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GENETIC PARAMETERS FOR COW WEIGHT AND HEIGHT USING A REPEATABILITY MODEL IN AMERICAN ANGUS CATTLE

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**ABSTRACT:** Estimates of genetic parameters were obtained from two samples of weights and heights of mature cows provided by the American Angus Association. The first sample consisted of 23,658 records for mature weight (MWT) and 13,012 for mature height (MHT) and the second sample consisted of 23,698 records for MWT and 13,310 for MHT. The four-generation pedigree file included 43,105 animals for the first sample and 44,141 animals for the second sample. Range in ages when cows were weighed was 2 to 11 years at the time of measurement. Variance components were estimated using the MTDFREML programs. Univariate and bivariate analyses were used to estimate genetic parameters for MWT, MHT, and the corresponding genetic correlation. The model included fixed effects of cow age and random cow permanent environmental, contemporary group (herd and year) and residual effects. Heritability estimates (SE) within contemporary group were 0.45 (0.012) for MWT and 0.64 (0.018) for MHT for sample 1 and 0.48 (0.011) for MWT and 0.62 (0.018) for MHT for sample 2. Estimates of repeatability were 0.64 and 0.77 for MWT and MHT, respectively for sample 1 and 0.66 and 0.70 for MWT and MHT, respectively for sample 2. The genetic and permanent environmental correlations between MWT and MHT were 0.80 and 0.75, respectively for sample 1 and 0.83 and 0.69 for sample 2. The estimates of genetic parameters will be used to estimate genetic changes in MWT and MHT from the complete data file.

**Key Words:** Angus, Cow Height, Cow Weight, Heritability

### Introduction

Cow weights and cow heights have been used to estimate lifetime growth curves (Johnson et al., 1990), influence of body size on efficiency (Morris and Wilton, 1976), production including maintenance requirements (Morris and Wilton, 1986), cow-calf profitability, reproduction (Olson et al., 1994), and cull cow value. Mature size can potentially impact the profitability of beef enterprises and thus should be considered in selection programs. Previous direct heritability estimates have been generally moderate to high using various models (Northcutt and Wilson, 1993; Kaps et al., 1999; Rumph et al., 2002).

The objective of the current study was to estimate genetic parameters and (co) variance components for mature weight and mature height of Angus cows using a repeatability model as a first step to estimate genetic trends.

### Materials and Methods

The cow weights and heights data and pedigree files used were supplied by the American Angus Association. Two samples were obtained from the complete data file based on the last digit of the herd code. The first sample contained 23,658 MWT and 13,012 MHT records (Table.1). The second sample contained 23,698 MWT and 13,310 MHT records. The four-generation pedigree files included 43,105 and 44,141 animals for samples 1 and 2, respectively. The records were from cows born between 1983 and 2006. The range in ages when cows were weighed was 2 to 11 years with the majority (80%) of records coming from cows between 2 and 6 years of age. Cows on average had 1.7 records for MWT.

### Animal Model

In matrix notation, the linear model equation for the vector of observations,  $y$ , is:

$$y = Xb + Z + Q + W + e,$$

where  $y$  is the vector of observed records,  $b$  is a vector of fixed effects of age when measured;  $a$  is a vector of random additive genetic effects;  $c$  is a vector of random contemporary group effects;  $W$  is a vector of random permanent environmental effects of the cows;  $X$ ,  $Z$ , and  $Q$  and  $W$  are incidence matrices relating  $Xb$ ,  $Q$ ,  $Z$ , and  $W$  to  $y$ ; and  $e$  is a vector of random residual effects. Univariate and bivariate analyses were used to estimate genetic parameters for MWT and MHT, with Henderson's (1977, 1984) augmented mixed model equations and the inverse of the four generation relationship matrix (Henderson, 1976; Quaas, 1976). Estimates were obtained using the MTDFREML programs (BOLDMAN et al., 1995).

### Results and Discussion

Estimates of variance and covariance components, heritability and repeatability for samples 1 and 2 are reported in Tables 2 and 3. Estimates of heritability for MWT were similar to those from previous reports. Johnson

et al. (1990) estimated heritability to be 0.38 but it was associated with a large standard error (0.30). Kaps et al. (1999) reported an estimate of 0.59 using a two-trait animal model with adjusted weaning weight and repeated mature weights, with fixed effects of weaning and cow contemporary groups, and direct genetic, maternal genetic and maternal permanent environment as random effects. Rumph et al. (2002) obtained heritability estimates ranging between 0.53 and 0.69 using 6 different models with the most optimal model being the full model that included direct and maternal genetic, direct permanent environment and maternal permanent environment as random effects.

For mature weight, Northcutt and Wilson (1993) reported estimates of heritability of 0.45 (0.10) and 0.48 (0.10) for weights adjusted for body condition score and unadjusted for body condition score, respectively, using a two-trait model for mature weight and mature height. For mature height, Northcutt and Wilson (1993) reported estimates of heritability of 0.83 (0.11) using the same model. Estimates of variance components and heritability reported by Northcutt and Wilson (1993) for the two-trait model were similar to those from the single trait analyses in the present study. Estimates of repeatability were 0.64 and 0.65 for cow weight for samples 1 and 2 and were 0.77 and 0.70 for cow height. Contemporary groups accounted for about 50% of phenotypic variance for both MWT and MHT.

Genetic correlations between weight and height were strong and positive (table 4). Previous studies have reported similar results, as shown by Northcutt and Wilson (1993) who estimated the Spearman rank correlation between weight and height to be 0.94. The permanent environmental correlations were also high, ranging from 0.69 to 0.75. In comparison with previous studies it may be important to note that in the present study, the number of animals with records and in the pedigree file were larger. Some of the small differences in estimates also may be caused by differences in models or statistical methods used in the analyses.

### Implications

Results from the current study, as expected, show that both MWT and MHT would respond favorably to selection and that changing one would lead to correlated response in the other. Selection would be more accurate for MHT than for MWT because heritability is greater and because less variation is due to permanent environmental effects. These results also show that selection for the total animal effect (genetic plus permanent environmental values) would be

considerably more accurate than selection for breeding value especially for MWT. The similarity of estimates of variance components for the two samples show that the data can be pooled in the second step of this project using the complete data file to determine if selection has been to increase or decrease MWT and MHT.

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