Estimating Heritability of Percentage of Intramuscular Fat and Ribeye Area Measures By Scan Session in Angus Bulls and Heifers

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Summary

The present study included 3,066 ultrasound-predicted percentage of intramuscular fat (UPFAT) and 4,502 ultrasound ribeye area (UREA) measures of bulls and heifers from the Iowa State University beef cattle breeding project. Data were collected over a four-year period between 1998 and 2001. The objective of the current study was to estimate variance components and heritability of UPFAT and UREA. Data were analyzed based on single- and multiple-trait animal models. Heritability of UPFAT increased from a minimum of 0.36 at a mean age of 37 weeks to a maximum of 0.54 at a mean age of 54 weeks. Heritability of UREA ranged from 0.30 at a mean age of 35 weeks to a maximum of 0.48 at a mean age of 50 weeks. Heritability of yearling UPFAT and UREA were 0.50 and 0.45, respectively. For the range of ages included in the present study the results suggest optimum heritability of UPFAT and UREA starting at about one year of age.

Introduction

National cattle evaluation programs use ultrasound-measured traits to compute animal expected progeny differences (EPD). Data for such evaluations come from bulls and developing heifers measured at about 12 and 14 months of age, respectively. The choice of these end-points is based on practical herd management and also to allow breeding cattle differentiate themselves genetically than earlier measurements. However, to maximize genetic response to selection, ultrasound data should be collected at the earliest possible time when individual animal phenotypic differences are best indicators of genetic ranking. Therefore, the general trend in variance components and genetic parameter estimates needs to be determined for a wide range of ages and production conditions.

The objective of this study was to estimate variance components and heritability of serially measured UPFAT and UREA in purebred Angus bulls and heifers.

Materials and Methods

Source of Data

Bulls and heifers in the present study came from the Iowa State University beef cattle breeding project. The project is designed to develop two lines of beef cattle for use as a research base to answer questions that influence genetic improvement of beef cattle. The two selection lines include a Quality line (Q-line) and a Retail line (R-line). Bulls in the Q-line are primarily selected for UPFAT EPD. Bulls in the R-line are selected primarily for ultrasound measured ribeye area (UREA) and percentage of retail product (PRP) EPD. In addition, bulls in both lines are required to meet birth weight EPD, fertility, and functional criteria.

The project was initiated in 1997 with the purchase of 285 spring 1996-born, purebred registered Angus heifers. Heifers were purchased from two herds in Nebraska and three herds in South Dakota. The heifers were randomly assigned to the two selection lines. Both lines were managed under similar conditions at the Rhodes research and demonstration farm located in central Iowa. Each year, breeding took place in June and July, with calving the following spring.

After weaning, bull calves were fed a 1.3 Mcal NEg /kg diet to allow a mean weight gain of 1.5kg /day. Replacement heifers were fed a 1.1 Mcal NEg/kg diet to allow a mean daily weight gain of 0.70 to 1.1 kg /d

Animals and Scanning Procedure

Serial ultrasound data were collected on progeny born at the Rhodes farm during the spring of 1998 to 2001. Each year the weaned bull and heifer calves were scanned four to eight times for ultrasound traits starting at a mean minimum age of 27 weeks, with an average interval of 4 to 6 weeks between scans. Bulls and heifers were scanned using an Aloka 500V real-time ultrasound machine, equipped with a 3.5-MHZ, 17.2 cm linear array transducer (Coromertics Medical Systems Inc., Wallingford, CT) or Classic Scanner-200, equipped with a 3.5-MHz, 18-cm transducer (Classic Ultrasound Equipment, Tequesta, FL).

Data Analysis

The current report includes information from two sets of data. Analysis of UPFAT was done based on 3,066 observations from 675 bulls and heifers born during the spring of 1998 to 2000 (data set I). However, UREA information included additional data from 248 spring 2001 born progeny (data set II). Ultrasound data were divided into groups based on scan sessions across years. Ultrasound-predicted percentage of intramuscular fat measures from the first five scans across years were used. Data from other scans were excluded due to small sample size and convergence problem. Data were analyzed using a single-trait animal model that included fixed effects of CG (birth year, sex, and pen), linear effect of age at measurement, random effects of animal, and an error term. A five-trait animal model was used to determine phenotypic and genetic correlation between consecutive scans.

However, the first six scan sessions were used in the analysis of UREA. All parameter estimates were obtained using a six-trait animal model that included the same fixed and random effects as UPFAT models.

Results and Discussion

Number of observations and other information used in the current analysis are provided in Tables 1 and 2. For both traits mean ultrasound measures increased with mean age.

Heritability (h^2) of UPFAT increased from a minimum of 0.36 at a mean age of 37 weeks (scan 1) to a maximum of 0.54 at a mean age of 54 weeks (scan 5). The increase in h^2 seems to be influenced by a relatively large increase in direct additive genetic variance with advancing scan sessions. Direct additive genetic variance increased by 163% from the first to the fifth scan. However, error variance values were nearly constant across scan sessions.

Table 2 shows a general increase in direct additive genetic variance for UREA measures with advancing scan sessions. Additive direct genetic variance values increased from 8.67 cm^4 at the first scan (35 weeks) to a maximum of 19.48 cm^4 at the sixth scan (56 weeks). Heritability of UREA ranged from 0.30 at a mean age of 35 weeks to a maximum of 0.48 at a mean age of 50 weeks. Heritability of yearling UPFAT and UREA were 0.50 and 0.45, respectively.

For both traits genetic association between scans decreased as the duration (distance) between scans increased. For instance, genetic correlation of UPFAT at 1st scan with measurements made in the 2nd, 3rd, 4th, and 5th scan were 0.93, 0.97, 0.90, and 0.88, respectively. Similarly, genetic correlation between yearling scan (scan 4) and UPFAT measures for the 2nd, 3rd, and 5th scans were 0.94, 0.96, and 0.99, respectively. For UREA measures, genetic correlation between yearling measures (scan 5) and those of scans 1, 2, 3, 4, and 6 were 0.91, 0.95, 0.96, 0.99, and 0.97, respectively.

For the range of ages included in the present study, results suggest a medium to high genetic control of UREA and UPFAT measures and that h^2 of both traits are at their optimum starting at about one year of age. The strong genetic association between scans suggests that measures at different scans are controlled by the same set of genes. Therefore, selecting for UPFAT and UREA at any of these mean ages would increase yearling measures. However, considering the relatively low h^2 of measures at earlier ages, individual selection based on earlier measures may reduce rate of genetic progress.

In the current analysis data were divided by scan sessions across years. However, this approach may not allow an efficient use of the entire data to generate trends in genetic parameter estimates. Hence, data pooled across years should be re-analyzed using random regression models.

Implications

Heritability of UPFAT and UREA in young Angus cattle are at their optimum at around one year of age. Therefore, phenotypic differences in yearling UREA and UPFAT are good measures of genetic potential for the receptive traits.

Table 1. Summary of results for UPFAT measures at different scan session across years.

Scan	n	Means (SD)		Estimates		
		UPFAT	Age , weeks	$\sigma_a^2 \pm$ SE	$\sigma_e^2 \pm$ SE	$h^2 \pm$ SE
1	587	3.64 (0.99)	36.97 (3.37)	0.24 ± 0.08	0.43 ± 0.07	0.36 ± 0.12
2	671	3.88 (0.92)	40.96 (3.70)	0.26 ± 0.07	0.38 ± 0.06	0.40 ± 0.10
3	658	4.16 (0.98)	47.67 (4.84)	0.35 ± 0.09	0.43 ± 0.07	0.45 ± 0.11
4	654	4.37 (1.15)	52.12 (4.95)	0.46 ± 0.11	0.47 ± 0.08	0.50 ± 0.11
5	496	4.67 (1.40)	54.33 (3.71)	0.63 ± 0.21	0.48 ± 0.16	0.54 ± 0.15

[a]UPFAT = ultrasound-predicted percentage intramuscular fat, σ_a^2 = direct additive genetic variance (%^{2}), σ_e^2 = error variance (%^{2}), h^2 = heritability.

Table 2. Summary of results for UREA measures at different scan session across years.

Scan	n	Means (SD)		Estimate		
		UREA	Ages, weeks	$\sigma_a^2 \pm$ SE	$\sigma_e^2 \pm$ SE	$h^2 \pm$ SE
1	863	47.52 (9.02)	34.90 (3.82)	8.67±2.33	20.59±2.02	0.30 ± 0.07
2	847	54.47 (9.17)	39.53 (4.05)	12.93±3.00	20.72±2.38	0.38 ± 0.08
3	835	62.16 (9.39)	45.48 (5.47)	13.79±3.18	23.06±2.53	0.37 ± 0.08
4	810	68.59 (8.94)	50.25 (5.43)	18.97±3.83	20.91±2.81	0.48 ± 0.08
5	656	75.37 (10.08)	52.90 (4.12)	18.24±4.21	22.72±3.23	0.45 ± 0.09
6	491	77.35 (11.62)	55.91 (3.46)	19.48±5.36	27.58±4.32	0.41 ± 0.10

[a]UREA = ultrasound ribeye area (cm^2), σ_a^2 = direct additive genetic variance (cm^4), σ_e^2 = error variance (cm^4), h^2 = heritability.