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## A prototype sire evaluation for New Zealand dairy cattle

D. J. GARRICK, B. L. HARRIS<sup>1</sup> P. SHANNON<sup>1</sup> AND C. SOSA-FERREYRA

Department of Animal Science, Massey University, Palmerston North, New Zealand.

### ABSTRACT

Genetic evaluation of dairy cattle in New Zealand is based on a system originally developed in the 1960s. Major developments in database capability and statistical techniques have taken place over the intervening years. From the mid-1980s a major redevelopment of the information and processing system for cows took place. In 1991, a major review of the sire evaluation system was initiated. A Best Linear Unbiased Prediction (BLUP) procedure has been developed based on an animal model. Implementation of a prototype system is being investigated.

In contrast to the existing technique, the prototype involves a concurrent evaluation of cows and sires in all breeds using a repeatability model. This model provides breeding values for every animal (cows with one or more performance records and ancestral animals). The Livestock Improvement database has information on some 10 million animals over more than 50 years.

Use of the prototype described in this paper will become routine for ranking of dairy sires from 1994 and will increase rate of genetic gain in the dairy industry by improved accuracy of evaluation and reduced bias. The improved accuracy will result from use of *all known* genetic relationships among animals. The current system: does not adjust the evaluation of a sire for the merit of its mates dam; ignores sons' evaluations in the evaluation of parents; ignores daughters information in the evaluation of dams. Reduced bias will result from concurrent evaluation across breeds. The current system compares animals to within-breed bases.

The assumed model is identical for sires and cows in the prototype system. Furthermore, partitioning of a breeding index (BI) into its components based on information from parents, individuals and progeny is simpler than the current system which uses a recursive method for updating evaluations. Additionally, partitioning of a BI into components will provide useful diagnostic information (particularly for progeny test bulls). Interpretations of PI (production index) and BI information on reports for farmers and AB companies will be similar to the current system.

**Keywords:** animal model, BLUP, dairy, sire evaluation.

### INTRODUCTION

A basic premise of animal breeding is that observable performance (or phenotype) is determined by genotype of the animal and by effects of the environment. Permanent improvement resulting from selection can be achieved by identifying those candidates that will pass on superior genes to their offspring and using these animals as the parents of the next generation. In the case of quantitative traits such as milk protein production, neither the genes themselves nor the genotypes can be observed with current technology. Selection of animals with superior phenotypes will result in some animals being retained as a result of superior environmental effects that are, by definition, not passed on to their progeny.

A major reason for recording pedigree and performance information is to apply statistical techniques to partition phenotypic performance according to genetic and various environmental influences. Estimates of the genetic effects can then be used as the basis of selection for future parents. The statistical approach requires knowledge of population parameters such as heritability (proportion of variation due to genetic effects) and repeatability (proportion of variation due to genetic and permanent environment effects). The statistical

procedure accounts for two facts relating to passage of genetic material between generations: (1) On average, progeny receive half the genetic superiority or inferiority of their parents. (2) Individuals deviate from parent average due to chance sampling effects at meiosis.

From an industry viewpoint, a major objective in setting up and financing a performance recording scheme should be to ensure that economically efficient genetic progress can be achieved. This involves processing and using information for timely identification of animals of high genetic and phenotypic merit to improve the net financial return to the farm business. Financial benefits accrue from superior production of selected animals or progeny of selected animals and costs accrue from data collection, manipulation, analysis and reporting. Statistical procedures developed and adopted by industry will develop over time with technological developments and changes in market returns and farm costs. The objective of this paper is to describe features of the current system, and a prototype animal model being considered for widespread adoption in 1994. A comparison and contrast of the operational and technical details of the two approaches follows.

<sup>1</sup>Livestock Improvement Corporation Ltd., Private Bag 3016, Hamilton, New Zealand.

## UNDERLYING PHILOSOPHY

Derivation of computing formulae for animal evaluation involves two steps. First, definition of the model (in a statistical sense) to describe the process(es) that influence the phenotype. The model includes a model equation, relevant means and variance parameters and perhaps distributional assumptions. Second, definition of the criterion for identifying a "good" predictor. For example, defining the prediction error as the difference between true genetic merit and predicted genetic merit, then the Best Predictor (BP) is that which minimises the variance of these errors. In many cases we limit ourselves to prediction formulae that involve linear functions of observations. In this case, our method of choice would be Best Linear Prediction (BLP; sometimes known as selection index) or Best Linear Unbiased Prediction (BLUP) (see for example, Henderson 1973; Garrick 1991).

A model equation commonly used for animal evaluation describes the phenotype as the sum of genetic and environmental effects. For example, a model equation for lactation yields may appear as follows:

$$y_{ijk} = \mu_i + a_j + p_j + e_{ijk} \quad [1]$$

where

$y_{ijk}$  is observation  $k$  on animal  $j$  in contemporary group  $i$  (e.g., herd-year);

$\mu_i$  is the fixed effect of contemporary group  $i$ ;

$a_j$  is the additive genetic value (or breeding value; BV) of animal  $j$ ;

$p_j$  is the permanent environmental effect of animal  $j$ . This includes environmental effects which are common to all records made by an individual; and

$e_{ijk}$  is the residual effect unique to observation  $k$  on animal  $j$  measured in contemporary group  $i$ . The residual effect encompasses all effects not included in the contemporary mean, nor part of the animal genetic or permanent environmental effect. It is sometimes described as a temporary environmental effect.

This model is known as a *repeatability* model due to the inclusion of the permanent environmental effect. The model definition is completed by defining the means and variances of effects in the model. The random effects,  $a_j$ ,  $p_j$ , and  $e_{ijk}$  have zero means and are mutually uncorrelated. Non-genetic effects  $p_j$  and  $e_{ijk}$  are uncorrelated between animals, with variances  $\sigma_p^2$  and  $\sigma_e^2$ , respectively. Further, residual effects ( $e_{ijk}$ ) are uncorrelated between records within animals. Genetic effects  $a_j$  are correlated between relatives and have variance  $A\sigma_a^2$  where  $A$  defines the numerator relationship matrix.

In New Zealand, estimated BVs are scaled and set to a base value (1960 average of 100 for Jersey and Holstein Friesian) before presentation as a breeding index (BI). The sum of estimates of the additive genetic value and the permanent environmental effect for an animal (i.e. the animal effect,  $\hat{a}_j + \hat{p}_j$ ) is an estimate of the producing ability of an animal. In New Zealand, an estimate of this animal effect is scaled, set to a base and known as a production index (PI).

## CURRENT SYSTEM

The current system was developed in the 1960s with some modification during intervening years. Distinctive features of the current system are first, that sires and cows are evaluated separately and second, evaluations involve successive updating, combining *prior* predictions and *new* phenotypic information. The model for sire evaluation includes an adjustment for preferential mating by accounting for the current estimate of merit of the dam.

$$y_{ijk} - 0.5\hat{a}_{dam(j)} = \mu_i + 0.5a_{sire(j)} + e_{ijk}^{\#} \quad [2]$$

where

$\hat{a}_{dam(j)}$  is the *estimated* merit of the dam, and  $e_{ijk}^{\#}$  is the random residual effect for model [2] which is equal to the sum of  $e_{ijk}$  from model [1], plus the effect of Mendelian sampling (deviation of the individual's merit from parent average) and permanent environmental effects. In some circumstances, models [1] and [2] will be equivalent for sire evaluation.

This currently-used model for sire evaluation makes no use of information from sons to predict the merit of a sire. Model equation [2] is fitted separately for first and later lactation records of daughters as if these are different traits with a genetic correlation of 0.8 between lactations. Evaluations for each lactation are subsequently combined into a single value using weights representing the relative contributions of each lactation to lifetime yield of daughters (Wickham and Stichbury, 1980).

## Cow Evaluation

In contrast to genetic assessment of sires, evaluation of cows assumes identical genes are involved in first and subsequent lactations. A repeatability of 60% is assumed, implying 40% of the variation in production records is due to temporary environmental effects. Information on daughters or sons are not used in the evaluation of a cow. In most cases, a cow would be aged or culled before progeny information was available. Evaluations on cows for BI and PI are obtained for one herd at a time, as herd test records are entered on the database, with intervals from four times per year down to once a month, depending on frequency of herd testing. The system for cow evaluation was rewritten in 1989 following a technical review of the procedures relating to the derivation of the Production Indexes (Harris *et al.*, 1989).

## Updating

Limitations in database capability and processing speed resulted in development of computing formulae for sire and cow evaluation whereby new predictions were obtained by simply updating current predictions as new information came to hand. Thus historical records are summarised in the current prediction and future evaluations are obtained without need to re-access old records (Shannon and Castle, 1970). This avoided the need for an extensive historical database. Furthermore, it reduced the computation involved at any one evaluation. Calves are assigned a BI based on their parent average BI. A reliability of the ancestral BI is calculated from the reliability of the parents. All subsequent evaluations and

reliabilities are obtained from updating. In general, the formulae for updates appear

$$\text{new BI} = (1-w) (\text{old BI}) + w (\text{yield deviation})$$

where  $w$  is a weighting factor based on the previous reliability of the BI prediction and the amount of new information incorporated in the yield deviation. The yield deviation is the difference ( $y_{ijk} - \hat{\mu}_i$ ) for cows or the ratio ( $y_{ijk} / \hat{\mu}_i$ ) for sires where  $\hat{\mu}_i$  is an estimate of the contemporary group effect. Reliabilities are updated using a different function although still involving prior reliability and the weighting factor. More extensive details of the current system are given by Wickham and Stichbury (1980) and Harris *et al.* (1989).

### PROTOTYPE ANIMAL MODEL SYSTEM

A technical review of the sire evaluation procedures was undertaken as a routine research and development exercise to identify any opportunities for enhancement to the system. This review was undertaken as a joint project between Livestock Improvement Corporation and the Department of Animal Science at Massey University.

Since initial development of the sire evaluation system, the national database for dairy cattle has been established (Wickham, 1984), and major advances in statistical methodology (Henderson, 1983) and computer power have occurred. These factors provide opportunities for improvement to the current system, such as better sire comparisons involving bulls sourced internationally and across-breed analysis. Furthermore, changes in computer hardware and operating systems would likely require a new implementation of the sire evaluation system, even if no major changes to computational procedures were to occur.

Given sufficient computing power, one approach is to directly fit the model in [1]. This has been routinely carried out for the Australian dairy population since 1982 and in the large United States Holstein-Friesian dairy population since mid-1989 (Wiggins and VanRaden, 1989). Computationally, this approach is demanding because it requires simultaneous solution of every contemporary group, animal genetic and permanent environmental effect. Furthermore, it requires access to both new and historical production records. The advantage of this *animal model* approach is that both sexes are solved concurrently, allowing optimal use of information on relatives. Furthermore, *all* relatives information can be used without increasing computational difficulty. In practice, the set of linear equations are solved iteratively, with each iteration involving reading all pedigree and performance information. An animal model with iterative solution is the basis of the prototype system developed for sire evaluation in New Zealand.

The solution for a single animal involves a linear function including the records on the animal, its relatives and herdmates contemporary with the animal and its relatives. The prediction formula for any animal can be readily summarised as a linear function involving three terms. These terms involve (i) the parent average genetic merit, (ii) the animal's own records (if applicable) deviated from their contemporary group effects, and (iii) the genetic merit of any progeny of the animal, adjusted for the genetic merit of the other parent of

the progeny. The estimated breeding value of animal  $i$  can be written as:

$$\hat{a}_i = \beta_1 \frac{(\hat{a}_{sm} + \hat{a}_{dam})}{2} + \beta_2 \left( \frac{\sum_{k=1}^m (w_k (y_{ik} - \hat{\mu}_i))}{\sum_{k=1}^m w_k} \right) + \beta_3 \left( \frac{\sum_{l=1}^n d_l (0.5 \hat{a}_l - 0.25 \hat{a}_{mm})}{\sum_{l=1}^n 0.25 d_l} \right) \quad [3]$$

with weights of:

$$\beta_1 = \frac{d_i \left( (1-r) + (r-h^2) \sum_{k=1}^n w_k \right)}{\left( h^2 \sum_{k=1}^m w_k + \delta_i (1-r) + \delta_i (r-h^2) \sum_{k=1}^m w_k \right)}$$

$$\beta_2 = \frac{h^2 \sum_{k=1}^m w_k}{\left( h^2 \sum_{k=1}^m w_k + \delta_i (1-r) + \delta_i (r-h^2) \sum_{k=1}^m w_k \right)}$$

$$\beta_3 = \frac{0.25 \sum_{l=1}^n d_l \left( (1-r) + (r-h^2) \sum_{k=1}^m w_k \right)}{\left( h^2 \sum_{k=1}^m w_k + \delta_i (1-r) + \delta_i (r-h^2) \sum_{k=1}^m w_k \right)}$$

$$\delta_i = d_i + 0.25 \sum_{l=1}^n d_l$$

where  $h^2$  is heritability,  $r$  is repeatability,  $n$  is number of progeny,  $m$  is the number of lactation records;  $w_k$  is the reciprocal of the residual variance of record  $k$ , and  $d_l$  takes values of 2, 4/3, or 1 depending whether animal  $i$  has both parents known, 1 parent known or both parents unknown, respectively.

The three weights sum to one, with values depending on the quantity and quality of available pedigree and performance information. Example values are shown in Table 1. Weights and information corresponding to the three terms are useful sources of diagnostic information. By comparing their values between subsequent evaluations computed over an animal's lifetime, it can readily be determined why estimates of BI may have changed from one evaluation to the next evaluation. For example, sires and cows obtain all information from their parent average in the absences of own or progeny records respectively. Accumulation of records on the individual cow will reduce weighting on the parent average and increase weighting on yields from 0.14 to 0.23 as the cow gains from one to five records. As records on progeny become available, there will be a decrease in weights for parent average and individual yields. For sires, almost all information arises from progeny and parent average weight decreases to 0.07 as progeny number reaches 80 daughters. These weights will alter depending on number of contemporaries and are only given here for indicative purposes.

**TABLE 1:** Indicative weights for parent average, individual deviation and progeny information in an animal model evaluation.

Sex	Parents	Information		Weights		
		No. records	No. progeny	Parents	Yield	Progeny
Cow	yes	0	0	1.00		
Cow	yes	1	0	0.86	0.14	
Cow	yes	5	0	0.77	0.23	
Cow	yes	5	1	0.69	0.20	0.11
Cow	yes	5	5	0.47	0.14	0.39
Bull	yes	-	0	1.00		
Bull	yes	-	20	0.23		0.77
Bull	yes	-	80	0.07		0.93

## FURTHER RESEARCH

Research has just been initiated in a number of areas to determine strategies for adoption in the 1994 implementation. These include the following.

### Grouping strategy.

Prior to obtaining performance information on an individual or any progeny, the best prediction of merit is the ancestral or parent average BI. In some cases, one or more parents may not be known, or in the case of imported animals, the animals may not have converted proofs for New Zealand conditions. Estimates of BI will be biased (usually downwards) if unknown parents are not accounted for. An appropriate strategy is to group like animals with unknown parents and include fixed group effects in the model equation (Wiggans and VanRaden, 1989). The difficulty arises in defining *like* (for example, country of origin by year of birth classes), without creating an excess of groups. Further work is required to determine optimal grouping strategies for foreign animals and animals with missing ancestral information.

### Heterogeneous variance.

The definition of BI in New Zealand as a proportional indicator of merit implies that genetic superiority is expressed in a scaled manner, the scaling being directly proportional to herd mean. This is currently accounted for in the sire evaluation, using the ratio of yield to contemporary group mean. The prototype animal model can readily account for defined heterogeneous residual variance. Further research is required to determine an appropriate technique for defining residual variance in each herd-year, perhaps as a function of estimated herd-year mean or phenotypic variance.

### Concurrent evaluation across all breeds.

Current evaluation of sires and cows provides estimates of BIs that are scaled to a within 1960 (most breeds) breed base of 100. Thus a BI of 140 indicates an animal is 40% better than an animal evaluated in 1960 of the same breed. Some farmers are choosing sires across breeds, on the basis of BI irrespective of the breed. Accordingly, every effort should be made to obtain across-breed evaluations.

### Part-lactation records.

Performance records may cover only a partial lactation because the lactation is still in progress at the time of evaluation or because lactations were terminated early (e.g. in a drought). Such records will have reduced genetic and environmental variance. Work is ongoing to determine an appropriate technique for including these part-lactation records.

## SUMMARY

Increases in computer memory and disk storage along with decreasing hardware costs have resulted in a rapid increase in the on-line information base for individual dairy cattle in New Zealand. Technological advances in statistics, computer software and numerical algorithms along with increased arithmetic speed has allowed information to be processed without need for simplifying assumptions applied in the past.

A unified model for all animals is simple to explain and understand. The animal model has advantages in accuracy and reduced bias relative to the current system. Furthermore, developments resulting from New Zealand and overseas research are more easily implemented in a single system than in separate models for cows and sires.

The opportunity now exists for the industry to make better use of available information by routine use of the prototype system based on the animal model. Associated diagnostic information will be a useful new addition to the evaluation system. Research currently underway will lead to on-going developments to provide AB companies and dairy farmers with more reliable information to assist in the selection of replacements and culling of existing animals so as to increase net farm income.

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