i) a multi-trait evaluation based on a linear model for all traits except calving ease and docility; and (ii) a threshold model analysis for calving ease and docility. Calving ease is evaluated jointly with gestation length and birth weight.

The basic model for the evaluation of all traits in the first and larger of these analyses is either

$$y_{ijklm} = [\mu + CG_i + a_j + m_k + pe_k + s_l * h_m + e_{ijklm}] \lambda_n \quad (1)$$

or

$$y_{ijlm} = [\mu + CG_i + a_j + s_l * h_m + e_{ijlm}] \lambda_n, \quad (2)$$

where y_{ijklm} is the pre-corrected phenotypic record of animal j raised by dam k in management group i in herd m; y_{ijlm} is a corresponding record when there are no maternal effects; μ is the overall mean of the trait; CG_i is the fixed effect of contemporary group i; a_j is the random additive genetic effect for animal j; m_k is the random maternal genetic effect for dam k; pe_k is the random permanent maternal environmental effect for dam k; $s_l * h_m$ is a random sire l by herd m interaction effect; e_{ijklm} is the residual associated with the observation $ijklm$; and λ_n is the heterogeneity adjustment for the nth level of residual variance based on herd × year × sex.

The first and second moments for terms in the analysis are:

$$E \begin{bmatrix} y \\ a \\ m \\ pe \\ s*h \\ e \end{bmatrix} = \begin{bmatrix} Xb \\ 0 \\ 0 \\ 0 \\ 0 \\ 0 \end{bmatrix} ; Var \begin{bmatrix} a \\ m \\ pe \\ s*h \\ e \end{bmatrix} = \begin{bmatrix} A\sigma_a^2 & A\sigma_{am} & 0 & 0 & 0 \\ A\sigma_{am} & A\sigma_m^2 & 0 & 0 & 0 \\ 0 & 0 & I\sigma_{pe}^2 & 0 & 0 \\ 0 & 0 & 0 & I\sigma_{sh}^2 & 0 \\ 0 & 0 & 0 & 0 & I\sigma_e^2 \end{bmatrix} \quad (3)$$

for traits containing a maternal effect, and

$$E \begin{bmatrix} y \\ a \\ s*h \\ e \end{bmatrix} = \begin{bmatrix} Xb \\ 0 \\ 0 \\ 0 \end{bmatrix} ; Var \begin{bmatrix} a \\ s*h \\ e \end{bmatrix} = \begin{bmatrix} A\sigma_a^2 & 0 & 0 \\ 0 & I\sigma_{sh}^2 & 0 \\ 0 & 0 & I\sigma_e^2 \end{bmatrix} \quad (4)$$

for traits without a maternal effect, with b a vector of fixed effects (contemporary group), X is a design matrix for fixed effects and A is the numerator relationship matrix.

Calving ease is evaluated with a threshold model with birth weight and gestation length as correlated traits; see Hoeschele *et al.* (1995) and Tier and Graser (1995) for details of the method. The model used is:

$$y_{ijklmn} = sex_i + dage_j + grade_k + CG_l + a_m + m_n + pe_n + e_{ijklmn}, \quad (5)$$

where y_{ijklmn} is the observed calving ease score of animal m with sex i from dam n in contemporary group l; sex_i is the effect of calf sex i (male and female); $dage_j$ is the effect of dam age class j; $grade_k$ is the effect of the dam breed percent class k; CG_l is the fixed effect of contemporary group l; and a, m, pe and e are as defined above.

Models used for birth weight and gestation length are similar to those defined for the multi-trait linear models although adjustment for heterogeneous residual variances and the sire × herd interaction term are omitted for computational reasons.

In the analysis of categorical data, such as calving ease, contemporary groups in which all animals have the same score are of no value in the analysis and the records of all such animals are omitted. To assist retention of data, calf sex is not included in the definition of contemporary group but modelled as a separate cross-classified effect. Birth weight and gestation length (if available) are included even where calving ease records are omitted. The resulting calving ease EBVs are expressed as + or – percent calves born unassisted using a threshold appropriate for 2-year-old cows with a male calf.

Pre-adjustment of phenotypes

From the models 1 and 2 above it is obvious that fixed effects like age of dam and age of animals are not included in the mixed model. Phenotypic records are pre-adjusted for these effects using breed by sex (and calving season) specific factors and several different adjustment methods (see Table 1). For age of calf, a sex and trait specific x-intercept, as presented by Raymond (1982), is used to calculate a multiplicative adjustment factor for each animal and weight to adjust the animal to the standard 200, 400 and 600 days of age. For age of dam, linear and quadratic regressions, including a heifer factor (Robinson 1996a) are used. These adjustment factors are regularly re-estimated using data from an individual breed or from a pooled group of breeds (e.g. Howarth and Johnston 1995; Meyer 1999). Adjustment factors are estimated from full genetic analyses commonly when estimating variance components. For small breeds where insufficient data exists to estimate specific adjustment factors and genetic parameters, values from a breed of similar phenotype and genetic background are used (e.g. Angus for Red Angus).

Contemporary group definition

Contemporary groups for most traits are initially formed by the concatenation of herd, sex, day of measurement and breeder-defined management group. Additional separations are made for twin calves (*v.* singles), and for ET calves by including breed of recipient. Animals are further subdivided by age in slices of 45 or 60 days depending on the trait. Age slicing minimises errors from age adjustments and reduces confounding between sires and season under natural mating and rapidly changing environmental conditions. Slices start

with the oldest animal in the contemporary group and gaps between slices can occur. Year of birth is not by default included in contemporary group definition as calving season in some environments spreads across calendar years. Day of recording is included to separate groups of animals recorded on adjacent days that are not recorded as separate management groups by breeders, and to separate animals in groups that may have been yarded overnight before records were taken.

The contemporary group defined through herd, sex and breeder-defined management group is carried forward as an animal gets older. Animals in different contemporary groups on this basis consequently are not compared for traits recorded later in life. Fertility and weight records of cows are an exception to this; for these traits, the definition of contemporary group does not include information from the juvenile stage. For analysis of days to calving from natural mating, as a trait of the cow, all cows mated to the same bull within a joining season are defined as a contemporary group and separations are also made for lactation status at the commencement of mating. For analysis of cow weight, measured at weaning of the calf, contemporary group is defined by the contemporary group of the calf at foot before age slicing.

Crossbred animals are included in either of 2 ways in the analysis depending on the desired outcome and data quality. Crossbred animals are separated into their own contemporary group by breed composition, thus avoiding the need to adjust for heterosis. Alternatively, records are pre-adjusted for heterosis using breed-combination specific multiplicative adjustment factors collated from the literature. The latter allows direct comparisons of genotypes of different breeds and will in the future allow the combining of data from different breeds into a single analysis. Australian field data do not allow the estimation of heterosis effects.

Maternal effects

Additive genetic, maternal genetic and permanent maternal environmental effects are included in the model for the analyses of gestation length, birth weight, weaning weight and yearling weight. With respect to the maternal effects, yearling weight is considered a repeated record of weaning weight. Maternal effects for embryo transfer and foster-calves are attributed to their recipient and foster dams, respectively. In an extreme case, an embryo transfer calf fostered after birth can contribute to 3 different dam equations: through the relationship matrix to the direct effects of its genetic mother, for birth weight and gestation length to maternal effects of the recipient dam and for weaning weight to the maternal effects of a foster dam, but

Table 1. Pre-adjustment processes and allowed age ranges for each trait analysed in the BREEDPLAN multi-trait model

QR, quadratic regression; INT, intercept; QR+H, quadratic regression plus additional adjustment for heifers; LR, linear regression; WC, regression to a standard weight (e.g. 300 kg carcass weight)
Age ranges are for the Angus breed, other breeds vary

| Trait | Adjustment method | | Age range (days) |
	Age of dam	Age of animal	
Gestation length	QR	—	0
Birth weight	QR	—	0
200-day weight	QR+H	INT	80–300
400-day weight	QR+H	INT	301–500
600-day weight	QR+H	INT	501–700
Mature cow weight	—	QR	870–3900
Scrotal size	QR	INT	300–700
Days to calving	—	QR	270–3650
Scan bull eye muscle area	QR	LR	300–800
Scan bull rib fat	QR	LR	300–800
Scan bull P8 fat	QR	LR	300–800
Scan bull intramuscular fat %	QR	LR	300–800
Scan heifer eye muscle area	QR	LR	300–800
Scan heifer rib fat	QR	LR	300–800
Scan heifer P8 fat	QR	LR	300–800
Scan heifer intramuscular fat %	QR	LR	300–800
Carcass weight	—	QR	300–1000
Carcass eye muscle area	—	WC	300–1000
Carcass rib fat depth	—	WC	300–1000
Carcass P8 fat depth	—	WC	300–1000
Carcass intramuscular fat %	—	WC	300–1000
Carcass retail meat yield %	—	WC	300–1000

embryo transfer calves are always separated from non-embryo transfer calves when forming contemporary groups.

Sire × herd interaction

Research by Notter *et al*. (1992), Robinson (1996*b*), Meyer (1997) and Bradfield *et al*. (1997) has shown that beef cattle data in Australia are affected by sire × herd interaction or sire × herd–year interactions, which can account for about 5–10% of the variation. While these interactions could be seen as genotype × environment interactions, sire × dam-line interactions might also contribute. Another source could be incorrect management group definition. Robinson (1996*b*), Meyer (1997) and Bradfield (1999) identified sire × herd interactions as 1 source contributing to negative correlations between direct and maternal effects for weaning weight. Including such a term in the model drastically reduced the magnitude of any negative correlation between those 2 terms. When the sire × herd interaction effect is included in the model the EBVs of sires with progeny in only 1 herd are most affected (Graser *et al*. 1999) as the separated interaction effect is least regressed.

Heterogeneous variances

Equations 3 and 4 suggest the existence of homogeneous variances for all animals. However, for many traits this is not the case. For example, for intramuscular fat the standard deviation increases with the contemporary group mean. Rather than standardise phenotypic data, the method by Reverter *et al*. (1997) is used to account for heterogeneous variances. This is an iterative procedure where within contemporary group residual variances are estimated regularly during the solving of the mixed model equations and, every 10 round of iterations, the right-hand sides are adjusted for each trait. The correlations among traits remain constant. The use of this adjustment is controlled by parameters and can be switched on and off as required.

Definition of traits

The set of 22 traits currently analysed in the multi-trait model are presented in Table 1. Not all breeds record all traits, and some still lack the data recording protocols to collect the necessary data to compute traits (e.g. days to calving, gestation length). The acceptable limits on valid trait ranges and ages can vary between breeds.

Growth traits

All growth traits are recorded by weighing animals, commonly with electronic scales. Various methods exist for weighing birth weight. Weights are generally recorded to the nearest kilogram or 0.5 kg. Birth weights are recorded within 24 h of birth, and the recommendation is that dead calves are also weighed. The number of animals born (e.g. single, twin, triplet) must be recorded.

Weights taken later in life include 200-, 400- and 600-day weights, and roughly coincide with weaning, yearling and sale/mating stages. Weighing is done on an entire management group when the average age of the group is about 200, 400 or 600 days. Note that weights are not recorded when each animal is 200 days of age. A second weight for each trait (i.e. 200, 400 or 600 days) is also accepted if it is measured within the set age ranges. Additional weights are analysed as a repeated measure, with specified residual covariances.

Cow weight is defined as the weight of the cow at weaning of her calf. Up to 4 weights on each cow are analysed using a repeatability model. Records can be taken as young as 2 years of age but the first record on a cow must occur before she is 5 years of age. Cow weight records are adjusted to a 5-year basis using the results by Johnston *et al*. (1996).

Ultrasound scanning traits

Real-time ultrasound scanning records on bulls and heifers (and steers) are recorded by accredited technicians who are required to pass a proficiency test at least every 3 years. The 4 traits commonly recorded are scanned fat depth at the 12/13th rib, fat depth at the P8 (rump) site, eye muscle area at the 12/13th rib and intramuscular fat percent (IMF%) at the 12/13th rib. For the analysis, traits measured on bulls are considered different, but correlated, traits to those measured on heifers and steers (Meyer and Graser 1999). Commonly, measurements are taken at the same time as measurement of the 400 or 600-day weight. However, to ensure suitable data for genetic analysis of fat traits, especially IMF%, breeders are advised not to scan when the average P8 fat depth of a group is less than 5 mm. For young bulls this generally requires scanning at older ages.

Carcass traits

Abattoir carcass traits are commonly recorded on groups of steers from either research herds or industry progeny tests. Hot carcass weight and carcass P8 fat depth are recorded on the kill floor, whereas carcass eye muscle area, rib fat and marbling score are recorded by trained AUSMEAT or Meat Standards Australia (MSA) technicians on the chilled carcass, commonly quartered at the 12/13th rib site. Intramuscular fat percent is determined from a meat sample collected at the abattoir and processed in a meat laboratory using either ether extract or near-infrared spectroscopy (Perry *et al*. 2001). Retail beef yield percent records derived especially from research projects of the Cattle and Beef Industry CRC are based on actual bone out yield (Perry *et al*. 2001). In the future, predicted yields from video image analysis may be used. Carcass traits, except weight, are adjusted to a 300 kg carcass weight basis using the procedure described by Reverter *et al*. (2000).

Reproductive traits

Gestation length for a calf is computed as the number of days between the AI date of its mother and the calf's date of

birth. The only additional recording requirement to allow the computation of this trait is the AI date. The gestation length data are screened and management groups with more than 50% gestation lengths being the same are excluded from the analysis.

A days to calving (DC) record for a cow is defined as the number of days from the bull-in date until the cow subsequently calves, as defined by Meyer *et al*. (1990). Penalty DC records (last calving date in a CG plus 21 days) are assigned to non-calving cows (Johnston and Bunter 1996). Up to 6 DC records per cow are analysed using a repeatability model. However, for any of these records to be used, the cow must have generated her first DC record before a given age, and these differ across breeds. The recording of DC requires a full female inventory recording system to ensure the capture of all mating records and of disposal codes for all females leaving the herd. Correct use of disposal codes, especially for cows culled for infertility, is critical for the evaluation of this trait. Currently only DC records from natural matings are used. Methods have been developed to use DC from AI matings (Robinson and Johnston 2003), but limitations in the structure of field data have so far prevented their implementation.

Scrotal size is the linear circumference (in cm) of the scrotum recorded on young bulls at ages within the ranges specified in Table 1.

Calving ease is scored at the birth of a calf in herds that observe their females daily during calving. Scores are recorded using a 5-point scale where 1 is unassisted; 2 is easy pull; 3 is hard pull; 4 is vet assistance; 5 is malpresentation. Unobserved calvings are not used, score 5 is excluded and scores 3 and 4 are combined for analyses, resulting in 2 thresholds.

Use of overseas EBVs

Australian beef seedstock breeders in all breeds are constantly searching overseas populations of their breed for genetic material that can improve their genetics and give them a wider gene pool. While the genetic evaluation uses genetic groups (further described below) to account for the different subpopulations involved, the genetic grouping strategy itself does not utilise any knowledge about the relative genetic values of animals from overseas. For many animals imported into Australia or for animals imported from another breed, considerable phenotypic information on progeny may exist in the exporting country or breed. It can sometimes take a cattle generation before a similar amount of performance data is available in Australia. The BREEDPLAN genetic evaluation system therefore utilises overseas EBVs for any trait for which overseas EBVs can be imported. The accuracy of imported EBVs, and an estimate of the genetic correlation between Australian and overseas rankings by trait, are used to weight differences in genetic value between animals relative to the data available in the Australian analysis. The procedure

is described by Tier *et al*. (1999). With increasing number of progeny recorded in Australia the imported EBVs receive less weight in the calculation of the EBVs in Australia. The overseas breeding values and their accuracies are used to construct contributions to the left- and right-hand sides of the mixed model equations. This requires knowledge of the units, variance components and models used overseas, as well as an indication of the genetic correlations between Australian and overseas data.

Genetic grouping

All breed data includes animals with different numbers of generations in their pedigree. In addition, new herds may join breed societies, animals may be imported from outside the country and, in the extreme, animals may be introduced from a different breed. An assumption that all unknown parents come from 1 base population with mean zero and variance σ_a^2, therefore, would be clearly violated. Thus genetic grouping is included for all analyses. The genetic grouping is incorporated through the numerator relationship matrix (NRM) using the method described by Westell *et al*. (1988). Formation of genetic groups is done on a breed-by-breed basis. The groups are formed making sure that the number of animals within a group, and number of descendants with records, are sufficient to estimate group effects with some accuracy. Genetic groups are formed for 5 separate classes of base animals. Of these, 3 classes are always used to assign groups, irrespective of the country in the analysis. The first group consists of all base animals born before 1985. Any sufficiently large herd joining since that time is allocated to its own group, and finally there are groups made up of more recent base animals coming from smaller herds, based upon 5–7-yearly periods until the present.

The remaining 2 classes of base animals are concerned with crossbred and immigrant animals. Some breeds have been established in Australia by a process of grading up from other breeds and some breeds are actively involved in crossbreeding. For these breeds, the base animals from other breeds are formed into groups by breed, or by type (British, European, *Bos indicus* or *Bos indicus*-derived breeds), depending upon the numbers of base animals. The final class relates to immigrant animals that provide genetic material (semen and embryos). There has been considerable importation of semen into Australian breeds. When the numbers of animals involved are sufficiently large, groups are formed for each country of origin. When the numbers are not large, countries are amalgamated on a continental basis.

Multiple sire groups

Under the extensive production systems common in much of northern Australia, it can be normal to mate more than a hundred cows to a team of sires. Increasingly, parentage of the progeny is established by DNA fingerprinting, but if not, these progeny are included in the pedigree, and in the NRM,

by assigning equal probabilities of being the sire to each bull in the team (Kerr *et al*. 1994). This adds some complexity to the mixed model equations, as the inverse of the NRM no longer has its usual sparse structure.

Population genetic parameters

Necessary estimates of population genetic parameters, including heritabilities, additive variances and genetic and residual covariances, are derived separately for all breeds and traits with sufficient data (e.g. Meyer *et al*. 2004). Where insufficient data are available, data are merged across breeds of similar type (e.g. British, European, *Bos indicus* and *Bos indicus*-derived breeds). Many of the breed societies publish the heritabilities and genetic correlations that are used, together with a detailed description of traits and other statistics (e.g. Anon. 2005). Most of the parameter estimates used have also been published in the scientific literature (e.g. Johnston and Bunter 1996; Johnston *et al*. 1996, 2003*b*; Meyer 1995; Meyer *et al*. 2004; Reverter *et al*. 2000). A number of these authors also discuss the identification of best models with which to evaluate individual traits, particularly those that involve maternal components (e.g. Meyer 1997; Robinson 1996*a*, 1996*b*) and sire × herd interactions (Meyer 2003).

Computing algorithms

The analytical software underlying BREEDPLAN consists of a sequence of programs which are controlled by parameter files that permit a wide range of different analyses to be undertaken. This includes allowing for alternative models, using subsets of traits, different methods of treating cross-bred data (either in separate contemporary groups by breed composition or pre-adjusted for heterosis), allowing pre-adjustment of data (see Table 1), building genetic groups, fitting heterogeneous variances (at the herd and/or year and/or sex level), fitting sire × herd (and/or year) interactions, and weighting information from overseas evaluations (depending upon the correlation between the overseas and local EBVs).

Data are adjusted, equations assigned to effects, inbreeding coefficients calculated and some components of the mixed model equations are built. The mixed model equations for an animal model are represented implicitly (Tier and Graser 1991) and are currently solved using an SOR (successive over-relaxation) algorithm, with considerable factoring out of common terms (Tier and Graser 1992). A new algorithm based upon the pre-conditioned conjugate gradient method (Tsuruta *et al*. 2001) for solving equations is being trialled. In the multi-trait analysis there are potentially 28 (18) observed values for traits of mature (young) females and 19 observations for males. The models for these observations require 25 genetic equations for each animal and an additional 3 equations for each cow's permanent environmental effects. A recent

analysis of a large breed in a trans-Tasman evaluation required solving 38.7 million simultaneous equations to analyse 3.4 million observations for 1.2 million animals. Right-hand sides are rebuilt regularly as the data are iteratively adjusted for heterogeneous residual variances.

Accuracies are approximated after the EBVs have been calculated. Numerous summary statistics, such as the number of progeny each parent has with observations for each trait, and genetic trends for the breed and each herd are also computed. All results are aggregated into a single file for loading into the breed society's database.

Accuracies

Accuracies of individual estimated breeding values are expressed as correlations between true and estimated breeding value, following the recommendation by McClintock *et al*. (1982). Accuracies can only be approximated due to the difficulty in calculating the diagonal of the inverse of the mixed model equations. The approximation used is based on an algorithm described by Graser and Tier (1997), where the information for a particular trait from the animal's own record, its parents and progeny information and records on correlated traits, are expressed as progeny equivalents and summarised before being translated as an accuracy.

Publishing EBVs

Publishing EBVs is the responsibility of each individual breed society. Minimum accuracies for publication of EBVs are required for all traits and by all breeds. However, these requirements vary from trait to trait and breed to breed. Also, the level of effort by different breed societies in publishing sire summaries in printed form varies between the societies. However virtually all societies now provide access to their EBVs through the internet. These can be accessed either through individual breed society websites or through the BREEDPLAN website (http://breedplan.une.edu.au/sireselect.htm). At each of these sites, pedigrees and EBVs can be interrogated for all recorded animals.

Selection indexes

With the increasing number of EBVs available it has become more difficult for seedstock breeders to combine all the information in the best way for deciding between animals for their breeding program. To overcome this difficulty, BreedObject, a software program which calculates economic values for a given market production environment, and which combines all available EBVs on an animal into an appropriate index, was developed for use with BREEDPLAN (Barwick *et al*. 1992). The method for constructing the indexes of economic merit from BLUP EBVs is described by Schneeberger *et al*. (1992). BreedObject has been used to develop indexes for most of the major Australian beef breeds (Barwick and Henzell 2005). It has also been implemented on the internet (http://breedobject.com), where there is the added

capacity for individual breeders and buyers of seedstock to derive their own 'customised' indexes. This is achieved by editing the market production system parameters used for the calculation of economic weights for the traits in the breeding objective (Barwick *et al*. 2001). Users can rank selected groups of animals, for example from their own herd or all animals in 1 or more sale catalogues, according to an index that is directed at their own needs, which is an important aid to the adoption of selection indexes. A detailed discussion of the development of beef selection indexes in Australia and of future issues for indexes is presented by Barwick and Henzell (2005).

Future developments

Genetic evaluation systems for livestock are constantly evolving to adapt to the changing needs of beef producers and to be able to incorporate new advances in genetics, animal breeding, recording practices, statistics and computing. The ongoing and fundamental aim of future developments for the Australian beef industry is to provide cost effective genetic evaluation that facilitates rapid rates of genetic progress. New traits are being researched that may be of more direct economic importance in the future or are correlated with such traits (e.g. meat tenderness). New statistical procedures are being developed to better describe the available data, for example random regression models (Meyer 2001), and advances in molecular research will provide new measures that can help selection for economic merit. Continual developments in computing will provide opportunities for analyses previously not possible or economically feasible.

New traits

Feed costs are the single greatest cost component of beef production in Australia, and Arthur *et al*. (2001) have identified genetic differences in feed requirements. Net feed intake (NFI) has been shown to be heritable in beef cattle and a correlated indicator trait has been identified in the IGF-I blood parameter (Johnston *et al*. 2002). For a number of years, trial EBVs for NFI have been computed for the Angus and Hereford breeds using net feed intake records of research herds and seedstock breeders, as well as IGF-I measurements from blood samples of many thousands of calves. It is intended to include these traits (i.e. NFI, IGF-1) in the BREEDPLAN multi-trait evaluation utilising new knowledge of genetic parameters between these and other traits (Moore *et al*. 2005). Availability of NFI EBVs will also add to the ability of BreedObject selection indexes to account for genetic variation between animals in feed utilisation.

Other new traits are also being considered. For example, detailed structural soundness data are being collected by accredited scorers using a linear scoring system on up to 15 traits related to the physical structure (e.g. feet, legs, udder) of an animal. Trial EBVs will be calculated for these traits once sufficient records are available. In addition,

collection and analysis of cow performance data, including cow survival, across a range of environments will enable the provision of enhanced genetic evaluations for cow traits, including the possibility of a cow longevity EBV.

Incorporating gene based information

Utilising DNA marker information in genetic evaluation systems has the potential to increase the accuracy of EBVs and increase rates of genetic progress for economic merit. While use of marker information is desirable it requires a level of measurement and recording that is only just being reached in the Australian beef industry. Currently, there is some recording of seedstock animals for several traits, including at least 2 gene markers for meat tenderness. In addition, several thousand phenotypic records of tenderness (e.g. mechanical shear force and Meat Standards Australia consumer tenderness scores) have been recorded in the Beef CRC on pedigree recorded animals, along with a large number of flight time records (Burrow and Corbet 2000), a trait that has been shown to be genetically correlated with tenderness (Reverter *et al*. 2003). These data will be combined to provide an EBV for meat tenderness. The flight time and related data may also be used to develop an EBV for temperament that addresses ease of cattle handling.

Across breed genetic evaluation

There is a demand for across breed genetic evaluation, especially from commercial producers who need to compare bulls across, as well as within, breeds. First methods have been developed for comparing the EBVs of 4 Australian breeds for growth traits (Johnston *et al*. 2003*a*). Expansion to other breeds and other traits is dependent on the availability of suitable data. These data will also allow joint across-breed evaluation from combined breed datasets.

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