

## MULTITRAIT ANALYSIS OF A BEEF CATTLE HERD WITH THE REDUCED ANIMAL MODEL

J.I. WELLER,<sup>1</sup> R.L. QUAAS, and J.S. BRINKS<sup>2</sup>  
Department of Animal Science, Cornell University  
Ithaca, New York 14853, USA

### SUMMARY

Weaning weight, gain on test, and feed consumption of the beef cattle herd at the San Juan Basin Research Center were analyzed with the reduced animal model. Only males were scored for gain on test and feed consumption. Of the 5145 animals with valid records for weaning weight, only 1463 had valid records for all three traits. Random effects were direct genetic effects for these three traits and maternal genetic and environmental effects on weaning weight. Fixed effects were inbreeding level and birth year for all three traits and effects of sex and dam's age and inbreeding level on weaning weight. Because animals that were not parents were absorbed into parents' equations, total number of mixed model equations was only 8095 compared with 22,111 for the complete model. Genetic effects of nonparents were derived by back solution. Variance and covariance components were estimated by Henderson's Method 3. A sire model was used to estimate direct genetic and environmental variance and covariance components. Maternal variance components for weaning weight were estimated with a model that included effects of sire, dam, and maternal grandsire. For all three traits, genetic trends were positive, and environmental trends were not significant. Genetic correlation between gain on test and feed consumption was .81.

### INTRODUCTION

Analysis of beef cattle production records with a multitrait animal model has several advantages over alternative methods. All relationships can be used in calculation of genetic evaluations, and nonrandom mating of animals is considered. Because both genetic and environmental covariances among traits are included in the animal model, records for one trait impact on evaluations for other traits. Breeding values are estimated for all animals for all traits, including animals without records for some or all of the traits analyzed. Difficulties in applying the animal model are 1) programming complexity, 2) computing limitations, and 3) accurate estimation of required parameters.

In a complete animal model analysis, number of equations will be more than total number of recorded animals times number of traits analyzed. In the reduced animal model (Quaas and Pollack, 1980), equations of animals without progeny are absorbed into their parents' equations, which results in approximately one-third the number of equations. Although back solutions must be derived for nonparents, the reduced and complete animal models are equivalent models. The reduced animal model has the added advantage that convergence should be more rapid than with the complete model because diagonal elements of the coefficient matrix are augmented relative to off-diagonal elements.

For beef cattle populations, the only data generally available for most animals are weaning and slaughter weights; paternity usually is unknown. Data from the San Juan Basin Research Center is unique in that both paternity and maternity are known for nearly all animals, and individual feed consumption and weight gain after weaning are recorded for most male calves. Thus, genetic evaluations could be derived for gain on test and feed consumption in addition to weaning weight. Because complete pedigree was known for most animals, estimating maternal genetic and environmental effects on each calf's weaning weight also was possible.

<sup>1</sup>Current address: Institute of Animal Science, ARO, Volcani Center, Bet Dagan 50250, Israel.

<sup>2</sup>Department of Animal Science, Colorado State University, Fort Collins, Colorado 80523, USA.

The goals of this study were to demonstrate feasibility of the reduced animal model for routine genetic analysis, estimate genetic and environmental trends in the research center herd, estimate genetic and environmental parameters of beef production traits, and assess consequences of selection for growth rate.

## MATERIALS AND METHODS

Data were weaning weights of 6941 calves born between 1946 and 1980 and test weights and feed consumption of 2525 bull calves weaned from 1956 through 1980. Gain on test and feed consumption were measured five times over 140 days. Feed consumption was measured as food given minus food remaining. Feed was sufficient for all calves to consume *ad libitum*. Data from animals were not included in the analysis if 1) breed was other than Hereford, 2) weaning weight was unknown or invalid, 3) sex was unknown, 4) either parent was unknown, or 5) dam's age was unknown. Records for gain on test were included only if the calf had valid records for weaning weight and all five test weights. Records for feed consumption were included only if the calf had valid records for weaning weight, gain on test, and all five feed consumption weights. Of the 5145 animals with records included in the analysis, 3623 had records only for weaning weight, 59 had records for weaning weight and gain on test, and 1463 had records for all three traits.

A multitrait mixed-linear model was used:

$$y_{wijklmno} = s_i + a_j + d_k + q_{wl} + t_{wm} + u_{wn} + v_o + p_o + e_{wijklmno}$$

$$y_{glmn} = q_{gl} + t_{gm} + u_{gn} + e_{glmn}$$

$$y_{flmn} = q_{fl} + t_{fm} + u_{fn} + e_{flmn}$$

where  $y$  is trait value for weaning weight ( $w$ ), gain on test ( $g$ ), or feed consumption ( $f$ );  $s_i$  is effect of sex  $i$ ,  $a_j$  is effect of dam's age  $j$ , and  $d_k$  is effect of level  $k$  of dam's inbreeding on weaning weight;  $q$  is fixed effect of level  $l$  of animal's inbreeding and  $t$  is fixed effect of animal's birth year  $m$  on the measured trait;  $u$  is random direct breeding value of calf  $n$  for the measured trait;  $v_o$  is maternal genetic effect of dam  $o$  on her calf's weaning weight;  $p_o$  is maternal permanent environmental effect; and  $e$  is random residual for each trait.

Known additive genetic relationships were assumed to be the only source of covariance among different animals for genetic effects;  $v$  was assumed to have no covariance with other genetic effects, and  $p$  was assumed to have no covariance with any other effect. Covariances among  $e$  for different animals were assumed to be 0. Solution of Henderson's mixed model equations for a multitrait analysis (Henderson and Quaas, 1976) includes inverse of the variance-covariance matrices for genetic and permanent environmental effects [ $\text{Var}(\mathbf{u})$ ]:

$$[\text{Var}(\mathbf{u})]^{-1} = \begin{bmatrix} \mathbf{G}^{-1} \otimes \mathbf{A}^{-1} & \mathbf{0} \\ \mathbf{0} & \mathbf{I} \otimes (1/r_p) \end{bmatrix}$$

where  $\mathbf{G}$  is the 4x4 genetic variance-covariance matrix for the three direct effects and the maternal genetic effect on inbreeding,  $\mathbf{A}$  is the numerator relationship matrix,  $\mathbf{I}$  is an identity matrix,  $r_p$  is variance of  $p$ , and  $\otimes$  denotes a kronecker product. Inverse of  $\mathbf{A}$  was calculated from a list of progeny and their parents using the algorithm of Quaas (1976), which also accounts for inbreeding. Solution of mixed model equations also includes inverse for residuals [ $\text{Var}(\mathbf{e})$ ]: [ $\text{Var}(\mathbf{e})$ ] $^{-1} = \mathbf{R}^{-1} \otimes \mathbf{I}$  where  $\mathbf{R}$  is the 3x3 residual variance-covariance matrix for each individual.

Variance components were estimated by Henderson's method 3 (Henderson, 1953). A sire model was used for gain on test and feed consumption. Direct genetic variance was calculated as 4 times the sire variance component; residual variance for the reduced animal model was calculated as residual for the sire model minus 3 times sire variance. This model was used to estimate variance components for weaning weight:

$$w = Xf + Z_s s + Z_m m + Z_d d + e$$

where  $w$  is a vector of weaning weights;  $f$  is the vector of fixed effects for weaning weight;  $s$ ,  $m$ , and  $d$  are vectors of sire, maternal-grandsire, and dam effects;  $X$ ,  $Z_s$ ,  $Z_m$ , and  $Z_d$  are known incidence matrices, and  $e$  is a vector of random residuals. Solutions for  $f$ ,  $s$ , and  $m$  were computed by direct inversion of the coefficient matrix after absorption of  $d$ . Back solutions then were calculated for  $d$ . The four variance components were computed from appropriate reductions of sums of squares. A matrix ( $C$ ) was derived to relate variance components from Henderson's method 3 to animal model variance components. Estimates for animal model variance components were computed as the vector of variance components from Henderson's method 3 multiplied by  $C^{-1}$ . Covariance components were computed by the method of Searle and Rounsaville (1974).

In the reduced animal model analysis of the complete edited data set, block diagonal structure of the coefficient matrix was exploited to compute only the nonzero elements of the coefficient matrix, and only these elements and the right-hand sides (RHS) of the equations were stored. Gauss-Siedel iteration was continued until mean squared deviation between actual and computed RHS was less than  $10^{-8}$  of mean squares of the actual RHS. Phenotypic trends were estimated as regression of measured trait on birth year. Genetic trends were estimated as regression of each animal's breeding value on its birth year; environmental trends were estimated as regression of year effects on birth year weighted by number of animals born each year.

## RESULTS AND DISCUSSION

All variance component estimates were within parameter space except for  $r_p$ . However, the estimated value of  $-1.7 \text{ kg}^2$  was not significantly different from 0. For the reduced animal model,  $20.7 \text{ kg}^2$  was substituted arbitrarily for this negative value. All four weaning weight variance components then were multiplied by .964 so that total variance for weaning weight would not be affected. Corrected variance components for direct effects are in Table 1. Maternal genetic variance was  $193 \text{ kg}^2$ .

**Table 1.** Variance components using Henderson's method 3 for weaning weight ( $w$ ), gain on test ( $g$ ), and feed consumption ( $f$ ).

Trait	Genetic			Environmental		
	w	g	f	w	g	f
	$\text{kg}^2$	$\text{kg}^2$	$\text{kg}^2$	$\text{kg}^2$	$\text{kg}^2$	$\text{kg}^2$
w	150	76	600	238	43	660
g		270	1246		179	540
f			8765			6931

Table 2 shows heritabilities, genetic correlations, and environmental correlations. Because of the high genetic correlation between gain on test and feed consumption, selection for gain should have a marked effect on consumption.

**Table 2.** Heritabilities (diagonal) and genetic (above diagonal) and environmental (below diagonal) correlations for weaning weight (w), gain on test (g), and feed consumption (f).

Trait	w	g	f
w	.39	.37	.52
g	.21	.60	.81
f	.51	.49	.56

The number of equations was 8095 for the reduced animal model compared with 22,111 for the complete model. The convergence criteria was met after 160 rounds of Gauss-Siedel iteration, but estimates obtained after 100 rounds were only marginally different from final estimates.

Genetic, environmental, and phenotypic trends are in Table 3. Genetic trends were positive, whereas environmental trends were not significantly different from 0. For all three traits, sum of genetic and environmental trends approximated actual phenotypic trends, which indicates that the main factors affecting these traits were have been included in the model.

**Table 3.** Genetic, environmental, and phenotypic trends for weaning weight (w), gain on test (g), and feed consumption (f).

Trait	Trend		
	Genetic	Environmental	Phenotypic
	kg/yr	kg/yr	kg/yr
w, direct	.60	-.22	.63
w, maternal	.38	.00	...
g	.70	.13	.96
f	3.90	3.76	8.24

#### REFERENCES

- HENDERSON, C.R. 1953. *Biometrics* 9: 226-234.  
HENDERSON, C.R. and QUAAS, R.L. 1976. *J. Anim. Sci.* 43: 1188-1197.  
QUAAS, R.L. 1976. *Biometrics* 32: 949-953.  
QUAAS, R.L. and POLLACK, E.J. 1980. *J. Anim. Sci.* 51: 1277-1287.  
SEARLE, S.R. and ROUNSAVILLE, T.R. 1974. *Amer. Stat.* 28: 67-68.