

DEVELOPING EFFECTIVE GENETIC EVALUATION SYSTEMS FOR BEEF CATTLE

Bruce Tier and Hans-Ulrich Graser
Animal Genetics and Breeding Unit*
University of New England
Armidale, NSW Australia 2351

INTRODUCTION

Before discussing the development of genetic evaluation systems it is worth noting some fundamental differences between the way beef is produced on different continents. In North America there is a clear division between the cow-calf producers who are responsible for selection decisions and other operators involved with 'finishing' cattle; widespread use is made of crossbreeding, and most animals are finished under an intensive feeding regime. In Europe beef production is mainly a by-product of the dairy industry, where calves are weaned early and fed intensively from a young age; limited use is made of crossbreeding. In Australia, most cattle are purebred or synthetic and finished by the breeder on pasture, although there are trends to the use of cross breeding and intensive feeding of cattle destined for high quality export markets. On all continents we find a relatively small, but highly influential, seedstock sector. It can be difficult to extend the idea and principles of genetic evaluation to parts of this sector who receive very high prices for breeding stock without any predictions of genetic merit. As production systems have developed in different ways we can expect genetic evaluation systems to do similarly.

Accurate and timely predictions of an animal's genetic merit are an important tool in the cattlemen's hands to continually improve the productivity of their livestock. Predictions must be available for all prospective parents. Predictions are not solely for breeders; a description of the genetic potential of livestock will become important to lot feeders and other cattlemen in the business of 'finishing' cattle.

Good predictions depend upon quality data, appropriate models and good estimates of (co)variances. They should be made using all the available data and allow valid comparison of animals across space and time. The use of these predictions requires a level of understanding by the producers. They need to learn how genes act, interact and are inherited. They need to understand how the management of their livestock affect the quality of the data. They need to understand the uncertainty of our predictions.

In this paper we examine how accurate predictions can be made and put to practical use by seedstock and commercial cattlemen. Most of our remarks will be confined to the situations found in North America and Australia.

TRAITS

The first task to develop a genetic evaluation system is to identify and define all traits of economic importance or traits well correlated to them, not simply those which are easily measured and/or highly heritable. It is not simply meat, but meat of a certain quality, that is the end product of the beef industry and it has to be produced at the least possible cost. There are a variety of different markets for beef throughout the world. Typically they are specified by characteristics such as weight, sex, age, subcutaneous and intramuscular fatness, muscularity, (lean) meat and fat colour. Table 1 illustrates the specifications provided to Australian cattle producers for a high grade Japanese market, a high grade European Community market and the Australian domestic market.

If these traits formed the basis of payment for commercial cattlemen then they would be the logical starting point for traits to observe and predict. There are problems associated with this approach: firstly, these traits do not form the basis of payment to commercial cattlemen, at least at the moment; secondly, few data useful

to genetic prediction services are recorded by the commercial sector of the industry; and thirdly, few stud animals are slaughtered and hence useful data on some of these traits are unavailable - although, in the hands of a trained operator, images obtained using ultra-sound can provide good measures of fatness and muscularity in real time.

Table 1. Target live specifications for some markets available to Australian producers. (extracted from Australian Beef Improvement News, February 1994).

Trait	Market		
	Japan Chilled Longfed	EC High Quality Chilled	Australian Supermarket Yearling
Liveweight	>600kg	<600kg	>300kg
Sex	Male	Male or Female	Male
Muscle:Fat (Scores)	A,B:2-3	A,B,C:3-4	A,B,C:2-3
Genetics	British, some crossbreds	British, European and some of their crosses	Beef breeds only
Age (months)	<42	<36	<24
Production System	>180 days grain fed	Improved pasture, crop or some grain (>100 days) Free of Hormonal Growth Promotants	Supplementary feed or grain finished

Other traits are also economically important to producers. Besides 'final product' traits, traits which relate to the performance of the breeding herd assume importance to the breeder. The high maintenance cost and low reproductive rate of cows makes mature weight and fertility traits very important. Fertility traits for analysis could include one or more of gestation length and calving traits - days-to-calving, pregnancy test results, calving success/failure, age at first-calving, age-at-puberty. Calving difficulty (or ease) - a trait of the calf and the cow - is also important. Unfortunately most of these traits are not very heritable, some are difficult and/or expensive to record and complicated to analyse. Traits relating to structural soundness of the animal are also important to breeders so that the breeding animals can perform efficiently throughout their lives. Other traits which affect the health and welfare of both animals for breeding and slaughter - such as disease or parasite resistance, or temperament - can be important to some breeds and/or production systems.

Precise definition of traits will prevent the analysis of data observed on two similar but different traits as the same trait e.g. fat depth should be measured at a common site. While precise definition of traits is important, the prediction service should not lose sight of the management and economic problems facing breeders. For example, most growth rate observations require that the age of the calf be known which implies that birth dates must be observed. Birth dates are normally required for registration in the seedstock sector but in large and/or extensive enterprises this may be sufficient to deter the breeder from recording any data.

DATA

All traits need to be recorded using common terms and measures. They must be recorded at ages when there is sufficient expression of the trait (limited use can be made of ultra-sound measurements of fat depth taken on grass fed yearling bulls as there is almost no fat to measure). Many continuously recorded traits have convenient scales - kg, lb, mm. For traits which don't have a convenient scale and use a scoring system (e.g. calving ease) standard scores and recording procedures are required.

For data to be useful to a genetic evaluation process they must meet certain requirements. Our current evaluation procedures are based upon contrasting the performance of an animal with that of others which have

been treated in like manner. We need to know which animals have been treated differently - including grown in different pastures. Differential treatment that goes unreported can bias predictions and lead to biased estimates of variance components.

Another requirement of our evaluation procedures is that data which form the basis of selection be included in our multiple trait analyses. For this reason alone the cost structure for recording data should not encourage selective reporting of observations. This suggests that a data recording system should be based upon an inventory of cows, with relatively high charges for cows to be re-admitted once they have been removed from the inventory. The cost per cow should include the basic cost of recording its progeny. The data system and the genetic prediction system must be easily accessible to the users. Data should be capable of being readily transferred to and from the data system electronically, magnetically, or on paper. On entry to the system, data should be verified to avoid simple errors. Verification of data is not solely the responsibility of the data recording system. Owners of the data should receive a (printed) copy of any raw data they have recorded. It is easy to make a case for breed societies to monitor some recording operations of their members.

Breeders need to understand that our prediction systems can make best use of data which are contrasted with many others i.e. large groups with descendants from a variety of parents. They need to appreciate this so that they manage as many animals (offspring of different sires) as contemporaries as possible. They also need to know the reasons why data are rejected from any analysis so they can avoid making those errors in the future.

It is essential for animals to maintain their identity throughout their life - both in the field and in the data system. Publication of two, different sets of predictions for the same animal is undesirable. For this reason it is also important to identify all the calves resulting from splitting embryos. We also need information that will allow the data to be adjusted for any systematic effects - such as age when observed, the age of the dam and the breed and sex of the animal.

Relationships and genetic correlations allow the observation of one trait on an animal to contribute to the prediction of another trait on a relative. Hence knowledge of each animal's pedigree is useful. Integration of performance information with pedigree information is necessary to reduce the incidence of identification errors which occur all too frequently when different systems are employed. In some areas where the industry is more extensive joining a number of sires to large groups of cows is common (multiple sire joining). Data collected in such production systems will have the dams identified and modifications to the numerator relationship matrix, A , (Henderson 1988) allow its analysis, if the sires in the groups are identified.

Performance data for carcase traits needs to be gathered in the commercial sector. This will require commitment from the commercial sector which perceives little benefit but significant costs associated with performance recording. It will also require commitment from the stud sector to allow the inclusion of data from non-stud herds into their databases. Most importantly, if these data are to be useful then the identity of the animals must be preserved as ownership is transferred and the subsequent management and performance recorded. The commercial sector will need a reward to collect these data. Ideally, this will come through the markets differentiating between genotypes. More suitable genotypes will become more profitable (reduce costs by meeting market specifications sooner) and therefore be preferred by the commercial sector. That is a long run view and its realisation may require some assistance (education) from the seedstock sector.

From a scientific viewpoint additional data will lead to better predictions. Practically, there is a cost to the measurement of animals and recording of the data. When one trait is highly correlated with another it may make little sense to record both. Conversely, there are times when cattle are being handled when it may be relatively inexpensive to record some additional data which can improve the accuracy of the predictions. Costs of recording performance include costs associated with the handling of cattle, the cost of measuring equipment

(scales, scanner), sometimes the cost of a trained operator and finally the costs associated with recording the data with the database. Analytical costs may not be trivial. Further research is required to help breeders maximise the benefits of recording under different production systems.

ANALYTICAL PROCEDURES

The two significant breakthroughs that allowed the widespread application of best linear unbiased prediction (BLUP) procedures to livestock industries were the ability to write A^{-1} directly from a pedigree list (Henderson 1976) and advances in computing power. The latter continues unabated and it is now possible to predict the genetic worth of large populations using multiple trait animal models which incorporate many correlated traits, quickly and frequently.

Artificial insemination allows many herds to use the same sires. This establishes genetic links between herds and sub-populations of the same breeds within and across countries. There is already demand for genetic evaluations that transcend national and breed boundaries, which is being addressed.

Base animals can be assigned to genetic groups which are incorporated into the analysis using the method of Westell et al. (1988). The criteria used to establish genetic groups should reflect shared ancestry. Immigration of genetic material - often semen from sires with many progeny in other populations - is an ongoing process. Problems with genetic groups can arise when there are too few animals to form a group.

Only through the use of animal models can biases in the genetic predictions that result from non-random mating be removed. Before the use of BLUP, when genetic predictions for sire were made by contemporary comparison, one requirement for participants in recording schemes was that cows be randomly assigned to the chosen bulls. This requirement limited the usefulness of the prediction service at that time because many breeders were unwilling to randomly assign cows and either didn't participate or, if they did, finished with biased results.

Using multiple trait animal models allow observation of one trait to contribute to the prediction of others. When the observations that form the basis of selection are included in an analysis, a multiple trait model can account for biases which can result from selection (Sorensen and Kennedy 1984). Given the power and cheapness of computers available currently there is little excuse for not using multiple trait animal models as a matter of course.

Recently (Hoeschele et al., 1994) developed a multiple continuous trait, single categorical trait for the analysis of calving ease together with a number of continuously distributed growth, carcass and fertility traits. In the future Markov chain Monte Carlo methods will allow joint analysis of a number of categorical traits and continuous traits.

Cheap computational power available to genetic prediction services allows the provision of regular, timely and up-to-date predictions to breeders. These could result from a continuous evaluation system or simply from regular (e.g. monthly) analyses. This would require close marriages between the data and analytical systems, uncommon in North America, but avoid production of interim predictions. Publication of formal sire summaries could still be made annually.

Modelling of systematic effects can be problematical when environmental conditions fluctuate from year to year. In parts of Australia, it is not uncommon for daily growth rates to 200 days to vary by 0.5kg from group to group within and across years. Similar variation can be found for other traits. Fitting one covariate to remove the effect of being observed at different ages will induce biases in the predictions. Some animals will be over

adjusted, some under. Research into the improvement of prediction models is a necessary but unglamorous function of genetic prediction services.

(CO)VARIANCES

Good estimates of genetic parameters are required. As new data are collected and new traits added to multiple trait models so new genetic parameters need to be estimated and old ones re-estimated periodically (say every other generation). Packages are available in the public domain for estimating (co)variance components, but they are computationally intensive. New developments in estimation algorithms (Smith 1994, Meyer 1994) will allow the analysis of larger sets of data and more complicated models.

Collecting data for estimating variance components can be an expensive process. Most producers are loath to record information which they perceive as having little benefit to them in the short run. Significant quantities of data and extensive pedigrees are required to disentangle some parameters such as the covariance between the maternal effects for birth and 200-day weights.

REPORTS

Once the data have been analysed the breeders are furnished with a number of reports. These include predictions of genetic merit together with an approximate accuracy for all the traits in the analysis on their animals. Results for active and young sires in the breed are generally made available through a sire summary. Nothing more typifies the nature of animal breeding than a list of animals with publications of genetic merit for a number of traits - animals are bundles of genes. We cannot select the genes for good yearling weight from one animal and combine them with genes for easy calving of another and those for a high level of fertility of a third; at least not in one generation. We can only select whole animals. Breeders are faced with the question of combining information on their traits of interest before ranking animals. The advantage of index selection compared to other forms of selection are well known. While desirable carcasses are defined by market specification, improvement in other traits can vary in importance among producers of the same breed of cattle. Producers involved with 'finishing' cattle have no interest in fertility, but female fertility has a high economic value to breeders.

Theory for constructing selection indexes is also well known, but requires as a starting point a set of economic values related to the traits in the objective. The derivation of these economic values is not a trivial task (Barwick 1993). All traits in the objective need economic values and they need to be derived using data from the production system. Economic rewards are not always linear - carcasses are classified into grades with differing rewards. Different traits express themselves at different times and some form of discounting may be necessary to reflect different timing. Any set of index weights implies a set of economic assumptions. Users of indexes need to understand how robust the index weights are to changes in the underlying economic assumptions.

Other summary reports are often provided by genetic prediction services. These can include genetic and environmental trends, distributions of the predictions for all or some classes of animals, descriptions of the numbers of animals and observations used in each analysis, tables that allow the reader to translate measures of accuracy into confidence intervals and tables of genetic parameters used in the analysis. Together with these tables is the information that breeders and buyers need to interpret them.

SITUATION

Unlike the dairy industry the data bases for North American beef breeds are decentralised; generally owned and operated by breed societies. In Australia through its National Beef Recording Scheme, most breed societies use a combined pedigree and performance recording system developed and operated by the Agricultural Business Research Institute - a fully owned company of the University of New England.

As can be seen in Table 2 most genetic prediction services in North America and Australia use animal models for most of their analyses. A variety of methods exist for adjusting observations to standards for comparison (e.g. age) in different countries and for different breeds and traits. Methods used include multiplicative and additive adjustments. Sometimes, when expression of a trait is governed by grade of animal, data are scaled to account for heterogeneous variances.

Table 2. Types of random effects fitted for analyses of various traits in North America and Australia (A = animal, M = maternal, P = Permanent environmental, S = sire, MGS = maternal grandsire), parentheses indicate observations are used but predictions not published.

Trait	Australia	North America
Growth		
Birth weight	A, (M), (P)	A (M,P for some breeds)
200/205 day weight	A, M, (P)	A,M,(P)
Yearling weight/gain	A, (M*), (P*)	A
Later weights	A	
Mature cow weights		A
Hip height		A
Fertility		
Calving ease	A,M,(P)	S,MGS
Scrotal size	A	A
Days-to-calving	A	
Gestation length	A,(M),(P),	A
Carcase		
	[Ultra sound measures on live animals]	[Direct measures]
Weight	(A)	S,MGS
Eye muscle area (EMA)	A	S,MGS
Fat depth (rib)	A	
Fat depth (rump)	A	
Marbling		S,MGS
Estimated total meat yield	A	
Estimated meat yield %	A	

* Same effect as 200-day weight

In North America birth weight, 205 day weight and yearling gain are often analysed with the one multiple trait model. A variety of models are used for the analysis of calving ease, and sometimes it is analysed as a threshold trait in a multiple trait model together with birth weight as a marker trait, at other times it is analysed using a single trait linear model. A multiple trait model is used to analyse carcass weight, marbling and rib-eye area.

In Australia, growth and all fertility traits (excluding calving ease) are analysed with the one multiple trait analysis which includes a total of seven animal, three maternal and three permanent environmental effects for each animal. Calving ease is analysed jointly with birth weight and gestation length as marker traits for some breeds.

CONCLUDING REMARKS

In the future we will see the addition of new traits to help describe the genetic merit of animals more completely. The development of more objective methods for marketing beef will lead to a demand for evaluation of new traits. More sophisticated models for analysis (e.g. to incorporate marker information) and tools to help breeders with their selection decisions will be developed. We will see an improved level of understanding of genetic principles among cattlemen.

Genetic improvement has significant potential for improving productivity in the beef industry. The aim of any genetic prediction service must be to provide their clients with the information they need, at the right time to allow them to make the most profitable/utilitarian decisions about their enterprises. The essence of the problem is to determine which traits to record, clearly define them, establish sound practices in relation to the observing and recording of data, integrate recording systems with the analytical and reporting systems, provide access to the recording and reporting systems, provide good estimates of population parameters, compute predictions of genetic merit and finally, but most importantly, provide the information that will allow the decision maker to understand how to use the information.

REFERENCES

- BARWICK, S.A. (1993) In *Animal Breeding: The Modern Approach*. eds Hammond, K., Graser, H.-U. and McDonald C.A. 121-140.
- HENDERSON, C.R. (1976) *Biometrics* 32:69-88.
- HENDERSON, C.R. (1988) *J. Anim. Sci.* 66:1614-1621.
- HOESCHELE, I., TIER, B., GRASER, H.-U. (1994) *J. Anim. Sci.* (Submitted).
- MEYER, K. (1994) *Proc. 5th World Congr. Genet. Appl. Livestock Prod.*
- SMITH, S.P. (1994) *J. Comp. Graph Stat.* (Submitted).
- SORENSEN, D.A. and KENNEDY, B.W. (1984) *Theor. Appl. Genet.* 66:217-220.
- WESTELL, R.A., QUAAS, R.L., VAN VLECK, L.D. (1988) *J. Dairy Sci.* 71:1310-1318.