

# New Developments in Beef Cattle Genetic Evaluation in Australia

*D.J. Johnston, H.-U. Graser and B. Tier*

*Animal Genetics and Breeding Unit, University of New England, Armidale, NSW 2351, Australia*

## Introduction

Genetic evaluation of beef cattle in Australia uses a flexible and evolving system based on best linear unbiased prediction. Estimated breeding values (EBV) are computed from multiple trait animal models. A comprehensive description of the traits, methods and models used can be found in Graser *et al.* (2005). The genetic evaluation system known as BREEDPLAN was first released in Australia in 1984 and is currently used to evaluate 27 breeds within Australia (including 9 breeds with combined data with New Zealand) and breeds from 9 other overseas countries. The BREEDPLAN analytical software, and its associated systems (e.g. BreedObject), have been developed by the Animal Genetics and Breeding Unit (AGBU) primarily funded through a series of research grants by Meat and Livestock Australia. The BREEDPLAN analytical software is licensed to the Agricultural Business Research Institute (ABRI) and they provide genetic evaluation services to a large number of clients. The software uses pedigree and performance data recorded predominantly by seedstock breeders. These data are commonly channeled through a number of Breed Societies to the databases of the National Beef Recording Scheme at ABRI.

Research and development of the BREEDPLAN system involves a team of AGBU scientists and students. Discussed briefly below are six key areas of research and development that have either recently been completed or are currently underway and these include: new and improved methods; incorporation of DNA based data; inclusion of new traits; selection indexes; pooled evaluations; system audits.

### 1) New and improved methods

Research and development of new and improved methods is ongoing, with the aim of

providing the Australian beef industry with cost effective genetic evaluations that facilitates rapid genetic progress and profitable beef production. New work has included advances in both the fields of prediction and estimation. In prediction, we are currently investigating the use of more complex models (e.g. dominance effects) and advantages of reducing the number of equations using principal components (e.g. Meyer 2007). We have also recently implemented a new solver using the preconditioned conjugate gradient method that delivers a level of convergence previously not commercially viable using Gauss-Seidel iteration. In the area of estimation, new REML software (called WOMBAT, Meyer, 2006) has been developed (and freely available) and provides efficient procedures for estimation of variance components, particular from large data sets and complex, multiple trait models.

### 2) Incorporating DNA based data

Utilising DNA marker information has the potential to increase the accuracy of beef genetic evaluation, particularly for traits that are difficult to measure (e.g. feed efficiency) and those expressed at later ages. Research is underway into methods of incorporating the marker genotype into the existing EBVs and selection indexes. Also required, in parallel to the research, is the design of databases to house the marker data and provide extracts to allow its incorporation into the current genetic evaluation framework. The challenge is to use the DNA data efficiently and effectively given the relatively small number of animals currently with genotypes known. The other critical information to enable the incorporation of markers into the existing evaluations is accurate estimates of the size of effects of each marker on all traits in the evaluations. We are currently collaborating in a research project to estimate the size of effects of 12 commercially available beef DNA markers in approximately

14,000 animals with a comprehensive range of economically important phenotypes. Research is also underway into the potential use of SNP data from whole genome scans where suites of SNP have the potential to explain a significant amount of the additive variance of many traits.

### 3) New trait development

Genetic evaluations systems are constantly evolving to adapt to the changing needs of beef producers and developments in recording technology. The development and incorporation of a new trait into the existing genetic evaluation involves many steps, including: initial recommendations on the records collected (e.g. when to measure and which groups of animals), innovative breeders recording the new measures, data editing, modeling appropriate fixed effects, estimation of variance components (e.g. heritability), assessment of usefulness, continued and increased recording, re-estimation of variance and covariance, software development to incorporate the new trait, output modifications for the new EBV, and industry education.

Currently we are researching and developing evaluations for several new traits that are either of direct economic importance or are correlated with such traits. Areas of research include: the refinement of trial net feed intake (NFI) EBVs (i.e. a measure of feed efficiency) to include different trait definitions of NFI and re-estimated correlations with IGF-I; a threshold model approach for the analysis of linear physical structural assessment scores of feet and leg structure in young bulls and heifers (Jeyaruban *et al.* 2007); meat tenderness EBV using a combined approach of direct tenderness measures, correlated traits (e.g. flight time and meat colour) and DNA markers; flight time temperament EBV. Flight time is one measure of the temperament that can be easily and cheaply measured on large numbers of cattle. We now have more than 5000 records recorded by seedstock breeders in some tropically adapted breeds where temperament is considered to be more of an issue. We will start our part of the research shortly to develop an EBV for flight time.

Another important economic trait in beef production is female reproductive performance. Currently in our evaluations we used the trait called days to calving. The phenotypes are generated from natural mating record and requires recording of all cows mated. However, difficulties in data collection and the low heritability have generally limited genetic change in this trait in most breeds. Research as part of the Beef CRC program has recently been completed into the measurement and analysis of age at puberty in tropically adapted beef heifers. The research is ongoing to allow estimation of the genetic relationships between age at puberty with postpartum reconception interval, lifetime reproductive performance and cow longevity. These data will allow research into enhanced trait definition and evaluation methods for female reproductive traits.

### 4) Selection Indexes

With the large number of EBVs available and the diversity of our markets and production systems in Australia the construction of selection indexes is very important tool for breeders and bull buyers. The BreedObject software program calculates economic values for a given system and combines the BREEDPLAN EBVs into an EBV for economic merit. Currently there are 25 breed standard \$Indexes for Australian breeds and the facility exists via the web for individuals to construct fully customized indexes.

The BreedObject system is continually updated in line with developments in the genetic evaluation (e.g. new traits, re-estimated variance components) and is also undertaking research to improve its methodology (e.g. non-linear economic values) and various aspects of its functionality e.g. customized web delivery (see Barwick and Henzell 2005). There is ongoing consultation with industry on the modification of existing \$Indexes (i.e. periodically to accommodate changing markets and production costs) and to develop new \$Indexes for other breeds.

## 5) Pooled evaluations

Currently our genetic evaluations provide comparisons of animals across herds but research is underway to allow across country comparisons and also across breed comparisons. Several research projects are in progress investigating the feasibility of across country comparisons. The research involves developing software for combining phenotypic data across countries, estimation of across country genetic correlations, a web based database for the ongoing recording of the identities of across country animals, and software programs to build and solve the system of equations for multi-country, multi-trait evaluation.

Across breed (or multi-breed) evaluations are also under investigation primarily to allow the direct comparison of animals across breed, and also the computation on EBVs on hybrid animals. The initial component of this work used limited number of records (and traits) from experimental herds to compute adjustment factors between breed evaluations. It is hoped that with modifications to data recording systems, industry data from herds running more than one breed can be captured to supplement the research herd data on an ongoing basis. This will enable in the future the ability to combine breed databases and compute a single set of multi-breed EBVs.

## 6) System audits

There are three key initiatives in the area of system audits. It is our aim to improve the genetic evaluation system by developing software and analyses that perform a series of checks. The first piece of software recently developed is called TakeStock. This software uses existing input and output files to perform a genetic audit of genetic progress in a breed and across herds (for a breed nominated \$Index). The analysis identifies variables that explain differences in the rate of progress across herds for animals born in defined periods. Herds are then benchmarked against the significant explanatory variables and compare to the breed average (Johnston 2007). A “report card” is produced for each eligible herd and this allows herds to identify possible

reasons for slower rates of genetic gain and areas of their performance recording and/or selection practices that could be improved.

The next important area of work in the audit area is the current development of data auditing software. This software allows a breed to assess the completeness and quality of data entering their genetic evaluation. The software uses existing files to examine feature of the data on each herd over a nominated set of years (e.g. numbers born, pedigree known, sex ratios). The next step is to quantify the level of performance recording for each trait and the quality of these records. All the computed variables are then collated, allowing each herd to be rated and compared to a breed average. Further work is underway to quantify and evaluate the loss of data and record effectiveness. This will assist breeders in identifying any shortfalls in their performance recording practices that could be improved.

To investigate the suitability of an assumed heritability used in the genetic evaluation, analyses have been performed where data from a given set of years for a breed and a particular trait (e.g. birth weight) are excluded and then regressed on the sire EBVs computed from the remaining data. The estimated regression coefficient is compared against its expectation (i.e. 0.5). Finally, a recent investigation on the magnitude of GxE across states (i.e. Victoria and Queensland) was undertaken to check that combining data across regions in the current evaluation was suitable for a wide range of growth, carcass and reproductive traits. Results showed little or no evidence of GxE across the range of traits in Angus (i.e. genetic correlations across states close to one), with the possible exception of scan intramuscular fat in bulls and the maternal component of 200d weight. In general, the outcomes demonstrated the current practice of pooling of data across states is appropriate.

## Conclusions

The BREEDPLAN genetic evaluation system and associated software are being continually improved to meet the ever changing needs of the Australian beef breeding sector and the rapid advances in the fields of genetics and computing.

## References

- Barwick, S.A. & Henzell, A.L. 2005. Development successes and issues for the future in deriving and applying selection indexes for beef breeding. *Aust. J. Expt. Agric.* 45, 923-933.
- Graser, H-U., Tier, B., Johnston, D.J. & Barwick, S.A. 2005. Genetic evaluation for the beef industry in Australia. *Aust. J. Expt. Agric.* 45, 913-921.
- Jeyaruban, M.G., Johnston, D.J. & Graser, H.U. 2007. Development of a genetic evaluation system for structural soundness traits in Angus cattle. *Proc. Assoc. Advmt. Anim. Breed. Genet.* 17 (in press)
- Johnston, D.J. 2007. Genetic trends in Australian beef cattle – making real change. *Proc. Assoc. Advmt. Anim. Breed. Genet.* 17 (in press)
- Meyer, K. 2006. “WOMBAT” – Digging deep for quantitative genetics analyses by restricted maximum likelihood. *Proc. 8<sup>th</sup> World Congr. Genet. Appl. Livest. Prod.* N. 27-14.
- Meyer, K. 2007. Multivariate analyses of carcass traits for Angus cattle fitting reduced rank and factor-analytic models. *J. Anim. Breed. Genet.* 124, 50-64.