Partitioning Variation in Measurements of Beef Carcass Traits Collected Using Ultrasound

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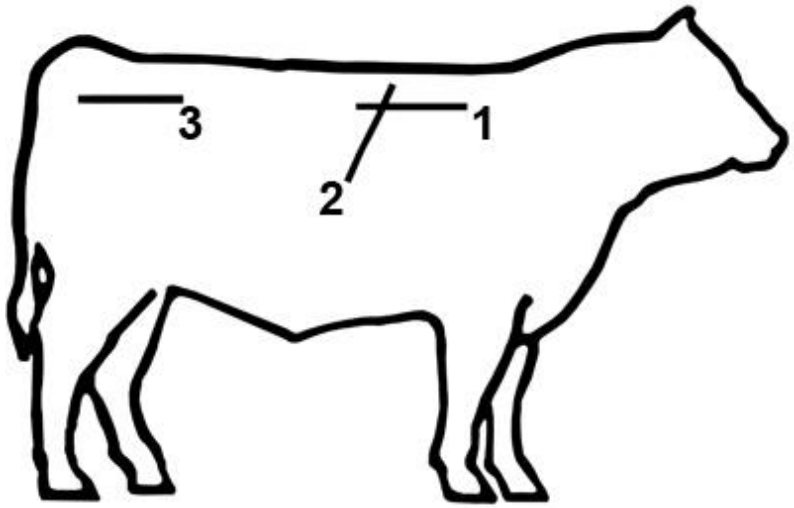
Excellence in Research and Development

ULTRASOUND

- Method of measuring carcass traits
- Utilized since the 1950's
- Quick, relatively inexpensive, non-invasive
- Readily incorporated into multiple-trait genetic prediction

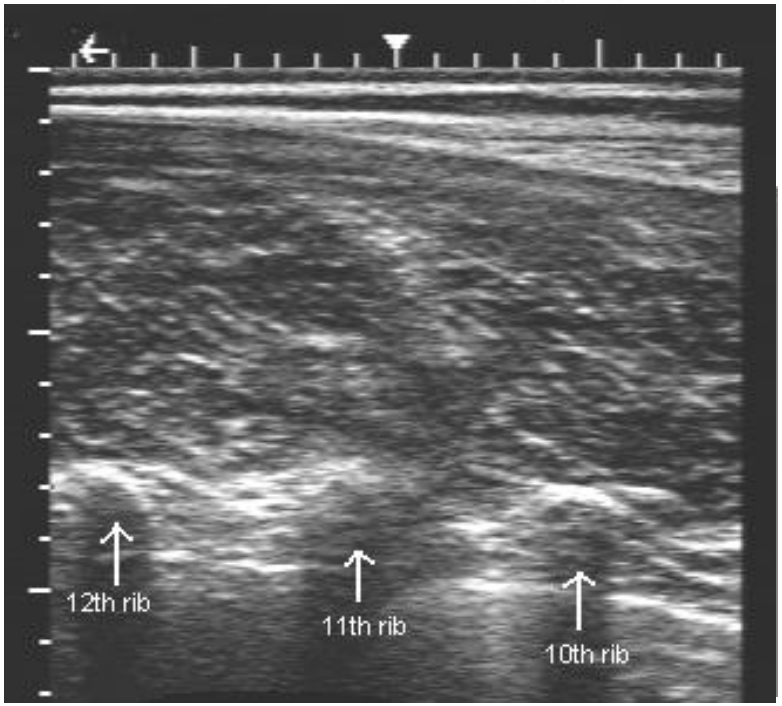
American Hereford Association

CARCASS ULTRASOUND



Measurements

- Intramuscular Fat (IMF)
- Longissimus Muscle Area
- Subcutaneous Fat
- Rump Fat

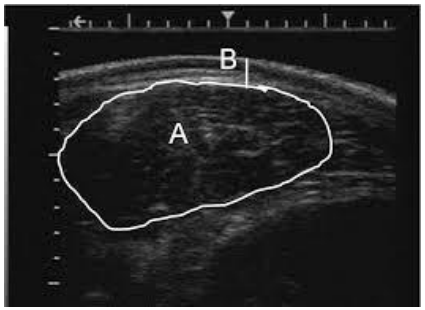


Top: University of Georgia Extension, 2018
Bottom: Carr et al., Ultrasound and Carcass Merit of Youth Market Cattle, University of Florida Extension

FLOW OF ULTRASOUND DATA

Ultrasound Technician

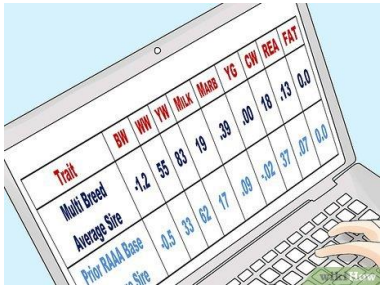
Imaging Laboratory



Breed Associations

AMERICAN ANGUS ASSOCIATION
THERE'S MORE PROFIT WITH ANGUS

EPDs



Genetic Selection

INTRODUCTION

- Abundant attention given to incorporation of data into systems of genetic evaluation
- Far less attention given to the underlying assumptions
- Technician and interpretive laboratory effects are assumed to be small due to UGC certification
- Homogeneity of additive genetic and residual variances

HYPOTHESES

- Homogeneity of within technician variances
- Technician variance = 0
- Homogeneity of additive genetic and residual variances across imaging laboratories
- Within trait, genetic correlations between imaging laboratories = 1

Informally, *it does not matter who scans the cattle or which laboratory interprets the images*

DATA USED

ANGUS THE BUSINESS BREED

American HEREFORD ASSOCIATION

SimGenetics PROFIT THROUGH SCIENCE American Simmental Association

- Collected from 2015 to 2017
- Previously incorporated into national cattle evaluation
  - Animal ID
  - Contemporary group
  - Technician ID (includes technology)
  - Imaging laboratory
  - Longissimus muscle area (LMA)
  - Intramuscular fat (IMF)
  - Subcutaneous fat depth (SFD)

All of the data came from images that had passed the QC of the interpretation laboratory and the breed association

DESCRIPTION OF DATA - ANGUS

Trait	Interpretation Laboratory	Number of scanning technicians - cor… gr…	N…	Phenotypic …ard …on
LMA, cm^2	1	61 – 2435	34952	15.2
	2	14 – 1641	14719	16.3
	3	18 – 1415	16288	13.8
SFD, mm	1	61 – 2435	34952	2.77
	2	14 – 1641	14719	2.80
	3	18 – 1415	16288	2.72
IMF, %	1	61 – 2435	34960	1.30
	2	14 – 1641	14719	1.31
	3	18 – 1415	16288	1.51

N=5491

N≈65953

DESCRIPTION OF DATA - HEREFORD

Trait	Interpretation Laboratory	Number of scanning technicians - cor… gro…	…	Phenotypic
LMA, cm^2	1	45 – 2211	23122	14.3
	2	12 – 1496	11490	15.5
	3	9 – 865	8546	13.9
SFD, mm	1	45 – 2214	21465	2.59
	2	13 – 1499	10366	2.51
	3	9 – 865	7914	2.71
IMF, %	1	45 – 2209	23120	0.98
	2	12 – 1498	11492	0.76
	3	9 – 867	8568	1.20

N=4572

N≈43158

DESCRIPTION OF DATA - SIMMENTAL

Trait[1]	Interpretation Laboratory	Number of scanning technicians - cont… gr…	…mbe…	Phenotypic …d
LMA, cm^2	1	53 – 1963	25799	14.7
	2	11 – 780	6018	16.2
	3	23 – 1675	16481	15.6
SFD, mm	1	53 – 1963	25799	2.40
	2	11 – 780	6018	2.07
	3	23 – 1675	16481	2.34
IMF, %	1	53 – 1963	25799	1.02
	2	11 – 780	6018	0.81
	3	23 – 1675	16481	1.14

N N=4418 N=48298

STATISTICAL MODEL

$$y_{ijk} = \mu + t_i + c_{ij} + a_{ijk} + e_{ijk}$$

y_{ijk} = Ultrasound carcass phenotype for k^{th} animal

μ = Overall mean

t_i = Effect of i^{th} technician

c_{ij} = Effect of j^{th} contemp. group scanned by i^{th} technician

a_{ijk} = Effect of additive genetics by the k^{th} animal

e_{ijk} = Residual deviation from model effects

Linear model fitted using MTDFREML

All effects, except μ, were considered <u>random</u>

$$t \sim N(0, \sigma_t^2) \qquad c \sim N(0, \sigma_c^2) \qquad a \sim N(0, A\sigma_a^2) \qquad e \sim N(0, \sigma_e^2)$$

MULTIVARIATE MODEL

$$\begin{bmatrix} y_1 \\ y_2 \\ y_3 \end{bmatrix} = \begin{bmatrix} 1\mu \\ 1\mu \\ 1\mu \end{bmatrix} + \begin{bmatrix} Z_1 t_1 \\ Z_2 t_2 \\ Z_3 t_3 \end{bmatrix} + \begin{bmatrix} Z_4 c_1 \\ Z_5 c_2 \\ Z_6 c_3 \end{bmatrix} + \begin{bmatrix} Z_7 a_1 \\ Z_8 a_2 \\ Z_9 a_3 \end{bmatrix} + \begin{bmatrix} e_1 \\ e_2 \\ e_3 \end{bmatrix}$$

$$Var\begin{bmatrix} t_1 \\ t_2 \\ t_3 \end{bmatrix} = \begin{bmatrix} I\sigma^2_{t_1} & 0 & 0 \\ 0 & I\sigma^2_{t_2} & 0 \\ 0 & 0 & I\sigma^2_{t_3} \end{bmatrix} \qquad Var\begin{bmatrix} c_1 \\ c_2 \\ c_3 \end{bmatrix} = \begin{bmatrix} I\sigma^2_{c_1} & 0 & 0 \\ 0 & I\sigma^2_{c_2} & 0 \\ 0 & 0 & I\sigma^2_{c_3} \end{bmatrix}$$

$$Var\begin{bmatrix} e_1 \\ e_2 \\ e_3 \end{bmatrix} = \begin{bmatrix} I\sigma^2_{e_1} & 0 & 0 \\ 0 & I\sigma^2_{e_2} & 0 \\ 0 & 0 & I\sigma^2_{e_3} \end{bmatrix} \qquad Var\begin{bmatrix} a_1 \\ a_2 \\ a_3 \end{bmatrix} = \begin{bmatrix} A\sigma^2_{a_1} & A\sigma_{a_1 a_2} & A\sigma_{a_1 a_3} \\ A\sigma_{a_2 a_1} & A\sigma^2_{a_2} & A\sigma_{a_2 a_3} \\ A\sigma_{a_3 a_1} & A\sigma_{a_3 a_2} & A\sigma^2_{a_3} \end{bmatrix}$$

SE of genetic correlations (Bijma and Bastiaansen, 2014)

RESULTS

Estimates of heritability assuming $\sigma_p^2 = \sigma_a^2 + \sigma_e^2$				
Breed	Lab	LMA	SQF	IMF
Angus				
	1	0.32 ± 0.02	0.37 ± 0.02	0.48 ± 0.02
	2	0.27 ± 0.03	0.33 ± 0.03	0.67 ± 0.04
	3	0.38 ± 0.03	0.43 ± 0.03	0.55 ± 0.04
Hereford				
	1	0.35 ± 0.02	0.26 ± 0.02	0.34 ± 0.02
	2	0.35 ± 0.03	0.25 ± 0.03	0.49 ± 0.03
	3	0.34 ± 0.03	0.29 ± 0.03	0.42 ± 0.03
Simmental				
	1	0.41 ± 0.02	0.47 ± 0.02	0.55 ± 0.02
	2	0.45 ± 0.05	0.41 ± 0.05	0.52 ± 0.05
	3	0.50 ± 0.03	0.45 ± 0.03	0.54 ± 0.03

Partitioning phenotypic variance of longissimus muscle area

	Variance components and percentages of phenotypic variance							
	σ_a^2	%	σ_t^2	%	$\sigma_{c:t}^2$	%	σ_e^2	%
Angus								
Lab 1	16.87	7 ± 1	53.98	23 ± 4	124.13	54 ± 3	35.06	15 ± 1
Lab 2	16.65	6 ± 1	42.58	16 ± 6	162.95	61 ± 4	45.10	17 ± 1
Lab 3	17.41	9 ± 1	13.40	7 ± 3	129.10	68 ± 2	29.28	15 ± 1
Hereford								
Lab 1	18.85	9 ± 1	34.24	17 ± 4	120.75	59 ± 3	30.50	15 ± 1
Lab 2	20.45	8 ± 1	15.57	6 ± 3	169.03	70 ± 2	35.97	15 ± 1
Lab 3	14.75	8 ± 1	8.14	4 ± 3	143.16	74 ± 2	28.11	14 ± 1
Simmental								
Lab 1	27.31	13 ± 1	57.21	26 ± 5	93.89	43 ± 3	38.60	18 ± 1
Lab 2	33.35	13 ± 2	60.64	23 ± 8	126.81	49 ± 5	40.31	15 ± 2
Lab 3	30.57	12 ± 1	49.98	20 ± 6	133.84	55 ± 4	30.67	13 ± 1

Partitioning phenotypic variance of subcutaneous fat depth

	Variance components and percentages of phenotypic variance							
	σ_a^2	%	σ_t^2	%	$\sigma_{c:t}^2$	%	σ_e^2	%
Angus								
Lab 1	0.98	13 ± 1	1.48	19 ± 3	3.58	47 ± 2	1.64	21 ± 1
Lab 2	0.87	11 ± 1	0.92	12 ± 5	4.26	54 ± 3	1.79	23 ± 2
Lab 3	1.08	15 ± 2	1.44	19 ± 6	3.46	47 ± 4	1.42	19 ± 2
Hereford								
Lab 1	0.86	13 ± 1	0.64	10 ± 2	3.18	47 ± 2	2.04	30 ± 1
Lab 2	0.80	13 ± 2	0.33	5 ± 3	3.27	52 ± 2	1.93	31 ± 2
Lab 3	0.74	10 ± 2	1.68	23 ± 9	3.16	43 ± 5	1.75	24 ± 3
Simmental								
Lab 1	1.43	25 ± 2	1.15	20 ± 4	1.58	28 ± 2	1.59	28 ± 2
Lab 2	0.92	22 ± 3	0.70	16 ± 6	1.35	31 ± 3	1.32	31 ± 3
Lab 3	0.93	17 ± 2	1.24	23 ± 6	2.17	39 ± 3	1.15	21 ± 2

Partitioning phenotypic variance of percent intramuscular fat

	Variance components and percentages of phenotypic variance							
	σ_a^2	%	σ_t^2	%	$\sigma_{c:t}^2$	%	σ_e^2	%
Angus								
Lab 1	0.34	20 ± 2	0.43	25 ± 4	0.56	33 ± 2	0.37	22 ± 1
Lab 2	0.52	30 ± 3	0.21	12 ± 5	0.73	43 ± 3	0.26	15 ± 2
Lab 3	0.51	22 ± 2	0.33	15 ± 5	1.03	45 ± 3	0.41	18 ± 2
Hereford								
Lab 1	0.16	16 ± 1	0.21	22 ± 4	0.37	34 ± 2	0.27	28 ± 2
Lab 2	0.15	26 ± 2	0.07	12 ± 5	0.23	39 ± 3	0.13	23 ± 2
Lab 3	0.24	17 ± 2	0.20	14 ± 6	0.69	48 ± 4	0.32	22 ± 2
Simmental								
Lab 1	0.28	27 ± 2	0.27	27 ± 4	0.26	25 ± 2	0.23	22 ± 2
Lab 2	0.17	26 ± 3	0.10	16 ± 6	0.22	34 ± 3	0.16	25 ± 3
Lab 3	0.31	24 ± 2	0.18	14 ± 4	0.55	42 ± 2	0.26	20 ± 2

LONGISSIMUS MUSCLE AREA

Estimates of genetic correlation and rank correlation of sires evaluated by pairs of interpretation laboratories (Number of sires)				
		Lab 1	Lab 2	Lab 3
Angus				
	Lab 1		0.99 (417)	0.99 (501)
	Lab 2	0.94 ± 0.04		0.99 (327)
	Lab 3	0.96 ± 0.04	0.94 ± 0.04	
Hereford				
	Lab 1		0.95 (245)	1.00 (199)
	Lab 2	0.92 ± 0.06		0.96 (251)
	Lab 3	0.98 ± 0.06	0.88 ± 0.06	
Simmental				
	Lab 1		0.88 (341)	0.94 (510)
	Lab 2	0.78 ± 0.06*		0.93 (320)
	Lab 3	0.85 ± 0.05	0.80 ± 0.06*	

SUBCUTANEOUS FAT DEPTH

Estimates of genetic correlation and rank correlation of sires evaluated by pairs of interpretation laboratories (Number of sires)				
		Lab 1	Lab 2	Lab 3
Angus				
	Lab 1		0.99 (418)	0.98 (501)
	Lab 2	0.93 ± 0.04		0.98 (327)
	Lab 3	0.92 ± 0.04*	0.92 ± 0.04*	
Hereford				
	Lab 1		0.82 (232)	0.77 (185)
	Lab 2	0.70 ± 0.11*		0.49 (238)
	Lab 3	0.58 ± 0.14*	0.26 ± 0.14*	
Simmental				
	Lab 1		0.95 (341)	0.99 (510)
	Lab 2	0.82 ± 0.05*		0.93 (341)
	Lab 3	0.94 ± 0.04	0.79 ± 0.06*	

PERCENT INTRAMUSCULAR FAT

Estimates of genetic correlation and rank correlation of sires evaluated by pairs of interpretation laboratories (Number of sires)				
		Lab 1	Lab 2	Lab 3
Angus				
	Lab 1		0.99 (418)	0.99 (501)
	Lab 2	0.95 ± 0.03		0.97 (327)
	Lab 3	0.94 ± 0.03*	0.89 ± 0.03*	
Hereford				
	Lab 1		0.97 (245)	0.97 (200)
	Lab 2	0.89 ± 0.06*		0.93 (251)
	Lab 3	0.87 ± 0.07*	0.80 ± 0.06*	
Simmental				
	Lab 1		0.94 (341)	0.97 (320)
	Lab 2	0.79 ± 0.05*		0.96 (510)
	Lab 3	0.88 ± 0.04*	0.87 ± 0.05*	

SUMMARY #1

- Considerable variation among technicians; for all traits it is as large or larger than additive genetic merit

- Within technician estimates of variance are significantly heterogeneous (Bartlett's test) for all traits

SUMMARY #2

- Estimates of additive genetic variance are generally homogenous among the interpretation laboratories; but there may be exceptions
- Likewise, with exceptions the estimates of residual variance are generally homogenous among interpretation laboratories
- Genetic correlations among interpretation laboratories suggest that results reported from different laboratories may be slightly different "traits"; particularly for subcutaneous fat depth and IMF

RECOMMENDATIONS

- UGC should revisit the certification standards for both field technicians and image interpretation laboratories
- There may be merit in standardized methods of image interpretation that can be deployed across laboratories
- Breed associations should dive deeper into the data they receive, relative to carcass traits measured with ultrasound, to insure that they are meeting the BLUP assumptions of homogenous variance

CLOSING THOUGHTS

- There is work to do to make ultrasound the most valuable tool it can be for genetic improvement of beef cattle
- Data currently being collected using ultrasound technology is of unquestioned value in prediction of breeding values for carcass traits
- Rank correlations for sires having progeny with images interpreted in more than one laboratory indicate generally excellent agreement in their evaluations

ACKNOWLEDGEMENTS

Thank You

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