ESTIMATES OF HERITABILITIES AND GENETIC CORRELATIONS IN POLLED HEREFORD CATTLE SELECTED FOR FEED CONVERSION

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Summary

Performance records of 1459 Polled Hereford cattle were analyzed to estimate heritabilities and genetic correlations of beef cattle traits from birth to maturity. Estimates of heritability (h^2) for birth weight (BWT), weaning weight (WWT), yearling weight (YWT), scrotal circumference (SC), yearling height (YHT), mature height (MHT), and mature weight (MWT) were moderate to high, with the exception of WWT ($h^2 = .14$), and ranged from .38 to .72. The traits associated with feed conversion, daily feed intake (INT), average daily gain (ADG), and feed conversion (CONV) had heritabilities of .24, .25, and .14, respectively. Genetic correlations (r_g) between the growth traits (BWT, WWT, YWT, YHT, MHT, MWT, and SC) were positive and ranged from .20 to .88. The $r_g=.99$ between milk production (MILK) and maternal weaning weight (MWW) indicates that the traits are essentially the same and supports the method in which many breed associations calculate and report expected progeny differences (EPDs) for milk production. The $r_g = .42$ between ADG and INT, $r_g = .27$ between INT and CONV, and the $r_g = -.82$ between ADG and CONV suggest that faster gaining cattle have greater feed intakes and are more efficient.

(Key Words: Selection, Feed Conversion, Growth Traits, Heritability, Genetic Correlation, Polled Hereford.)

Introduction

Feed costs represent a significant economic input to beef producers. To attain greater efficiency in production systems, beef producers should consider including feed conversion in selection programs. Reported heritabilities suggest that selection for more efficient cattle can be effective. However, one of the major stumbling blocks in selecting feed for conversion is the difficulty with which it is measured. It requires measurement of individual animal feed intakes and weight gains, a process that is expensive and not feasible for most beef producers. Therefore, beef producers need to identify traits that have favorable genetic associations with feed conversion, are easily and cost effectively measured, and can be incorporated readily into a selection program. Our purpose was to estimate the heritabilities and genetic correlations of beef cattle traits from birth to maturity and provide producers with an indirect means for improving feed conversion.

Experimental Procedures

The data set examined in this study contained the performance records of 1459 Polled Hereford cattle born from the spring of 1967 through the spring of 1979. These data were the result of a project conducted at Kansas State University in which animals were selected on the basis of improved feed conversion. This herd was assembled in 1967 using animals donated by breeders from several states. The original animals (42 females and 5 males) represented 34 herds

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from Colorado, Illinois, Kansas, Missouri, Oklahoma, and Pennsylvania. From 1967 to 1971, animals in the herd were mated randomly to increase the size of the herd and to provide a foundation herd from which the selection and control herds would be established. Beginning with the 1971 breeding season, cows were assigned randomly to either the selection or control herds. Once these herds were established, they were closed, and no other genetic material was introduced. Each year in the selection herd, the two bulls exhibiting the best feed conversion (feed/gain) were selected as herd sires and used for 2 consecutive years. In the control herd, the first bull born to the oldest herd sire was selected to replace his sire. These bulls were used in the control herd for approximately 6 years.

Cows in both the selection and control herds were maintained on native Kansas tall-grass prairie throughout the year and were supplemented in the winter. Cows were bred to calve in March and April. Breeding was primarily by natural service during a 60 to 70 day breeding season. Progeny were weaned in the fall at approximately 200 days of age. Following a 3 to 4 week weaning period, bull calves were placed on an individual 140-day postweaning performance test, which allowed for the selection for feed conversion. The ration consisted of 25% prairie hay, 15% dehydrated alfalfa, 43% corn, 12.5% soybean meal, 4% molasses, and .5% salt. Heifers were group fed and not selected on the basis of improved feed conversion. In both the selection and control herds, cows were culled if they: (1) were not pregnant at the end of the breeding season, (2) had severe structural problems, or (3) were horned. Birth weight (BWT), weaning weight (WWT), yearling weight (YWT), yearling height (YHT), daily feed intake (INT), average daily gain (ADG), feed conversion (CONV), scrotal circumference (SC), scanned ribeye area (REA), scanned backfat thickness (FAT), mature height (MHT), mature weight (MWT), and milk production (MILK) records were available for analysis. The number of observations, means, and standard deviations are presented in Table 1.

A multiple-trait, derivative-free, restricted maximum likelihood procedure (MTDFREML) was used to analyze the data generated in this study. A full animal model was used to calculate the genetic and phenotypic (co)variances. The fixed effects used in the model included age of dam (2, 3, 4, 5-10, and >10 years) and contemporary group (sex and year of birth). For the analyses of MHT and MWT, age of cow was the only fixed effect included in the model. Year of milking and age at milking were the fixed effects used in the analyses of milk production. Ages at which various measurements were recorded were used as covariates for the respective trait. Average weight maintained over the 140-day test period was used as a covariate in the analyses of INT and CONV. Maternal and permanent environmental effects were included as random effects in the analyses of BWT and WWT.

Results and Discussion

Heritabilities (h^2) provide an indication of the amount of genetic change that can be made through selection. The heritabilities that were estimated for the traits in this study generally would be considerate moderate to high (Table 2). The traits associated with weight, BWT, WWT, YWT, and MWT, had heritabilities of .38, .14, .39, and .47, respectively; generally within the range of reported estimates. The maternal heritabilities for BWT and WWT were .14 and .18, respectively. Traits related to structure usually have high heritabilities. The same held true for our study. Yearling height had a heritability of .52, and MHT had a heritability of .72. In this study, the traits associated with feed conversion (feed/gain) included ADG, INT, and CONV, which had heritabilities of .25, .24, and .14, respectively. Ultrasound technology allows for the measurement of various beef cattle traits without slaughter. Scanned backfat thickness ($h^2 = .25$) and REA ($h^2 = .19$) were moderately heritable. Scrotal circumference was found to be highly heritable, with an estimate of .48. The heritability estimate for MILK in this study was .19.

Genetic correlations (r_g) measure the strength of the relationship between the breeding values of two traits. They provide an estimate of how traits will react in a selection program. The genetic correlations estimated for the traits in this study are presented in Table 2. The genetic correlations between growth traits (BWT, WWT, YWT, MWT, YHT, and MHT) were found to be strong and positive, ranging from .33 to .88. The strength of these correlations was expected, because many of the same genes are involved in the expression of the growth traits and also because of the part-whole relationship that many of the traits share. The genetic correlations between traits associated with feed conversion (INT, ADG and CONV) and other traits in the study were of various magnitudes and signs. The r_g = .42 between ADG and INT, r_g = .27 between INT and CONV, and the r_g = -.82 between ADG and CONV suggest that faster gaining cattle have greater feed intakes and are more efficient. Average daily gain on test had negative associations with BWT (r_g = -.01) and WWT (r_g = -.22) and positive associations with YWT (r_g = .49) and MWT (r_g=.72). This indicates that animals with poor preweaning performance had greater average daily gains during the postweaning test period. Animals with greater postweaning gains were heavier when yearling and mature weights were measured. Larger framed animals had greater postweaning average daily gains, as evidenced by the genetic associations between ADG and YHT (r_g=.65) and between ADG and MHT (r_g=.97). Negative genetic correlations were found between INT and BWT (r_g = -.35) and between INT and WWT (r_g = -.61), suggesting that animals with poor preweaning performance had greater feed intakes during the postweaning performance test period. The positive genetic association between INT and YWT (r_g = .59) indicates that those animals with greater feed intakes during the post-weaning period had heavier weights at the end of the test. The genetic associations between SC and many of the growth traits (BWT, WWT, YWT, YHT, and ADG) were positive. Scrotal circumference had a positive association (r_g = .25) with MHT and a negative (r_g = -.11) association with MWT. This suggests that animals with larger scrotal circumferences reached maturity sooner and had lighter mature weights. The genetic correlations between REA and other growth traits (BWT, WWT, YWT, YHT, ADG, and SC) ranged from .18 to .70. These correlations suggest that faster growing cattle have the propensity to have larger REA. The genetic association between MILK and maternal WWT was found to be very strong (r_g = .99). This suggests that these traits are essentially the same. Milk expected progeny differences (EPDs), published by many breed associations, are calculated as maternal weaning weight. The strong correlation between MILK and MWW lends support for this method of estimating an animal's genotype for milk production.

Table 1. Summary of Traits Analyzed

Traits[a]	N	Mean	SD	Minimum	Maximum
BWT (lb)	1369	73.24	9.63	36.99	99.01
WWT (lb)	1284	383.80	68.23	150.00	590.00
YWT (lb)	1045	715.07	145.42	325.01	1047.99
YHT (in)	774	41.43	1.97	31.00	49.00
INT (lb)	486	16.67	2.36	9.11	24.29
ADG (lb)	534	2.80	.42	.68	3.77
CONV (lb)	486	5.93	.82	3.95	13.40
SC (cm)	259	32.57	2.62	25.90	41.00
REA (in²)	806	8.56	1.94	4.50	14.38
FAT (in)	806	.20	.10	.01	.76
MHT (in)	136	46.86	1.77	42.22	51.67
MWT (lb)	156	1025.22	107.06	757.00	1350.00
MILK (lb)	115	2498.63	859.94	964.46	8641.46

[a]BWT = birth weight; WWT = weaning weight; YWT = yearling weight; YHT = yearling height; INT = daily feed intake; ADG = average daily gain; CONV = feed/gain; SC = scrotal circumference; REA = scanned ribeye area; FAT = scanned backfat thickness; MHT = mature height; MWT = mature weight; MILK = 205-day milk production.

Table 2. Heritabilities and Genetic Correlations of Traits Analyzed[a]

Traits[b]	BWT	MBW	WWT	MWW	YWT	YHT	INT	ADG	CONV	SC	REA	FAT	MHT	MW	MILK
BWT	**.38**														
MBW	-.35	**.14**													
WWT	.69	.36	**.14**												
MW	-.39	.73	-.10	**.18**											
YWT	.33	.83	.70	.89	**.39**										
YHT	.44	.39	.60	.51	.68	**.52**									
INT	-.35	-.03	-.61	-.60	.59	.05	**.24**								
ADG	-.01	.88	-.22	.58	.49	.65	.42	**.25**							
CONV	.08	-.95	.53	.46	-.73	-.40	.27	-.82	**.14**						
SC	.35	.20	.49	.53	.32	.40	-.25	.01	.06	**.48**					
REA	.55	.48	.41	.75	.70	.35	-.02	.18	.24	.18	**.19**				
FAT	.70	.26	.01	.64	.37	.15	-.02	-.06	.37	.48	.30	**.25**			
MHT	.58	.40	.69	.51	.79	1.0	.12	.97	.64	.25	.82	.02	**.72**		
MWT	.47	.61	.67	.18	.69	.73	-.36	.72	-.95	-.11	.73	-.47	.88	**.47**	
MILK	.38	-.57	.01	.99	.45	.16	-1.0	-.27	-.46	.15	.31	.43	-.15	-.16	**.19**

[a]Heritabilities (bold, underlined) lie on the diagonal; Genetic correlations lie below the diagonal.
[b]BWT = birth weight; MBW = maternal birth weight; WWT = weaning weight; MWW = maternal weaning weight; YWT = yearling weight; YHT = yearling height; INT = daily feed intake; ADG = average daily gain; CONV = feed/gain; SC = scrotal circumference; REA = scanned ribeye area; FAT = scanned backfat thickness; MHT = mature height; MWT = mature weight; MILK = milk production.