

GENETIC EVALUATION OF BRITISH PEDIGREE BEEF CATTLE BREEDS

R.E. Crump¹, G. Simm¹, D. Nicholson², R.H. Findlay², J.G.E. Bryan³ and R. Thompson²

¹ Scottish Agricultural College, West Mains Road, Edinburgh, EH9 3JG, U.K.

² Roslin Institute (Edinburgh), Roslin, Midlothian, EH25 9PS, U.K.

³ Meat and Livestock Commission, PO Box 44, Winterhill House, Snowdon Drive, Milton Keynes, MK6 1AX, U.K.

SUMMARY

Genetic evaluation of pedigree beef cattle using multivariate individual animal model BLUP has been introduced in the UK. On-farm records of weight traits, ultrasonic fat depth and visual muscle score appraisal are included in the analyses. In this paper information is presented on analytical procedures and results for estimated genetic gain in the weight traits are given.

INTRODUCTION

The Meat and Livestock Commission (MLC) records the performance of pedigree beef cattle in Britain as an aid to selection by pedigree breeders. Records of performance have been collected both on-farm and, until the mid 1980s, at central performance testing stations. The early schemes concentrated on recording birth weights and weights at approximately 100 day intervals thereafter, up to 400 or 500 days of age. Since the 1970s, other optional measurements have been added periodically, including calving ease, ultrasonic fat depth, muscling score and ultrasonic muscle depth. Food intake was recorded at central test stations.

Until the mid 1980s these records were adjusted for age and fixed effects such as dam age, and results were presented to breeders as within-herd or within-test contemporary comparisons. From the mid 1980s a selection index was also available to breeders. The selection objective of this index was to maximise the margin between saleable meat yield and feed costs, taking into account the cost of calving difficulty (Allen and Steane, 1985).

A major limitation of this method was that comparisons between animals could only be made within a herd or test group. In common with most other European countries, the average size of pedigree beef herds in Britain is very low (5 to 12 cows for the major beef breeds; Simm *et al*, 1990). Hence, there are few contemporary animals, leading to low accuracies of estimated breeding values (EBVs). Also, potentially high rates of inbreeding reduce the scope for the use of homebred males.

Best Linear Unbiased Prediction (BLUP) is now the method of choice for genetic evaluation of farm animals. BLUP in general, and animal model BLUP in particular (i) make maximal use of information from relatives; (ii) are the most effective methods of separating genetic and environmental effects and (iii) permit across-herd and across-year evaluations, provided there are genetic links between herds or years (Henderson, 1973; Henderson and Quaas, 1976). Approximately 20 to 50% of births in the major beef breeds in Britain are the result of artificial inseminations (AI), which helps to create strong genetic links between herds and years (Simm *et al*, 1990). Hence BLUP evaluations could substantially improve genetic progress in British beef breeds, as a result of improved accuracy, but particularly by allowing comparison of EBVs across herds and years, thus increasing selection intensity. With this in mind the MLC has contracted the Scottish Agricultural College and the AFRC Roslin Institute to test appropriate statistical models, to develop software for routine use and to do the first BLUP evaluations for the numerically most important beef breeds in Britain. This paper outlines the procedures used and the results of these first evaluations (full details are given by Crump *et al*, 1994a).

MATERIALS AND METHODS

Data: Records of performance collected from 1970-1991 for the Simmental, Limousin, Charolais, South Devon and Aberdeen Angus breeds were obtained from the MLC. Data on birth weight, 200 day weight and 400 day weight were available, together with a much smaller number of records on ultrasonic fat depth and visually assessed muscling score. The number of records, means and standard deviations for the weight traits only are shown in Table 1. Pedigree data for the recorded animals and their ancestors were obtained from the

relevant breed society. In some cases supplementary records of birth weight were also available from the breed society. Data validation was carried out at the MLC.

Table 1. Number of observations (obs), means (\bar{x} , in kg) and standard deviations (sd, in kg) for the three weight traits recorded in five beef breeds

Breed	Birth weight			200 day weight			400 day weight		
	obs	\bar{x}	sd	obs	\bar{x}	sd	obs	\bar{x}	sd
Charolais	84 073	42.9	4.6	48 238	282	37	23 699	522	49
Simmental	40 748	40.3	3.9	34 923	286	33	18 613	518	44
Limousin	49 846	37.0	3.4	31 046	251	29	17 375	459	39
Aberdeen Angus	5 898	31.7	3.5	22 019	208	29	11 711	390	38
South Devon	4 110	43.8	5.8	20 629	253	36	8 314	441	50

The data for weight traits and ultrasonic fat depth were corrected for heterogeneity of variance between herds using the methodology of Brotherstone and Hill, 1986. The standardisation procedure scaled data so that the within-herd variance moved towards the population mean within-herd variance for that trait. The weight given to the within-herd variance estimate in the scaling factor for any herd depended on the number of degrees of freedom associated with the estimate. Data values were corrected for contemporary group means and least squares estimates of fixed effects, the residuals were standardised and records were recreated by adding fixed effects and contemporary group means back on.

Assignment of records to contemporary groups: An algorithm to assign records to contemporary groups within herds was produced which took account of the within herd calving pattern and recorded information on management groups, where available. Simple methods were used to investigate the effect of assigning records to contemporary groups in different ways. The accuracy of mass selection is $r = h(1-1/n)^{1/2}$, where h is the square root of the heritability and n is the size of the contemporary groups. The number and size of contemporary groups affects the magnitude of r . When there are many small contemporary groups r will be lower than when there are few large contemporary groups. The heritability estimate is also dependent upon the number and size of contemporary groups. Considering additive direct effects only, $h = \sigma_d/(\sigma_d + \sigma_e)$. If we assume that all variance changes due to contemporary groups affect environmental rather than additive genetic variance, then when there are many small contemporary groups σ_e will be reduced, compared to when there are few large contemporary groups, because variance between contemporary group means is accounted for. Reducing σ_e causes an increase in h and a corresponding increase in r . The balance between h and r can be investigated for different contemporary grouping strategies.

The optimum values of the parameters controlling the contemporary group assignment algorithm were assessed by investigating the ratio r/σ_a (Crump *et al.*, 1994b) for various contemporary grouping strategies for 200 day weight. Phenotypic variances were estimated using the residual variance after fitting of fixed effects using least-squares and the accuracy of mass selection was calculated using a weighted estimate of $(1-1/n)$.

Statistical models: Least-squares analysis was used to select the fixed effect models to be fitted in the BLUP evaluations. There were only minor differences in the results across breeds, and as a result the same fixed effect structure was applied to each breed. Table 2 contains information on the fixed effects fitted for the three weight traits evaluated.

Table 3 shows the parameters used in the BLUP evaluations for each of the five breeds. These were derived from an extensive literature review. Ideally, parameters would be obtained from the population of animals under evaluation. However, there is no evidence of systematic differences between breeds in genetic parameters for growth traits (see for example Mohiuddin, 1993). There are relatively few parameter estimates for fat and muscle measurements or maternal components of growth, and so it is difficult to assess whether there are breed differences. Partly for this reason, and because of the small number of records available, the results for maternal EBVs for growth traits and for ultrasonic fat and muscle score, are not presented here.

Table 2. Fixed effect model fitted to all breeds

	Birth weight	200 day weight	400 day weight
Contemporary group - excluding sex	✓	✓	
Contemporary group - including sex			✓
Month of birth	✓	✓	✓
Sex	✓	✓	
Embryo transfer calf	✓		
Foster calf		✓	
Birth type	✓	✓	✓
Breed of mother at birth	✓		
Breed of mother at weaning		✓	✓
Percent purebred	✓	✓	✓
Age of dam (linear and quadratic)	✓	✓	✓

Table 3. Genetic parameters used in BLUP evaluations. Heritabilities on diagonal, genetic correlations above diagonal and phenotypic correlations below diagonal.

	BW	W200	W400	FAT	MSC	BWm	W200m
Birth weight (BW)	0.41	0.49	0.53	0.00	0.00	-0.38	-0.15
200 day weight (W200)	0.35	0.28	0.82	0.00	0.00	0.00	-0.32
400 day weight (W400)	0.38	0.72	0.41	0.21	0.10	0.00	0.00
Backfat depth (FAT)	0.00	0.24	0.36	0.29	0.00	0.00	0.00
Muscling score (MSC)	0.00	0.10	0.30	0.10	0.25	0.00	0.00
Birth weight - maternal (BWm)						0.06	0.42
200 day wt - maternal (W200m)							0.07

For all of the breeds, there was some importation of animals from different countries and breeds. In order to take some account of possible differences in the average genetic merit of different populations, genetic groups (Westell *et al*, 1988, Quaas, 1988) were included in the model.

BLUP evaluations: The BLUP evaluations were performed within breed, fitting a multivariate Individual Animal Model to the five available traits. In addition to additive direct genetic effects, additive maternal genetic and permanent environmental effects were included for birth weight and 200 day weight. The algorithm used was an adaptation of the multivariate Reduced Animal Model BLUP algorithm of Schaeffer and Wilton (1987).

Accuracy evaluations: Univariate accuracies were calculated as $(1-PEV/\sigma_i)^{1/2}$, where PEV is the prediction error variance of effect i for the individual and σ_i is the variance associated with effect i . The method of Thompson *et al* (1994) was used to invert the coefficient matrix and obtain prediction error variances for all effects. Univariate accuracies were converted to 'pseudo-multivariate' accuracies for each animal. In order to estimate prediction error covariances between traits for a given animal, it was assumed that the effective number of records for trait j (eff_j) was a subset of the effective number of records for trait k (eff_k) (where $eff_k > eff_j$). This allows an approximate set of multivariate mixed model equations to be created for an animal from which the 'pseudo-multivariate' accuracies can be derived.

Comparison of EBVs from consecutive evaluations: For animals with large observed changes in EBVs between evaluations at times t and $t+1$, confidence intervals for $EBV_{t+1}-EBV_t$ are produced using $PEV_t PEV_{t+1}$ as the variance of $EBV_{t+1}-EBV_t$. The confidence intervals take account of information included in the previous evaluation and give an indication of whether any new information available reasonably explains the observed change in EBVs. Phenotypic information for the animal and close relatives is also summarised.

RESULTS

Additive direct EBVs for all five recorded traits plus additive maternal EBVs for 200 day weight are presented to breeders alongside an index calculated from the five additive direct EBVs. The goal of the Index is essentially similar to that of Allen and Steane (1985), but with new methods for calculating the economic values of goal traits. All EBVs are expressed relative to the average EBV of calves born in 1980 and are accompanied by an accuracy value. The regression coefficients of EBV on year of birth are shown in Table 4.

Table 4. Regressions of EBV on year of birth from 1980 to 1992

Trait	Simmental	Limousin	Charolais	South Devon	Aberdeen Angus
Birth weight	0.09	0.07	0.11	0.05	0.17
200 day weight	0.84	0.59	0.84	0.57	1.33
400 day weight	1.53	1.04	1.59	1.19	2.49

DISCUSSION

National BLUP evaluations for pedigree beef cattle are now in place for the numerically most important beef breeds in the UK. As the use of EBVs by breeders in making breeding decisions increases, so should the rates of genetic progress achieved.

The genetic parameter estimates used were assumed constant across breeds. Between breed differences in the observed genetic trends are therefore due to differences in (i) selection policies; (ii) true genetic parameters and (iii) phenotypic variances of traits.

In setting up the evaluations, the structure of the UK pedigree beef population has been considered. The small herd size, and hence low contemporary group size, prompted the consideration of contemporary grouping strategies which help to maximise the accuracy of evaluations. In countries where contemporary group size is usually much higher this would not be of such concern. Conversely, the low herd size is partly responsible for the high use of AI in the UK, which has provided high numbers of genetically connected contemporary groups, across which EBVs can be compared.

ACKNOWLEDGEMENTS

We are grateful to the Meat and Livestock Commission for funding this work.

REFERENCES

- ALLEN, D.M. and STEANE, D.E. (1985) British Cattle Breeders Club Digest No. 40, pp 63-70
- BROTHERSTONE, S. and HILL, W.G. (1986) *Animal Production*, 42 : 297-303
- CRUMP, R.E., SIMM, G., NICHOLSON, D., FINDLAY, R.H., BRYAN, J.G.E. and THOMPSON, R. (1994a) (in preparation)
- CRUMP, R.E., WRAY, N.R., THOMPSON, R. and SIMM, G. (1994b) (in preparation)
- HENDERSON, C.R. (1973) Proc. Anim. Breed. Genet. Symp. in honour of J.L. Lush, Am. Soc. Anim. Sci., 10-41
- HENDERSON, C.R. and QUAAS, R.L. (1976) *Journal of Animal Science*, 43 : 1188-1197
- MOHIUDDIN, G. (1993) *Animal Breeding Abstracts*, 61 : 495-522
- QUAAS, R.L. (1988) *Journal of Dairy Science*, 71(suppl. 2) : 91-98
- SCHAEFFER, L.R. and WILTON, J.W. (1987) Proc. Conf. Genet. Eval. Beef Cattle, Kansas City, pp 25-49
- SIMM, G., STEANE, D.E. and WRAY, N.R. (1990) Proc. 4th World Cong. Genet. Appl. Livest. Prod., XV : 231-243
- THOMPSON, R., WRAY, N.R. and CRUMP, R.E. (1994) *Journal Anim. Breed. and Genet.* (submitted)
- WESTELL, R.A., QUAAS, R.L. and VAN VLECK, L.D. (1988) *Journal of Dairy Science*, 71 : 1310-1318