

**Multibreed herd, growth, feed efficiency, ultrasound, carcass, genetic-genomic research**

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**The UF Multibreed Herd**

**Data Recording System**

**Mating System**

**Genetics Research**

**Genomics Research**





**The UF Multibreed Herd**  
**Data Recording System**  
**Mating System**  
**Genetics Research**  
**Genomics Research**

### Data Recording: Types of Data

- Pedigree:** Animal, Sire, Dam, Mgs, Mgd, breed fractions
- Mating Data:** AI & NS sires, AI Dates, NS Dates
- Phenotypic Data:** {Growth, Reproduction, Survival, Feed Intake, Ultrasound, Carcass} {Dates and Traits}
- Genomic Data:** Alleles for all SNP in a chip {3K, 50K, 770K, Complete Sequence}

### Data Recording: Database Files

<b>Calves (yearly, accumulated)</b>	<b>Pedigree, Breed Fractions, Survival, Growth, Ultrasound, Feed Efficiency, Carcass, Meat Palatability</b>
<b>Dams (yearly, accumulated)</b>	<b>Pedigree, Breed Fractions, Reproduction, Weights, Condition Scores, ELISA ParaTBC</b>
<b>Sires (yearly, accumulated)</b>	<b>Pedigree, Breed Fractions, Semen Dosages, Sire Usage</b>
<b>Genotypes (accumulated)</b>	<b>Illumina3K, Illumina50K, IlluminaHD, Complete DNA Sequence</b>

### Calf File 2011: Pedigree Data

YEAR	CALF	DIR	CG	AI	NS	CHLDR	CMC	SS	AI	NS	DIR	CG	AI	NS	CHLDR	CMC	ASSR	NAME	DAM	DIR	CG	AI	NS	CHLDR	CMC	MSISE	DOC	AI	NS	MSUM	DOC	AI	NS	CHLDR	CMC	ASSR	NAME	DATE	
2011	1100001	1	1	24	0	250	0	20	12	255	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0

### Calf File 2011: PreWean Growth Data

YEAR	CALF	DATE	WT	BL	DATE	WT	BL	DATE	WT	BL	DATE	WT	BL	DATE	WT	BL	DATE	WT	BL	DATE	WT	BL	DATE	WT	BL	DATE	WT	BL	DATE	WT	BL	DATE	WT	BL	DATE	WT	BL	DATE	WT	BL			
2011	1100001	2011	206	520	2011	460	520	2011	512	520	2011	512	520	2011	512	520	2011	512	520	2011	512	520	2011	512	520	2011	512	520	2011	512	520	2011	512	520	2011	512	520	2011	512	520	2011	512	520

### Calf File 2011: Feed Efficiency Data

### Calf File 2011: Ultrasound Data

### Calf File 2011: Carcass Data

### Calf File 2011: Meat Palatability Data

### Cow File 2011: Ped & Mating Data

### Cow File 2011: NS & Calving Data

## Cow File 2011: WT, CS, ELISA Data

This screenshot shows a Microsoft Excel spreadsheet titled "Cow File 2011: WT, CS, ELISA Data". The spreadsheet has columns for "YEAR", "DATA", "CWT", "CS", "ELISA", and "WT". The data is organized into rows for each cow, with columns for different data points. The spreadsheet is color-coded with yellow and green highlights for certain columns.

## Sire File 2012

This screenshot shows a Microsoft Excel spreadsheet titled "Sire File 2012". The spreadsheet has columns for "SIRE", "MATING FORMS", "AI NOM", "SEM", "ANF", "BIFR", "SEM", "M", "2005", "2006", "2007", "2008", "2009", "2010", "2011", "2012", "MATING FORMS", and "AI NOM". The data is organized into rows for each sire, with columns for different data points. The spreadsheet is color-coded with yellow and green highlights for certain columns.

## MAB File 2006-2010: Genotypic Data

This screenshot shows a Microsoft Excel spreadsheet titled "MAB File 2006-2010: Genotypic Data". The spreadsheet has columns for "Sire", "Dam", "A", "B", "C", "D", "E", "F", "G", "H", "I", "J", "K", "L", "M", "N", "O", "P", "Q", "R", "S", "T", "U", "V", "W", "X", "Y", "Z", "AA", "AB", "AC", "AD", "AE", "AF", "AG", "AH", "AI", "AJ", "AK", "AL", "AM", "AN", "AO", "AP", "AQ", "AR", "AS", "AT", "AU", "AV", "AW", "AX", "AY", "AZ", "BA", "BB", "BC", "BD", "BE", "BF", "BG", "BH", "BI", "BJ", "BK", "BL", "BM", "BN", "BO", "BP", "BQ", "BR", "BS", "BT", "BU", "BV", "BW", "BX", "BY", "BZ", "CA", "CB", "CC", "CD", "CE", "CF", "CG", "CH", "CI", "CJ", "CK", "CL", "CM", "CN", "CO", "CP", "CQ", "CR", "CS", "CT", "CU", "CV", "CW", "CX", "CY", "CZ", "DA", "DB", "DC", "DD", "DE", "DF", "DG", "DH", "DI", "DJ", "DK", "DL", "DM", "DN", "DO", "DP", "DQ", "DR", "DS", "DT", "DU", "DV", "DW", "DX", "DY", "DZ", "EA", "EB", "EC", "ED", "EE", "EF", "EG", "EH", "EI", "EJ", "EK", "EL", "EM", "EN", "EO", "EP", "EQ", "ER", "ES", "ET", "EU", "EV", "EW", "EX", "EY", "EZ", "FA", "FB", "FC", "FD", "FE", "FF", "FG", "FH", "FI", "FJ", "FK", "FL", "FM", "FN", "FO", "FP", "FQ", "FR", "FS", "FT", "FU", "FV", "FW", "FX", "FY", "FZ", "GA", "GB", "GC", "GD", "GE", "GF", "GG", "GH", "GI", "GJ", "GK", "GL", "GM", "GN", "GO", "GP", "GQ", "GR", "GS", "GT", "GU", "GV", "GW", "GX", "GY", "GZ", "HA", "HB", "HC", "HD", "HE", "HF", "HG", "HH", "HI", "HJ", "HK", "HL", "HM", "HN", "HO", "HP", "HQ", "HR", "HS", "HT", "HU", "HV", "HW", "HX", "HY", "HZ", "IA", "IB", "IC", "ID", "IE", "IF", "IG", "IH", "II", "IJ", "IK", "IL", "IM", "IN", "IO", "IP", "IQ", "IR", "IS", "IT", "IU", "IV", "IW", "IX", "IY", "IZ", "JA", "JB", "JC", "JD", "JE", "JF", "JG", "JH", "JI", "JJ", "JK", "JL", "JM", "JN", "JO", "JP", "JQ", "JR", "JS", "JT", "JU", "JV", "JW", "JX", "JY", "JZ", "KA", "KB", "KC", "KD", "KE", "KF", "KG", "KH", "KI", "KJ", "KL", "KM", "KN", "KO", "KP", "KQ", "KR", "KS", "KT", "KU", "KV", "KW", "KX", "KY", "KZ", "LA", "LB", "LC", "LD", "LE", "LF", "LG", "LH", "LI", "LJ", "LK", "LL", "LM", "LN", "LO", "LP", "LQ", "LR", "LS", "LT", "LU", "LV", "LW", "LX", "LY", "LZ", "MA", "MB", "MC", "MD", "ME", "MF", "MG", "MH", "MI", "MJ", "MK", "ML", "MN", "MO", "MP", "MQ", "MR", "MS", "MT", "MU", "MV", "MW", "MX", "MY", "MZ", "NA", "NB", "NC", "ND", "NE", "NF", "NG", "NH", "NI", "NJ", "NK", "NL", "NM", "NO", "NP", "NQ", "NR", "NS", "NT", "NU", "NV", "NW", "NX", "NY", "NZ", "OA", "OB", "OC", "OD", "OE", "OF", "OG", "OH", "OI", "OJ", "OK", "OL", "OM", "ON", "OO", "OP", "OQ", "OR", "OS", "OT", "OU", "OV", "OW", "OX", "OY", "OZ", "PA", "PB", "PC", "PD", "PE", "PF", "PG", "PH", "PI", "PJ", "PK", "PL", "PM", "PN", "PO", "PP", "PQ", "PR", "PS", "PT", "PU", "PV", "PW", "PX", "PY", "PZ", "QA", "QB", "QC", "QD", "QE", "QF", "QG", "QH", "QI", "QJ", "QK", "QL", "QM", "QN", "QO", "QP", "QQ", "QR", "QS", "QT", "QU", "QV", "QW", "QX", "QY", "QZ", "RA", "RB", "RC", "RD", "RE", "RF", "RG", "RH", "RI", "RJ", "RK", "RL", "RM", "RN", "RO", "RP", "RQ", "RR", "RS", "RT", "RU", "RV", "RW", "RX", "RY", "RZ", "SA", "SB", "SC", "SD", "SE", "SF", "SG", "SH", "SI", "SJ", "SK", "SL", "SM", "SN", "SO", "SP", "SQ", "SR", "SS", "ST", "SU", "SV", "SW", "SX", "SY", "SZ", "TA", "TB", "TC", "TD", "TE", "TF", "TG", "TH", "TI", "TJ", "TK", "TL", "TM", "TN", "TO", "TP", "TQ", "TR", "TS", "TT", "TU", "TV", "TW", "TX", "TY", "TZ", "UA", "UB", "UC", "UD", "UE", "UF", "UG", "UH", "UI", "UJ", "UK", "UL", "UM", "UN", "UO", "UP", "UQ", "UR", "US", "UT", "UU", "UV", "UW", "UX", "UY", "UZ", "VA", "VB", "VC", "VD", "VE", "VF", "VG", "VH", "VI", "VJ", "VK", "VL", "VM", "VN", "VO", "VP", "VQ", "VR", "VS", "VT", "VU", "VV", "VW", "VX", "VY", "VZ", "WA", "WB", "WC", "WD", "WE", "WF", "WG", "WH", "WI", "WJ", "WK", "WL", "WM", "WN", "WO", "WP", "WQ", "WR", "WS", "WT", "WU", "WV", "WW", "WX", "WY", "WZ", "XA", "XB", "XC", "XD", "XE", "XF", "XG", "XH", "XI", "XJ", "XK", "XL", "XM", "XN", "XO", "XP", "XQ", "XR", "XS", "XT", "XU", "XV", "XW", "XX", "XY", "XZ", "YA", "YB", "YC", "YD", "YE", "YF", "YG", "YH", "YI", "YJ", "YK", "YL", "YM", "YN", "YO", "YP", "YQ", "YR", "YS", "YT", "YU", "YV", "YW", "YX", "YZ", "ZA", "ZB", "ZC", "ZD", "ZE", "ZF", "ZG", "ZH", "ZI", "ZJ", "ZK", "ZL", "ZM", "ZN", "ZO", "ZP", "ZQ", "ZR", "ZS", "ZT", "ZU", "ZV", "ZW", "ZX", "ZY", "ZZ".

## MAB 2006-2010: FE & Genotypic Data

This screenshot shows a Microsoft Excel spreadsheet titled "MAB 2006-2010: FE & Genotypic Data". The spreadsheet has columns for "Colleague", "Sire", "Dam", "A", "B", "C", "D", "E", "F", "G", "H", "I", "J", "K", "L", "M", "N", "O", "P", "Q", "R", "S", "T", "U", "V", "W", "X", "Y", "Z", "AA", "AB", "AC", "AD", "AE", "AF", "AG", "AH", "AI", "AJ", "AK", "AL", "AM", "AN", "AO", "AP", "AQ", "AR", "AS", "AT", "AU", "AV", "AW", "AX", "AY", "AZ", "BA", "BB", "BC", "BD", "BE", "BF", "BG", "BH", "BI", "BJ", "BK", "BL", "BM", "BN", "BO", "BP", "BQ", "BR", "BS", "BT", "BU", "BV", "BW", "BX", "BY", "BZ", "CA", "CB", "CC", "CD", "CE", "CF", "CG", "CH", "CI", "CJ", "CK", "CL", "CM", "CN", "CO", "CP", "CQ", "CR", "CS", "CT", "CU", "CV", "CW", "CX", "CY", "CZ", "DA", "DB", "DC", "DD", "DE", "DF", "DG", "DH", "DI", "DJ", "DK", "DL", "DM", "DN", "DO", "DP", "DQ", "DR", "DS", "DT", "DU", "DV", "DW", "DX", "DY", "DZ", "EA", "EB", "EC", "ED", "EE", "EF", "EG", "EH", "EI", "EJ", "EK", "EL", "EM", "EN", "EO", "EP", "EQ", "ER", "ES", "ET", "EU", "EV", "EW", "EX", "EY", "EZ", "FA", "FB", "FC", "FD", "FE", "FF", "FG", "FH", "FI", "FJ", "FK", "FL", "FM", "FN", "FO", "FP", "FQ", "FR", "FS", "FT", "FU", "FV", "FW", "FX", "FY", "FZ", "GA", "GB", "GC", "GD", "GE", "GF", "GG", "GH", "GI", "GJ", "GK", "GL", "GM", "GN", "GO", "GP", "GQ", "GR", "GS", "GT", "GU", "GV", "GW", "GX", "GY", "GZ", "HA", "HB", "HC", "HD", "HE", "HF", "HG", "HH", "HI", "HJ", "HK", "HL", "HM", "HN", "HO", "HP", "HQ", "HR", "HS", "HT", "HU", "HV", "HW", "HX", "HY", "HZ", "IA", "IB", "IC", "ID", "IE", "IF", "IG", "IH", "II", "IJ", "IK", "IL", "IM", "IN", "IO", "IP", "IQ", "IR", "IS", "IT", "IU", "IV", "IW", "IX", "IY", "IZ", "JA", "JB", "JC", "JD", "JE", "JF", "JG", "JH", "JI", "JJ", "JK", "JL", "JM", "JN", "JO", "JP", "JQ", "JR", "JS", "JT", "JU", "JV", "JW", "JX", "JY", "JZ", "KA", "KB", "KC", "KD", "KE", "KF", "KG", "KH", "KI", "KJ", "KL", "KM", "KN", "KO", "KP", "KQ", "KR", "KS", "KT", "KU", "KV", "KW", "KX", "KY", "KZ", "LA", "LB", "LC", "LD", "LE", "LF", "LG", "LH", "LI", "LJ", "LK", "LM", "LN", "LO", "LP", "LQ", "LR", "LS", "LT", "LU", "LV", "LW", "LX", "LY", "LZ", "MA", "MB", "MC", "MD", "ME", "MF", "MG", "MH", "MI", "MJ", "MK", "ML", "MN", "MO", "MP", "MQ", "MR", "MS", "MT", "MU", "MV", "MW", "MX", "MY", "MZ", "NA", "NB", "NC", "ND", "NE", "NF", "NG", "NH", "NI", "NJ", "NK", "NL", "NM", "NO", "NP", "NQ", "NR", "NS", "NT", "NU", "NV", "NW", "NX", "NY", "NZ", "OA", "OB", "OC", "OD", "OE", "OF", "OG", "OH", "OI", "OJ", "OK", "OL", "OM", "ON", "OO", "OP", "OQ", "OR", "OS", "OT", "OU", "OV", "OW", "OX", "OY", "OZ", "PA", "PB", "PC", "PD", "PE", "PF", "PG", "PH", "PI", "PJ", "PK", "PL", "PM", "PN", "PO", "PP", "PQ", "PR", "PS", "PT", "PU", "PV", "PW", "PX", "PY", "PZ", "QA", "QB", "QC", "QD", "QE", "QF", "QG", "QH", "QI", "QJ", "QK", "QL", "QM", "QN", "QO", "QP", "QQ", "QR", "QS", "QT", "QU", "QV", "QW", "QX", "QY", "QZ", "RA", "RB", "RC", "RD", "RE", "RF", "RG", "RH", "RI", "RJ", "RK", "RL", "RM", "RN", "RO", "RP", "RQ", "RR", "RS", "RT", "RU", "RV", "RW", "RX", "RY", "RZ", "SA", "SB", "SC", "SD", "SE", "SF", "SG", "SH", "SI", "SJ", "SK", "SL", "SM", "SN", "SO", "SP", "SQ", "SR", "SS", "ST", "SU", "SV", "SW", "SX", "SY", "SZ", "TA", "TB", "TC", "TD", "TE", "TF", "TG", "TH", "TI", "TJ", "TK", "TL", "TM", "TN", "TO", "TP", "TQ", "TR", "TS", "TT", "TU", "TV", "TW", "TX", "TY", "TZ", "UA", "UB", "UC", "UD", "UE", "UF", "UG", "UH", "UI", "UJ", "UK", "UL", "UM", "UN", "UO", "UP", "UQ", "UR", "US", "UT", "UU", "UV", "UW", "UX", "UY", "UZ", "VA", "VB", "VC", "VD", "VE", "VF", "VG", "VH", "VI", "VJ", "VK", "VL", "VM", "VN", "VO", "VP", "VQ", "VR", "VS", "VT", "VU", "VV", "VW", "VX", "VY", "VZ", "WA", "WB", "WC", "WD", "WE", "WF", "WG", "WH", "WI", "WJ", "WK", "WL", "WM", "WN", "WO", "WP", "WQ", "WR", "WS", "WT", "WU", "WV", "WW", "WX", "WY", "WZ", "XA", "XB", "XC", "XD", "XE", "XF", "XG", "XH", "XI", "XJ", "XK", "XL", "XM", "XN", "XO", "XP", "XQ", "XR", "XS", "XT", "XU", "XV", "XW", "XX", "XY", "XZ", "YA", "YB", "YC", "YD", "YE", "YF", "YG", "YH", "YI", "YJ", "YK", "YL", "YM", "YN", "YO", "YP", "YQ", "YR", "YS", "YT", "YU", "YV", "YW", "YX", "YZ", "ZA", "ZB", "ZC", "ZD", "ZE", "ZF", "ZG", "ZH", "ZI", "ZJ", "ZK", "ZL", "ZM", "ZN", "ZO", "ZP", "ZQ", "ZR", "ZS", "ZT", "ZU", "ZV", "ZW", "ZX", "ZY", "ZZ".

The UF Multibreed Herd

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## Mating System: Diallel

Sires are mated to dams of all breed compositions

Computer Program

Assigns AI and NS sires to heifers and dams separately

Aims at producing enough replacements for purebred groups (Angus, Brangus, Brahman)

## Matings 2012

### 22 Sires

Angus	.75 A	Brang	.50A	.25A	Brah
4	3	4	3	3	5

### 322 Dams

Angus	.75 A	Brang	.50A	.25A	Brah
47	67	45	69	39	55



## Matings 2012



BGDam	Breed Group of Sire						All
	A	.75 A	Br	.50A	.25A	B	
A	22	5	8	4	3	5	47
.75 A	13	9	14	8	9	14	67
Br	5	5	25	3	4	3	45
.50A	12	11	14	10	9	13	69
.25A	8	6	10	5	5	5	39
B	2	2	2	2	4	43	55
All	62	38	73	32	34	83	322

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## Research: Statistical Genetics 1

Genetic evaluation methodology to evaluate animals in multibreed populations

Statistical Models (Multiple Trait, Additive, Non-Additive, Direct, Maternal Genetic Effects)  
 Estimation of variance and covariance components and genetic parameters  
 Computational Procedures (Direct, Iterative)  
 Computer Programs (Fortran, SAS)

## Research: Statistical Genetics 2

Angus-Brahman Multibreed Herd

Test and Validate  
 Multiple-Trait Multibreed Statistical Models  
 Computational Procedures (REML, GEM Algorithms)  
 MREMLEM Program  
 (Data Editing, Predictions, Estimation of VarCov Components & GenPar)  
 Growth Traits  
 Carcass Traits

## Research: Statistical Genetics 3

Romosinuano-Zebu (Colombia)  
 Sanmartinero-Zebu (Colombia)  
 Holstein-Other Breeds (Thailand)  
 Holstein-Chilean Friesian (Chile)

Multiple-Trait Multibreed Statistical Models  
 Dedicated Versions of MREMLEM  
 Growth Traits (Colombia)  
 Dairy Traits (Thailand, Chile)

## Research: Feed Efficiency & Postweaning Growth

HATCH & TSTAR Projects

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

## Objectives

Effect of breed composition and temperament (chute score, exit velocity) on RFI, DFI, FCR, PWG

Estimate genetic parameters for RFI, DFI, FCR, PWG





### Data Recording at FEF

Calves: Bulls, Heifers, Steers  
 AdjPeriod: 21 d; Trial: 70 d  
 Pens: 24; Calves/pen: 14 - 16


Intake: Feed, Water (Real time)  
 Growth: Dates, weights, Hip Ht (2 wk)  
 Temperament: Chute Score, Exit Vel (2 wk)  
 Ultrasound: UREA, UIMF, UBF

### Data

3 Herds: Brooksville, Gainesville, Marianna  
 2 Years: 2006 – 2007  
 Number Calves: 581

Brooksville (100 calves)  
 Gainesville (388 calves)  
 Marianna (93 calves)

### Calves 2006-2007 BKV-GNV-MAR




n = 581 BGDam	Breed Group of Sire					
	A	.75 A	Br	.50A	.25A	B
A	80	7	42	7	8	21
.75 A	18	9	7	9	12	11
Br	16	2	70	2	3	4
.50A	18	17	24	11	16	20
.25A	8	6	6	8	6	5
B	14	0	0	0	0	84

## Computation of RFI

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

## Definition of RFI groups

High = RFI > 0.9 kg DM/d

Med = - 0.9 kg DM/d ≤ RFI ≤ 0.9 kg DM/d

Low = RFI < - 0.9 kg DM/d

## Model for RFI

RFI  
=  
herd-year-pen + age of dam  
+ sex of calf + age calf  
+ BFcalf (sex) + Het calf (sex)  
+ mean chute score + mean exit velocity  
+ sire  
+ residual

## Residual Feed Intake

**Sex**  
Bulls similar RFI to Steers  
Heifers less efficient (higher RFI) than steers  
(1.24 ± 0.36 kg DM/d)

**Breed**  
Bulls and Steers: Similar RFI from A to B  
Heifers: RFI decreased as B % increased  
(-1.29 ± 0.28 kg DM/d; more efficient)

## Model for FCR, DFI, PWG

FCR, DFI, PWG  
=  
herd-year-pen + age of dam  
+ sex of calf + age calf  
+ RFI group + BF calf (rfigrp) + Het calf (rfigrp)  
+ mean chute score + mean exit velocity  
+ sire  
+ residual

## Feed Conversion Ratio

**Breed**  
FCR increased as B % increased (less efficient)  
High RFI Group = 1.41 ± 0.52 kg DM\*d<sup>-1</sup>/kg gain\*d<sup>-1</sup>  
Med RFI Group = 1.29 ± 0.47 kg DM\*d<sup>-1</sup>/kg gain\*d<sup>-1</sup>

**Heterosis**  
FCR increased as Het % increased (less efficient)  
High RFI Group = 0.92 ± 0.51 kg DM\*d<sup>-1</sup>/kg gain\*d<sup>-1</sup>



## Daily Feed Intake

### Breed

DFI decreased as B % increased (more efficient)  
 High RFI Group =  $-0.97 \pm 0.38$  kg DM/d  
 Med RFI Group =  $-0.90 \pm 0.33$  kg DM/d  
 Low RFI Group =  $-0.99 \pm 0.31$  kg DM/d

### Heterosis

DFI increased as Het % increased (less efficient)  
 High RFI Group =  $1.01 \pm 0.35$  kg DM/d  
 Med RFI Group =  $1.09 \pm 0.32$  kg DM/d

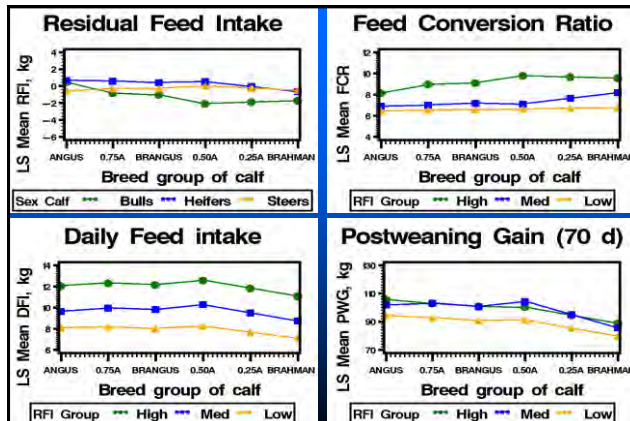
## Postweaning Gain (70 d)

### Breed

PWG decreased as B % increased (A better)  
 High RFI Group =  $-18.81 \pm 5.98$  kg  
 Med RFI Group =  $-16.18 \pm 5.28$  kg  
 Low RFI Group =  $-14.82 \pm 4.85$  kg

### Heterosis

PWG increased as Het % increased (favorable)  
 Med RFI Group =  $10.59 \pm 5.88$  kg



## Temperament

Mean Chute Score  
 No effect on any trait

Mean Exit Velocity  
 No effect on RFI, FCR, PWG  
 DFI ( $-0.29 \pm 0.09$  kg DM\*d<sup>-1</sup>/m\*sec<sup>-1</sup>)  
 Higher feed intake => lower EV

## Genetic Parameters (REML)

	RFI	DFI	FCR	PWG
RFI	$0.19 \pm 0.11$	$0.73 \pm 0.13$	$0.09 \pm 0.38$	$0.58 \pm 0.28$
DFI	$0.89 \pm 0.01$	$0.42 \pm 0.13$	$-0.05 \pm 0.31$	$0.88 \pm 0.12$
FCR	$0.55 \pm 0.03$	$0.37 \pm 0.04$	$0.24 \pm 0.11$	$-0.50 \pm 0.23$
PWG	$0.15 \pm 0.04$	$0.41 \pm 0.04$	$-0.57 \pm 0.03$	$0.40 \pm 0.13$

## Research: Feed Efficiency & Carcass and Meat Palatability

HATCH & TSTAR Projects

UF FE Facility, NFREC, Marianna, FL  
 Suwannee Farms  
 UF Meats Lab

## Objective

Effect of breed composition, RFI, and temperament (chute score, exit velocity) on carcass and meat palatability traits



## Carcass (2006-2007) UF Angus-Brahman Herd



n = 170 BGDam	Breed Group of Sire					
	A	.75 A	Br	.50A	.25A	B
A	17	2	2	2	3	4
.75 A	6	4	8	5	3	4
Br	2	1	18	1	1	2
.50A	5	10	10	6	5	5
.25A	5	3	2	4	1	2
B	0	0	0	0	0	27

## Model

$HCW, REA, BFAT, MAR, SF, TEND$   
 =  
 year-pen + age calf +  
 RFI group + BF calf (rfigrp) + Het calf  
 + mean exit velocity  
 + sire  
 + residual

## Regression of Carcass & Meat Quality traits on Brahman Fraction

Trait	P > F	High RFI	Medium RFI	Low RFI
HCW	0.0006	-65.7 ± 22.1 kg	-42.4 ± 23.5 kg	-43.3 ± 18.2 kg
REA	0.0001	-8.08 ± 5.0 cm <sup>2</sup>	-14.6 ± 5.3 cm <sup>2</sup>	-17.9 ± 4.1 cm <sup>2</sup>
BFAT	0.0207	-1.08 ± 0.4 cm	-0.4 ± 0.4 cm	-0.1 ± 0.3 cm
MAR	0.0001	-170.7 ± 44.1 units	-182.2 ± 46.7 units	-38.7 ± 36.3 units
SF	0.0003	1.3 ± 0.3 kg	0.6 ± 0.3 kg	0.2 ± 0.3 kg
TEND	0.0001	-0.9 ± 0.3 units	-1.7 ± 0.3 units	-0.9 ± 0.3 units

## Carcass Traits by Feed Efficiency Group

High RFI smaller REA than Low RFI  
(-11.0 ± 3.8 cm<sup>2</sup>)

High RFI higher MAR than Low RFI  
(116.0 ± 34.0 units)  
Medium RFI higher MAR than Low RFI  
(108.0 ± 29.9 units)

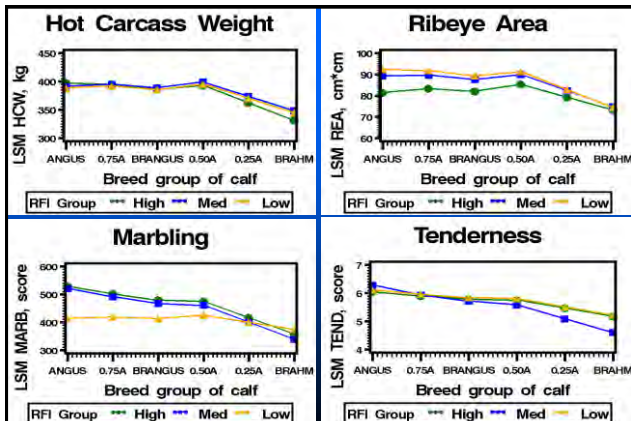
## In general ...

Less efficient steers (High RFI) had smaller REA than more efficient steers (Low RFI)

HCW, REA, BFAT, MAR, and TEND decreased as Brahman fraction increased

REA increased as heterozygosity increased

EV had no effect on carcass and meat quality traits



## Research: Breed Composition & Carcass, Meat Palatability

HATCH & TSTAR Projects

Complete Angus-Brahman Multibreed Dataset (1989 to 2009)  
1,367 Steers  
100% Angus to 100% Brahman

## Objective

Breed & Heterosis Effects in the Angus-Brahman Multibreed Population

Additive Angus – Brahman Differences  
Angus x Brahman Heterosis Effects

6 Carcass Traits: HCW, DP, REA, FOE, KPH, MAB  
6 Meat Palat Trt: WBSF, TEND, CTI, JUIC, FLAV, OFLAV

The UF Multibreed Herd

Data Recording System

Mating System

Genetics Research

Genomics Research

## Research: Feed Efficiency, PostWeaning Growth, Carcass, and Meat Palatability

HATCH & TSTAR Projects

UF FE Facility, NFREC, Marianna, FL  
Suwannee Farms  
UF Meats Lab  
New Mexico State University  
GeneSeek

## Objectives

Fraction of additive genetic variation explained by the Illumina Bovine3K Chip (2900 SNP)

Ranking of animals for RFI, DFI, FCR and PWG using genomic-polygenic, genomic, and polygenic models

Genetic trends from Angus to Brahman for RFI, DFI, FCR and PWG with the 3 models

## Genomic-Polygenic Model

$$\begin{aligned}
 & \text{RFI, FCR, DFI, PWG} \\
 & = \\
 & \text{year-pen} + \text{age of dam} \\
 & + \text{sex of calf} + \text{age calf} \\
 & + \text{BF calf} + \text{Het calf} \\
 & + \text{additive animal polygenic} \\
 & + \text{additive SNP genomic} \\
 & + \text{residual}
 \end{aligned}$$

## Genomic Model

$$\begin{aligned}
 & \text{RFI, FCR, DFI, PWG} \\
 & = \\
 & \text{year-pen} + \text{age of dam} \\
 & + \text{sex of calf} + \text{age calf} \\
 & + \text{BF calf} + \text{Het calf} \\
 & + \text{additive SNP genomic} \\
 & + \text{residual}
 \end{aligned}$$

## Polygenic Model

$$\begin{aligned}
 & \text{RFI, FCR, DFI, PWG} \\
 & = \\
 & \text{year-pen} + \text{age of dam} \\
 & + \text{sex of calf} + \text{age calf} \\
 & + \text{BF calf} + \text{Het calf} \\
 & + \text{additive animal polygenic} \\
 & + \text{residual}
 \end{aligned}$$

## Genomic-Polygenic Predictions

$$\begin{aligned}
 \text{Prediction} &= \text{Breed Solution} + \text{Sum SNP predictions} + \text{Polygenic prediction} \\
 \\
 \text{EBV}_{\text{animal}} &= \text{Prob (Alleles Brahman)} * (\text{Brahman}^\circ - \text{Angus}^\circ) \\
 &+ \text{Sum } [(\# \text{ "Alleles 2" at locus } i) * (\text{SNP}_i)], i = 1 \text{ to } 2,899 \\
 &+ \hat{a}_{\text{animal}}
 \end{aligned}$$

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 &+ \hat{a}_{\text{animal}}
 \end{aligned}$$

### Number of calves by breed group of sire x breed group of dam combination

Breed group of dam	Breed group of sire						
	Angus	¾ A ¼ B	Brangus	½ A ½ B	¼ A ¾ B	Brahman	All
Angus	46	10	18	7	7	17	105
¾ A ¼ B	24	21	31	26	14	16	132
Brangus	4	10	60	9	10	7	100
½ A ½ B	30	27	21	26	22	20	146
¼ A ¾ B	13	17	11	9	11	4	65
Brahman	1	2	1	0	0	68	72
All	118	87	142	77	64	132	620

### Additive Genetic and Genomic Variation for RFI, DFI, FCR and PWG

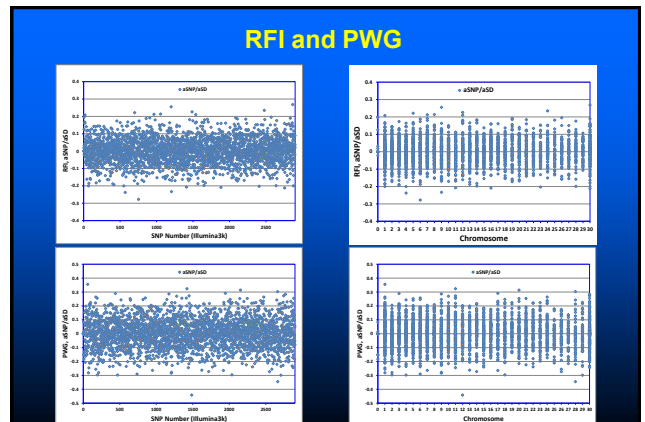
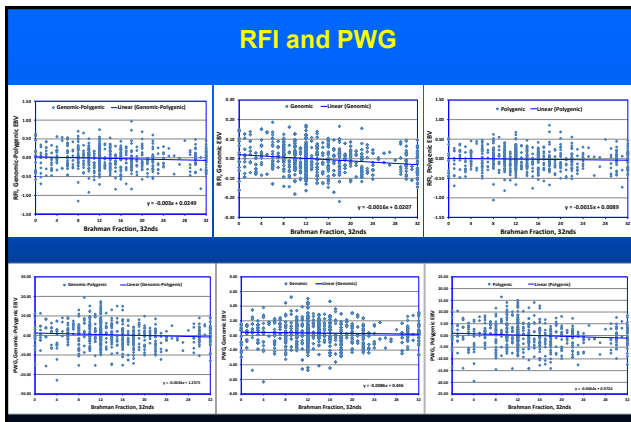
Trait	Parameter	AGVar	PhenVar	Heritability	AGOVAr/AGVar
RFI	Mean	0.37	1.79	0.21	0.14
	SD	0.15	0.11	0.08	0.11
DFI	Mean	0.80	2.43	0.33	0.10
	SD	0.24	0.15	0.09	0.08
FCR	Mean	1.32	6.50	0.20	0.26
	SD	0.56	0.40	0.08	0.17
PWG	Mean	89.74	240.97	0.37	0.16
	SD	25.85	15.09	0.10	0.11

### Rank correlations of animals evaluated for RFI, DFI, FCR, and PWG using genomic-polygenic, genomic, and polygenic models

Correlation	Trait			
	RFI	DFI	FCR	PWG
GP Model, G Model	0.65	0.62	0.66	0.74
GP Model, P Model	0.98	0.99	0.95	0.99
G Model, P Model	0.52	0.51	0.42	0.65

### Linear regression coefficients of genomic-polygenic, genomic, and polygenic EBV for RFI, DFI, FCR, and PWG on Brahman fraction of calf

Effect	Trait			
	RFI	DFI	FCR	PWG
Genomic-Polygenic	-0.0030	-0.0066	-0.0020	-0.0634
	P < 0.0311	P < 0.0070	P < 0.4812	P < 0.0274
Genomic	-0.0016	-0.0030	-0.0015	-0.0086
	P < 0.0001	P < 0.0001	P < 0.1529	P < 0.2825
Polygenic	-0.0015	-0.0040	-0.0007	-0.0664
	P < 0.2395	P < 0.1000	P < 0.7772	P < 0.0122



### Number and percentage of standardized predicted SNP values from the genomic-polygenic model

SDSNP Range	Trait							
	RFI		DFI		FCR		PWG	
	N	%	N	%	N	%	N	%
-0.4 to -0.5	0	0	0	0	0	0	1	0.03
-0.3 to -0.4	0	0	1	0.03	4	0.14	1	0.03
-0.2 to -0.3	8	0.28	19	0.66	60	2.07	66	2.28
-0.1 to -0.2	187	6.45	244	8.42	393	13.55	371	12.80
0 to -0.1	1204	41.53	1171	40.38	1007	34.74	998	34.43
0 to 0.1	1289	44.46	1169	40.32	1004	34.63	1010	34.84
0.1 to 0.2	202	6.97	277	9.56	379	13.07	376	12.97
0.2 to 0.3	9	0.31	18	0.62	48	1.66	72	2.48
0.3 to 0.4	0	0	0	0	4	0.14	4	0.14

### Summary for RFI, DFI, FCR and PWG

Fraction AddGenomVar/AddGenVar	Low: 0.10 to 0.26
Corr (GP Model, Genomic Model)	Medium: 0.62 to 0.74
Corr (GP Model, Polygenic Model)	Highest: 0.95 to 0.99
Corr (G Model, Polygenic Model)	Lowest: 0.42 to 0.65
Regr (EBV, B fraction of animal)	Low and Negative as B increased
"Influential" SNP	Throughout the genome

### Objectives

Fraction of additive genetic variation explained by the Illumina Bovine3K Chip (2900 SNP)

Ranking of animals for UREA, UBF, UPIMF, and UW using genomic-polygenic, genomic, and polygenic models

Genetic trends from Angus to Brahman for UREA, UBF, UPIMF, and UW with the 3 models

### Additive Genetic and Genomic Variation for UREA, UBF, UPIMF, and UW

Trait	Parameter	AGVar	PhanVar	Heritability	AGOVari/AGVar
UREA	Mean	20.14	58.30	0.39	0.09
	SD	6.00	3.58	0.10	0.07
UBF	Mean	0.994	0.022	0.25	0.38
	SD	0.002	0.001	0.08	0.17
UPIMF	Mean	0.29	0.59	0.53	0.06
	SD	0.08	0.04	0.12	0.05
UW	Mean	0.06	0.12	0.54	0.08
	SD	0.01	0.01	0.11	0.06

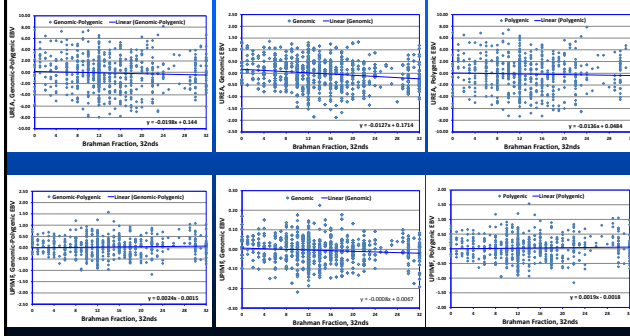
### Rank correlations of animals evaluated for UREA, UBF, UPIMF, and UW using genomic-polygenic, genomic, and polygenic models

Correlation	Trait			
	UREA	UBF	UPIMF	UW
GP Model, G Model	0.99	0.89	0.99	0.99
GP Model, P Model	0.58	0.51	0.60	0.65
G Model, P Model	0.65	0.79	0.64	0.70

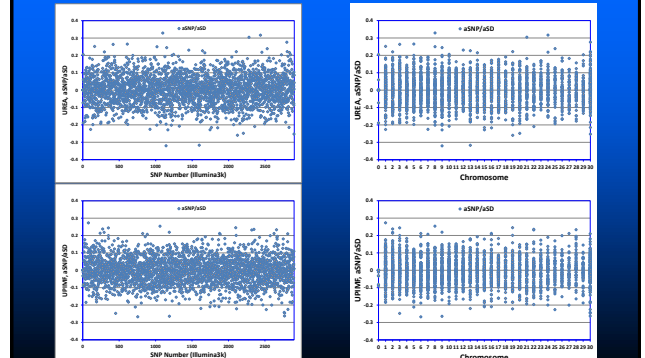
### Linear regression coefficients of genomic-polygenic, genomic, and polygenic EBV for UREA, UBF, UPIMF, and UW on Brahman fraction of calf

Effect	Trait			
	UREA	UBF	UPIMF	UW
Genomic-Polygenic	-0.0198	-0.0011	0.0024	-0.23
	P = 0.1778	P < 0.0001	P = 0.2222	P = 0.0133
Genomic	-0.0127	-0.0015	-0.0008	-0.17
	P < 0.0001	P < 0.0001	P = 0.0107	P < 0.0001
Polygenic	-0.0136	-0.0007	0.0019	-0.20
	P = 0.3321	P < 0.0001	P = 0.3256	P = 0.0252

## UREA and UPIMF



## UREA and UPIMF



## Number and percentage of standardized predicted SNP values from the genomic-polygenic model

SDSNP Range	Trait							
	UREA		UBF		UPIMF		UW	
	N	%	N	%	N	%	N	%
-0.3 to -0.4	2	0.07	11	0.38	0	0	6	0.21
-0.2 to -0.3	14	0.48	78	2.69	15	0.52	65	2.24
-0.1 to -0.2	276	9.52	419	14.45	245	8.45	359	12.38
0 to -0.1	1098	37.88	654	32.91	1217	41.98	1016	35.12
0 to 0.1	1190	41.05	920	31.74	1170	40.36	1006	34.7
0.1 to 0.2	296	10.21	415	14.32	234	8.07	370	12.76
0.2 to 0.3	20	0.69	83	2.86	18	0.62	70	2.41
0.3 to 0.4	3	0.1	17	0.59	0	0	5	0.17
0.4 to 0.5	0	0	2	0.07	0	0	0	0

## Summary for UREA, UBF, UPIMF, and UW

Fraction AddGenomVar/AddGenVar	Low: 0.09 to 0.38
Corr (GP Model, Genomic Model)	Highest: 0.89 to 0.99
Corr (GP Model, Polygenic Model)	Lowest: 0.51 to 0.65
Corr (G Model, Polygenic Model)	Medium: 0.64 to 0.79
Regr (EBV, B fraction of animal)	Near Zero (Pos or Neg) as B increased
"Influential" SNP	Throughout the genome

## Objectives

Fraction of additive genetic variation explained by the Illumina Bovine3K Chip (2900 SNP)

Ranking of animals for HCW, DP, REA, FOE, and MAB using genomic-polygenic, genomic, and polygenic models

Genetic trends from Angus to Brahman for HCW, DP, REA, FOE, and MAB with the 3 models

## Number of calves by breed group of sire x breed group of dam combination

Breed group of dam	Breed group of sire						All
	Angus	¼ A ¼ B	Brangus	½ A ½ B	¾ A ¾ B	Brahman	
Angus	19	3	6	1	2	4	35
¼ A ¼ B	6	2	9	11	4	3	35
Brangus	1	2	22	3	4	2	34
½ A ½ B	8	12	9	7	3	1	40
¾ A ¾ B	6	8	8	1	4	2	29
Brahman	0	2	0	0	0	27	29
All	40	29	54	23	17	39	202

### Additive Genetic and Genomic Variation for HCW, DP, REA, FOE, and MAB

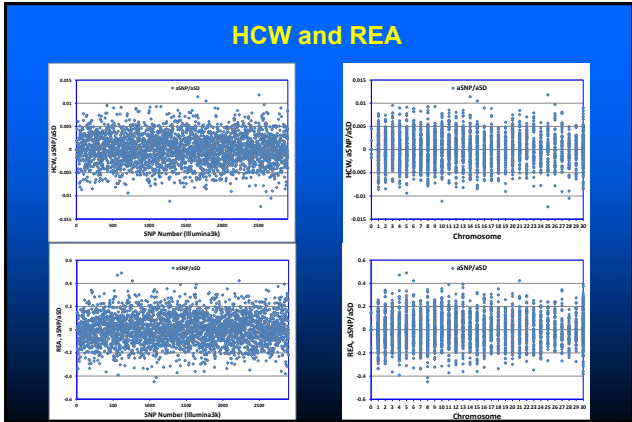
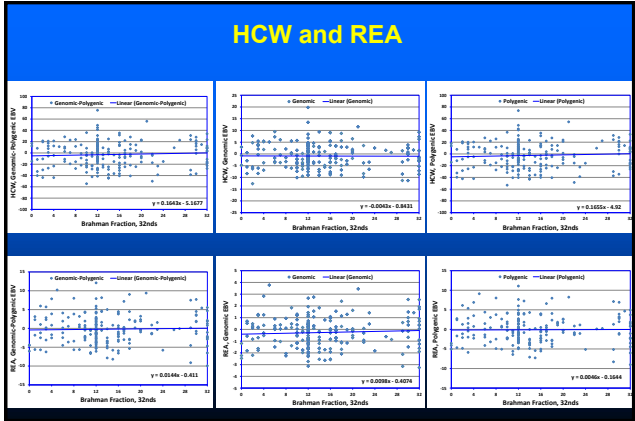
Trait	Parameter	AGVar	PhenVar	Heritability	AGOVari/AGVar
HCW (kg) <sup>2</sup>	Mean	895.86	1232.46	0.72	0.08
	SD	270.57	150.59	0.18	0.09
DP (%) <sup>2</sup>	Mean	5.03	19.24	0.25	0.47
	SD	3.89	2.39	0.17	0.26
REA (cm) <sup>4</sup>	Mean	39.02	71.73	0.53	0.19
	SD	18.74	9.17	0.22	0.16
FOE (cm) <sup>2</sup>	Mean	0.11	0.23	0.44	0.27
	SD	0.06	0.03	0.20	0.21
MAB (unit) <sup>2</sup>	Mean	3580.57	4739.93	0.75	0.23
	SD	980.23	572.93	0.16	0.16

### Rank correlations of animals evaluated for HCW, DP, REA, FOE, and MAB using genomic-polygenic, genomic, and polygenic models

Correlation	Trait				
	HCW	DP	REA	FOE	MAB
GP Model, G Model	0.85	0.95	0.84	0.84	0.90
GP Model, P Model	0.99	0.94	0.99	0.99	0.99
G Model, P Model	0.84	0.78	0.79	0.78	0.85

### Linear regression coefficients of genomic-polygenic, genomic, and polygenic EBV for HCW, DP, REA, FOE, and MAB on Brahman fraction of calf

Effect	Trait				
	HCW	DP	REA	FOE	MAB
Genomic-Polyg	0.1643	0.0050	0.0144	0.0000	0.2714
	P < 0.3869	P < 0.5414	P < 0.6643	P < 0.7554	P < 0.4904
Genomic	-0.0043	0.0016	0.0098	0.0000	0.2212
	P < 0.9226	P < 0.7556	P < 0.3806	P < 0.2290	P < 0.3326
Polygenic	0.1655	0.0057	0.0046	0.0144	0.0710
	P < 0.3742	P < 0.2286	P < 0.8798	P < 0.6643	P < 0.8457



### Number and percentage of standardized predicted SNP values from the genomic-polygenic model

SD Range	Trait									
	HCW		DP		REA		FOE		MAB	
	N	%	N	%	N	%	N	%	N	%
-0.4 to -0.5	0	0	0	0	2	0.07	0	0	0	0
-0.3 to -0.4	0	0	2	0.07	23	0.79	0	0	0	0
-0.2 to -0.3	0	0	37	1.28	124	4.28	0	0	0	0
-0.1 to -0.2	0	0	308	10.62	474	16.38	0	0	0	0
0 to -0.1	1437	48.67	1080	37.25	837	28.87	1446	49.88	1504	51.88
0 to 0.1	1462	50.43	1083	37.36	798	27.53	1453	50.12	1395	48.12
0.1 to 0.2	0	0	346	11.94	464	16.01	0	0	0	0
0.2 to 0.3	0	0	42	1.45	143	4.93	0	0	0	0
0.3 to 0.4	0	0	1	0.03	30	1.03	0	0	0	0
0.4 to 0.5	0	0	0	0	4	0.14	0	0	0	0



## Summary for HCW, DP, REA, FOE, and MAB

Fraction AddGenomVar/AddGenVar	Low: 0.88 to 0.47
Corr (GP Model, Genomic Model)	Medium: 0.84 to 0.90
Corr (GP Model, Polygenic Model)	Highest: 0.94 to 0.99
Corr (G Model, Polygenic Model)	Lowest: 0.78 to 0.85
Regr (EBV, B fraction of animal)	Near Zero (Pos or Neg) as B increased
"Influential" SNP	Throughout the genome

## Remarks

The low fraction of Add Genetic Variation accounted for by the Illumina Bovine3K Chip indicates that this chip should be used in combination with higher density chips for genomic evaluation

If genotypes from the Illumina Bovine3K Chip were available, then a genomic-polygenic model should be used

If imputation from a low density chip (e.g., 3K, 7K) to a higher density chip (e.g., 50K) were used in a multibreed population, animals from various breed groups would need to be genotyped with the higher density chip

Genomic results here should be taken with caution due to the small number of animals and the large number of predicted SNP effects (even with a low density chip)

## Next Steps

Continue to collect multibreed phenotypic information

Collaborate with researchers at institutions with similar goals and available phenotypes and genotypes

Genotype animals in the multibreed population with a combination of Illumina Bovine7K, Bovine50K and BovineHD (770K) Chips

Strengthen genetic links with straightbred and multibreed cattle herds where Brahman is one of the component breeds

Collaborate with researchers working in physiological genomics

## Research Team

University of Florida  
Animal Sciences  
Large Animal Clinical Sciences  
North Florida Research & Education Center  
Beef Research Unit  
Pine Acres

New Mexico State University  
University of Georgia  
National University of Colombia, ICA, &  
CORPOICA (Colombia)  
Kasetsart University (Thailand)  
University of Chile (Chile)

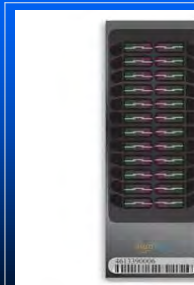
## Illumina Bovine3k BeadChip



Number of Markers	2,908
Samples per BeadChip	32
DNA Requirement	250ng
Assay	Infinium HD
Instrument	iScan, HiScanSQ, or BeadArray Reader

[http://www.illumina.com/products/bovine\\_snp50\\_whole-genome\\_genotyping\\_kits.ilmn](http://www.illumina.com/products/bovine_snp50_whole-genome_genotyping_kits.ilmn)


## Illumina BovineSNP50 v2 BeadChip



Number of Markers	54,608
Samples per BeadChip	32
DNA Requirement	200ng
Assay	GoldgenGate
Instrument	iScan or HiScanSQ

[http://www.illumina.com/products/bovine\\_snp50\\_whole-genome\\_genotyping\\_kits.ilmn](http://www.illumina.com/products/bovine_snp50_whole-genome_genotyping_kits.ilmn)

# Illumina BovineSNP<sup>HD</sup> BeadChip

	Number of Markers	771,943
	Samples per BeadChip	8
	DNA Requirement	200ng
	Assay	Infinium HD
	Instrument	iScan or HiScanSQ

[http://www.illumina.com/products/bovinehd\\_whole-genome\\_genotyping\\_kits.ilmn](http://www.illumina.com/products/bovinehd_whole-genome_genotyping_kits.ilmn)

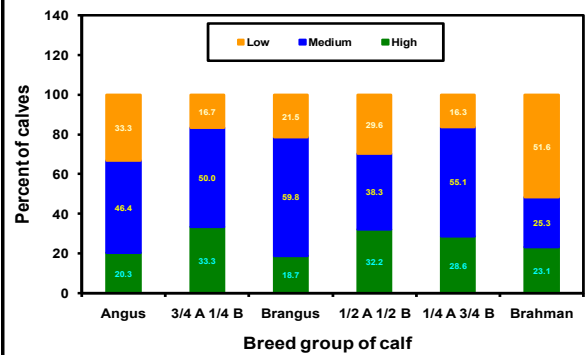


## People

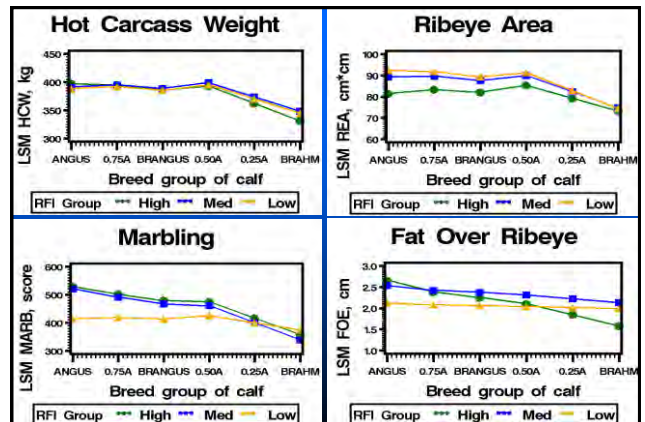
**University of Florida**  
 Don Wakeman, Jerry Wasdin, Paul Dixon, Danny Driver  
 Roger West, Dwain Johnson, Lee McDowell, Owen Rae, Gary Hansen, Cliff Lamb, Tim Olson

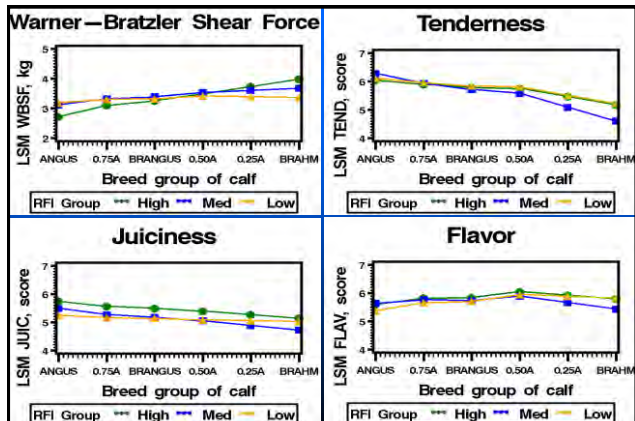
**New Mexico State University:** Milton Thomas  
**University of Georgia:** Ignacy Misztal  
 Colombia: Carlos Manrique, German Martinez, Gustavo Ossa  
 Thailand: Skorn Koonawootrittriron, Sornthep Tumwasorn, Thanathip Suwanasopee  
 Chile: Nelson Barria, Alejandro Jara

## Residual Feed Intake



Effect	Trait			
	RFI	DPI	FCR	PWG
Hard year pen	< 0.0001	< 0.0002	< 0.0001	< 0.0001
Age of dam	0.41	0.12	0.65	0.28
Sex of calf	0.003	< 0.0001	< 0.0001	< 0.0001
Age of calf	0.06	0.01	0.0004	0.04
RFI group		< 0.0001	0.78	0.09
Brahman fraction nested within sex of calf	< 0.0001			
Heterosis nested within sex of calf	0.24			
Brahman fraction nested within RFI group		0.0009	0.0073	0.0004
Heterosis nested within RFI group		0.0002	0.22	0.20
Mean Chute Score	0.39	0.42	0.11	0.33
Mean Exit Velocity	0.89	0.0012	0.34	0.31





## Research: Breed Composition & Carcass, Meat Palatability

HATCH & TSTAR Projects

Complete Angus-Brahman Multibreed Dataset (1989 to 2009)  
1,367 Steers  
100% Angus to 100% Brahman

## Objective

Breed & Heterosis Effects in the Angus-Brahman Multibreed Population

Additive Angus – Brahman Differences  
Angus x Brahman Heterosis Effects

6 Carcass Traits: HCW, DP, REA, FOE, KPH, MAB  
6 Meat Palat Trt: WBSF, TEND, CTI, JUC, FLAV, OFLAV

### Number of steers by breed group of sire x breed group of dam combination

Breed group of dam	Breed group of sire						All
	Angus	¼ A ¼ B	Brangus	½ A ½ B	¼ A ¼ B	Brahman	
Angus	116	16	34	17	27	32	242
¼ A ¼ B	47	23	30	26	29	32	140
Brangus	28	6	134	17	20	21	245
½ A ½ B	54	50	61	46	49	46	280
¼ A ¼ B	29	20	32	21	24	45	197
Brahman	28	15	26	11	10	144	235
All	302	130	137	138	160	320	1367

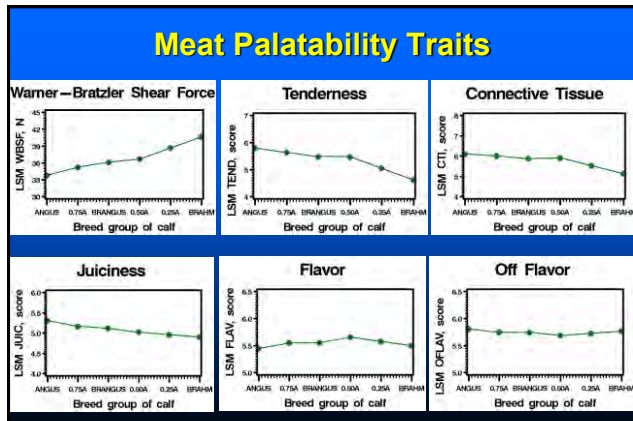
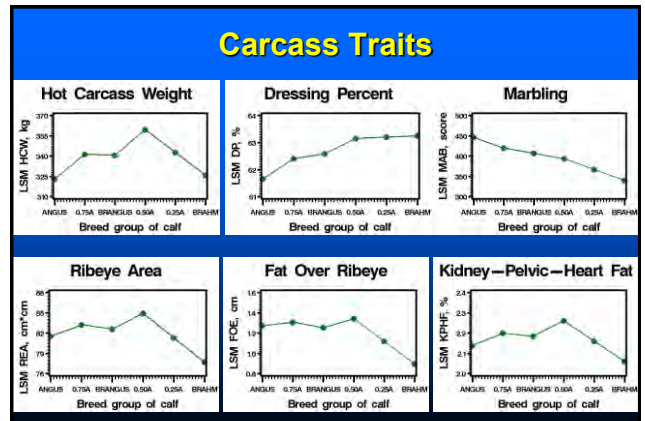
## Model

HCW, DP, MAR, REA, FOE, KPH  
WBSF, TEND, JUC, FLAV, OFLAV  
=  
year + age at slaughter +  
BF calf + Het calf  
+ sire  
+ residual

### Breed differences and heterosis effects for carcass traits

Trait	n	Effect	Estimate	SE	Pr >  t
HCW, kg	1359	Brahman – Angus	2.85	3.44	0.44
DP, %	1359	Brahman – Angus	1.60	0.25	<0.0001
MAB, units	1357	Brahman – Angus	-105.97	7.68	<0.0001
REA, cm <sup>2</sup>	1328	Brahman – Angus	-3.82	0.93	<0.0001
FOE, cm	1353	Brahman – Angus	-0.38	0.05	<0.0001
KPH, %	1275	Brahman – Angus	-0.08	0.05	0.15
HCW, kg	1359	Heterosis	35.01	3.95	<0.0001
DP, %	1357	Heterosis	0.69	0.29	0.017
MAB, units	1328	Heterosis	0.26	8.83	0.98
REA, cm <sup>2</sup>	1353	Heterosis	5.31	1.08	<0.0001
FOE, cm	1275	Heterosis	0.26	0.05	<0.0001
KPH, %	1359	Heterosis	0.16	0.06	0.01

Breed differences and heterosis effects for meat palatability traits					
Trait	n	Effect	Estimate	SE	Pr >  t
WBSF, kg	662	Brahman - Angus	0.70	0.11	<0.0001
TEND, units	352	Brahman - Angus	-1.18	0.13	<0.0001
CTI, units	352	Brahman - Angus	-0.97	0.14	<0.0001
JUIC, units	352	Brahman - Angus	-0.40	0.12	0.001
FLAV, units	352	Brahman - Angus	0.05	0.09	0.56
OFLAV, units	352	Brahman - Angus	-0.04	0.07	0.57
WBSF, kg	662	Heterosis	-0.06	0.14	0.68
TEND, units	352	Heterosis	0.26	0.17	0.13
CTI, units	352	Heterosis	0.29	0.16	0.062
JUIC, units	352	Heterosis	-0.09	0.14	0.54
FLAV, units	352	Heterosis	0.18	0.10	0.08
OFLAV, units	352	Heterosis	-0.10	0.08	0.22



### In short ...

- Brahman carcasses had similar HCW and KPH, but higher DP, lower MAB, smaller REA, and thinner FOE than Angus carcasses
- DP and WBSF increased as Brahman fraction increased
- MAB, REA, FOE, TEND, CTI, and JUIC decreased as Brahman fraction increased
- HCW, DP, REA, and FOE increased as heterozygosity increased