Feed Efficiency and Subclinical ParaTBC Research at UF

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- The UF Multibreed Herd
- Mating Plan
- Data Recording
- Postweaning Feed Efficiency
- Subclinical Paratuberculosis

Angus-Brahman Multibreed Herd

- Diallel Mating Plan
- Managed as a commercial beef herd
- Typical data recording scheme
  - Dates and {data}
  - Date AI1, sire, …
  - Date, weight, condition score, …

Diallel Mating Plan 2005-2006

21 Sires

Angus	.75 A	Brang	.50A	.25A	Brah
4	3	4	3	3	4

282 Dams (2005); 297 Dams (2006)

Angus	.75 A	Brang	.50A	.25A	Brah
58	52	28	74	35	35
54	57	35	82	33	36

Calves 2006-2007 UF Angus-Brahman Herd


n = 335	Breed Group of Sire					
BGDam	A	.75 A	Br	.50A	.25A	B
A	29	7	9	7	8	14
.75 A	18	5	13	9	9	9
Br	2	2	28	2	3	2
.50A	16	16	15	11	15	17
.25A	4	3	6	8	4	5
B	0	0	0	0	0	39

Data

- Calves, Sires, Dams
  - Pedigree, breed fractions
- Calves
  - Growth: Dates, wts, cs, hht, fi, fe, temp, ubf,urea
  - Carcass: Date, hcw, bf, rea, yg, etc
- Dams
  - Dates, wts, cs, ParaTBC score

Postweaning Feed Efficiency

2006 - 2010
HATCH Project (5 years)
(200 calves/year)

NFREC GrowSafe FE Facility
Marianna, FL
20 pens – 16 - 20 calves/pen

Measurements at NFREC FE Facility

Weights – weekly (3 wk adj + 7 wk trial)
Feed Intake – real-time (weekly file)
Temperament – Chute score, Exit Vel
Ultrasound – foe, rea (70th d)

Blood Samples (@ Marianna)

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Usual Model for RFI

Daily feed intake
=
Avge daily gain
+
Metabolic Mid-wt
+
Residual feed intake

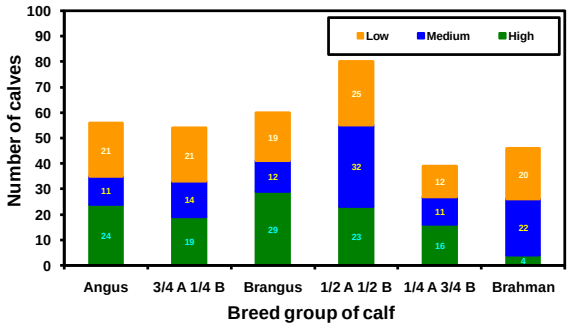
RFI groups

High = Calf RFI > mean + 0.5 SD

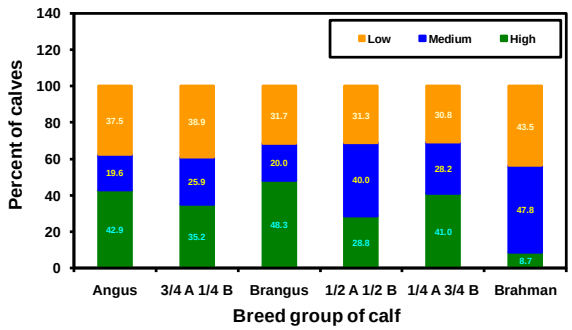
Med = mean - 0.5 SD ≤ RFI ≤ m + 0.5 SD

Low = Calf RFI < mean - 0.5 SD

Residual Feed Intake



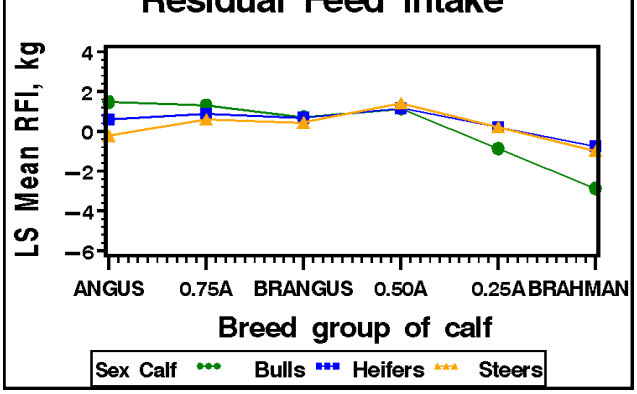
Residual Feed Intake



Model for RFI

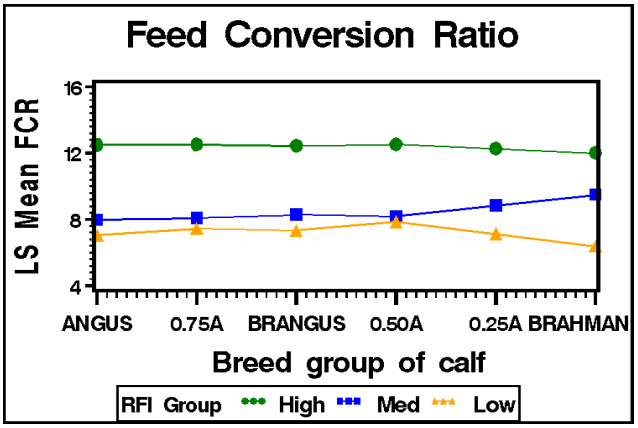
RFI
=
year*pen + age of dam
+ sex of calf + age calf
+ BFCalf(sex)+ Hetcalf(sex)
+ mean chute score + mean exit velocity
+ ELISA Score for ParaTBC
+ sire + residual

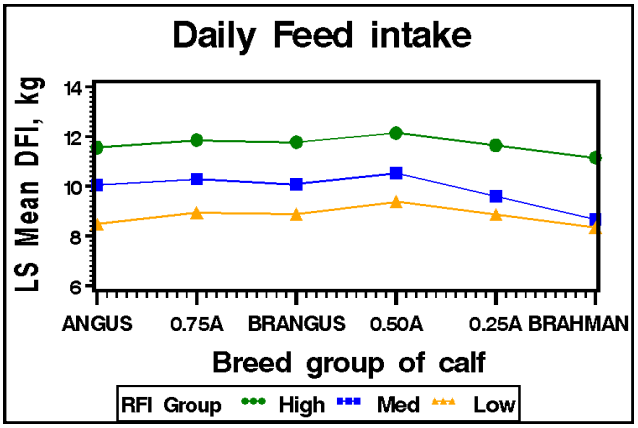
Residual Feed Intake

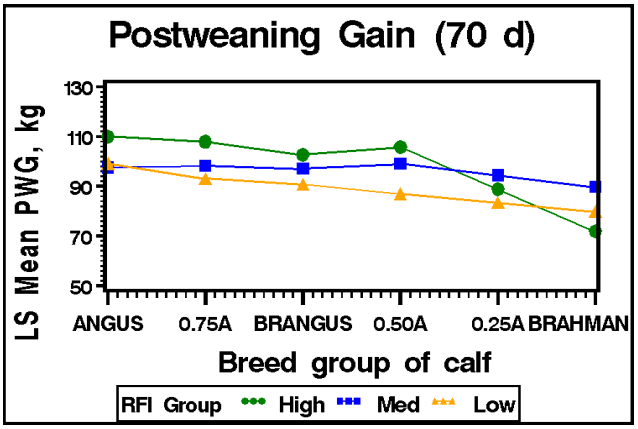


Model for Feed Efficiency Traits

FCR, DFI, PWG
=
year*pen + age of dam
+ sex of calf + age calf +
RFI group + BFcalf(rfigrp) + Hetcalf(rfigrp)
+ mean chute score + mean exit velocity
+ ELISA Score for ParaTBC
+ sire + residual

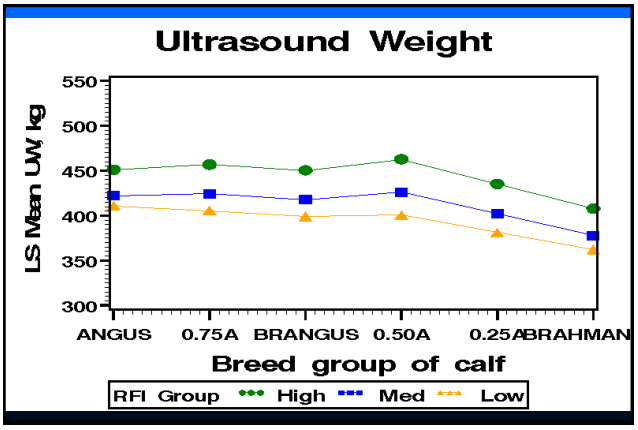


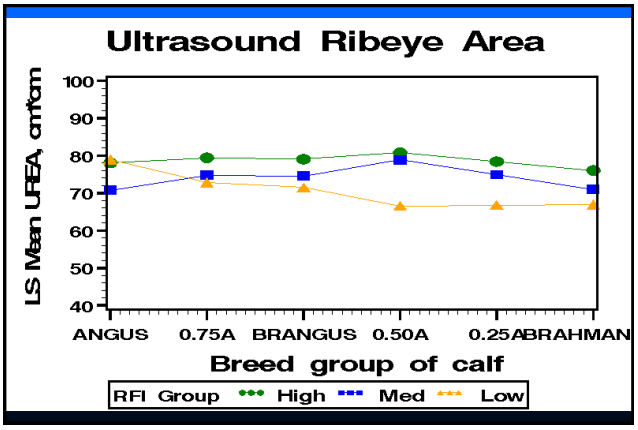


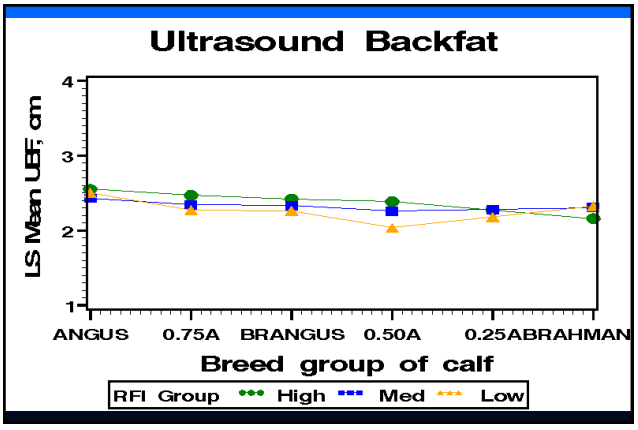


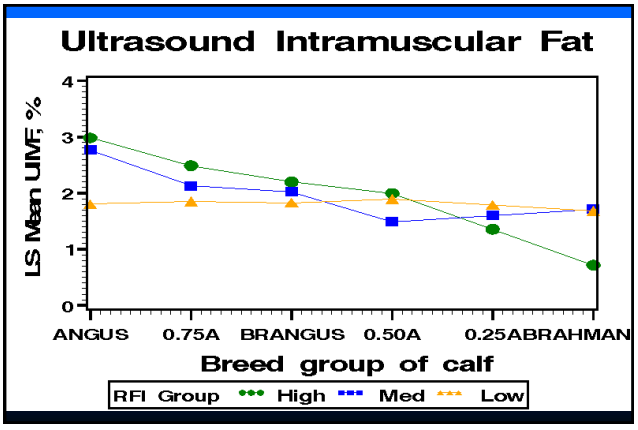
Model for Ultrasound Traits

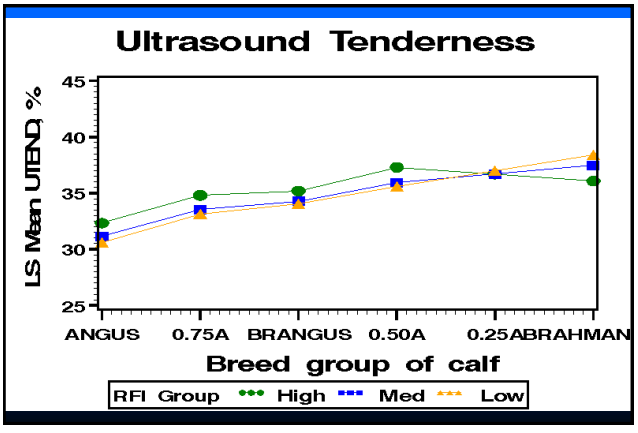
UW, UREA, UBFAT, U%IMFAT, UTEND
=
year*pen + age of dam
+ sex of calf + age calf +
RFI group + BFcalf(rfigrp) + Hetcalf(rfigrp)
+ mean chute score + mean exit velocity
+ ELISA Score for ParaTBC
+ sire + residual









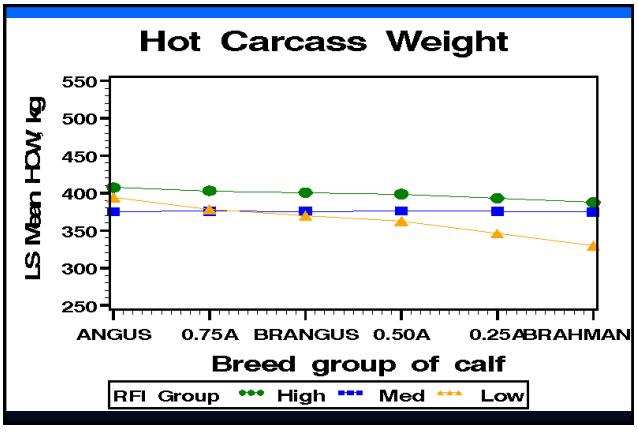


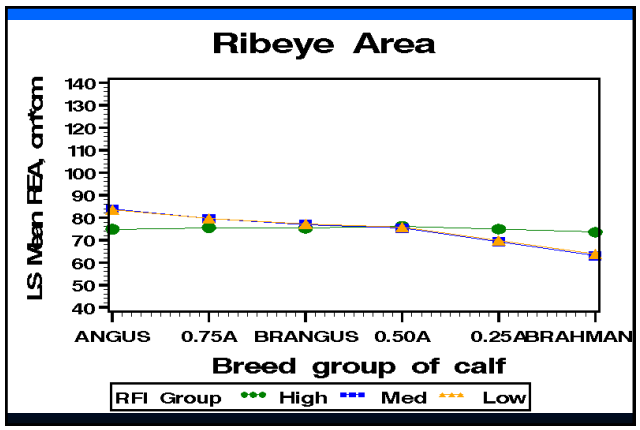
Calves 2006 - Carcass
UF Angus-Brahman Herd

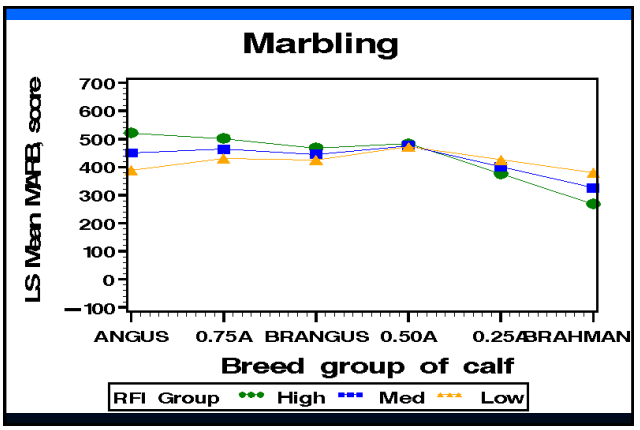
n = 88	Breed Group of Sire					
BGDam	A	.75 A	Br	.50A	.25A	B
A	7	2	1	1	3	3
.75 A	4	1	4	3	1	2
Br	1	0	11	0	0	0
.50A	0	4	7	3	4	2
.25A	1	2	1	4	1	2
B	0	0	0	0	0	13

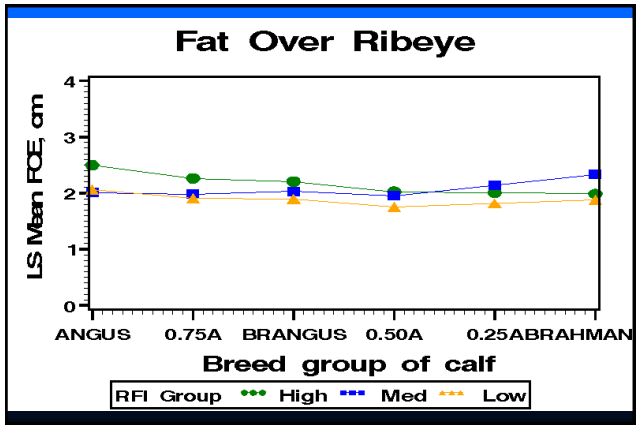
Model for Carcass Traits

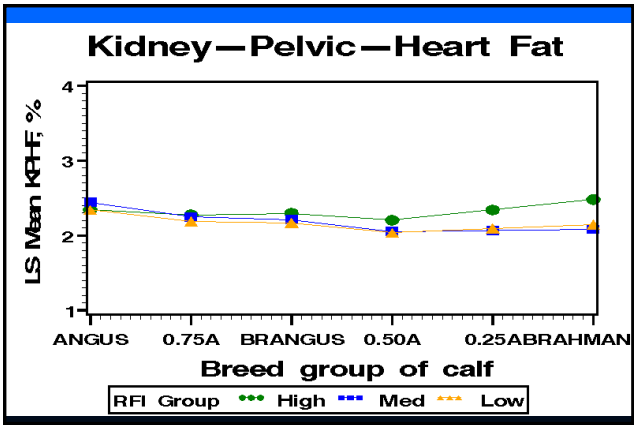
HCW, REA, BFAT, MARB, WBSF, TEND
=
year*pen + age of dam
+ sex of calf + age calf +
RFI group + BFcalf(rfigrp) + Hetcalf
+ mean exit velocity
+ ELISA Score for ParaTBC
+ sire + residual

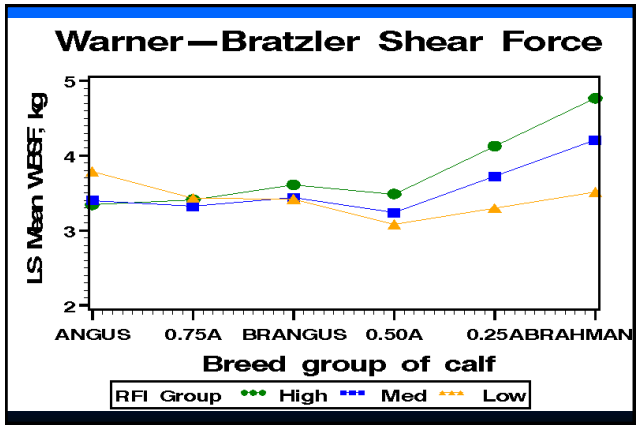


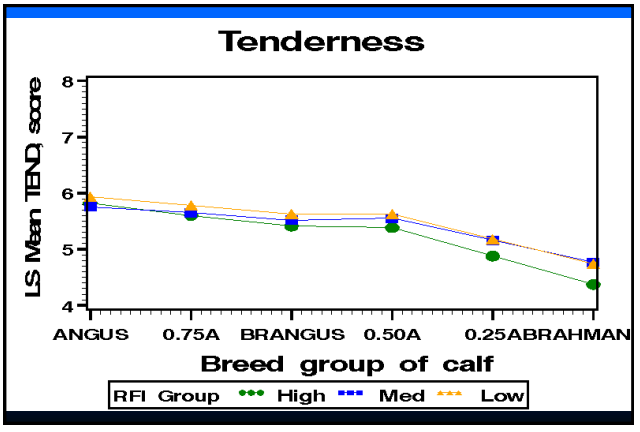

Ribeye Area
LS Mean REA, cm²/cm
140
130
120
110
100
90
80
70
60
50
40
ANGUS
0.75A
BRANGUS
0.50A
0.25A
BRAHMAN
Breed group of calf
RFI Group
High
Med
Low


Marbling
LS Mean MARB, score
700
600
500
400
300
200
100
0
−100
ANGUS
0.75A
BRANGUS
0.50A
0.25A
BRAHMAN
Breed group of calf
RFI Group
High
Med
Low


Fat Over Ribeye
LS Mean FOE, cm
4
3
2
1
0
ANGUS
0.75A
BRANGUS
0.50A
0.25A
BRAHMAN
Breed group of calf
RFI Group
High
Med
Low


Kidney—Pelvic—Heart Fat
LS Mean KPH, %
4
3
2
1
ANGUS
0.75A
BRANGUS
0.50A
0.25A
BRAHMAN
Breed group of calf
RFI Group
High
Med
Low


Warner—Bratzler Shear Force
LS Mean WBSF, kg
5
4
3
2
ANGUS
0.75A
BRANGUS
0.50A
0.25A
BRAHMAN
Breed group of calf
RFI Group
High
Med
Low


Tenderness
LS Mean TEND, score
8
7
6
5
4
ANGUS
0.75A
BRANGUS
0.50A
0.25A
BRAHMAN
Breed group of calf
RFI Group
High
Med
Low

Temperament

No effect on most traits

Mean Chute Score – No effect on any trait
Mean Exit Velocity
ADG (P < 0.02)
YWT (P < 0.001)
KPHF (P < 0.03)

Subclinical ParaTBC

No effect on
Post-weaning Growth Traits
Carcass Traits

Paratuberculosis

(Johnes' Disease)

Cows 2002-2006
UF Angus-Brahman Herd

n = 502	Breed Group of Sire					
BGDam	A	.75 A	Br	.50A	.25A	B
A	45	7	14	11	15	15
.75 A	16	12	13	16	18	17
Br	12	3	31	5	6	6
.50A	25	13	19	10	15	19
.25A	15	11	6	9	12	13
B	5	1	4	1	6	56

Calves 2002-2006
UF Angus-Brahman Herd

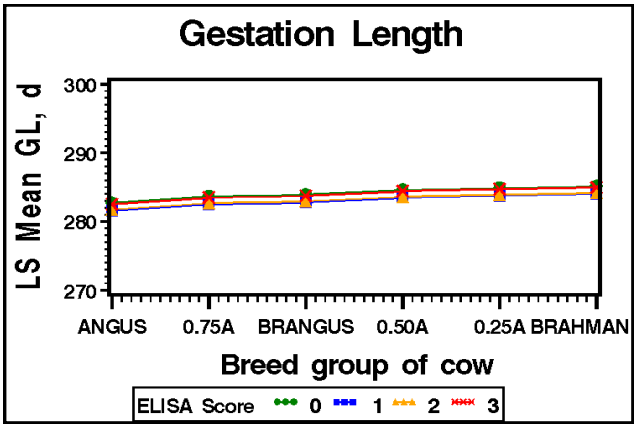
n = 956	Breed Group of Sire					
BGDam	A	.75 A	Br	.50A	.25A	B
A	76	19	26	16	20	28
.75 A	40	22	31	23	32	27
Br	9	3	78	12	8	9
.50A	51	37	43	31	40	38
.25A	14	12	19	23	20	39
B	2	0	3	0	5	100

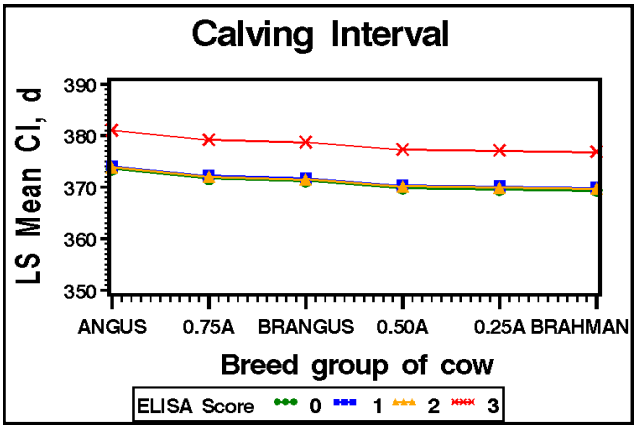
Model for cow and calf traits

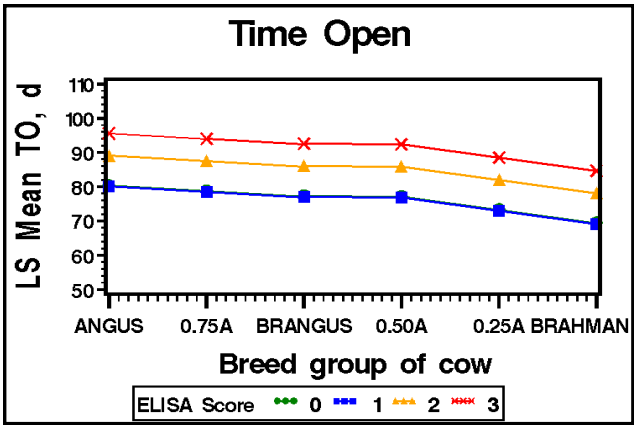
GL, CI, TO, WC, BW, WW205
=
year + age of dam + sex of calf
+ Brahman fraction of sire and dam
+ Heterosis of calf and dam
+ ELISA score for ParaTBC
+ sire (GL, BW, WW) + dam
+ residual

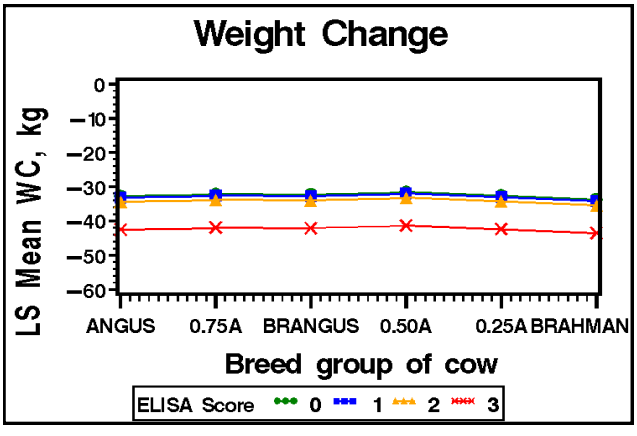
Regression of cow and calf traits on cow ELISA scores

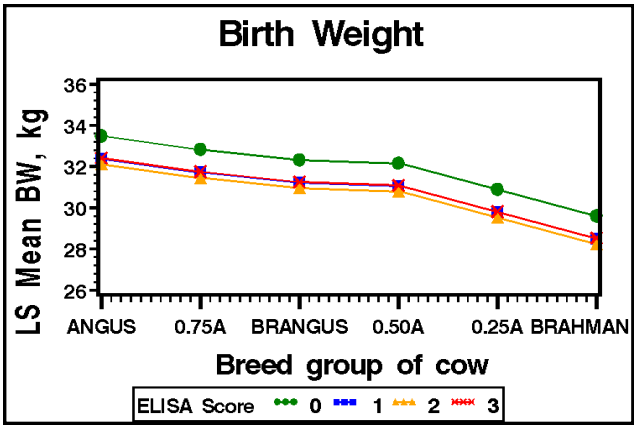
	Cow traits				Calf traits	
	Gestation Length	Calving Interval	Time Open	Weight Change	Birth Weight	Weaning WT 205
ELISA score	-0.2	1.7	4.8	-2.8	-0.4	-2.3
SE	0.4	1.6	1.4	1.2	0.2	0.9
P > |t|	0.66	0.29	0.001	0.02	0.04	0.01
No. records	580	605	358	931	953	921
No. sires	45	69	455	78	78	78
No. cows	312	252	185	363	373	362

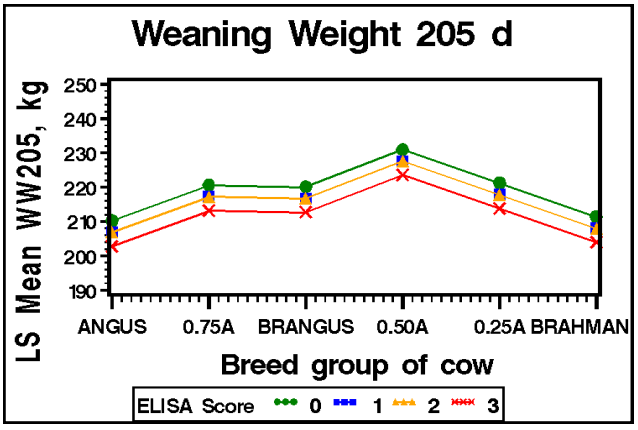












Research Areas

- Differences in gene expression between animals that show wide differences in FE
- Fine mapping of FE QTL regions
  Identify candidate genes
- Analyze associations between candidate genes (SNP) and FE
- Functional characterization of candidate genes associated with FE

Research Areas

- Use markers to determine the "actual" breed composition of animals in the multibreed herd (Improve accuracy of genetic predictions)
- Evaluate activity of genes associated with growth traits at various ages (birth to slaughter)
- Evaluate genes associated with FE in animals from 100% Angus to 100% Brahman
- Evaluate association of DNA markers, ELISA, Fecal Culture with Subclinical ParaTBC effects