DEVELOPMENT OF A PREDICTION EQUATION FOR RETAIL BEEF YIELD PERCENTTO BE USED IN NATIONAL GENETIC EVALUATION SCHEMES

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SUMMARY

Boning room dissection data from 3,084 carcasses were examined to determine which commercial primal cuts would provide a reduced set of cuts to best measure retail beef yield percent (RBY %). Animals were part of the Beef CRC straightbred program and consisted of 2,251 steers and 833 heifers from temperate and tropically adapted breeds. Potential predictors were 10 retail cuts, carcass weight and subcutaneous fat depth at the rib and rump sites. Only 6 primal cuts and the carcass weight appeared in the final equation (R^2 = 89.2 %) which also included the fixed effect of contemporary group defined as herd of origin, sex, and kill. Although the investigation of residuals did not reveal any anomalies, the final prediction equation tended ($P < 0.05$) to overestimate values at the lower end of the scale, and vice versa. The estimate of genetic correlation between predicted and actual RBY % was 0.92.

Keywords: Carcass, genetic evaluation, beef cattle

INTRODUCTION

BREEDPLAN, the National Australian genetic evaluation for cattle produces several carcass EBVs, including percent of retail beef yield (RBY %). Collection of actual yield data is not only costly in terms of labour but also causes considerable disruption to the abattoir labour force. The Cooperative Research Centre for the Cattle and Beef Industry (Beef CRC) has developed a bone-out procedure which involves the measurement of lean meat and fat from individual commercial cuts in addition to clean bone weights (Wt). However, this procedure is not viable under normal commercial conditions.

Most studies on prediction of RBY % include subcutaneous fat depth and/or eye muscle area among their predictors (Gwartney *et al.* 1994; Dikeman *et al.* 1998). However, such predictors are not suitable for the purpose of this study as they are also traits included in National genetic evaluation programs. The objective of this study was to develop an equation with a reduced set of primal cuts to accurately predict RBY % to be used in National genetic evaluation schemes.

MATERIALS AND METHODS

The Beef CRC database contains boning room records on 3,084 animals. Table 1 shows descriptive statistics for actual RBY % by breed type (temperate v tropical) and sex. Temperate breeds included Angus, Hereford, Murray Grey and Shorthorn. Tropically adapted breeds were Brahman, Belmont Red and Santa Gertrudis. Within these breeds, progeny from 229 different sires were represented, with progeny per sire per sire ranging between 1 and 65.

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* AGBU is joint institute of Agriculture and The University of New England

Table 1. Descriptive statistics for retail beef yield percent

Breed type	Sex	N	Mean (%)	STD (%)	Minimum (%)	Maximum (%)
Tropical	Heifer	548	66.87	3.05	58.50	76.77
	Steer	611	68.12	3.16	59.14	76.59
Temperate	Heifer	285	66.70	3.76	54.00	77.16
	Steer	1,640	67.09	3.68	55.00	77.02

Details of the design of the breeding and management regimes used by the Beef CRC have been presented by Robinson (1995). RBY was measured as the total Wt of 17 trimmed boneless retail cuts, plus the Wt of adjusted manufacturing trim, expressed as a percentage of recovered side Wt (Wolcott *et al.* 1997). Cuts were trimmed to a maximum coverage of 3 mm of subcutaneous fat and accessible inter-muscular fat was removed. Because the collection of individual Wt of 17 primals proved to be extremely costly in both time and labour, it was decided to reduce the number of primals to ten. Potential predictors were hot carcass Wt and the individual Wt of ten retail primal cuts (Table 2) from the left side of the carcass. Because of different quartering points at the various abattoirs, cube roll and striploin were combined. Additionally, subcutaneous fat depths at the 12th/13th rib and P8 rump sites (Table 2) were also included to test whether or not it would improve the model.

Table 2. Descriptive statistics for predictor traits

Predictor	Mean	STD	Minimum	Maximum
Outside flat (kg)	4.848	0.911	2.305	8.415
Eye round (kg)	1.955	0.374	0.845	3.382
Rump (kg)	4.416	0.852	2.200	7.940
Cube roll + Striploin (kg)	6.901	1.356	3.235	11.766
Blade (kg)	6.649	1.290	3.360	11.390
Topside (kg)	7.245	1.260	3.670	12.165
Thick flank (kg)	0.610	0.131	0.195	1.930
Knuckle (kg)	4.422	0.722	2.415	7.575
Tenderloin (kg)	1.873	0.380	0.485	3.555
Hot carcass weight (kg)	261.7	52.8	124.0	445.5
12th/13th Rib fat depth (mm)	8.115	4.529	1.000	34.000
P8 Rump fat depth (mm)	10.867	4.770	1.000	36.000

Procedures GLM and REG of SAS (1991) were used to develop the prediction equation. Following Draper and Smith (1998), mean square errors (MSE) were explored to select the best model from the optimum cutoff point for the number of variables in regression. The algorithm used follows:

Step 1. Fit the "full" model with the 12 predictors (Table 2) with linear and quadratic components (thus a total of 24 predictors), and contemporary group (CG) defined as herd of origin, sex, and kill code (*ie.* slaughter house and date, also confounded with finishing and market).

Step 2. Adjust observations on RBY % for CG with the BLUE resulting from the model in Step 1.

Step 3. Obtain $S^2(p)$, the average MSE of all the possible "reduced" regression models with 1, 2, ..., up to 24 predictors (p).

Step 4. Plot $S^2(p)$ over p to obtain an estimate of the optimum number of predictors (p_o) to be included in the final prediction equation.

Step 5. Select the prediction equation with the smallest MSE among those with p_0 predictors.
Step 6. Fit a model with the fixed effect of CG and the predictors selected from Step 5.

Finally, genetic parameters were estimated by REML using VCE 4.2 software from Groeneveld and Garcia-Cortés (1998). Special emphasis was given to the estimate of the genetic correlation (r_g) between actual and predicted RBY %. To assess the predictive capability of the proposed equation, the 3,084 carcasses were randomly split into two groups. One group contained the actual RBY % measure and the other the predicted one. The estimated r_g was then recorded. This process was repeated 10 times. The model for genetic analysis included carcass Wt as covariate, the fixed effect of CG, and the random effects of additive genetic and residual. Ancestors were traced back 5 generations yielding a relationship matrix with 5,458 individuals.

RESULTS AND DISCUSSION

All measures of retail primal cut Wt, carcass Wt, and subcutaneous fat depth were significantly ($P<0.05$) and moderately to strongly correlated with RBY %. The model containing the 12 predictors (Table 2) with linear and quadratic components and the fixed effect of CG accounted for 90.7 % of the variance in RBY % with a residual standard deviation (σ_e) of 1.39 %. This indicates the upper limit of achievable predictive ability.

The plot of $S^2(p)$ against p indicated that only six predictor variables should be included. The resulting prediction equation for RBY % as developed from the final model (including the fixed effect of CG) yielded an R^2 of 89.2 % with a σ_e of 1.45 % and was as follows:

$$\begin{aligned}\text{Predicted RBY \%} = {} & 66.5807 - 0.1286 * \text{Hot Carcass Wt} + 2.5517 * \text{Eye Round Wt} \\ & + 0.8667 * (\text{Cube Roll} + \text{Striploin})\text{ Wt} + 1.1957 * \text{Blade Wt} \\ & + 1.5276 * \text{Topside Wt} + 2.2983 * \text{Tenderloin Wt}\end{aligned}$$

Even though both measurements of fat depth (rib and rump) had one of the strongest raw correlations with RBY % (around -0.6), neither appeared in the final equation. This was attributed to fat depth being positively correlated with all the other predictors and their inclusion did not significantly ($P>0.05$) improve prediction models. By not including any measurements of subcutaneous fat depth, the resulting equation appears suitable for National genetic evaluation schemes without the risk of inflating prediction error covariance and/or removing genetic variation. An additional appeal of the presented equation is the even distribution of cuts across the carcass. Using a slightly different set of primals, Hartjen *et al* (1993) concluded that dissection of the brisket, flat-ribs and thin flank can be used effectively to estimate total carcass composition.

Working with a subset (N = 977) of the data used in the present study, Wolcott *et al* (1997) reported R^2 values for predicting RBY % between 44 % and 70 % for six different market and finishing categories. In their equations, the authors included live weight and real time ultrasound measurements of rib fat depth and eye muscle area as predictors. More recently, Dikeman *et al* (1998) working with steer crosses, reported R^2 values of 93 % for predicting RBY % for an equation including carcass weight, and other indirect measures of yield such as subcutaneous and inter-muscular fat trim percent, marbling score and kidney fat percentage.

In spite of the large R^2 and the exploration of residuals not showing any evident anomaly, our equation tended ($P < 0.05$) to bias values in the lower and upper ends of the scale. The largest overestimation, by 1.71 % on average, occurred for tropical heifers. At the other extreme, temperate steers suffered an underestimation by 0.69 % on average. Similarly, prediction of RBY % for animals finished at feedlots were more likely ($P < 0.05$) to be overestimated (by 0.4 % on average) than those for animals finished on pasture. Also, prediction of RBY % for animals slaughtered for the export market (namely Korean and Japanese) were overestimated by 0.68 % on average, whilst an underestimation by 0.86 % was observed for those animals slaughtered for the domestic market.

Estimates of heritability for actual and predicted RBY % were 0.57 ± 0.06 and 0.47 ± 0.06, respectively. Genetic correlation (r_g) was estimated to be 0.92 ± 0.03, which guarantees an optimum ranking of sires regardless of the measurement used. However, phenotypic variance for predicted RBY % was about half that for true RBY % (1.97 $\%^2$ against 4.23 $\%^2$). When the data were randomly split into two groups, one with the actual RBY % and the other the predicted one, and the process repeated 10 times, the estimated r_g averaged 0.88 and ranged from 0.69 to 1.00.

Results indicate that RBY % can accurately be predicted using a limited number of valuable primal cuts. However, the equation developed here could be of limited use to both producers and abattoirs as an on-line prediction of carcass yield as these groups do not always have access to all predictors. Computerised weighing of individual cuts from identified animals is being considered by some abattoirs, and under these conditions the proposed equation would be of great value. The accuracy of different equations for each breed by sex by market combination is yet to be explored. Further work is also required to test our model on an independent non-CRC data set.

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