# **Carcass EPDs from Angus Heifer Real-time Ultrasound Scans**

### A.S. Leaflet R1736

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#### Summary

The objective of this research was to use developing Angus heifer real-time ultrasound records to estimate genetic parameters and calculate carcass EPD for external 12-13<sup>th</sup> rib fat (FAT), rump fat thickness (RFAT), ribeye area (REA), and % intramuscular fat (%IMF). Heritability estimates are all of a moderate level  $(\geq .40)$  and are higher than the estimates determined previously with bull-only ultrasound data. Genetic correlations are generally of the same magnitude and same sign as previously reported with the bull-only ultrasound data. Angus breeders need to be alerted to the fact that developing heifers can be scanned to accurately predict carcass merit in steer-mate half-sibs. The results of this research indicate that the heifer data may be more accurate than the half-sib yearling bulls findings because the heritability estimates from the heifer data are higher than those estimated from the yearling bull data.

#### Introduction

Iowa State University has just completed a two-year research project with the American Angus Association dealing with using real-time ultrasound to scan young seed stock animals for body composition traits. One of the primary objectives of this research project was to address the genetic aspects of ultrasound measured traits and to develop expected progeny differences (EPD) for carcass traits. The objective of this research was to use developing Angus heifer real-time ultrasound records to estimate genetic parameters and calculate carcass EPD for external 12-13<sup>th</sup> rib fat thickness (FAT), rump fat thickness (RFAT), ribeye area (REA), and % intramuscular fat (% IMF).

#### **Materials and Methods**

Scans were collected over the calendar years of 1998-9. There were 9,720 heifers represented in the unedited data set. After edits, there were 8,630 observations used for the analysis. Edits included removal of animals with missing trait measures, removal of measures taken outside of the age windows, and removal of single-progeny sire records. Adjustments to the raw records were accomplished according to current adjustment procedures being used by the American Angus Association. The adjustment endpoint is 390 days of age. Means of the measures of the unedited data set by equipment type (Classic Scanner 200-CS200 and Aloka 500-A500) and for the edited across equipment data set are presented in Table 1.

Variance components for the adjusted traits of scan weight (SWT), FAT, RFAT, REA, % IMF and percent retail product (% RP) were estimated using restricted maximum likelihood (REML) procedures. The model was a sirematernal grandsire multiple trait mixed-model fitting contemporary groups as a fixed effect. A contemporary group is defined by herd, weaning contemporary group, and scanning contemporary group. Expected progeny differences (EPD) are a by-product of the variance component estimation algorithm. These procedures are the same as those used previously with the carcass data and yearling bull ultrasound data.

Trait	A500		CS200		Combined (edited)	
	Mean	STD	Mean	STD	Mean	STD
Age, d	398	31	386	30	395	30
Gain, lbs/d	1.55	.52	1.53	.38	1.56	.48
Scan wt, lbs	842	121	835	101	846	112
Adjusted scan wt, lbs	831	111	841	93	834	102
% IMF, %	4.22	.96	3.69	.91	4.07	.97
Adjusted % IMF, %	4.17	.96	3.71	.88	4.05	.96
Ribeye area, sq. in.	9.10	1.46	9.11	1.27	9.17	1.38
Adjusted ribeye area, sq. in.	9.15	1.40	9.28	1.21	9.25	1.32
12-13 <sup>th</sup> rib fat thickness, in.	.21	.11	.22	.10	.22	.10
Adjusted 12-13 <sup>th</sup> rib fat thickness,	.21	.11	.22	.10	.22	.10
in.						
Rump fat thickness, in.	.28	.12	.33	.11	.30	.12
Adjusted rump fat thickness, in.	.28	.12	.34	.11	.30	.12
Adjusted percent retail product, %	65.2	1.4	65.1	1.3	65.1	1.37
Number of animals	7,349		2,371		8.630	

## Table 1. Live animal and ultrasound measures for developing Angus heifers (1998-9).

#### **Results and Discussion**

Heritability estimates, genetic correlations and phenotypic correlations are presented in Table 2. Product-moment ( $r_p$ ) and Spearman-rank correlations ( $r_s$ ) between the ultrasound EPD and the Spring 2000 Angus carcass EPD are presented in Table 3 for three accuracy levels (.40, .70, and .85). The carcass database is primarily composed of steer progeny; however, there are some heifer progeny records in the data.

Heritability estimates are all of a moderate level ( $\geq$  .40) and higher than the estimates determined previously with

bull-only ultrasound data. Genetic correlations are of generally the same magnitude and same sign as previously reported with the bull-only ultrasound data.

Carcass EPD based ultrasound scans of developing heifers compare favorably with the carcass EPD (based primarily steer progeny data). As accuracy increases (more progeny), both the product moment and rank correlations improve to moderately high levels.

Table 2. Heritability estimates,	genetic correlations and	phenotypic correlations	for developing	Angus heifers
(390-day endpoint).				

Trait	SWT	FAT	RFAT	REA	% IMF	% RP
SWT	.50 <sup>a</sup>	.21 <sup>b</sup>	.20	.34	19	33
FAT	.33°	.48	.74	.23	.09	53
RFAT	.33	.64	.56	.18	01	40
REA	.43	.28	.29	.40	.04	.56
%IMF	.00	.18	.14	.00	.42	.08
%RP	29	51	29	.57	11	.46

<sup>a</sup>Heritability estimates on the diagonal.

<sup>b</sup>Genetic correlations upper off-diagonals.

<sup>c</sup>Phenotypic correlations lower off-diagonals.

Table 3.	<b>Comparison of ultrasou</b>	nd and carcass EPI	) for ranking sires	s for the traits of FAT	<b>F. REA and %IMF</b>
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		Traits					
		FAT	FAT REA		A	% IMF	
Accuracy	No. of	r <sub>p</sub>	r <sub>s</sub>	r <sub>p</sub>	r <sub>s</sub>	r <sub>p</sub>	r <sub>s</sub>
level	Sires	-		-		-	
.40	197-207	.44	.42	.42	.43	.49	.46
.70	52-53	.52	.53	.68	.70	.55	.53
.85	17-20	.62	.72	.65	.76	.69	.69

#### Implications

Angus breeders need to be alerted to the fact that developing heifers can be scanned to accurately predict carcass merit in steer-mate half-sibs. The results of this research indicate that the heifer data may be more accurate than half-sib yearling bulls findings because the heritability estimates from the heifer data are higher than those estimated from the yearling bull data.

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