The Effectiveness of the Best Linear Unbiased Prediction of Beef Sires Using Field Data Collected from Small Farms[1]

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ABSTRACT: Beef sire evaluation using BLUP was investigated under field conditions at small-scale farms. The 6,848 records on fattened Japanese Black cattle steers were obtained from 1981 through 1987. The average number of steers in the subclass of market-year-farm was 5.2. A sire-maternal grandsire mixed model with relationships was used to analyze the data to yield BLUP for the sire and maternal grandsire effects. The regression coefficients of the realized value of progeny on the predicted value calculated using BLUP procedures for daily gain, carcass weight, and marbling score were 1.027, 1.054, and .917, respectively (i.e., the regression almost equaled 1). Therefore, BLUP was shown to be very effective in predicting offspring performance, even using field records collected from small-scale farms.

Key Words: Best Linear Unbiased Prediction, Genetic Models, Small Farms, Beef Cattle, Carcass Quality

Introduction

In Japan, the domestic breed of beef cattle is called Wagyu. They were developed from ancient native cattle that were mixed with some European breeds and were used as draft cattle. Today, they are used for meat production. Among the Wagyu, there are several established breeds; Japanese Black cattle are the largest breed in the Wagyu population.

The Japanese Black cattle are not genetically uniform. They are divided into subpopulations on a prefectural basis (Nomura and Sasaki, 1988). The genetics of each subpopulation depends on which European breed was used and the breeding program adopted by each prefecture.

Cattle numbers are small, in general, within prefectures, herd size is small, and the carcass markets are not large. Usually prefectures conduct a sire evaluation program in which progeny number per sire is small. Accurate sire evaluation is difficult. Therefore, the mixed-model method developed by Henderson (1973) was selected as the best choice to address the difficulties caused both by the number of animals and by the small contemporary group size.

The purpose of this study was to evaluate the effectiveness of the sire evaluation program using a sire-maternal grandsire mixed model in the context of the Japanese situation.

Materials and Methods

The data used were from the Ohita Prefectural Record of Performance Program, which collected records from finished steers of Japanese Black cattle from 1981 to 1987. The finished steers were shipped from the farms in Ohita Prefecture to carcass markets where the steers were slaughtered and sold. Average age of the steers was 853 d. The data were edited to be connected across subclasses such that each market-year subclass had ≥ 100 steers and each farm had ≥ 20 steers. The final number of steers was 6,848. Table 1 gives the numbers by carcass market and year. There were 20 market-year subclasses, 62 farms, and 93 sires. The average number of steers in the market-year-farm subclass was 5.2.

Table 1. Numbers of records used for the present research by year
and by carcass market where the records were collected

Carcass market	Year							Total
	1981	1982	1983	1984	1985	1986	1987	
Ohita	126	99	213	—	—	—	—	438
Osaka	265	207	243	164	197	426	447	1,949
Matsubara	651	644	725	447	383	607	521	3,978
Tokyo	93	247	143	—	—	—	—	483
Total	1,135	1,197	1,324	611	580	1,033	968	6,848

Sires were evaluated using single-trait BLUP with a sire-maternal grandsire model (Everett et al., 1979; Quaas et al., 1979). The numerator relationship among sires and maternal grandsires was used. However, no genetic groups were included. The fixed effects in the model were market-year, farm, fattening period, and slaughter age. The fattening period and slaughter age were included as covariates as follows:

$$y_{ijklm} = M_i + F_j + S_k + (1/2)S'_l + p(P_{ijklm} - \overline{P}) + a_1 (A_{ijklm} - \overline{A}) + a_2(A_{ijklm} - \overline{A})^2 + e_{ijklm},$$

where y_{ijklm} = a record on the average daily gain (kilograms per day), carcass weight (kilograms), or marbling score; M_i = the fixed effect of the ith market-year; F_j = the fixed effect of the jth fattening farm; S_k = the random effect representing one-half of the breeding value of the kth sire; S'_l = the random effect representing one-half of the breeding value of the lth sire as a maternal grandsire; p = linear partial regression of the y_{ijklm} on fattening period of a particular steer; P_{ijklm} and $\overline{P}$ = the fattening period from the start of fattening to shipping to market in number of days of the particular steer and its average, respectively; a_1 and a_2 = linear and quadratic partial regression of the y_{ijklm} on slaughter age of a particular steer; A_{ijklm} and $\overline{A}$ = the slaughter age in days of the particular steer and its average, respectively; and e_{ijklm} = a random residual effect associated with a particular record.

Daily gain was regressed linearly on fattening period and linearly and quadratically on slaughter age. Carcass weight was regressed linearly on both. Marbling score was regressed linearly only on slaughter age. These choices of linear and quadratic terms were based on the statistical significance of the effect as determined by the least squares analysis of variance (Sasaki and Sasae, 1988).

The heritabilities for daily gain, carcass weight, and marbling score used in the mixed-model analysis of the data were .16, .23, and .27, respectively, as reported by Sasaki et al. (1986).

The data were divided into two sets, DATA 1 and DATA 2. This was carried out to confirm the results of selection of sire and maternal grandsires based on their EPD from DATA 1, using the realized values of progeny in DATA 2 of the selected sires and maternal grandsires. The sires were in one of three groups, as shown in Figure 1. Sires of the S_B group had their progeny only in DATA 1, and sires of the S_A group had their progeny only in DATA 2. Sires of the S_C group had their progeny both in DATA 1 and DATA 2.

Best linear unbiased prediction was performed on DATA 1 and compared with realized results from DATA 2. As in the first step, sires in the S_B and S_C groups were evaluated using DATA 1. Then, the sires with $\geq$ 10 progeny and the maternal grandsires with $\geq$ 50 grandsons in the S_C group of DATA 1 were listed in the sire summary with their EPD for the three traits.

The records of steers shipped in 1986 and 1987 (i.e., DATA 2) were corrected for the nongenetic effects of market-year, fattening farm, fattening period, and slaughter age, using the best linear unbiased estimates (BLUE) for the effects obtained from an analysis of all data.

Finally, a certain percentage of sires was selected based on the EPD for each trait from sires listed in the sire summary beforehand. The selection rates equaled 100, 50, 30, 20, or 10%. Maternal grandsires were also selected as well as sires, so that the rates equaled 100, 90, 80, 70, 60, 50, 40, 30, or 20%. Then, steers that had either the selected sire as their father or the selected sire as their father and the selected maternal grandsire as their maternal grandfather were chosen from the adjusted DATA 2, and the average of the steers chosen was calculated to form the realized value for each combination of sires selected with a certain selection rate and maternal grandsires with a certain selection rate.

The predicted value for steers with both sire and maternal grandsire was calculated as follows:

$$\alpha = \frac{\sum_{k=1}^{n} \{S_k + \frac{1}{2}S'_k\}}{n}$$

S i r e Group Number	DATA 1 (1981 - 1985)	DATA 2 (1986 - 1987)
S$_B$ 58	Progeny	
S$_C$ 18	Progeny	Progeny
S$_A$ 17		Progeny

Figure 1. Composition of the data used for the analysis. S$_A$ — group of sires that had their progeny only in DATA 2. S$_B$ — group of sires that had their progeny only in DATA 1. S$_C$ — group of sires that had their progeny both in DATA 1 and DATA 2.

where a is the average predicted value of steers produced from the matings between the selected sires and the daughters of the selected maternal grandsires, n is the number of steers, S$_k$ is the selected sire's EPD of the kth steer, and S$'_k$ is the selected maternal grandsire's EPD of the kth steer. When the maternal grandsire was not listed in the sire summary, S$'_k$ was assumed to be zero.

The value realized in the progeny was calculated as follows:

$$p = \frac{\sum_{k=1}^{n} \hat{Y}_k}{n}$$

where p is the average realized value of the steers, n is the number of steers and $\hat{Y}_k$ is the adjusted measurement of the kth steer.

The realized and the predicted value pairs were calculated for all combinations of the selection rates on the side of sire with those on side of maternal grandsire. The linear regression equation of the realized value on the predicted value and the correlation coefficients between them were calculated by the GLM and CORR procedures of SAS (1985).

Results and Discussion

One of the more difficult problems in animal breeding is to appraise whether a method for the genetic prediction of animals is effective. The problem is that the true genetic values are unknown, and, consequently, predictions by alternative methods cannot be compared with these true values to see which method is more accurate.

Correlation coefficients between the genetic

predictions by different methods have been used to compare them (Miller et al., 1968; Kennedy and Moxley, 1975; Kress et al., 1977; Pollak et al., 1977; Schneeberger et al., 1977; Dempfle and Hagger, 1979; Sasaki and Iwaisaki, 1980; Danell and Eriksson, 1982). However, the correlation coefficient does not describe which method gives the more accurate prediction but merely estimates the
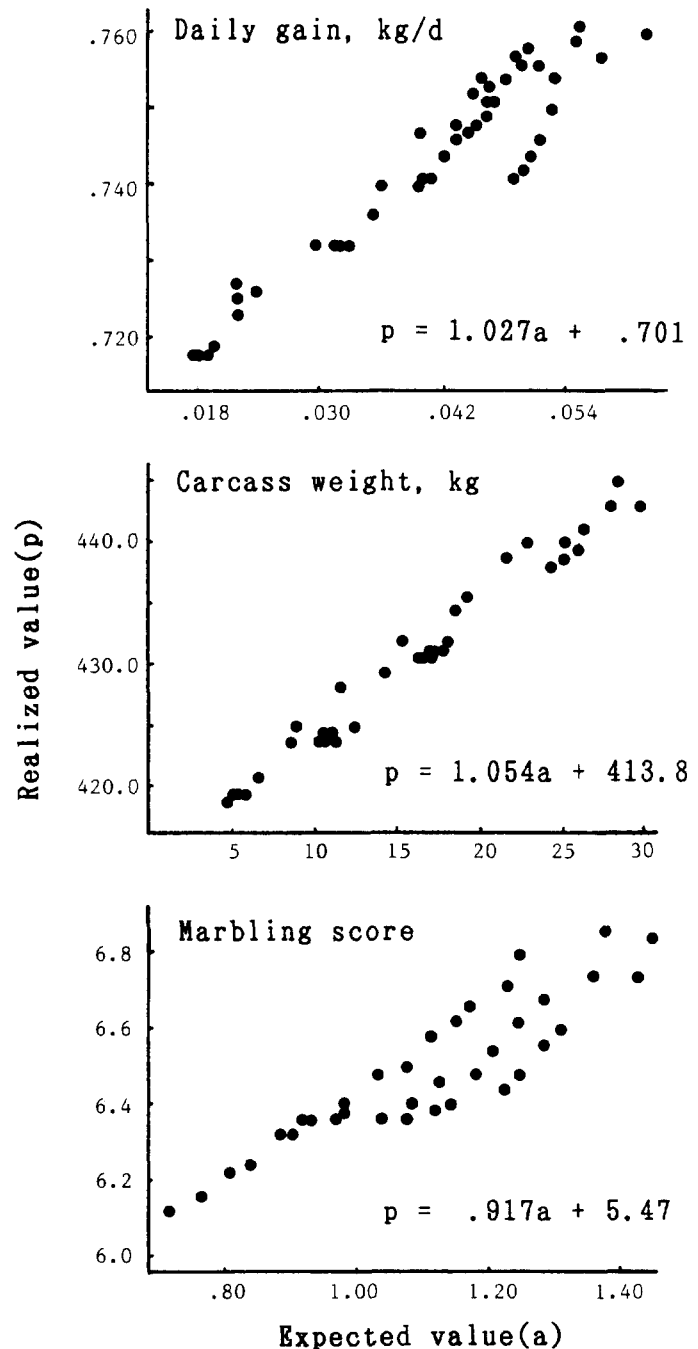

Figure 2. Scatter diagrams and regression equations of average daily gain, carcass weight, and marbling score of the realized-to-expected value pairs. A point is each combination of a selection rate on the side of sire with one on the side of maternal grandsire.

Table 2. Correlation coefficient $r_{(EV)(RV)}$ between the expected value and the realized value

Trait	$r_{(EV)(RV)}$
Daily gain	.95
Carcass weight	.99
Marbling score	.91

degree of closeness of the linear relationship between two predictions.

Error variances of predictions for animals can be compared among methods (Kennedy and Moxley, 1975; Pollak et al., 1977; Sasaki and Sasae, 1988). This seems to be effective to determine which method is more suitable under the given condition but not to appraise whether a method is appropriate or not.

A selection experiment is required to appraise appropriateness. However, this is prohibitive with cattle in terms of time and cost. The idea of comparing predictions with realized values was suggested by Heidhues et al. (1961) and Dempfle and Hagger (1979). Heidhues et al. (1961) compared the sire proofs with the performance of large numbers of subsequent progeny. Dempfle and Hagger (1979) divided the whole data into two parts randomly and compared the sire proofs obtained from the two parts.

Theoretically, if the EPD was accurate and unbiased and the number of the steers chosen was large, the regression line of the realized value on the predicted value should be linear and the coefficient should be close to 1. Underestimation or overestimation should not occur.

The results of our study are as shown in Figure 2. The expected to realized values are plotted for daily gain, carcass weight, and marbling score. Clearly, the trend of the realized with the expected value is upward and roughly linear for the three traits.

Then, the relationships were regressed for the same traits. The regression equations are given in Figure 2. None of the regression coefficients is significantly different from the value 1. This suggests that the EPD obtained using BLUP with the sire-maternal grandsire model give an unbiased prediction of one-half of the true breeding value of a sire and one-fourth of the true breeding value of the maternal grandsire. This prediction accounts for three-fourths the genetic difference. The fact that the regression is close to 1 suggests that in the predicted and the realized value the remainder of the genetic effects are random and this would give a regression of 1. Random mating of grandams to grandsires is a cause. Usually the randomness does not describe the mating system employed in cattle populations correctly. However,

Wagyu cattle had been selected based on visual appraisal until recently and, therefore, grandparents are likely to be mated randomly in terms of performance (i.e., no assortative mating among grandparents seems to have been practiced).

The simple correlation coefficients between the predicted value and the realized value were high (.95 for daily gain, .99 for carcass weight, and .91 for marbling score, see Table 2). We expect that the coefficients become virtually equal to 1 when n is large, as shown in the lower left part of the diagrams in Figure 2, which corresponds to the low selection intensity and a large number of steers.

Implications

This study demonstrates the effectiveness of the sire evaluation program using a sire-maternal grandsire mixed model, even when the average subclass size is small. The use of this method for similar situations can be recommended.

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